Abstract

The term coevolution describes the situation when two or more species or biomolecules reciprocally affect each others’ evolution. On the protein level, it is thought to be the main mechanism ensuring correct folding, interactions and function of a protein, and it can be observed both on the level of interacting protein families and individual amino acid residues. Coevolution studies have been proved to be a powerful tool for prediction of protein structure, function, interaction partners, etc. In this thesis, different algorithms used for detection of protein coevolution are described, as well as their applications and limitations.

Keywords: coevolution, protein family, protein structure prediction, interaction partners, correlated mutations, mirrortree, mutual information, direct coupling analysis