

Computing Reachable States for Nonlinear Biological Models

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Summary

- ▶ We propose a computer-aided methodology to help analyzing certain biological models
- ▶ Domain of applicability: **biochemical reactions** modeled as **differential equations**. State variables denote **concentrations**
- ▶ We propose **reachability computation**, a kind of **set-based simulation**, that may replace uncountably-many simulations
- ▶ The continuous analogue of **algorithmic verification** (model-checking), emerged from more than a decade of research on **hybrid systems**
- ▶ Since this is not part of the local culture, we first introduce the domain and only later move to the contribution of this paper

Outline

- ▶ **Under-determined** dynamical models and their biological relevance
- ▶ **Continuous dynamical systems** and abstract reachability
- ▶ **Effective representation** of sets and concrete algorithms for **linear** systems
- ▶ Treating **nonlinear** systems via **hybridization**
- ▶ **Dynamic hybridization**: idea and preliminary results
- ▶ Conclusions

Dynamical Models with Nondeterminism

- ▶ Dynamical system: state space X and a rule $x' = f(x, v)$
- ▶ The **next state** as a function of the **current state** and some **external influence** (or unknown parameters) $v \in V$
- ▶ In discrete domains: a transition system with input (alphabet)
- ▶ System becomes nondeterministic if input is projected away
- ▶ Given initial state, many possible evolutions (“runs”)
- ▶ **Simulation**: picking **one** input and generating **one** behavior
- ▶ **Symbolic verification**: magically computing **all** runs in parallel
- ▶ **Reachability computation**: adapting these ideas to systems defined by **differential equations** or **hybrid automata** (differential equations with mode switching)

Why Bother?

- ▶ Differential models of biochemical reactions are **very** imprecise for many reasons:
- ▶ They are obtained by measuring populations, not individuals
- ▶ Kinetic parameters are based on isolated experiments not always under same conditions
- ▶ Etc.
- ▶ It is nice to match an experimentally-observed behavior by a deterministic model, but can we do better?
- ▶ After all, biological systems are supposed to be **robust** under **variations** in environmental conditions and parameters
- ▶ Showing that **all** trajectories corresponding to a **range** of parameters exhibit the same **qualitative behavior** is much stronger

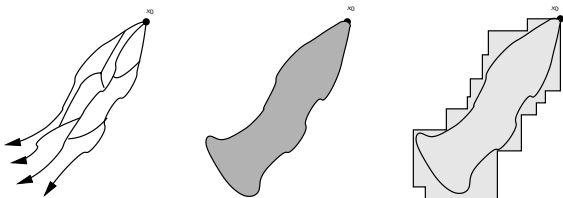
Preliminary Definitions and Notations

- ▶ A time domain $T = \mathbb{R}_+$, state space $X \subseteq \mathbb{R}^n$, input space $V \subseteq \mathbb{R}^m$
- ▶ **Trajectory**: partial function $\xi : T \rightarrow X$, **Input signal**: $\zeta : T \rightarrow V$ both defined over an interval $[0, t] \subset T$
- ▶ A continuous dynamical system $S = (X, V, f)$
- ▶ Trajectory ξ with endpoints x and x' is the **response** of S to input signal ζ if
- ▶ ξ is the solution of $\dot{x} = f(x, v)$ for initial condition x and $v(\cdot) = \zeta$, denoted by $x \xrightarrow{\zeta/\xi} x'$
- ▶ $R(x, \zeta, t) = \{x'\}$ denote the fact that x' is reachable from x by ζ within t time, that is, $x \xrightarrow{\zeta/\xi} x'$ and $|\zeta| = |\xi| = t$

Reachability

- ▶ $R(x, \zeta, t) = \{x'\}$ speaks of **one** initial state, **one** input signal and **one** time instant
- ▶ Generalizing to a **set** X_0 of initial states, to **all** time instants in an interval $I = [0, t]$ and **all** admissible input signals:

$$R_I(X_0) = \bigcup_{x \in X_0} \bigcup_{t \in I} \bigcup_{\zeta} R(x, \zeta, t)$$



- ▶ Depth-first vs. breadth-first

$$\bigcup_{\zeta} \bigcup_{t \in I} R(x, \zeta, t) = \bigcup_{t \in I} \bigcup_{\zeta} R(x, \zeta, t)$$

Abstract Reachability Algorithm

- ▶ The reachability operator satisfies the semigroup property:

$$R_{[0,t_1+t_2]}(X_0) = R_{[0,t_2]}(R_{[0,t_1]}(X_0))$$

- ▶ We can choose a time step r and apply the following iterative algorithm:

Input: A set $X_0 \subset X$

Output: $Q = R_{[0,L]}(X_0)$

$P := Q := X_0$

repeat $i = 1, 2 \dots$

$P := R_{[0,r]}(P)$

$Q := Q \cup P$

until $i = L/r$

- ▶ Remark: we look at bounded time horizon and do not mind about reaching a fixpoint

From Abstract to Concrete Algorithms

- ▶ The algorithm performs operations on **subsets** of \mathbb{R}^n which, mathematically speaking, can be weird objects
- ▶ Like any **computational** geometry we restrict ourselves to classes of subsets (boxes, polytopes, ellipsoids, zonotopes) having nice properties:
 - ▶ **Finite** syntactic representation
 - ▶ Effective decision procedure for membership
 - ▶ **Closure** (or approximate closure) under the reachability operator
- ▶ In this talk we use **convex polytopes** and their finite unions

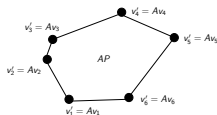
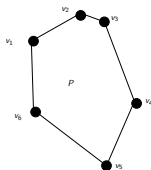
Convex Polytopes

- ▶ **Halfspace:** all points x satisfying a linear inequality $a \cdot x \leq b$
- ▶ **Convex polyhedron:** intersection of finitely many halfspaces;
Polytope: bounded convex polyhedron
- ▶ **Convex combination** of a set of points $\{x_1, \dots, x_l\}$ is any $x = \lambda_1 x_1 + \dots + \lambda_l x_l$ such that $\sum_{i=1}^l \lambda_i = 1$
- ▶ The **convex hull** $\text{conv}(\tilde{P})$ of a set \tilde{P} of points is the set of all convex combinations of elements in \tilde{P}
- ▶ Polytope representations:
 - ▶ **Vertices:** a polytope P admits a finite minimal set \tilde{P} (vertices) such that $P = \text{conv}(\tilde{P})$.
 - ▶ **Inequalities:** a polytope P admits a canonical set of halfspaces/inequalities such that $P = \bigwedge_{i=1}^k a^i \cdot x \leq b^i$

Autonomous (Closed, Deterministic) Linear Systems

- ▶ Systems defined by linear differential equations of the form $\dot{x} = Ax$ where A is a matrix are the most well-studied
- ▶ There is a standard technique to fix a time step r and work in discrete time, a **recurrence equation** of the form $x_{i+1} = Ax_i$
- ▶ The image of a set P by the linear transformation A is $AP = \{Ax : x \in P\}$ (one-step successors)
- ▶ It is easy to compute, for example, for polytopes represented by vertices:

$$P = \text{conv}(\{x_1, \dots, x_l\}) \Rightarrow AP = \text{conv}(\{Ax_1, \dots, Ax_l\})$$



Algorithm 1: Discrete-Time Linear Reachability

- ▶ **Input:** A set $X_0 \subset X$ represented as $\text{conv}(\tilde{P}_0)$
- ▶ **Output:** $Q = R_{[0..L]}(X_0)$ represented as a list $\{\text{conv}(\tilde{P}_0), \dots, \text{conv}(\tilde{P}_L)\}$

```
 $P := Q := \tilde{P}_0$   
repeat  $i = 1, 2 \dots$   
   $P := AP$   
   $Q := Q \cup P$   
until  $i = L$ 
```

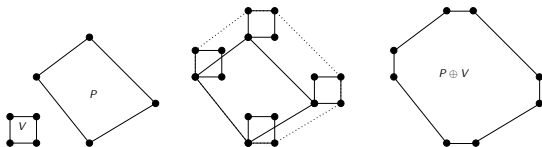
- ▶ Complexity assuming $|\tilde{P}_0| = m_0$ is $O(m_0 LM(n))$ where $M(n)$ is the complexity of matrix-vector multiplication in n dimensions: $\sim O(n^3)$
- ▶ Can be applied to other representations of objects closed under linear transformations

Linear Systems with Input

- ▶ Systems define by $x_{i+1} = Ax_i + v_i$ where the v_i 's range over a bounded convex set V
- ▶ The one-step successor of P is defined as

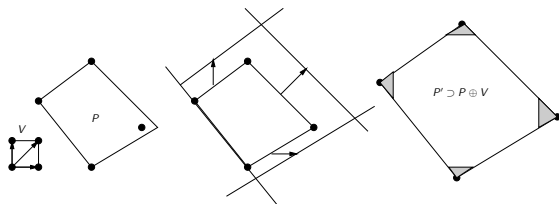
$$P' = \{Ax + v : x \in P, v \in V\} = AP \oplus V$$

- ▶ Minkowski sum $A \oplus B = \{a + b : a \in A \wedge b \in b\}$
- ▶ Same algorithm can be applied but the Minkowski sum increases the number of vertices in every step



Alternative: Pushing Facets

- ▶ Over-approximating the reachable set while keeping its complexity more or less fixed
- ▶ Assume P represented as intersection of halfspaces
- ▶ For each halfspace $H^i : a^i x \leq b^i$, let $v^i \in V$ be the input vector which pushes it in the “outermost” way
- ▶ Apply $Ax + Bv^i$ to H^i and the intersection of the pushed halfspaces over-approximates $AP \oplus V$



- ▶ The problem: over-approximation errors accumulate (the “wrapping effect”)

Linear Reachability: State of the Art

- ▶ New algorithmics by C. Le Guernic and A. Girard
- ▶ Efficient computations: linear transformation applied to fixed number of points in each iteration
- ▶ No accumulation of over-approximation errors
- ▶ Initially used **zonotopes**, a class of sets closed under both linear operations and Minkowski sum; Can be applied to any “lazy” representation of the sequence of the computed sets
- ▶ Based on the observation that two consecutive sets

$$\begin{aligned}P_k &= A^k P_0 \oplus A^{k-1} V \oplus A^{k-2} V \oplus \dots \oplus V \\P_{k+1} &= A^{k+1} P_0 \oplus A^k V \oplus A^{k-1} V \oplus \dots \oplus V\end{aligned}$$

share a lot of terms

- ▶ Can compute within few minutes the reachable set after 1000 steps for linear systems with 200 (!) state variables

Linear Reachability: Some Credits

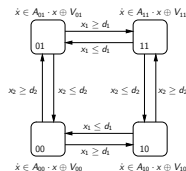
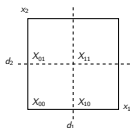
- ▶ Algorithmic analysis of hybrid systems started with tools like **Kronos** and **HyTech** for timed automata and “linear” hybrid automata: **HenzingerSifakisYovine** and **HenzingerHoWongtoi** - very simple continuous dynamics, summarized in **ACH⁺95**
- ▶ Verifying differential equations: **Greenstreet96**
- ▶ Reachability for linear differential equations and hybrid systems: **ChutinanKrogh99**, **AsarinBournezDangMaler00** (polytopes) **KurzhanskiVaraiya00**, **BotchkarevTripakis00** (ellipsoids), **MitchellTomlin00** (level sets)
- ▶ Pushing faces and treating inputs: **DangMaler98**, **Varaiya98**
- ▶ Using zonotopes: **Girard05**
- ▶ New algorithmic scheme **Girard LeGuernic06-09**

The Nonlinear Challenge

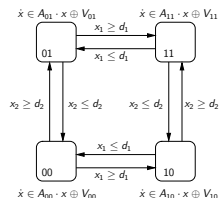
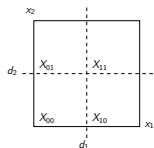
- ▶ Ok, bravo, but linear systems were studied to death by everybody. Real interesting models, biological included, are **nonlinear**
- ▶ What about systems of the form $x_{i+1} = f(x_i, u_i)$ or even $x_{i+1} = f(x_i)$ where f is an arbitrary continuous function, say a polynomial ?
- ▶ Convexity-preservation property of linear maps doesn't hold
- ▶ You can make small time steps, use a **local linear approximation** and bloat the obtained set to be safe
- ▶ This approach will either accumulate **large errors** or require expensive computation in **every step**

Hybridization: Asarin, Dang and Girard 2003

- ▶ Take a nonlinear system $x_{i+1} = f(x_i)$ and partition the state space into boxes (linearization domains)
- ▶ In each box X_q find a matrix A_q and a convex polytope V_q s.t. $f(x) \in A_q x \oplus V_q$ for every $x \in X_q$
- ▶ A_q is a **local linearization** of f with error bounded by V_q
- ▶ The new dynamics is $x_{i+1} \in A_q x \oplus V_q$ iff $x \in X_q$
- ▶ A piecewise-(linear-with-input) systems, a restricted type of a hybrid automaton, which over-approximate f in terms of inclusion of trajectories

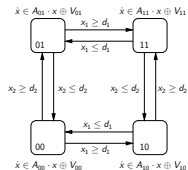
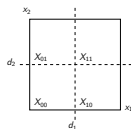


Hybridization (cont.)

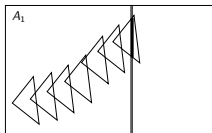


- ▶ In the hybrid automaton, x evolves according to the linear dynamics $A_q x \oplus V_q$ as long as it **remains** in X_q
- ▶ Reaching the **boundary** between X_q and $X_{q'}$, it takes a **transition** to q' and evolves according to $A_{q'} x \oplus V_{q'}$
- ▶ Linearization and error are computed only in the passage between blocks, **not** in every step
- ▶ Quality can be improved by making boxes smaller

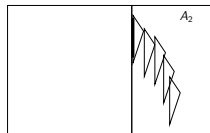
Hybrid Reachability



- ▶ Compute in one domain a sequences of sets using linear techniques until a set intersects with a boundary
- ▶ Take the intersection as initial set in next domain with the next linearization



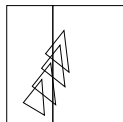
(a)



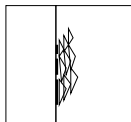
(b)

Between Theory and Practice

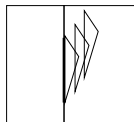
- ▶ First problem: intersection may be spread over many steps:



(a)

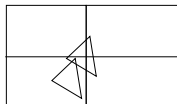


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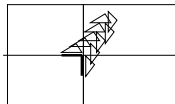


(c)

- ▶ Either **explosion** or union of intersections, **error** accumulation
- ▶ Major problem: a set may leave a box via **many facets**:



(a)

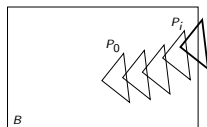


(b)

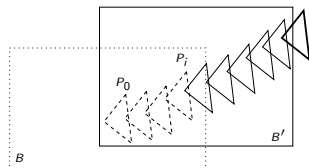
- ▶ Splitting is an **artifact** of the **fixed grid** imposed on the system
- ▶ Consequently, static hybridization is practically impossible beyond 3 dimensions

Our Contribution (at Last!)

- ▶ A **dynamic** hybridization scheme **not** based on a fixed grid
- ▶ In this scheme we do not need intersection **at all** and we allow the linearization domains to **overlap**
- ▶ When we leave a domain, we backtrack one step and define a new linearization domain around the previous set and continue with the new linearized dynamics from there



(a)

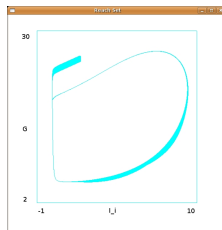
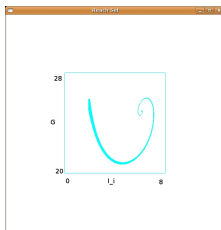


(b)

- ▶ And it works!

Example: E. Coli Lac Operon

$$\begin{aligned}\dot{R}_a &= \tau - \mu * R_a - k_2 R_a O_f + k_{-2}(\chi - O_f) - k_3 R_a I_i^2 + k_8 R_i G^2 \\ \dot{O}_f &= -k_2 r_a O_f + k_{-2}(\chi - O_f) \\ \dot{E} &= \nu k_4 O_f - k_7 E \\ \dot{M} &= \nu k_4 O_f - k_6 M \\ \dot{I}_i &= -2k_3 R_a I_i^2 + 2k_{-3} F_1 + k_5 I_r M - k_{-5} I_i M - k_9 I_i E \\ \dot{G} &= -2k_8 R_i G^2 + 2k_{-8} R_a + k_9 I_i E\end{aligned}$$



- We can also do a 9-dimensional highly-nonlinear **aging** model

Conclusions

- ▶ Disclaimer: we do **not** bring any new biological insight on any concrete system at this point
- ▶ Our goal is to develop **tools**, as **general-purpose** as possible, that can aid in the analysis of **many** non-trivial systems
- ▶ **Problem specificity** cannot be avoided of course: it will come up at the particular modeling and exploration phases
- ▶ Current version is a **prototype**:
 - ▶ Fixed-size boxes as linearization domains and other heuristics. Can be improved in efficiency and accuracy;
 - ▶ It is based on the old algorithmics for linear systems;
 - ▶ Improving all these aspects is on our immediate agenda
- ▶ We also explore alternative approaches for parameter synthesis based on simulation and sensitivity analysis **Donze et al09**
- ▶ Methodological aspects of the use of such tools in the **biological context** should be worked out

Thank You