Effect on Domain Combination based Protein Interaction Prediction Method by Adjusting an eValue of InterPro

Hee-Young, Hur1    Dong-Soo, Han1
1School of Engineering, Information and Communications University, Deajeon, Korea
Email: hyerue@icu.ac.kr, dshan@icu.ac.kr

ABSTRACT

Domain based protein interaction prediction methods have been actively studied for many years. Among these domain based approaches, domain combination based protein-protein interaction possibility ranking method is superior to others in terms of its prediction accuracy. However, this kind of prediction methods which is using a learning set can not use whole of domain interaction databases because of the properties of the method. Furthermore, when the system finds domain information from biological databases, it shows the same domains even though they are portions of proteins which have different functions. These make a defect of the prediction system that different proteins are treated as having same domain composition because of the lack of domain information. Domain information using in domain combination method is based on InterPro which is results of InterProScan. An evalue is used when InterProScan filters insufficient elements after integration process of databases. In this paper, we adjust this evalue and get more data that used in the learning set. Evaluation is done by using domain combination based protein-protein interaction possibility ranking method comparing with original database from InterPro and adjusted database which changed its evalue. As a result, it can enhance not sequence coverage but the scope of prediction range.