Tolque: A Tool for Algorithmic Algebraic Model Checking

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Motivated by the need for scalable symbolic reasoning methodologies aimed at systems biology, as well as the novel opportunities made possible by powerful hybrid automata models of biochemical networks, we have embarked upon the Algorithmic Algebraic Model Checking (AAMC) project that combines symbolic computation with model checking to analyze biochemical systems. Briefly, AAMC aims to identify a decidable (ultimately, practical) component of a theory for systems biology by examining the connections between semi-algebraic hybrid automata, modal logic, computability and systems biology, starting with a characterization based on Semi-Algebraic Hybrid Automata [5]. Tolque is a continually evolving practical implementation of this emerging theoretical framework.

In Semi-Algebraic Hybrid Automata, the continuous dynamics and discrete jump conditions are defined by first-order formulæ whose terms are polynomials over the reals. Consequently, they can exploit a series of real algebraic techniques, based on Tarski's result on the decidability of real quantifier elimination, to study the possible evolutions of the system entirely symbolically. Beyond decidability of Timed Computation Tree Logic (TCTL) [4], we studied Semi-Algebraic Constant Reset Automata [2] and Independent Dynamics Automata [1] whose resets were constrained to be constant or identity.

Tolque [4], a preliminary version of the algebraic dense-time model-checker for semi-algebraic hybrid automata, was implemented in C/C++. Inspired by the success over small examples and by the substantial theoretical progress since the prototypical implementation, in this abstract, we describe its multi-faceted expansion, which is in progress. The entire gamut of TCTL queries will now be supported (rather than just $\exists\mathcal{F}$), allowing nesting of operators and specification of nesting degrees as well. An improved Tolque will automatically perform symbolic Taylor series approximation of the differential equations. The most significant enhancement of Tolque will be the ability to over / under approximate semi-algebraic sets by rectangular grids and polytopes [3]. The user will then be able to choose from a set of transition relations which interpret time discretization differently. A Lisp-based symbolic algebra backbone will optimize the computations and employ heuristics to choose between different quantifier elimination tools such as Qepcad, Redlog and AQCS.

Integration with Simpathica is planned in order to allow biochemical networks to be easily represented, stored and analyzed, in keeping with our initial "Systems Biology" motivation. We have applied the AAMC approach to the Delta-Notch protein interaction [4] and the run-and-tumble bacterial chemotaxis [1] examples, and are in the process of integrating kinetic mass action and flux balance analysis to develop a general algebraic framework for metabolic networks.

References

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