

Seamless Logic-based and Analysis-based Hybrid Systems with Application to Bio-molecular Networks

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The possibility to mathematically model hybrid systems with dynamics over domains of very distinct types is realizable with the tools of analysis on the spaces occurring as objects in a Cartesian closure of the category of topological spaces. That is simply the mathematical setting in which such hybrid models live, yet it is only a setting, with the tools of category theory itself not required for constructing a system and verifying its properties. The domains in such systems are called convergence spaces. Although convergence spaces are not well-known, the subject reaches back through the work of Bourbaki, and their use arose repeatedly in applications through the intervening years since then, and notably has arisen as a basis for functional analysis, (Beattie and Butzman, 2002.) Convergence spaces provide a way to *uniformly* define the notion of limit in function spaces since the limit notion in a function space Y^X , as a convergence space, uniformly depends on the limit notions in X and Y , which is unlike the circumstance with topological spaces. This uniformity allows to define continuity in discrete and continuous hybrid structures, and allows to define differentiability as well, in perfect agreement with these notions as we already know them in e.g. familiar vector spaces. The use of convergence spaces enables us to have a notion of differentiation that is native to the domains over which differentiation is defined, and therefore not dependent on encodings of differentiation into familiar spaces. In our short presentation/poster we present the definition of a convergence space and define continuity and differentiability. As examples we present as convergence spaces the space of real numbers with its usual metric, a simple directed graph, and a hybrid structure. We present differentiability with an example; and present a very simple hybrid dynamical system that is uniformly defined differentially using derivatives of both boolean and real variables with respect to time that models a reversible reaction enzymatically catalyzed in one direction (Breitling, et.al., 2008) with the enzyme's presence discretely dependent on one of the reaction products. The example includes a generalization of a normal logic program clause, with Boolean and real variables in the body, in which the head is a Boolean variable differentiable with respect to time. We also point out that our application to bio-molecular networks arose from observing the swimming behavior of a microscopic organism, *Chlamydomonas reinhardtii*. The dynamics of the the organism's swimming is not fully understood and we believe the analysis of the dynamics is likely to be furthered using the convergence space approach.

Keywords: convergence space, bio-molecular networks, logic-based

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