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Dissertation

Title *Protein Domain Linker Prediction: A Direction for Detecting Protein-Protein Interactions*
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Abstract

Protein chains are generally long and consist of multiple domains. Domains are the basic elements of protein structure that can exist, evolve, and function independently. The accurate identification of protein structural domains and their interactions has significant impacts in protein research fields. The accurate prediction of protein domains is a fundamental step in experimental and computational proteomics. The knowledge of domains is useful in classifying proteins, understanding their structures, functions and evolution, and predicting protein-protein interactions. The identification of interactions among proteins and their associated structural domains provide a global picture of the cellular functions and the biological processes. In this research work we introduce novel solutions for two main research problems. First, we present a method for the prediction of inter-domain linkers solely from the amino acid sequence information. This is achieved by introducing the concept of amino acid compositional index. Unlike previous approaches, we use the predicted inter-domain linkers to identify the actual structural domains. Second, we utilize the structural domain knowledge to predict protein-protein interactions. The proposed framework is evaluated against several state-of-the-art approaches and demonstrated that it provides a noticeable improvement. The higher accuracy achieved is a valid argument in favor of the proposed framework.

Keywords: Protein domain identification, domain-linker prediction, compositional index, physiochemical properties, protein-protein interaction prediction, PPI, domain-domain interactions.

Research Relevance and Potential Impact

The identification of protein-protein interaction is crucial to the understanding of the molecular events under normal and abnormal physiological conditions. It leads to significant applications for the diagnosis and treatment of diseases such as cancer and diabetes which are relevant to the UAE.

Relevant Publications

- Maad Shatnawi and Nazar Zaki (2015) Inter-domain linker prediction using amino acid compositional index. Computational Biology and Chemistry (CBAC) 55: 23- 30, April 2015. (ISI IF 1.595)
- Maad Shatnawi, Nazar Zaki, and Paul D. Yoo (2014) "Protein inter-domain linker prediction using random forest and amino acid physiochemical properties." BMC Bioinformatics 15 (Suppl 16): S8, December 2014. (ISI IF 2.670)
- Maad Shatnawi and Nazar Zaki (2015) Novel domain identification approach for protein-protein interaction prediction. 2015 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology, Niagara Falls, Canada, August 2015.

Career Aspirations

To have an academic position within a reputable institution, to be an active team player within interdisciplinary research groups, and to extend knowledge to young generation.