

# Invariant Verification of Nonlinear Hybrid Automata Networks of Cardiac Cells<sup>\*</sup>

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**Abstract.** Verification algorithms for networks of nonlinear hybrid automata (HA) can aid us understand and control biological processes such as cardiac arrhythmia, formation of memory, and genetic regulation. We present an algorithm for over-approximating reach sets of networks of nonlinear HA which can be used for sound and relatively complete invariant checking. First, it uses automatically computed input-to-state discrepancy functions for the individual automata modules in the network  $\mathcal{A}$  for constructing a low-dimensional model  $\mathcal{M}$ . Simulations of both  $\mathcal{A}$  and  $\mathcal{M}$  are then used to compute the reach tubes for  $\mathcal{A}$ . These techniques enable us to handle a challenging verification problem involving a network of cardiac cells, where each cell has four continuous variables and 29 locations. Our prototype tool can check bounded-time invariants for networks with 5 cells (20 continuous variables, 29<sup>5</sup> locations) typically in less than 15 minutes for up to reasonable time horizons. From the computed reach tubes we can infer biologically relevant properties of the network from a set of initial states.

**Keywords:** Biological networks, hybrid systems, invariants, verification.

## 1 Introduction

Central to understanding and controlling behavior of complex biological networks are invariant properties. For example, synchronization of the action potentials of cardiac cells and neurons is responsible for normal functioning of the heart and for formation of memory [6, 16], and maintenance of synchrony is an invariant property. Real-time prediction of loss of synchrony can enable automatic deployment of counter-measures. For instance, embedded defibrillator devices are being designed to preempt possible cardiac arrest that arises

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<sup>\*</sup> The authors are supported by NSA SoS grant (W911NSF-13-0086), AFOSR YIP grant (FA9550-12-1-0336), NSF CAREER grant (CNS 10-54247), the ERC AdG VERIWARE, ERC PoC VERIPACE, and the Institute for the Future of Computing, Oxford Martin School.

from loss of synchrony. Offline invariant checks can aid in debugging pacemakers and brain-machine interfaces. Checking invariant properties for networks of dynamical systems is challenging. Analytical results exist only for modules with relatively simple dynamics and on special types of topologies such as scale-free and random graphs [7, 9, 38, 40, 43]. These approaches cannot be applied to modules with nonlinear and hybrid dynamics such as the models of cardiac cells in [11, 20]. Aside from the nonlinearities in the modules, the complete network model involves shared continuous variables between modules (ion-channels) which have limited support in analytical and verification approaches. In the absence of analytical approaches, one performs simulation experiments which are computationally inexpensive but fall short of providing guarantees and are of limited utility in studying invariants for sets of initial states or parameter values. For example, if we wanted to know if the voltage of an action potential stays within some range from a set of initial states, then a finite number of simulations cannot give us a provably correct answer.

In this paper, we present an algorithm for verifying bounded-time invariant properties of networks of deterministic nonlinear hybrid automata. The underlying principle is simulation-based verification which combines numerical simulations with formal analysis [5, 14, 15]. First, a simulation  $\psi$  is computed from a single initial state  $\mathbf{v}$ . This  $\psi$  is then bloated by *some factor* to over-approximate all executions from a neighborhood  $B_{\mathbf{v}}$  of  $\mathbf{v}$  of non-zero measure. By repeating this process for different  $\mathbf{v}$ 's, all behaviors from a set of initial states can be over-approximated and robust invariants can be checked. In [15], we used user-provided model annotations (*discrepancy functions*) to statically compute the bloating factor in a way that can make the over-approximations arbitrarily precise. The resulting algorithm enjoys scalability and relative completeness: if the system satisfies the invariant robustly, then the algorithm is guaranteed to terminate. The burden of finding discrepancy functions for large models is partly alleviated in [26] for nonlinear differential equations. That paper proposes *input-to-state (IS)* discrepancy functions for each module  $\mathcal{A}_i$  of a larger system  $\mathcal{A} = \mathcal{A}_1 \parallel \dots \parallel \mathcal{A}_N$ . These user-provided, albeit modular, annotations are used to construct a lower-dimensional nonlinear time-varying system whose trajectories give the necessary bloating factor for the trajectories of the system  $\mathcal{A}$ .

These previous results do not extend to hybrid systems with guards and resets, and their applicability is still limited by the annotation required from the user. One challenge is that individual simulations capture a particular sequence of locations. However, the states reached in a bloated version of the simulation may intersect with many other guards and visit a completely different sequence of locations. Our contributions address this and other technical hurdles, demonstrating a promising approach for invariant verification of nonlinear hybrid networks. (a) We present a new simulation-based verification algorithm for nonlinear hybrid networks that uses modular input-to-state (IS) discrepancy functions. Modular annotations and the simulation-based approach make it scalable. The algorithm is sound; it systematically discovers possible transitions and then generates new simulations for different location sequences. We identify

general robustness conditions that yield relative-completeness. (b) We develop a set of techniques for automatically computing input-to-state discrepancy functions for a general class of nonlinear hybrid models. (c) The performance of our prototype implementation in checking bounded-time invariants of complex Simulink models of cardiac cell networks illustrate the promise of the approach [25]. For networks with 5 cells, each with 4 dimensions and 29 locations, and multi-affine dynamics (total of 20 continuous variables,  $29^5$  locations), invariants for up to reasonable time horizons are established typically in less than 15 minutes. In two minutes, it finds counter-examples of networks with 8 cells. All of this enables us to check biologically relevant properties for cardiac cells networks.

Section 2 provides background for hybrid automata, whereas Section 3 introduces IS discrepancy and techniques for computing them. Section 4 describes the main algorithm and Section 5 presents its applications in checking cardiac networks. Finally, Section 6 discusses related works and concludes the paper.

## 2 Hybrid Automata Modules and Networks

*Hybrid Input/Output Automata.* (HA) is a framework for specifying interacting modules that evolve discretely and continuously and share information over continuous variables and discrete transitions [31, 34, 35]. Please see the full version [25] for related definitions and notations.

For a variable  $v$ , its type, denoted by  $\text{type}(v)$ , is the set of values that it can take. For a set of variables  $\mathcal{V}$ , a *valuation*  $\mathbf{v}$  maps each  $v \in \mathcal{V}$  to a point in  $\text{type}(v)$ . Given a valuation  $\mathbf{v}$  for  $\mathcal{V}$ , the valuation of a particular variable  $v' \in \mathcal{V}$ , denoted by  $\mathbf{v}.v'$ , is the restriction of  $\mathbf{v}$  to  $v'$ ; for a set  $V \subseteq \mathcal{V}$ ,  $\mathbf{v}.V$  is the restriction of  $\mathbf{v}$  to  $V$ .  $\text{Val}(\mathcal{V})$  is the set of all valuations for  $\mathcal{V}$ . A *trajectory* for  $\mathcal{V}$  models continuous evolution of the values of the variables over a closed interval  $[0, T]$  called the *domain*. A trajectory  $\xi$  is a map  $\xi : [0, T] \rightarrow \text{Val}(\mathcal{V})$ . Restriction of  $\xi$  to a subset of variables  $\mathcal{X} \subseteq \mathcal{V}$  is denoted by  $\xi \downarrow \mathcal{X}$ . For a trajectory  $\xi$  of  $\mathcal{V} \cup \mathcal{U}$  with domain  $[0, T]$ , we define  $\xi.\text{fstate}$  as  $(\xi \downarrow \mathcal{V})(0)$  and  $\xi.\text{lstate}$  as  $(\xi \downarrow \mathcal{V})(T)$ . A variable is *continuous* if all its trajectories are piece-wise continuous and it is *discrete* if its trajectories are piece-wise constant. A HA has a set of continuous variables  $\mathcal{X}$  that evolve along trajectories (defined by differential equations with inputs  $\mathcal{U}$ ) and can be reset, and a set of discrete variables  $\mathcal{L}$  that change with transitions.

**Definition 1.** A Hybrid I/O Automaton (HA)  $\mathcal{A}$  is a tuple  $(\mathcal{L}, \mathcal{X}, \mathcal{U}, \Theta, \mathcal{D}, \mathcal{T})$  where (a)  $\mathcal{L}$  is a set of discrete variables.  $\text{Val}(\mathcal{L})$  is the set of locations. (b)  $\mathcal{X}$  is a set of real-valued continuous variables.  $\mathcal{V} := \mathcal{X} \cup \mathcal{L}$  is the set of state variables;  $\text{Val}(\mathcal{V})$  is the state space. (c)  $\mathcal{U}$  is a set of real-valued input variables;  $\text{Val}(\mathcal{U})$  is the input space. (d)  $\Theta \subseteq \text{Val}(\mathcal{V})$  is a set of start states; (e)  $\mathcal{D} \subseteq \text{Val}(\mathcal{V}) \times \text{Val}(\mathcal{V})$  is a set of discrete transitions. (f)  $\mathcal{T}$  is the set of trajectories for  $\mathcal{V} \cup \mathcal{U}$  that is closed under prefix, suffix, and concatenation [31]. Over any trajectory  $\xi \in \mathcal{T}$ ,  $\mathcal{L}$  remains constant. For any state  $\mathbf{v}$  and piece-wise continuous input trajectory  $\eta$ , there exists a state trajectory  $\xi$  such that  $\xi.\text{fstate} = \mathbf{v}$  and either (i)  $\xi \downarrow \mathcal{U} = \eta$ , or (ii)  $\xi \downarrow \mathcal{U}$  matches a prefix of  $\eta$  with a transition enabled at  $\xi.\text{lstate}$ .

A transition  $(\mathbf{v}, \mathbf{v}') \in \mathcal{D}$ , for any two states  $\mathbf{v}, \mathbf{v}'$ , is written as  $\mathbf{v} \rightarrow_{\mathcal{A}} \mathbf{v}'$  or as  $\mathbf{v} \rightarrow \mathbf{v}'$  when  $\mathcal{A}$  is clear from the context. The transitions of  $\mathcal{A}$  are specified for pairs of locations in the guard-reset style. For each pair  $(\ell, \ell')$  of locations the guard  $G_{\ell, \ell'} \subseteq \text{Val}(\mathcal{X})$  is the set of states from which a transition from location  $\ell$  to  $\ell'$  is enabled and the reset map is a continuous function  $\text{Val}(\mathcal{X}) \rightarrow \text{Val}(\mathcal{X})$ .

For location  $\ell \in \text{Val}(\mathcal{L})$ , the trajectories of  $\mathcal{A}$  are defined by a *trajectory invariant*  $I_{\ell} \subseteq \text{Val}(\mathcal{X})$  and a set of ordinary differential equations (ODEs) involving the variables in  $\mathcal{X}$  and  $\mathcal{U}$ . The ODE is specified by a Lipschitz continuous function called *dynamic mapping*  $f_{\ell} : \text{Val}(\mathcal{X}) \times \text{Val}(\mathcal{U}) \rightarrow \text{Val}(\mathcal{X})$ . Given an input trajectory  $\eta$  of  $\mathcal{U}$  and a state  $\mathbf{v} \in \text{Val}(\mathcal{V})$ , a state trajectory from  $\mathbf{v}$  with  $\eta$  is a function  $\xi_{\mathbf{v}, \eta} : [0, T] \rightarrow \text{Val}(\mathcal{V})$  satisfying: (a)  $\xi_{\mathbf{v}, \eta}(0) = \mathbf{v}$ , (b) for any  $t \in [0, T]$ , the time derivative of  $\xi \downarrow \mathcal{X}$  at  $t$  satisfies the differential equation  $\frac{d(\xi \downarrow \mathcal{X})(t)}{dt} = f_{\ell}((\xi \downarrow \mathcal{X})(t), \eta(t))$ , and (c)  $(\xi \downarrow \mathcal{X})(t) \in I_{\ell}$  and  $(\xi \downarrow \mathcal{L})(t) = \ell$ . As in the last two statements, we will drop the subscripts of a trajectory when the dependence on the initial state and the input is clear. Because of the invariant  $I_{\ell}$ , in some location  $\ell \in \text{Val}(\mathcal{L})$  all the trajectories might be of finite duration. Conditions (i) and (ii) in Definition 1 make the HA *input enabled*, that is, from any state  $\mathcal{A}$  is able to consume any input  $\eta$  completely (i) or up to some time at which it reacts with a transition (ii).

A HA without inputs ( $\mathcal{U} = \emptyset$ ) is *closed*; otherwise, it is *open*. A HA with a single location and no transitions is called a *dynamical system*. We denote the components of HA  $\mathcal{A}$  by  $\mathcal{L}_{\mathcal{A}}, \mathcal{X}_{\mathcal{A}}, \mathcal{U}_{\mathcal{A}}, \Theta_{\mathcal{A}}, \mathcal{D}_{\mathcal{A}}, \rightarrow_{\mathcal{A}}$  and  $\mathcal{T}_{\mathcal{A}}$ , and for  $\mathcal{A}_i$  its components are denoted by  $\mathcal{L}_i, \mathcal{X}_i, \mathcal{U}_i, \Theta_i, \mathcal{D}_i, \rightarrow_i$  and  $\mathcal{T}_i$ .

*Semantics.* We assume that the discrete transitions are urgent and deterministic. That is, from any state  $\mathbf{v} = (\mathbf{x}, \ell)$  at most one of following two things can happen: (a) a transition to a unique state  $(\mathbf{x}', \ell')$ , or (b) a trajectory  $\xi_{\mathbf{v}}$  of non-zero duration. A bounded execution of  $\mathcal{A}$  records the evolution of the variables along a particular run. A *bounded execution fragment* is a finite sequence of trajectories  $\xi_{(0)}, \xi_{(1)}, \dots$ , such that, for each  $i$ ,  $\xi_{(i)} \in \mathcal{T}$  and  $\xi_{(i)}. \text{lstate} \rightarrow \xi_{(i+1)}. \text{fstate}$ . A *bounded execution* is an execution fragment with  $\xi_{(0)}. \text{fstate} \in \Theta$ . A state  $\mathbf{v}$  is *reachable* if it is the last state of some execution. We denote the set of reachable states of  $\mathcal{A}$  by  $\text{Reach}_{\mathcal{A}}$ . The reachable states up to a bounded time horizon  $T > 0$  are denoted by  $\text{Reach}_{\mathcal{A}}(T)$ . The reachable states from a subset of initial states  $\Theta' \subseteq \Theta$  up to  $T$  are denoted by  $\text{Reach}_{\mathcal{A}}(\Theta', T)$ . A set  $\text{Inv} \subseteq \text{Val}(\mathcal{V})$  is an *invariant* of a closed HA  $\mathcal{A}$  if  $\text{Reach}_{\mathcal{A}} \subseteq \text{Inv}$ . Checking invariants corresponds to verifying safety properties. Computing  $\text{Reach}_{\mathcal{A}}$  exactly is undecidable but for the simplest classes of hybrid automata [1, 23, 32, 44].

For relative completeness, we define robustness of HA. A HA  $\mathcal{A}(c)$  is a *c-perturbation* of  $\mathcal{A}$  if  $\mathcal{A}(c)$  is obtained by perturbing the initial set and dynamical mappings of  $\mathcal{A}$  by at most  $c$ . That is,  $\mathcal{A}$  and  $\mathcal{A}(c)$  are identical except that (i)  $d(\Theta_{\mathcal{A}}, \Theta_{\mathcal{A}(c)}) \leq c$  where  $d(\cdot, \cdot)$  is the Hausdorff distance and (ii) for every location  $\ell$  and any continuous state  $\mathbf{x} \in \text{Val}(\mathcal{X})$ , the dynamical mappings of the two HA satisfy  $|f_{\ell, \mathcal{A}}(\mathbf{x}) - f_{\ell, \mathcal{A}(c)}(\mathbf{x})| \leq c$ . The *c-perturbed reach set* of  $\mathcal{A}$ , denoted by  $c\text{-Reach}_{\mathcal{A}}$ , is the set of states reachable by some  $c$ -perturbation of  $\mathcal{A}$ . For a time bound  $T > 0$ ,  $\text{Inv}$  is a *robust invariant* up to time  $T$  if there exists

a positive constant  $c > 0$  such that  $c\text{-Reach}_{\mathcal{A}}(T) \subseteq \text{Inv}$ . In this paper we will present semi-decision procedures for bounded-time robust invariant checking of networks of deterministic nonlinear HA.

*Composition.* Large and complex models can be created by *composing* smaller automata. The composition operation identifies (“plugs-in”) the input variables of one automaton  $\mathcal{A}_i$  with the state variables of another automaton<sup>1</sup>. A pair of HAs  $\mathcal{A}_1$  and  $\mathcal{A}_2$  are *compatible* if their state variables are disjoint  $\mathcal{V}_1 \cap \mathcal{V}_2 = \emptyset$ .

**Definition 2.** *Given a pair of compatible HAs  $\mathcal{A}_1$  and  $\mathcal{A}_2$  the composed automaton  $\mathcal{A} = \mathcal{A}_1 \parallel \mathcal{A}_2$  is  $\langle \mathcal{L}, \mathcal{X}, \mathcal{U}, \Theta, \mathcal{D}, \mathcal{T} \rangle$ , where (a)  $\mathcal{L} := \mathcal{L}_1 \cup \mathcal{L}_2$ , (b)  $\mathcal{X} := \mathcal{X}_1 \cup \mathcal{X}_2$ , (c)  $\Theta = \Theta_1 \times \Theta_2$ , (d)  $\mathcal{U} = U_1 \cup U_2 \setminus (\mathcal{V}_1 \cup \mathcal{V}_2)$ , (e)  $\mathcal{D}: \mathbf{v} \rightarrow \mathbf{v}'$  iff either  $\mathbf{v}.\mathcal{V}_1 \rightarrow_1 \mathbf{v}'.\mathcal{V}_1$  and  $\mathbf{v}.\mathcal{V}_2 = \mathbf{v}'.\mathcal{V}_2$ , or  $\mathbf{v}.\mathcal{V}_2 \rightarrow_2 \mathbf{v}'.\mathcal{V}_2$  and  $\mathbf{v}.\mathcal{V}_1 = \mathbf{v}'.\mathcal{V}_1$ , and (f) A trajectory  $\xi$  of  $\mathcal{V} \cup \mathcal{U}$  is in  $\mathcal{T}$  iff  $\xi \downarrow (\mathcal{V}_i \cup \mathcal{U}_i) \in \mathcal{T}_i$  for each  $i \in \{1, 2\}$ .*

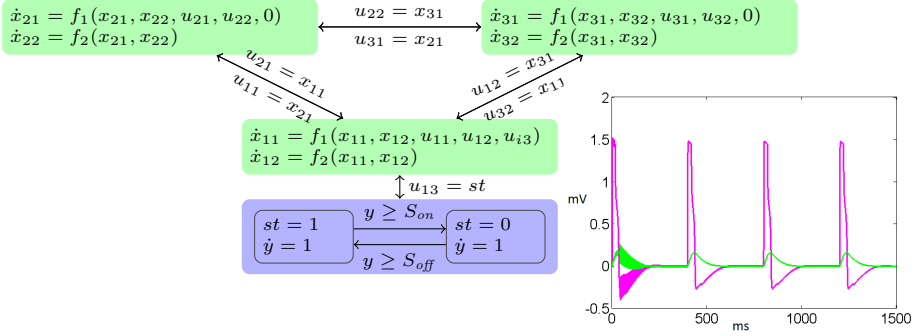
Note that the composition of two or more HA will define a *network*.  $\mathcal{A}$  satisfies the requirements for Definition 1 and can be constructed by syntactically combining the guards, resets, and ODEs of its components.

*Example 1.* In the 2-dimensional FitzHugh-Nagumo (FHN) cardiac cell network, the  $i^{\text{th}}$  cell automaton  $\mathcal{A}_i$  has a single location, two continuous variables  $\mathcal{X} = \{x_{i1}, x_{i2}\}$  corresponding to fast and slow currents, and inputs  $(u_{i1}, u_{i2})$ , corresponding to diffusion from neighboring cells, and  $u_{i3}$ , a stimulus. The evolution is given by the ODEs (dynamic mapping):  $\dot{x}_{i1} = (a - x_{i1})(x_{i1} - 1)x_{i1} - x_{i2} + u_{i3} + \frac{D}{h^2}(u_{i1} + u_{i2} - 2x_{i1})$ ,  $\dot{x}_{i2} = \epsilon(\beta x_{i1} - \gamma x_{i2} - \delta)$ , where  $a, \beta, \delta, \gamma, \epsilon$  are parameters of the cell, the  $u_{i3}$  term models direct stimulus input, and the  $\frac{D}{h^2}(\cdot)$  term models the effect of the diffusion coupling with neighboring cells. In Figure 1, three FHN cells  $\mathcal{A}_1, \mathcal{A}_2$  and  $\mathcal{A}_3$  are interconnected in a ring and with a pulse generator. In each cycle, the pulse is activated for  $S_{on}$  time and stays off for  $S_{off}$  time. The composed system is defined by identifying input variables of one automaton with the state variables of another. For example,  $u_{11} = x_{21}, u_{12} = x_{31}$  defines the part of the ring where  $\mathcal{A}_1$  gets diffused current inputs from its neighbors and  $u_{13} = st$  connects the output of the pulse generator to  $\mathcal{A}_1$ .

### 3 Annotations for Modules in a Network

We proposed simulation-based robust invariant verification of dynamical and switched systems in [15]. The approach requires the designers to provide special annotations called *discrepancy functions* for each location of the automaton. The algorithm first computes a validated numerical simulation from an initial state, say  $\mathbf{v}$ , and then bloats the simulation using the discrepancy function to compute arbitrarily precise over-approximations of  $\text{Reach}_{\mathcal{A}}(B_{\delta}(\mathbf{v}), T)$ . Repeating this over a set of initial states  $\mathbf{v}$  and with varying precision  $\delta$ , one obtains a decision procedure for robust invariant checking. Towards our goal of verifying hybrid networks, in this section we present new techniques for computing discrepancy functions for such models.

<sup>1</sup> We do not allow HA to interact via transition synchronization as in [31, 35].



**Fig. 1.** Ring of 3 FHN-modules with a simple pulse generator. Reach set from a set of initial states projected on  $x_{11}$  and  $x_{12}$ .

### 3.1 IS Discrepancy and Approximations

First of all, we will use the definition of Input-to-State (IS) discrepancy function [26], which enables us to use annotations for individual modules in a dynamical system to then check invariants of the composed system. The IS discrepancy function for a location  $\ell$  of  $\mathcal{A}$  (or for a dynamical system) bounds the distance between two trajectories in location  $\ell$  from different initial states, as a function of time and the inputs they receive.

**Definition 3.** For a HA  $\mathcal{A} = (\mathcal{L}, \mathcal{X}, \mathcal{U}, \Theta, \mathcal{D}, \mathcal{T})$ , a continuous function  $V : Val(\mathcal{X})^2 \rightarrow \mathbb{R}_{\geq 0}$  is an input-to-state discrepancy function for a location  $\ell$  if

- (a)  $\exists$  class- $\mathcal{K}$  functions (see [26])  $\underline{\alpha}, \bar{\alpha}$ , s.t.,  $\forall \mathbf{x}, \mathbf{x}' \in Val(\mathcal{X}), \underline{\alpha}(|\mathbf{x} - \mathbf{x}'|) \leq V(\mathbf{x}, \mathbf{x}') \leq \bar{\alpha}(|\mathbf{x} - \mathbf{x}'|)$ , and
- (b)  $\exists \beta : \mathbb{R}_{\geq 0} \times \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$  and  $\gamma \in \mathcal{K}$  such that for any  $\mathbf{x}, \mathbf{x}'$ , any pair of input trajectories  $u, u' : \mathcal{U}$ , and any  $t \in \mathbb{R}_{\geq 0}$ ,

$$V(\xi_{\mathbf{x}, \ell, u}(t), \xi_{\mathbf{x}', \ell, u'}(t)) \leq \beta(|\mathbf{x} - \mathbf{x}'|, t) + \int_0^t \gamma(|u(s) - u'(s)|) ds.$$

In addition,  $\beta(\cdot, \cdot)$  is of class- $\mathcal{K}$  in the first argument and  $\beta(\cdot, 0) = \bar{\alpha}(\cdot)$ .

Here  $\xi_{\mathbf{x}, \ell, u}$  denotes the trajectory of the continuous variables  $\mathcal{X}$  in location  $\ell$  from state  $\mathbf{x}$  and with the input trajectory  $u$ . The tuple  $(\underline{\alpha}, \bar{\alpha}, \beta, \gamma)$  is called the *witness* of the discrepancy function  $V$ . The first condition merely bounds  $V$  in terms of the norm of its arguments. The more important second condition ensures that the distance between the trajectories is bounded as a function of  $\beta$  and  $\gamma$ , and can be reduced arbitrarily by making  $\mathbf{x} \rightarrow \mathbf{x}'$  and  $u \rightarrow u'$ . IS discrepancy is related to integral input-to-state stability [2–4, 42]. However, for our verification algorithms, we do not require neighboring trajectories to converge over time. Using the IS discrepancy functions along with their witnesses, we construct a reduced order model  $M$  which can be employed to compute precise over-approximations of  $Reach_{\mathcal{A}}(T)$ . Given a dynamical system (HA with

one location)  $\mathcal{A} = \mathcal{A}_1 \parallel \mathcal{A}_2$  connected in a ring and IS discrepancy with witnesses for each of the modules, the IS approximation of  $\mathcal{A}$  is a  $(2+1)$ -dimensional closed deterministic dynamical system  $M$  defined as follows.

**Definition 4.** For a pair of nonnegative constants  $(\delta_1, \delta_2)$ , the  $(\delta_1, \delta_2)$ -IS approximation of  $\mathcal{A}$  is a closed dynamical system with three variables  $\mathcal{X} = \{m_1, m_2, clk\}$  initialized to  $\{\beta_1(\delta_1, 0), \beta_2(\delta_2, 0), 0\}$ , and dynamics  $\dot{\mathbf{x}} = f_M(\mathbf{x})$ , where

$$f_M(\mathbf{x}) = \begin{bmatrix} \dot{\beta}_1(\delta_1, \mathbf{x}(clk)) + \gamma_1 \circ \underline{\alpha}_2^{-1}(\mathbf{x}(m_2)) \\ \dot{\beta}_2(\delta_2, \mathbf{x}(clk)) + \gamma_2 \circ \underline{\alpha}_1^{-1}(\mathbf{x}(m_1)) \\ 1 \end{bmatrix}. \tag{1}$$

The variable  $clk$  tracks the real time, and both the initial state and the dynamics of  $M$  depend on the choice of the parameters  $\delta_1$  and  $\delta_2$ . It can be shown that the valuations of  $m_i$  along  $\mu$  (the trajectory of  $M$ ) give an upperbound on the distance between any trajectories of  $\mathcal{A}_i$  that start from initial states and are at most  $\delta_i$  apart. The following theorem establishes that the reach set of  $\mathcal{A}$  from a set of states can be precisely over-approximated by bloating an individual execution  $\xi$  of  $\mathcal{A}$  by a factor that is entirely determined by (a) a pair  $V = (V_1, V_2)$  of IS discrepancy functions of  $\mathcal{A}_1$  and  $\mathcal{A}_2$  along with their witnesses, and (b) the trajectory  $\mu$ .

**Theorem 1 (Theorems 5.4 and 5.7 from [26]).** Let  $\xi_{\mathbf{v}}$  be a trajectory of  $\mathcal{A}$ . For any nonnegative pair  $\delta = (\delta_1, \delta_2)$ , and any time  $T \geq 0$ , suppose  $\mu$  is the trajectory of the  $(\delta_1, \delta_2)$ -IS approximation  $M$ . Then  $\text{Reach}_{\mathcal{A}}(B_{\delta}(\mathbf{v}), T) \subseteq \bigcup_{t \in [0, T]} B_{\mu(t)}^V(\xi_{\mathbf{v}}(t))$ . Further, for any  $\epsilon > 0$  and  $T > 0$ ,  $\exists \delta_1, \delta_2 > 0$  such that, for the  $(\delta_1, \delta_2)$ -IS approximation  $M$ ,  $\bigcup_{t \in [0, T]} B_{\mu(t)}^V(\xi_{\mathbf{v}}(t)) \subseteq \epsilon\text{-Reach}_{\mathcal{A}}(B_{\delta}(\mathbf{v}), T)$ .

The precision of the over-approximation can be improved by reducing the parameters  $\delta_1$  and  $\delta_2$ , and thus creating a finer covering of the initial set  $\Theta_{\mathcal{A}}$ . The result is generalized to dynamical systems with  $N$  modules connected in general network topologies [26], where the IS approximation is  $(N + 1)$ -dimensional.

For a hybrid system  $\mathcal{A} = \mathcal{A}_1 \parallel \mathcal{A}_2$ , instead of providing annotations for the total of  $|Val(\mathcal{L}_1)| \times |Val(\mathcal{L}_2)|$  locations of  $\mathcal{A}$ , the user has to provide IS discrepancy functions for  $|Val(\mathcal{L}_1)| + |Val(\mathcal{L}_2)|$  locations. From there, our algorithm automatically constructs  $|Val(\mathcal{L}_1)| \times |Val(\mathcal{L}_2)|$  IS approximations corresponding to each location-pair of  $\mathcal{A}$ . For cardiac cell networks, where all the automata modules are identical, this means working with  $|Val(\mathcal{L}_1)|$  IS discrepancy functions. The next proposition gives a technique for computing IS discrepancy functions.

**Proposition 1.** For a dynamical system with linear input  $\dot{\mathbf{x}} = f(\mathbf{x}) + B\mathbf{u}$ , where  $B$  is a matrix,  $V(\mathbf{x}_1, \mathbf{x}_2) = |\mathbf{x}_1 - \mathbf{x}_2|$  is an IS discrepancy function with

$$V(\xi_1(t), \xi_2(t)) \leq e^{\lambda_{max}t} |\mathbf{x}_1 - \mathbf{x}_2| + \int_0^t M|B| |(v_1(\tau) - v_2(\tau))| d\tau,$$

where  $\lambda_{max}$  is the largest eigenvalue of the Jacobian matrix  $J = \frac{1}{2}(\frac{\partial^T}{\partial \mathbf{x}} f(\mathbf{x}) + \frac{\partial}{\partial \mathbf{x}} f(\mathbf{x}) + I)$ ,  $M = \sup_{s \in [0, t]} e^{\lambda_{max}s}$  is the supremum of an exponential function of

$\lambda_{max}$ , and  $\xi_i$  is the state trajectory from  $\mathbf{x}_i$  with input trajectory  $v_i$ . Specifically, for a linear time invariant system  $\dot{\mathbf{x}} = \mathbf{A}\mathbf{x} + \mathbf{B}\mathbf{u}$ ,  $\lambda_{max}$  is the largest eigenvalue of the matrix  $\mathbf{A}$ , and  $M = \sup_{s \in [0, t]} |e^{\mathbf{A}s}|$ .

For linear dynamical systems, we use the special case to obtain tight IS discrepancy functions by solving Linear Matrix Inequalities. The more general case establishes IS discrepancy functions for a larger class of non-linear systems for which the Jacobian matrix has bounded eigenvalues. For the nonlinear dynamic maps in this paper, computing the maximum eigenvalue of the Jacobian is solved using the MATLAB optimization toolbox or by a sum of squares solver [41].

## 4 Checking Bounded Invariants of HA Networks

First we define simulations for hybrid automata, and then we describe the verification algorithm that uses simulations and IS discrepancy functions.

### 4.1 Simulations of Dynamical Systems

For a closed dynamical system  $\mathcal{A}$  with an initial state  $\mathbf{v}$ , validated ODE solvers [10, 12, 37] can compute a sequence of sets  $R_0, \dots, R_l \subseteq \text{Val}(\mathcal{X})$  such that the trajectory  $\xi_{\mathbf{v}}$  of  $\mathcal{A}$  is contained in  $R_k$  over the interval  $[(k-1)\tau, k\tau]$ , where  $\tau$  is the simulation time-step. We formalize this as follows:

**Definition 5.** Consider a deterministic closed HA  $\mathcal{A}$ , an initial state  $\mathbf{v}$ , an error bound  $\epsilon > 0$ , and time step  $\tau > 0$ . Let the location of  $\mathbf{v}$  be  $\ell$  and  $\xi_{\mathbf{v}}$  be the execution of  $\mathcal{A}$  starting from  $\mathbf{v}$ . A  $(\mathbf{v}, \epsilon, \tau)$ -simulation fragment is a finite sequence  $\rho = (R_0, t_0), \dots, (R_l, t_l)$  where, for each  $k \in \{0, \dots, l\}$ , (a)  $0 < t_k - t_{k-1} \leq \tau$ , (b)  $R_k$  is contained in the invariant  $I_{\ell}$  except possibly the last  $R_l$ , (c)  $\text{dia}(R_k) \leq \epsilon$ , and (d) for any time  $t \in [t_{k-1}, t_k]$ ,  $\xi_{\mathbf{v}}(t) \cdot \mathcal{X} \in R_k$ .

For relative completeness of verification, we will require that for a desired error bound  $\epsilon > 0$  the diameter of  $R_k$  can be made smaller than  $\epsilon$  by reducing the step size  $\tau$ . A simulation for a HA is a sequence of simulation fragments (for different locations) that captures all the transitions of at least one execution.

**Definition 6.** Consider a HA  $\mathcal{A}$ , an initial state  $\mathbf{v}$ , an error bound  $\epsilon > 0$ , a time bound  $T > 0$ , a transition bound  $l$ , and a time step  $\tau > 0$ . Let  $\xi_{\mathbf{v}}$  be the execution from  $\mathbf{v}$  with  $\xi_{\mathbf{v}}.\text{dur} \leq T$ , where  $\xi_{\mathbf{v}}.\text{dur}$  is the time duration of the trajectory  $\xi_{\mathbf{v}}$ , and with  $l$  transitions at times  $\sigma_1, \dots, \sigma_l \in \mathbb{R}_{\geq 0}$ ; let  $\sigma_0 = 0$ . A  $(\mathbf{v}, \epsilon, \tau, T, l)$ -simulation is a finite sequence  $\psi = \rho_0, \dots, \rho_l$  where (a) each  $\rho_k = (R_{k(1)}, t_{k(1)}), \dots, (R_{k(m_k)}, t_{k(m_k)})$  is a  $(\xi(\sigma_k), \epsilon, \tau)$ -simulation fragment with  $m_k$  samples, (b)  $t_0 = 0$ ,  $t_{l(m_l)-1} = T$ , and for each  $k > 0$ ,  $t_{k(m_k)} \geq t_{(k+1)(1)}$ , and (c)  $\sigma_k \in [t_{(k+1)(1)}, t_{k(m_k)}]$ .

A  $(\mathbf{v}, \epsilon, \tau, T, l)$ -simulation  $\psi$  is a sequence of  $l$  simulation fragments where each fragment  $\rho_k$  has  $m_k$  elements with indices  $k(1), \dots, k(m_k)$ . The  $k^{\text{th}}$  transition on the actual execution  $\xi_{\mathbf{v}}$  has to occur between the last sample period of  $\rho_{k-1}$  and



the first sample interval of  $\rho_k$  (condition (c)). In addition,  $\rho_k$  is a  $(\xi_{\mathbf{v}}(\sigma_k), \epsilon, \tau)$ -simulation fragment, that is, it *contains* the trajectory of  $\mathcal{A}$  starting from the post state  $\xi_{\mathbf{v}}(\sigma_k)$  of the  $k^{\text{th}}$  transition. In Algorithm 2, the subroutine *Simulate* computes a simulation of HA of the above type. The simulation  $\psi$  represents other executions that start near  $\mathbf{v}$ . Formally, we say an execution fragment  $\xi$  is *captured* by  $\psi$  if duration of  $\xi$  is at most  $T$ ,  $\xi$  experiences exactly the same sequence of locations as recorded in some prefix of  $\psi$ , and its  $k^{\text{th}}$  transition occurs in the intervals  $[t_{k(m_k)}, t_{(k+1)(1)}]$ .

## 4.2 Verification Algorithm

We sketch the key ideas that enable the checking of bounded-time invariants of closed networks of hybrid automata. The main inputs of *InvVerify* (Algorithm 1) are the specification of the composed automaton  $\mathcal{A} = \mathcal{A}_1 \parallel \dots \parallel \mathcal{A}_N$ , the open unsafe set  $\mathbb{U}$ , and the collection of discrepancy functions and witnesses *ISD* for every location of each subsystem. The variable  $\mathcal{C}$  (line 2) is initialized to a collection of tuples  $\{(\mathbf{v}_k, \delta, \epsilon, \tau)\}_{k \in |\mathcal{C}|}$ , such that  $\{\mathbf{v}_k\}$  is a  $\delta$ -cover of  $\Theta$ , that is,  $\Theta \subseteq \cup_{k \in |\mathcal{C}|} B_\delta(\mathbf{v}_k)$ , and  $(\delta, \epsilon, \tau)$  are parameters. For each  $(\mathbf{v}, \delta, \epsilon, \tau)$  in  $\mathcal{C}$ , the subroutine *ReachFromCover* (Algorithm 2) computes *flag* and a set  $S$ . The *flag* is set to SAFE if all executions from  $B_\delta(\mathbf{v})$  are disjoint from  $\mathbb{U}$  up to time  $T$  and in that case  $\mathbf{v}$  is removed from  $\mathcal{C}$ . The *flag* is set to UNSAFE if at least one execution reaches  $\mathbb{U}$ , and in that case *InvVerify* returns UNSAFE and  $\mathcal{R}$ . Finally, if the *flag* is set to REFINE then  $\mathbf{v}$  is replaced by a finer cover of  $\Theta \cap B_\delta(\mathbf{v})$ . In addition to having  $\delta/2$ -radius balls covering  $B_\delta(\mathbf{v})$ , the parameters  $\epsilon$  and  $\tau$  are also halved to compute more precise over-approximations. The sets  $S$  and  $\mathcal{R}$  compute over-approximations of  $\text{Reach}_{\mathcal{A}}(B_\delta(\mathbf{v}), T)$  and  $\text{Reach}_{\mathcal{A}}(T)$ , respectively. *ReachFromCover* checks safety with respect to  $\mathbb{U}$  of the states reachable from  $B_\delta(\mathbf{v})$  up to time  $T$  and with at most  $n > 0$  transitions. First, it computes an over-approximation ( $\mathcal{R}$ ) of  $\text{Reach}_{\mathcal{A}}(B_\delta(\mathbf{v}), T)$  with certain precision

---

**Algorithm 1.** *InvVerify*( $\mathcal{A}, \text{ISD}, \mathbb{U}, T, \epsilon_0, \delta_0, n_0$ ): Verifies invariants of hybrid networks.

---

```

1 end  $\mathcal{R} \leftarrow \emptyset; \delta \leftarrow \delta_0; \epsilon \leftarrow \epsilon_0; \tau \leftarrow \tau_0; n \leftarrow n_0;$ 
2  $\mathcal{C} \leftarrow \{(\mathbf{v}, \delta, \epsilon, \tau) \mid \{\mathbf{v}\} \text{ is a } \delta\text{-Cover}(\Theta)\};$ 
3 while  $\mathcal{C} \neq \emptyset$  for each  $(\mathbf{v}, \delta, \epsilon, \tau) \in \mathcal{C}$  do
4    $(\text{flag}, S) \leftarrow \text{ReachFromCover}(\mathcal{A}, \mathbf{v}, \delta, \epsilon, \tau, T, \text{ISD}, n);$ 
5   switch flag do
6     case SAFE:  $\mathcal{C} \leftarrow \mathcal{C} \setminus \{(\mathbf{v}, \delta, \epsilon, \tau)\}; \mathcal{R} \leftarrow \mathcal{R} \cup S$  case UNSAFE: return
7       (UNSAFE,  $\mathcal{R}$ ) case REFINE:
8          $\mathcal{C} \leftarrow \mathcal{C} \setminus \{(\mathbf{v}, \delta, \epsilon, \tau)\}; \delta \leftarrow \delta/2; \epsilon \leftarrow \epsilon/2; \tau \leftarrow \tau/2; n \leftarrow 2n;$ 
9          $\mathcal{C} \leftarrow \mathcal{C} \cup \{(\mathbf{v}, \delta, \epsilon, \tau) \mid \{\mathbf{v}\} \text{ is a } \delta\text{-Cover}(\Theta \cap B_\delta(\mathbf{v}))\};$ 
10        end
11    end
12 return (SAFE,  $\mathcal{R}$ );
```

---

---

**Algorithm 2.** *ReachFromCover*( $\mathcal{A}, ISD, \mathbb{U}, \mathbf{v}, \delta, \epsilon, \tau, T, n$ ): Over-approx  $\text{Reach}_{\mathcal{A}}(B_{\delta}(\mathbf{v}))$ .

---

```

1  $\mathcal{R} \leftarrow \emptyset; \mathcal{C} \leftarrow \{(\mathbf{v}, 0)\}; \text{count} \leftarrow 0;$ 
2 while  $\mathcal{C} \neq \emptyset$  for each  $(\mathbf{v}, t_0) \in \mathcal{C}$  do
3    $r \leftarrow \delta; \psi \leftarrow \text{Simulate}(\mathcal{A}, \mathbf{v}, T - t_0, \epsilon, \tau); \text{count} \leftarrow \text{count} + 1;$ 
4   for  $k = 0 : l$ , where  $\psi = \rho_0, \rho_1, \dots, \rho_l$  do
5      $(S_k, r) \leftarrow \text{BloatWithISD}(\rho_k, ISD, r, \epsilon, \tau, \mathcal{A});$ 
6   end
7   if a transition  $(\ell, \ell')$  is enabled from  $S_j$  but is not captured by  $\psi$  then
8      $\mathcal{C} \leftarrow \mathcal{C} \cup \{(\mathbf{v}, t_0) \mid \{\mathbf{v}\} \text{ is the } \delta\text{-Cover}(R_{\ell, \ell'}(S_k \cap G_{\ell, \ell'})),$ 
9        $t_0 \text{ is the first time } (\ell, \ell') \text{ is enabled}\};$ 
10  if a transition is captured by  $\psi$  but is not enabled for a subset  $S'_k \subseteq S_k$  then
11     $\mathcal{C} \leftarrow \mathcal{C} \cup \{(\mathbf{v}, t_0) \mid \{\mathbf{v}\} \text{ is the } \delta\text{-Cover}(S'_k),$ 
12       $t_0 \text{ is the first time the transition is captured}\};$ 
13  end
14  if  $(\cup_j s_j \cap \mathbb{U} = \emptyset) \wedge (\text{count} < n)$  then  $\mathcal{R} \leftarrow \mathcal{R} \cup (\cup_j s_j); \mathcal{C} \leftarrow \mathcal{C} \setminus \{(\mathbf{v}, t_0)\}$ 
    else if  $(\exists R_j \subseteq \mathbb{U}) \wedge (\text{count} = 1)$  then return (UNSAFE,  $\mathcal{R}$ ) else
    return (REFINE,  $\mathcal{R}$ )
15 end
16 return (SAFE,  $\mathcal{R}$ );
```

---

(determined by the parameters  $\delta, \epsilon$ , and  $\tau$ ). If this over-approximation is sufficient to prove/disprove safety with respect to  $\mathbb{U}$  then it sets the *flag* to SAFE or UNSAFE, and otherwise it returns REFINE. If it detects that more than  $n$  transitions are possible within time  $T$ , then also it returns REFINE.

In computing  $\mathcal{R}$  in *ReachFromCover*, the set  $\mathcal{C}$  stores a set of state-time pairs that are yet to be processed. If  $(\mathbf{v}, t_0) \in \mathcal{C}$  then  $\text{Reach}_{\mathcal{A}}(B_{\delta}(\mathbf{v}), T - t_0)$  is yet to be evaluated and added to  $\mathcal{R}$ . For each  $(\mathbf{v}, t_0)$  in the cover  $\mathcal{C}$ , a  $(\mathbf{v}, \epsilon, \tau, T, l)$ -simulation  $\psi = \rho_0, \dots, \rho_l$  is computed. The variable *count* tracks the number of new simulation branches initiated in a run of the algorithm. Let  $\xi$  be the actual execution starting from  $\mathbf{v}$  and  $G_{\ell, \ell'}$  be the guard from location  $\ell$  to  $\ell'$ . By Definition 6, each  $\rho_k$  of  $\psi$  is a simulation fragment. By Definition 4, the IS approximation is a (small) dynamical system, whose trajectory gives an upper bound of the distance between continuous trajectories of  $\mathcal{A}$ . The subroutine *BloatWithISD*( $\rho_k, ISD, r, \epsilon, \tau, \mathcal{A}$ ) (i) creates an IS Approximation  $M$  of  $\mathcal{A}$  using the discrepancy functions in  $ISD$  that correspond to the location of  $\rho_k$ , (ii) generates a  $(r, \epsilon, \tau, T, 0)$ -simulation of  $M$ , say  $\mu$ , (iii) bloats each set  $R_j$  in  $\rho_k$  with the valuation of  $\mu(t_j)$  to obtain a set  $s_j$ , (iv) returns the sequence of sets  $S_k = (s_{k(1)}, t_{k(1)}), \dots, (s_{k(m)}, t_{k(m)})$ , and finally (v) applies the transition between  $\rho_k$  and  $\rho_{k+1}$  on the set  $s_{k(m)}$  and returns  $r$  as the radius of image of the reset function. From Theorem 1,  $S_k$  contains all continuous trajectories of  $\mathcal{A}$  that start from  $B_r(R_{k(1)})$ . It can be checked that  $\cup_j s_j$  precisely over-approximates all the executions from  $B_r(\mathbf{v})$  that are captured by  $\psi$  (Proposition 2-3).

To over-approximate the states reached via executions from  $B_{\delta}(\mathbf{v})$  that are *not* captured by  $\psi$ , the algorithm generates new simulations (line 7-13) and adds up *count*. The algorithm transverses  $S_k$  and generates and checks two possible

cases as described in line 7 and 10. Then the algorithm decides whether the computed over-approximation  $\mathcal{R}$  is safe, unsafe, or needs further refinement.

### 4.3 Soundness and Relative Completeness

We will state the key propositions of the algorithms that are used for proving correctness. The details of the proofs are given in the technical report [25]. In what follows, all the program variables refer to their valuations at the  $p^{\text{th}}$  iteration of the **while** loop of *ReachFromCover*, unless otherwise stated. That is,  $(\mathbf{v}, t_0)$  is the time-state pair being explored in the  $p^{\text{th}}$  iteration. Propositions 2 and 3 follow from straightforward inductive application of Theorem 1, the fact that  $\psi$  is a simulation from  $\mathbf{v}$  with the properties stated in Definition 6, and the continuity of the reset functions for all location pairs.

**Proposition 2.** *Let  $\psi$  be a simulation from  $\mathbf{v}^{(p)}$ . For any execution fragment  $\xi$  starting from a state in  $B_\delta(\mathbf{v}^{(p)})$ , if the transition sequence of  $\xi$  is captured by  $\psi$  then, for any  $t \in [0, T - t_0^{(p)}]$ ,  $\xi(t) \in \cup_{j=1}^{l(m_i)} s_j$ . Recall that  $l(m_i)$  denotes the last index of  $\rho_l$  and thus the total number of elements in  $\psi$ .*

**Proposition 3.** *For the execution  $\xi_{\mathbf{v}}$  from  $\mathbf{v}$ , and any  $r > 0$ , there exists sufficiently small  $\delta, \epsilon, \tau$ , such that  $\cup_{j=1}^{l(m_i)} s_j \subseteq \cup_{t \in [0, T - t_0]} B_r(\xi_{\mathbf{v}}(t))$ .*

Using Proposition 2, we can prove the soundness of the algorithm. We show that every execution from  $\Theta$  can be decomposed into execution segments that are captured by some simulation generated during the **while** loop of *ReachFromCover*.

**Theorem 2 (Soundness).** *If *InvVerify* returns SAFE then  $\mathcal{A}$  is safe with respect to  $\mathbb{U}$  up to  $T$ , and if it returns UNSAFE then  $\mathcal{A}$  is unsafe.*

We establish termination of *InvVerify* under the following robustness assumption.

**Assumption 1.** *(i)  $\mathcal{A}$  has an average dwell time [24]. That is, there exists  $N' \geq 0$  and  $\tau' > 0$  such that, for any execution fragment  $\xi$  of  $\mathcal{A}$ , the number of transitions occurring in  $\xi$  is upperbounded by  $N' + \frac{\xi.\text{dur}}{\tau'}$ . (ii) One of the following conditions hold: (a)  $\bar{\mathbb{U}}$  is a robust invariant of  $\mathcal{A}$  up to time  $T$ . (b) There exists  $c > 0$ , such that all  $c$ -perturbations of  $\mathcal{A}$  reach  $\mathbb{U}$  with in  $T$ .*

Assumption 1(i) is standard for well-designed systems and can be automatically checked for certain model classes [36]. Part (ii) is a robustness condition with respect to the invariant  $\bar{\mathbb{U}}$  (complement of  $\mathbb{U}$ ) such that the satisfaction of the invariant remains unchanged under sufficiently small perturbations to the models. Since the over-approximation can be computed up to arbitrary precision (Proposition 3), *InvVerify* is guaranteed to terminate.

**Theorem 3 (Relative completeness).** *Under Assumption 1, *InvVerify* terminates.*

## 5 Checking Invariants for Cardiac Cell Networks

We present a challenging case study modeling a cardiac cell that involves nonlinear HA networks. The purpose of the case study is to demonstrate the effectiveness of *InvVerify*. Our case study is the minimal ventricular (MV) model of Bueno-Orovio et al. [11] that generates action potential (APs) on cardiac rings [17]. Unlike the FHN model of Example 1, the MV model can reproduce realistic and important AP phenomena, e.g. alternans [22], and yet is computationally more efficient than some of the other models in the literature. Using the techniques from Grosu et al. [19], we abstract the MV model into a network of multi-affine hybrid (MAH) automata (see Figure 2). On the resulting network we check a key invariant property.

### 5.1 The MAH Cardiac Cell Network Model

The MV model describes the flow of currents through a cell. The model is defined by four nonlinear PDEs representing the transmembrane potential  $x_1(\mathbf{d}, t)$ , the fast channel gate  $x_2(\mathbf{d}, t)$ , and two slow channel gates,  $x_3(\mathbf{d}, t)$  and  $x_4(\mathbf{d}, t)$ . All of the four variables are time and position  $\mathbf{d} := (d_x, d_y, d_z) \in \mathbb{R}^3$  dependent. For one dimensional tissue, i.e.,  $\mathbf{d} := d_x$ , the evolution of transmembrane potential is given by:

$$\frac{\partial x_1(d_x, t)}{\partial t} = D \frac{\partial^2 x_1(d_x, t)}{\partial d_x^2} + e(x_1, t) - (J_{fi} + J_{so} + J_{si}), \quad (2)$$

where  $D \in \mathbb{R}$  is the diffusion coefficient,  $e(\mathbf{d}, t)$  is the external stimulus applied to the cell,  $J_{fi}$  is the fast inward current,  $J_{si}$  is the slow inward current and  $J_{so}$  is the slow outward current. The currents  $J_{fi}$ ,  $J_{so}$  and  $J_{si}$  are described by Heaviside function. To define the propagation of the action potential on a cardiac ring of length  $L$ , we set the boundary conditions to:  $x_i(0, t) = x_i(L, t)$  for all  $i \in \{0, \dots, 4\}$  and  $t \in \mathbb{R}$ .

*MAH approximation.* One alternative to solving these highly nonlinear PDEs is to discretize space and hybridize the dynamics. The result is the MAH model. Following the approach of [19] we first hybridize the dynamics and obtain a HA with 29 locations. The basic idea is to approximate the Heaviside function from  $J_{fi}$ ,  $J_{so}$  and  $J_{si}$  with a sequence of ramp functions. Each location of the resulting HA contains a multi-affine ODE such as:

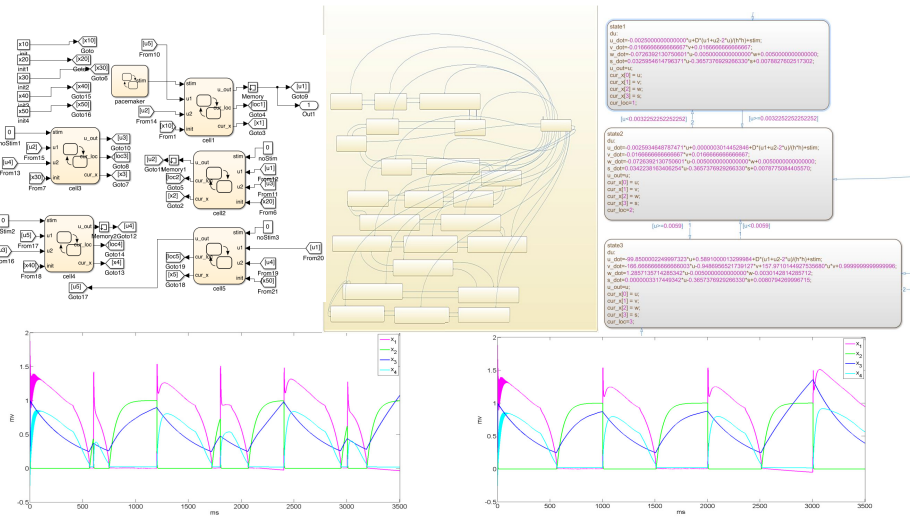
$$\begin{aligned} \dot{x}_1 &= -0.935x_1 + 12.70x_2 - 8.0193x_1x_2 + 0.529x_3x_4 + 0.87 + st \\ \dot{x}_2 &= -0.689x_2; \quad \dot{x}_3 = -0.0025x_3; \quad \dot{x}_4 = 0.0293x_1 - 0.0625x_4 + 0.0142, \end{aligned}$$

where  $st$  is the time-varying stimulus input. Urgent transitions from each location  $\ell_i$  to the next (and predecessor) location  $\ell_{i+1}$ ,  $i \in [29]$ , are enabled by the guards of the form  $x_1 \geq \theta'_i$  and  $x_1 < \theta_i$ , where  $\theta_i, \theta'_i$  are the constants arising from ramp approximations of the Heaviside functions.

Next, we discretize the 2nd order derivative  $D \frac{\partial^2 x_1(d_x, t)}{\partial d_x^2}$  from Eq. (2) with a discretization step of  $\Delta$  using 2nd order central difference method and obtain  $D \frac{x_1(d_x + \Delta, t) - 2x_1(d_x, t) + x_1(d_x - \Delta, t)}{\Delta^2}$ . Informally,  $\Delta$  represents the spatial discretization and corresponds to the length of the cell in the ring. This 2nd order central difference term is added to the right hand side of the dynamic mapping for  $x_1$  (in each location) to obtain the final MAH model of a single cardiac cell. Note that by using the central difference method the approximation error for the original MV model is of the order  $\mathcal{O}(\Delta^2)$ . To check invariants of a cardiac ring of length  $L$ , we connect all of the  $\lfloor \frac{L}{\Delta} \rfloor$  HA into a network such that the input variables of every HA  $\mathcal{A}_i, i \in [1, \lfloor \frac{L}{\Delta} \rfloor]$ , are identified with the variable  $x_{(i+1)1}$  of the successor  $\mathcal{A}_{i+1}$  and the state variable  $x_{(i-1)1}$  of  $\mathcal{A}_{i-1}$  in the ring. We consider scenarios where one HA in the ring gets a sequence of stimuli from a pulse generator and for the remaining HA  $st(t) := 0$ .

### 5.2 Experimental Results

For understanding the effect of stimuli on cardiac tissue (cell networks) the key invariant properties of interest are of the form  $x_1 \leq \theta_{max}$ , where  $\theta_{max}$  is a threshold voltage value. Other properties about timing of action potentials can be constructed using these building block invariants and additional timers. We implemented the algorithms of Section 4 in MATLAB programs that take as input Simulink/Stateflow models of FHM and MAH networks (see Figure 2). For



**Fig. 2.** Top left: top-level Simulink/Stateflow model for a ring of five MAH cells; the *Pacemaker* block stimulates one cell. Center: Stateflow model of a single MAH cell. Top right: dynamics and guards in 3 locations of a single cell. Bottom: reach set projected on  $x_{11}$  (AP) for stimulation period of 1000 msec (left) and 600 msec (right) with x-axis for time and y-axis for voltage.

**Table 1.** (a) Scaling with network size.  $N$ : number of cells in the ring network,  $\theta_{max}$ : threshold voltage defining invariant, Sims: number of simulations, Refs: max. number of refinements, RT: running time in seconds. (b) Verification of FHM networks with time horizon  $T=1200$  ms, initial set uncertainty  $\pm 0.01$  mV. (c) Comparison of running time with S-taliro over 3 cell MAH networks for cases where both tools find counter-examples.

N	$\theta_{max}$	Sims	Refs	RT(s)	$x_{i1} \leq \theta_{max}$
3	2	16	0	104.8	✓
3	1.65	16	0	103.8	✓
3	1.55	17	1	110.6	✓
3	1.5	NA	NA	9.0	×
5	2	3	0	208.0	✓
5	1.65	5	1	281.6	✓
5	1.65	170	125	945.0	✓
5	1.5	NA	NA	63.4	×
8	2	3	0	240.1	✓
8	1.65	73	9	2376.5	✓
8	1.5	NA	NA	119.7	×

(a)

N	$\theta_{max}$	Sims	Refs	RT	$x_{i1} \leq \theta_{max}$
3	1.5	1	0	1.5	✓
3	1.0	16	1	20.4	✓
5	1.5	8	2	9.2	✓
5	1.0	NA	NA	1.1	×
8	1.5	1	0	1.8	✓
8	1.0	24	3	33.5	✓

(b)

T	S-taliro	Our tool
100	24.2	3.1
1000	27.4	9.3
10000	55.5	62.9

(c)

all the locations the IS-discrepancy functions are computed using the techniques of Section 3. The cells being identical, essentially  $Val(\mathcal{L})$  IS discrepancy functions are sufficient. We computed the Jacobian matrices for each location by hand. Exploiting the loose coupling of the variables, in this case, we are able to find a closed form upperbound for the maximum eigenvalue for the Jacobians. The results presented here are based on experiments performed on a Intel Xeon V2 desktop computer using Simulink's ode45 simulation engine. Table 2(a) shows typical running times of our prototype on MAH networks of size 3, 5, and 8 cells with different invariant properties (defined by  $x_1 \leq \theta_{max}$ ). These are for a time horizon ( $T$ ) of 1200 ms with a stimulus of 5 ms exciting one of the cells every 600 ms. The uncertainty in the initial set is  $\pm 0.0001$  mV for each of the cells in the network (for comparison, the invariant ranges for the first few locations are 0.003 mV), except for the  $2^{nd}$  network with 5 cells, where the initial set has higher uncertainty of  $\pm 0.0001$  mV. With this larger initial set, even with the same threshold, the algorithm requires many more refinements and simulations to prove the invariant. Analogous results for 3, 5, and 8 cell FHN networks are shown in Table 2(b), with the longer time horizon  $T = 10000$  ms and greater uncertainty in the initial set of  $\pm 0.01$  mV. The two orders of magnitude faster running time (even for the same number of simulations) can be explained by the lower dimension (2) of FHN cells, and the absence of any transitions which spawn new branches in the execution of MAH -simulations. A comparable tool that can check for counter-examples in this class of HA models models is S-taliro [5]. We were able to find counter-examples using S-taliro for the 3 cell MAH networks with similar initial states (running times shown in Table 2(c)).

On average, for smaller time horizons ( $T$ ) S-taliro found counter-examples faster, but for longer  $T$  (and appropriate initial sets) the running times were comparable to our prototype.

It is known that electrical alternans initiate and destabilize reentrant waves which may induce cardiac arrhythmia such as ventricular fibrillation [27]. The electrical alternans involve long-short beat-to-beat alternation of AP duration at fast pacing rates. In Figure 2 (bottom left) we plot the reach set from a set of initial states with pacing rate of 1000 msec and observe that the AP durations do not change, whereas at a pacing rate of 600 msec (bottom right) the AP durations alternate. The reach set approximations computed by our tool enable us to prove absence of alternans over bounded-time horizons and also to find initial states from which they may arise.

## 6 Related Work, Discussion and Conclusions

Networks of timed automata to model the propagation of APs in human heart are employed in the Virtual Heart Model [28–30, 39] and hybrid automata are used in [8, 45]. In [18, 33], the authors develop a model of the cardiac conduction system that addresses the stochastic behavior of the heart, validated via simulation. However, the hybrid behavior of the heart is not considered. Grosu et al. [21] carry out automated formal analysis of a realistic cardiac cell model. In [19] a method to learn and to detect the emergent behavior (i.e. the spiral formation) is proposed. Simulation-based analysis of general nonlinear HA has been investigated in [5], where a search for counter-examples is carried out using sampling and stochastic optimization. Our approach is designed to prove bounded-time invariants. Other promising tools include Breach [14] and *Flow\** [13]; their application to cardiac cell networks will be an interesting direction to explore once support for these types of Simulink/Stateflow models is established.

In this paper, we present an algorithm to check robust bounded-time invariants for networks of nonlinear hybrid automata. We used automatically computed input-to-state discrepancy functions for individual locations of individual automata modules to over-approximate reachable states of the network. All of the developed techniques and the symmetry in the network of cells enabled us to check key invariants of networks of nonlinear cardiac cells, where each cell has four continuous variables and 29 locations. We will extend our algorithms to support richer classes of properties specified in metric or signal temporal logic. These results also suggest new strategies for pacemaker control algorithms, for example, for avoiding alternans and other undesirable behavior.

## References

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