ConPred: An Web-based Consensus Protein Secondary Structure Prediction System

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Protein structure prediction is one of the most significant problems in bioinformatics because the structure of protein determines its functions. Currently, there are tools such as *Sigcleave*, *tmap*, *helixturnhelix*, and *Garnier* that can predict protein secondary structure, or find protein structural motifs and some specific structure segments. However, sometimes their results are not identical or even contradictory for some proteins.

We propose to develop a consensus protein structure prediction system named *ConPred* to integrate the above results together in order to have an overall consensus protein secondary structure prediction that can have higher prediction accuracy. This system is being developed. Conpred is a web-based prediction system that can let users submit query amino acids sequence from web browser, and the prediction results are sent back to users by email. Moreover, Conpred is implemented on a high performance 164-processor Sun cluster in the faculty of Computer Science.