

Searching essential proteins in dynamic protein networks based on an improved H-index algorithm

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SUBJECT AREAS

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essential proteins; dynamic protein network; attenuation coefficient; improved H-index algorithm

Abstract

The essential proteins in protein networks play an important role in complex cellular functions and their evolution. Therefore, searching essential proteins in protein networks can help to explain the structure, function and dynamics of basic cellular networks. The existing dynamic protein network regards the protein situation at all times as the same, but in fact, the role of proteins varies at different times. In order to improve the accuracy of essential protein searching, an improved H-index algorithm based on attenuation coefficient method is proposed in this paper, which incorporates the neglected node information into consideration to improve the accuracy of essential protein searching. The experiments show that the essential proteins found on the basis of this model are more effective than other similar methods.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed.

However, the manuscript can be downloaded and accessed as a PDF.

Figures

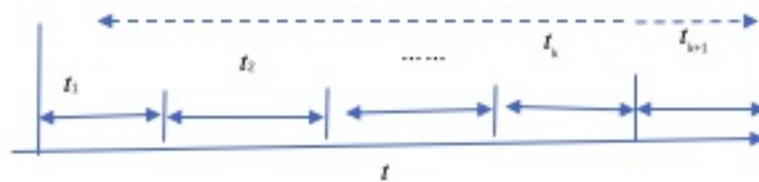


Figure 1

Time series diagram of dynamic protein network

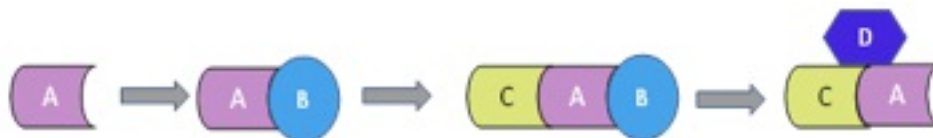


Figure 2 Simple Protein Evolution

Figure 2

Simple Protein Evolution

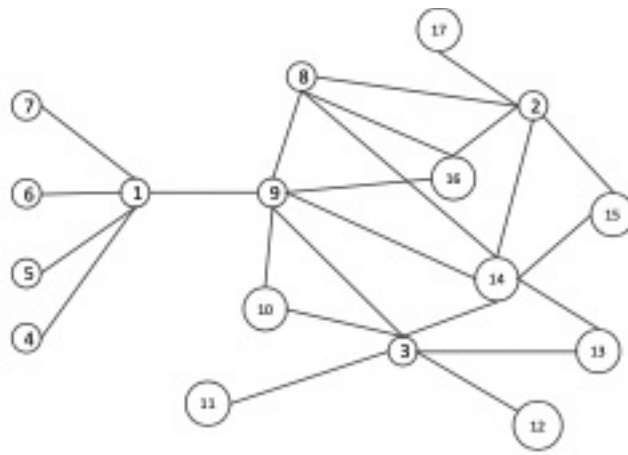
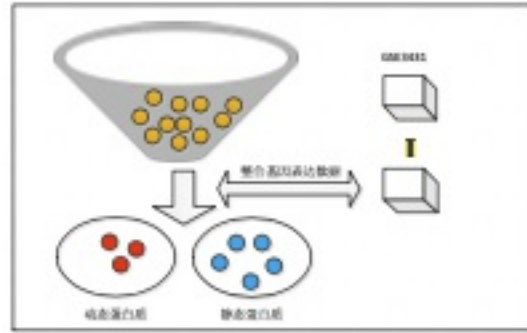
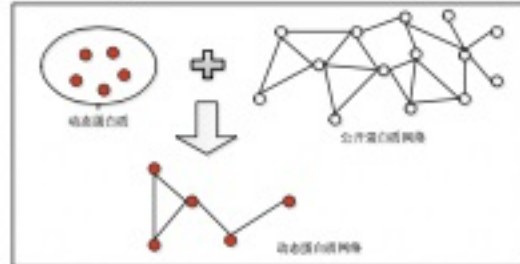


Figure 3

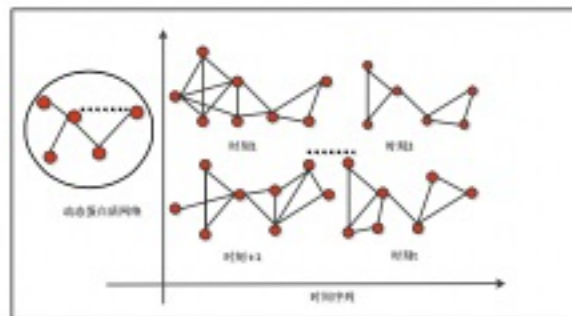
The example of node centrality



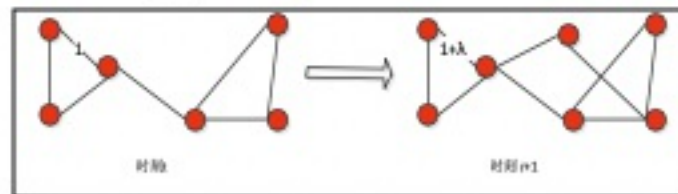
a. Integrating gene expression data and extracting dynamic proteins



b. Combining open protein network and dynamic protein to form dynamic protein network



c. Constructing dynamic protein networks at different times



d. The weight of the same edge at adjacent time

Figure 4

Construction of dynamic protein network based on attenuation coefficient

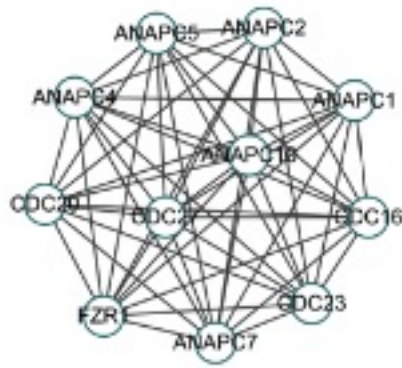


Figure 5

Part of yeast protein network

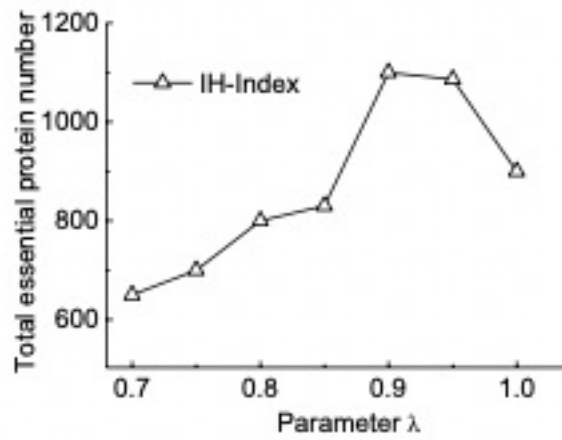


Figure 6

The effect of attenuation coefficient on the essential protein number

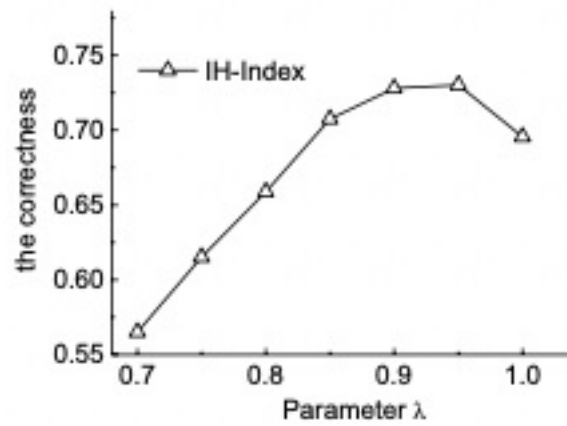


Figure 7

The correctness changes with the attenuation coefficient changes

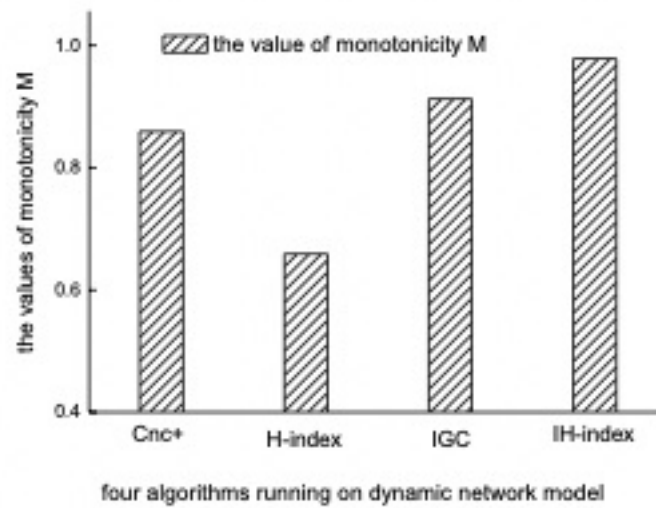


Figure 8

Monotonicity values of different essential protein search algorithms

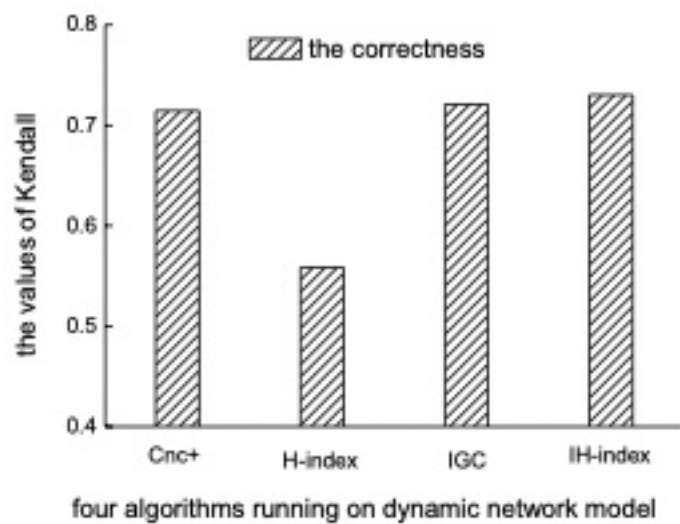


Figure 9

Correctness of different essential protein search algorithms