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Proteins domain classification and prediction from protein secondary structure

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Abstract

Prediction of protein function is of significance in studying biological processes. The prediction of protein function is one of the most demanding tasks in the study of bioinformatics. One approach for function prediction is to classify a protein into functional family. Classification of protein structures helps to understand relationships between protein structure and function. Machine learning methods greatly help to improve the classification of protein function. This paper presents a method for classifying the proteins based on the secondary structure. Support vector machine (SVM) is a useful method for such classification, which may involve proteins with diverse sequence distribution. We have developed SVM classification of a protein into functional domains from its secondary structure.

Biography

Habes M. Alkhraisat is Assistant Professor of Computer Science in the Department of Computer Science at the **Al-Balqa Applied University**. He received his BA from **Al-Balqa Applied University** in 2001, master degree of computer science from University of Jordan in 2003, and a Ph.D. from Saint Petersburg Electro Technical University in 2008.