Important Nodes Detection in Biological Networks: A Graph Kernel based Approach

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Abstract: In this paper, a new hybrid method proposed based on both graph kernels and principal component analysis for identification of important nodes in biological networks, which is indeed an important challenge to understand processes such as cancerogenesis, designing drugs or how to deal with diseases. Variouse measures such as centrality and motif based method have been proposed to investigate important nodes in these networks, but the main problem in most of them is low accuracy in these algorithms. In the proposed method we first extract appropriate features for each node in the network by using graph kernels, then the nodes are sorted based on these features by using PCA and finally the important nodes are identified. In order to evaluate the effectiveness of the proposed method, this method is compared with some common methods such as centrality measures and a motif based hybrid approach. The results of the experiments on real biological networks indicate that the proposed method has acceptable accuracy and can be used as an efficient method for identifying important nodes.

Key words: Complex Networks; Biological Networks; Identification of Important Nodes; Principal Component Analysis;Graph Kernel.