

Prediction of protein residue contact using support vector machine

Abstract :

Prediction of protein residue contact is one of the important two-dimensional prediction tasks in protein structure prediction. The residue contact map of protein contains information which represents three-dimensional conformation of protein. However the accuracy of the prediction is dependent on the type of protein information used to distinguish between contacts or non-contacts. According to CASP (Critical Assessment of Techniques of Protein Structure Prediction) the accuracy of protein contact map prediction is still low due to the behaviour of the predictors developed where the predictors only effective against specific type of protein structure. In order to further improve the performance of the predictor, effective features must be identified and used. Therefore, this research is conducted to determine the effectiveness of the existing features used in protein contact map prediction.