

On the Analysis of Numerical Data Time Series in Temporal Logic

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- Introduction
- LTL with constraints
- LTL constraint solving problem
- LTL constraint solving algorithm
- Biologically relevant patterns
- Discussion

- Logical paradigm for systems biology

Biological model = Transition system

Biological property = Temporal logic formula

Biological validation = Model checking

- Implemented in Biological Abstract Machine BIOCHAM
- The goal is to extract biological properties from experimental data

- Kripke structure is a triplet (S, R, L) , where S is a set of states, $R \subseteq R \times R$ is a transition relation and L is a labeling function.
- state: a vector of molecule concentrations
- transitions between two consecutive time points
- atomic propositions: constraints on molecular concentrations and their derivatives
- traces have the form $\langle t_i, x_i, dx_i/dt, d^2x_i/dt^2 \rangle$
- the step size $t_{i+1} - t_i$ is not constant

Constraint LTL syntax

$$\begin{aligned} C - Itl = & Atom \quad | \quad F(C - Itl) \\ & | \quad G(C - Itl) \quad | \quad X(C - Itl) \\ & | \quad (C - Itl)U(C - Itl) \quad | \quad (C - Itl) \wedge (C - Itl) \\ & | \quad (C - Itl) \vee (C - Itl) \quad | \quad (C - Itl) \Rightarrow (C - Itl) \\ & | \quad not(C - Itl) \end{aligned}$$
$$Atom = Value \ Op \ Variable \quad | \quad Value \ Op \ Value$$
$$Op = < \quad | \quad > \quad | \quad \leq \quad | \quad \geq$$
$$\begin{aligned} Value = & float \quad | \quad [molecule] \quad | \quad d[molecule]/dt \quad | \quad d^2[molecule]/dt^2 \\ & | \quad Value + Value \quad | \quad Value - Value \quad | \quad -Value \\ & Value \times Value \quad | \quad Value/Value \quad | \quad Value^{Value} \end{aligned}$$

- $F([A] > 10)$
- $G([A] + [B] < [C])$
- $F(d[M]/dt > 0 \wedge F((d[M]/dt < 0) \wedge F(d[M]/dt > 0)))$

- Given a trace T and a C-LTL formula ϕ with n variables, the *constraint solving problem* $\exists v \in \mathbb{R}^n$ such that $(\phi(v))$ is the problem of determining the valuation v of the variables for which ϕ is true in T .
- In other words, we look for the domain of validity $\mathcal{D}_\phi \subset \mathbb{R}^n$ such that $T \models_{LTL} \forall v \in \mathcal{D}_\phi (\phi(v))$.

- starting from the end of the trace, label each time point t_i by the subformula $F\psi$ (resp. $G\psi$, resp. $\psi_1 U \psi_2$) and its domain of validity $\mathcal{D}_{F\psi}(t_i) = \mathcal{D}_{F\psi}(t_{i+1}) \cup \mathcal{D}_\psi(t_i)$,
resp. $\mathcal{D}_{G\psi}(t_i) = \mathcal{D}_{G\psi}(t_{i+1}) \cap \mathcal{D}_\psi(t_i)$,
resp. $\mathcal{D}_{\psi_1 U \psi_2}(t_i) = \mathcal{D}_{\psi_2}(t_i) \cup (\mathcal{D}_{\psi_1 U \psi_2}(t_{i+1}) \cap \mathcal{D}_{\psi_1}(t_i))$
- label each time point t_i by the subformula $X\psi$ (resp. $\psi_1 \wedge \psi_2$, resp. $\psi_1 \vee \psi_2$) and its domain of validity $\mathcal{D}_{X\psi}(t_i) = \mathcal{D}_\psi(t_{i+1})$,
resp. $\mathcal{D}_{\psi_1 \wedge \psi_2}(t_i) = \mathcal{D}_{\psi_1}(t_i) \cap \mathcal{D}_{\psi_2}(t_i)$,
resp. $\mathcal{D}_{\psi_1 \vee \psi_2}(t_i) = \mathcal{D}_{\psi_1}(t_i) \cup \mathcal{D}_{\psi_2}(t_i)$
- return the non-empty domain $\mathcal{D}_\psi(t_i)$ for all time points t_i

Properties of the algorithm

- The algorithm is correct and complete: a valuation v makes ψ true at time t_i , $T, t_i \models_{LTL} (\psi(v))$ iff v is in the computed domain of ψ at t_i , $v \in \mathcal{D}_\psi(t_i)$.
- time complexity: $O(kn^{dv+1})$, where k, d, v are respectively the size, the depth and the number of variables of the C-LTL formula and n is the size of the trace.

- *Reachability*: $F([A] \geq p)$
- *Stability*: $G([A] \leq p_1 \wedge [A] \geq p_2)$: what is the range of values of $[A]$
- *Oscillation*:
 $F((d[A]/dt > 0 \wedge [A] > v_1) \wedge F(d[A]/dt < 0 \wedge [A] < v_2))$:
what amplitude $(v_1 - v_2)$ in at least one oscillation?
- *Influence*: $G(d[A]/dt \geq p_1 \Rightarrow d^2[B]/dt^2 \geq 0)$: above which threshold has A influence on B?

Thank you for you attention.
Questions?