MODULAR AND FUNCTIONAL ANALYSIS OF NON-MODEL ORGANISMS PROTEIN NETWORKS

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Proteins are essential macromolecules that play roles in most biological cell processes, which include gene expression, cell growth, intracellular communication, and apoptosis. Several processes are carried out by molecular machines composed of a large number of protein components organized by protein-protein interactions (PPI). These interactions have been studied by biochemistry, molecular dynamics, and signal transduction. All these analysis have been generating a huge amount of data, which enables the creation of protein interaction networks to organize the current knowledge on biochemical cascades on model organisms, as well as provide new pathways in non-model organisms. Taking into account the potential of protein network analysis, herein we propose the implementation of a new method of analysis of PPI data from non-model organisms. Three distinct networks of protein-protein interaction (PPI) were created for three different species: Rattus norvegicus, Aedes aegypti and Anopheles gambiae. Then, we implemented a methodology that swept each of the networks and identified 19 protein clusters of R. norvegicus, 18 of A. aegypti and 20 related to A. gambiae. Finally, the functional enrichment of each of the obtained modules, ie, the identification of cellular activities present in the module, was made through the online repository database called DAVID Bioinformatics Resources. The biological processes and molecular functions analysis (with p-value <10⁻¹⁰), related only to existing proteins in the modules, found 736 process/functions linked to R. norvegicus, 141 to A. aegypti and 158 to A. gambiae. The next stage of work will be the measurements of the overall metabolic performance of the organisms. This step will require the addition of protein microarray data on the networks, and it can provide new information of these non-model organisms.

Keywords: cluster, ppi, functional enrichment.