Boolean models and algorithms for analyzing gene expression data

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Abstract

We have been studying Boolean models and algorithms for analyzing gene expression data. We studied the sample complexity (the number of gene expression patterns) and algorithms for identifying genetic networks under the Boolean network model. We showed that if the indegree of each node is bounded by a constant, only $O(\log n)$ state transition pairs (from 2^n pairs) are necessary and sufficient to identify the original Boolean network of n nodes correctly with high probability. A similar property holds even for the Boolean network with small errors. We also studied algorithms for classification of tumor types of cells, based on a Boolean model. In particular, we studied methods for selection of informative genes (i.e., genes relevant to class distinction) and developed a heuristic algorithm.