

A NEW INTERPRETATION OF GENE EXPRESSION MICROARRAY DATA SETS USING FUZZY PETRI NET APPROACH

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Abstract

The analysis of high-throughput experimental data, such as microarray gene expression data, is currently seen as a promising way of finding gene regulatory networks. While increasing amount of microarray data sets are becoming available online, the integration of multiple microarray data sets from various data sources (e.g. different tissues, species, and conditions) for GRNs inference becomes very important in order to achieve more accurate and reliable GRNs modeling. In this paper, we introduce a fuzzy Petri net approach that allows a new interpretation of microarray data set and to infer gene regulatory networks. We validate our framework with an experimental study using microarray data sets. The results reported on gene regulatory network demonstrate the applicability and effectiveness of the proposed approach.

Keywords: bioinformatics, microarray data sets, Fuzzy Petri net.