

## Protein Remote Homology Detection and Fold Recognition by Combining Profiles with Kernel Methods

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**Abstract :** Protein remote homology detection and fold recognition are two most important tasks in protein sequence analysis, which is critical for protein structure and function studies. In this study, we combined the profile-based features with various string kernels, and constructed several computational predictors for protein remote homology detection and fold recognition. Experimental results on two widely used benchmark datasets showed that these methods outperformed the competing methods, indicating that these predictors are useful computational tools for protein sequence analysis. By analyzing the discriminative features of the training models, some interesting patterns were discovered, reflecting the characteristics of protein superfamilies and folds, which are important for the researchers who are interested in finding the patterns of protein folds.

**Keywords :** protein remote homology detection, protein fold recognition, profile-based features, Support Vector Machines (SVMs)

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