

Complex network study of the immune epitope database for parasitic organisms

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Background: Complex network approach allows the representation and analysis of complex systems of interacting agents in an ordered and effective manner, thus increasing the probability of discovering significant properties of them. In the present study, we defined and built for the first time a complex network based on data obtained from Immune Epitope Database for parasitic organisms. We then considered the general topology, the node degree distribution, and the local structure (triadic census) of this network. In addition, we calculated 9 node centrality measures for observed network and reported a comparative study of the real network with three theoretical models to detect similarities or deviations from these ideal networks. **Result:** The results obtained corroborate the utility of the complex network approach for handling information and data mining within the database under study. **Conclusion:** They confirm that this type of approach can be considered a valuable tool for preliminary screening of the best experimental conditions to determine whether the amino acid sequences being studied are true epitopes or not. © 2017 Bentham Science Publishers.

B-cells epitopes

Immune epitope database

Network theory

Parasitic organisms

Topological indices

Topological indices

epitope

epitope

amino acid sequence

Article

bioinformatics

comparative study

complex network approach

data analysis

data mining

factual database

information processing

mathematical analysis

nonhuman

parasite

system analysis

theoretical model

animal

artificial neural network

chemistry

immunology

parasite

Amino Acid Sequence

Animals

Data Mining

Databases, Factual

Epitopes

Neural Networks (Computer)

Parasites