BioDiVinE: A Tool for Parallel Analysis of ODE Models

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Abstract

THE use of model checking for the analysis of biological networks has attracted much attention recently. However, one of the practical limitations is the complexity of the model. Our work targets this issue by employing parallel on-the-fly LTL model checking.

1. Background

THIS work focuses on analysis of dynamic systems describing functionality of biological networks. In particular, the biological model is considered as a system of multi-affine ODEs. The continuous state space of the dynamic system is abstracted into a finite automaton by employing the *rectangular abstraction method* [3]. The analysis is performed on abstracted models. In particular, the state space reachable from given initial conditions (initial concentration of species) is automatically generated and analysed.

2. Related Work

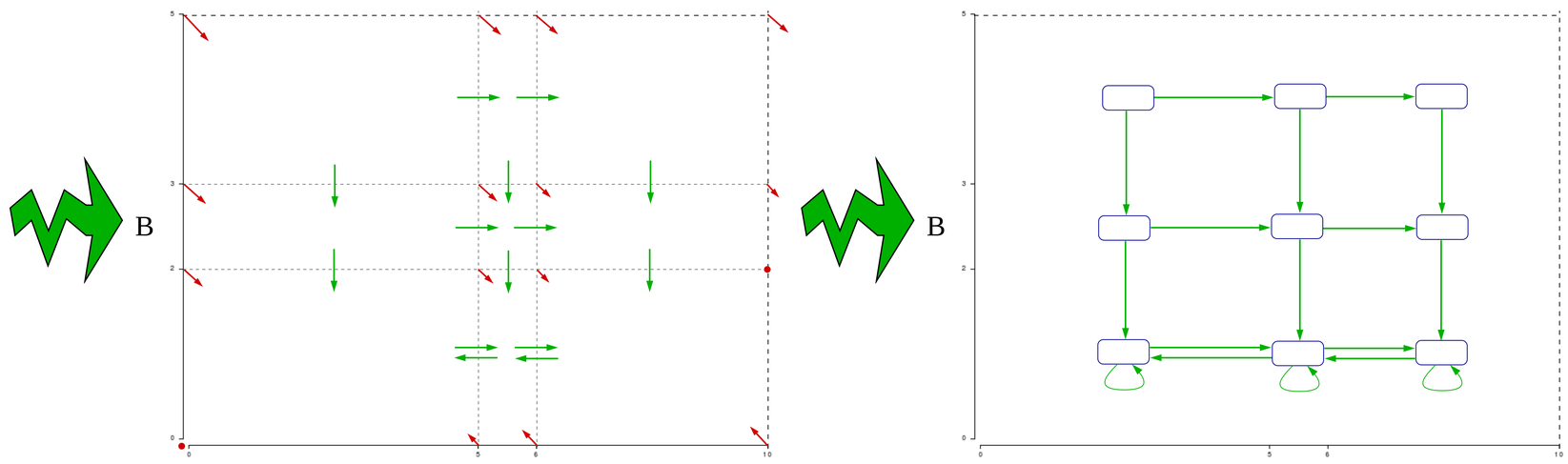
THERE is another work that employs rectangular abstraction for dynamic systems [2]. The framework is suitable for dynamic modelling of genetic regulatory networks where the non-linearities occur at the level of Hill functions. On the contrary, in our approach we consider dynamic systems in which non-linearities come from the law of mass action.

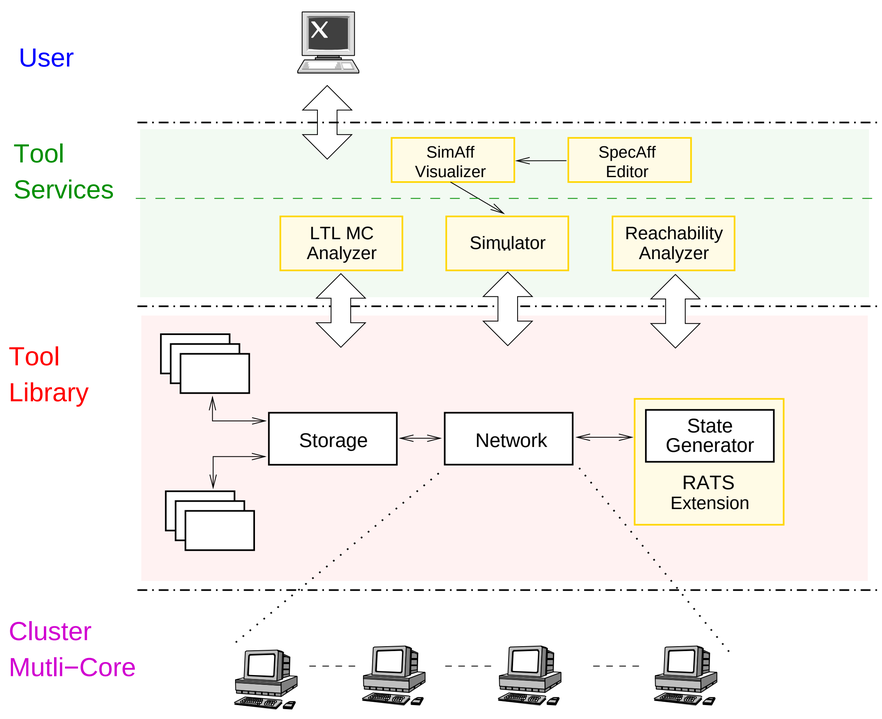
3. BioDiVinE Tool Description

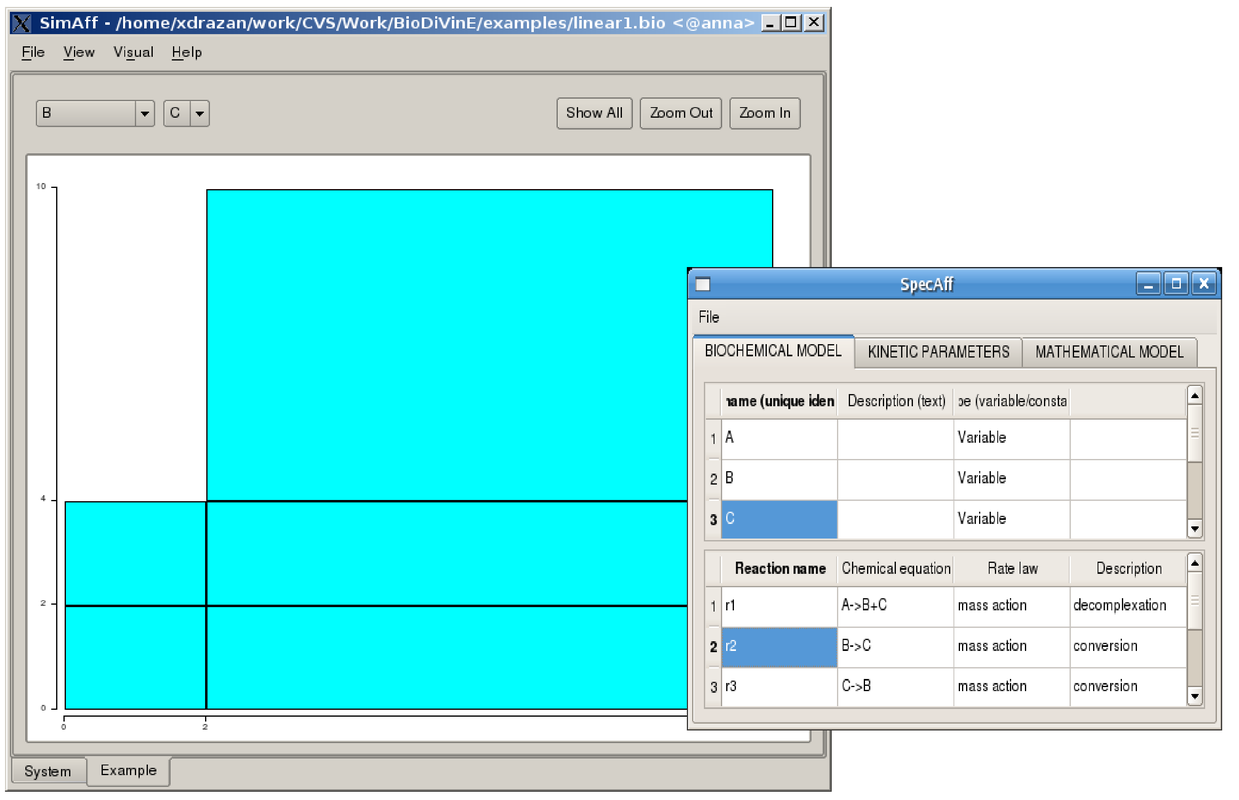
BIODIVINE tool considers the model in terms of chemical equations. The tool provides a user interface for specification of models as well as graphical environment for visualization of the abstracted state space. The central feature of the tool is a bunch of algorithms for LTL model checking analysis.

$$A \underset{k_2}{\overset{k_1}{\leftrightarrows}} B$$

$$\frac{dA}{dt} = -k_1 \cdot A + k_2 \cdot B$$
$$\frac{dB}{dt} = k_1 \cdot A - k_2 \cdot B$$





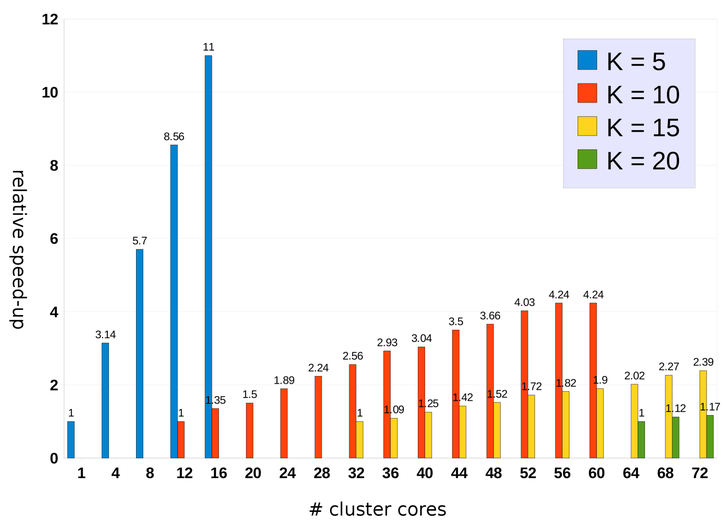


4. Experiments

WE have performed several experiments with BioDiVinE [1] in order to show scaling of the algorithms when distributed on several cluster nodes. The following graph shows scaling of model checking conducted on a simple model of a reaction network representing a catalytic reaction scaled for different numbers of intermediate products. We have considered a property expressing the consumption and consequent reaccumulation of the enzyme.

$$S + E \rightleftharpoons ES_1 \rightleftharpoons ES_2 \rightleftharpoons \cdots \rightleftharpoons ES_K \rightarrow P + E$$

$$E > 95 \wedge (E > 95 \mathbf{U} (E =< 95 \wedge (E <= 95 \mathbf{U} E > 95)))$$



References

[1] J. Barnat, L. Brim, I. Černá, S. Dražan, J. Fabriková, and D. Šafránek. Computational Analysis of Large-Scale Multi-Affine ODE Models. In *Proc. of High Performance Computational Systems Biology (HIBI 2009)*. IEEE Computer Society, 2009. Paper accepted.

[2] G. Batt, C. Belta, and R. Weiss. Model checking genetic regulatory networks with parameter uncertainty. *IEEE Transactions on Circuits and Systems and IEEE Transactions on Automatic Control, Special Issue on Systems Biology*, pages 215–229, 2008.

[3] C. Belta and L.C.G.J.M. Habets. Controlling a class of nonlinear systems on rectangles. *IEEE Transactions on Automatic Control*, 51(11):1749–1759, 2006.

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