Accurate and fast computational method for identifying protein function using protein-protein interaction data

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Abstract

A novel quantity called functional correlation was proposed to evaluate functional closeness of a protein with its neighbors in a PPI network. Each unclassified protein was assigned a functional probability distribution which specified the likelihood of an unclassified protein belonged to a specific function group. The functional probability distribution for all unclassified proteins were adjusted iteratively until functional correlation reached optimum. A function was assigned to an unclassified protein if its corresponding functional probability is higher than a chosen threshold. Our results showed that functional correlation optimization method(FCOM) is more robust to false protein interactions and insensitive to amount of known function proteins in a PPI network than other methods. FCOM method can be easily and usefully applied to organisms with rare known function proteins, disease genes, protein complexes, overlapped modular structures prediction and so on.

Keyword：protein-protein interaction network, function prediction