

利用混合方法預測蛋白質在細胞中的位置

Predicting Protein Subcellular Location Using Hybrid Approach

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Biologically, the function of a protein is highly related to its subcellular localization. It is necessary to develop a reliable method for protein subcellular localization prediction, especially when large-scale genome sequences are to be analyzed. Various methods have been proposed to perform the task. The results, however, are not satisfactory in terms of effectiveness and efficiency. A hybrid approach using naïve Bayesian classifier with information gain ratio and k -nearest neighbor classifier is presented. The total accuracy for a set of 17655 proteins can reach up to 91.5%.

Key Words: subcellular localization, function prediction