Efficient Computation of Steady States of Logical Models of Biological Systems

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Abstract: Logical models have been used to model biological systems and have significant applications to carry as much as possible qualitative information out from the system. Although the logical models have a relatively simple structure, but their analysis is not a trivial work at all. In this paper, we provide an efficient algorithm due to the novel computer algebraic tools to find steady states of a logical model. It is worth noting that the computer algebraic techniques are already employed to solve this problem, however their approach needs many evaluations of parameters which increases the volume of computations. More precisely, it needs 2^p computations of Gröbner basis where p is a prime number greater than all maximum expression level of nodes in the logical model. In our method, there is no need to several evaluation of parameters, as all possible cases will be analyzed at once and it needs to compute just one comprehensive Gröbner system. The efficiency of our method comes from the advantages and notable properties of comprehensive Gröbner system which is a novel computational tool in the context of computer algebra. The application of comprehensive Gröbner system is in fact, the analysis of a system of polynomial equations in which the coefficients contain some parameters. By applying comprehensive Gröbner systems, one can detect all cases for which a polynomial system has any solutions and provide all of the solutions. There are also a number of efficient algorithms and implementations to compute comprehensive Gröbner systems.

Keywords: Systems Biology; Logical Model; Steady State; Computer Algebra; Comprehensive Gröbner system

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