

Preface

Biological networks are an effective model for providing insights about biological mechanisms. Networks with different characteristics are employed for representing different scenarios. This powerful model allows analysts to perform many kinds of analyses which are proved to mine interesting information about underlying biological behaviors. This work intends to survey on biological networks as a model for subsequent analyses which are also presented and discussed. Then, it focuses on techniques for discovering exceptional patterns, a particular kind of analysis which is witnessing a great interest due to the importance of the knowledge it is able to mine, with a pattern accounting for local similarities and also collaborative effects involving interactions between multiple actors (for example, genes). Among exceptional patterns, of particular interest are discriminative ones, namely patterns which are able to discriminate between two input populations (for example, healthy/unhealthy samples). The work will also include discussions on the most recent proposal on discovering discriminative patterns, where there is a labeled network for each sample, resulting in a database of networks representing a sample set. Previous techniques are able to just consider an aggregated network of each population, thus allowing the analyst to get a much more fine analysis. In more details, edge-labeled networks are used and the discriminative power of a pattern is measured based on edge weights, which are representative of how much relevant is the co-expression between two genes.

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