A Complex Network Approach for the Analysis of Protein Units Similarity Using Structural Alphabet 董其樺, Jose C. Nacher Bioinformatics Computer Science and Informatics chihua.tung@chu.edu.tw

Abstract

In this paper we present a network approach based on the recent developed 3D-BLAST method of rapid protein structure search. We defined new local segments that represent structural feature of proteins named units of structural alphabet (USA). Each USA is composed of two protein secondary structures, and one loop located between these two secondary structures. We performed all-against-all structural comparison of USA and recognized the USA-based similarity network. The analytical result shows that the network with a power degree distribution is called scale free. These results not only suggest the existence of organizing principles in the local protein structure but also allow us to identify potential key fragments that could be useful for future new drug development and design.

Keyword:Local structure similarity network, network biology, protein modularity