IPM-POLYTECHNIQUE-WPI Workshop on Bioinformatics and Biomathematics, April 11-21, 2005, IPM, Tehran

Prediction of Protein Surface Accessibility Based on Residue pair Types and Accessibility States Using Dynamic programming algorithm

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Prediction of residue surface accessibility from protein sequence gives helpful information about structure and function of protein and it can be used as an intermediate step in predicting of protein tertiary structure. We have used a statistical approach for solvent accessibility prediction based on information theory and simultaneously taking into consideration pairwise residue types and accessibility states. A score system for residue pair in particular accessibility states is derived for adjacent neighbors up to nine residues apart in sequence. Since the prediction of residue accessibility by one residue widow sliding make ambiguity in accessibility prediction, we used a dynamic programming algorithm to find the path with maximum score. The prediction accuracy of this method for two and three states is better than 75, 69 % respectively. This result is better than methods based on evolutionary information and neuralnetwork.