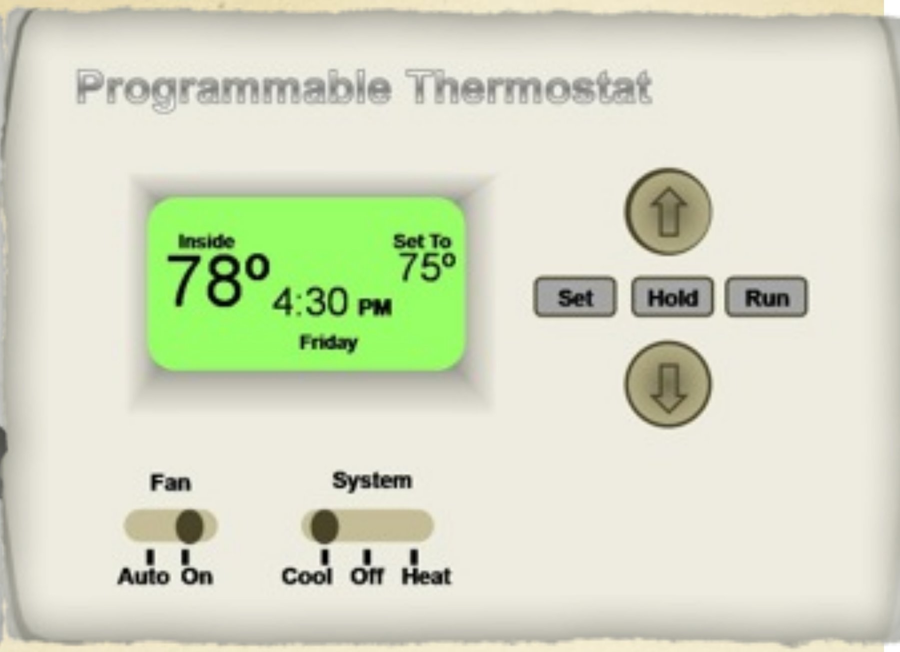
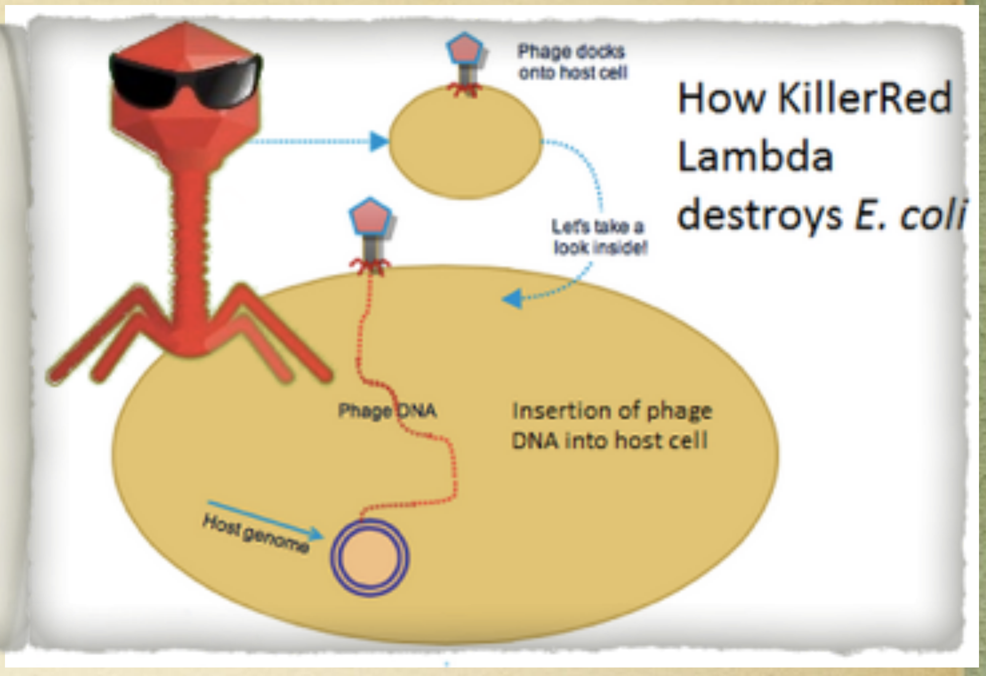




# SReach:

# A Probabilistic Bounded δ-Reachability Analyzer for Stochastic Hybrid Systems*

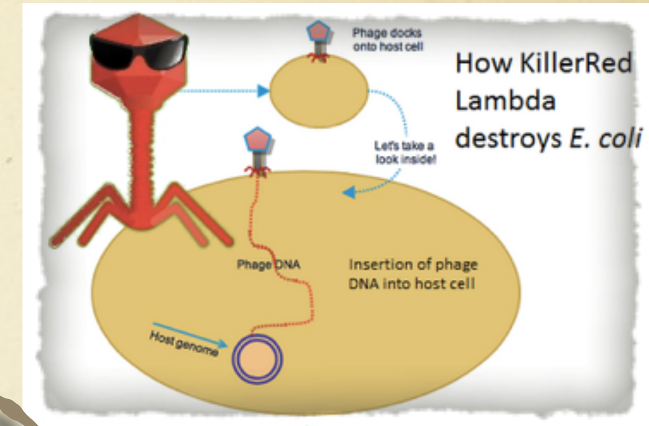
*Qinsi Wang*

**Qinsi Wang, Paolo Zuliani, Soonho Kong, Sicun Gao, and Edmund Clarke. SReach: A Probabilistic Bounded δ-Reachability Analyzer for Stochastic Hybrid Systems. CMSB 2015*

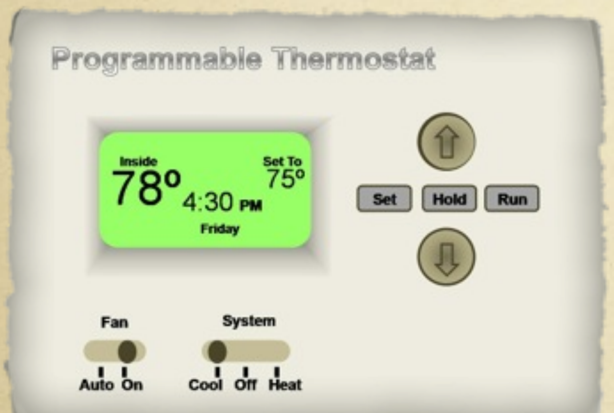
# SReach

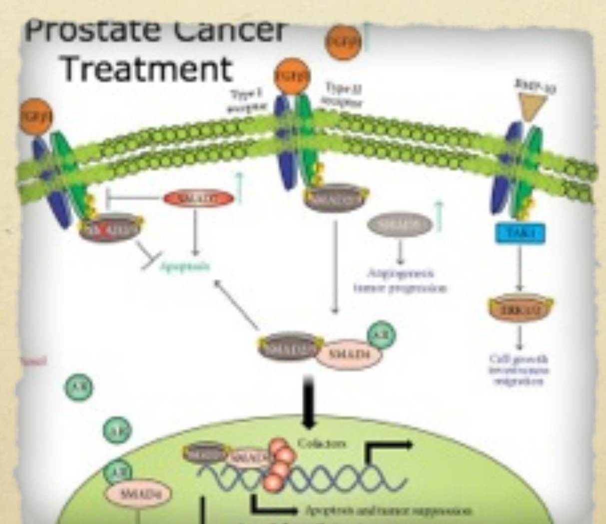
# Probabilistic Bounded Reachability Analysis of Stochastic Hybrid Systems

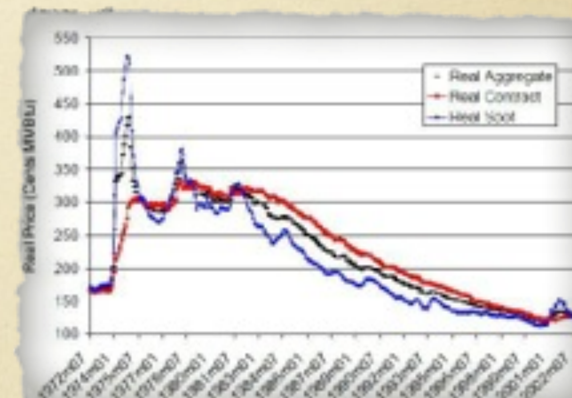
# Stochastic Hybrid Systems

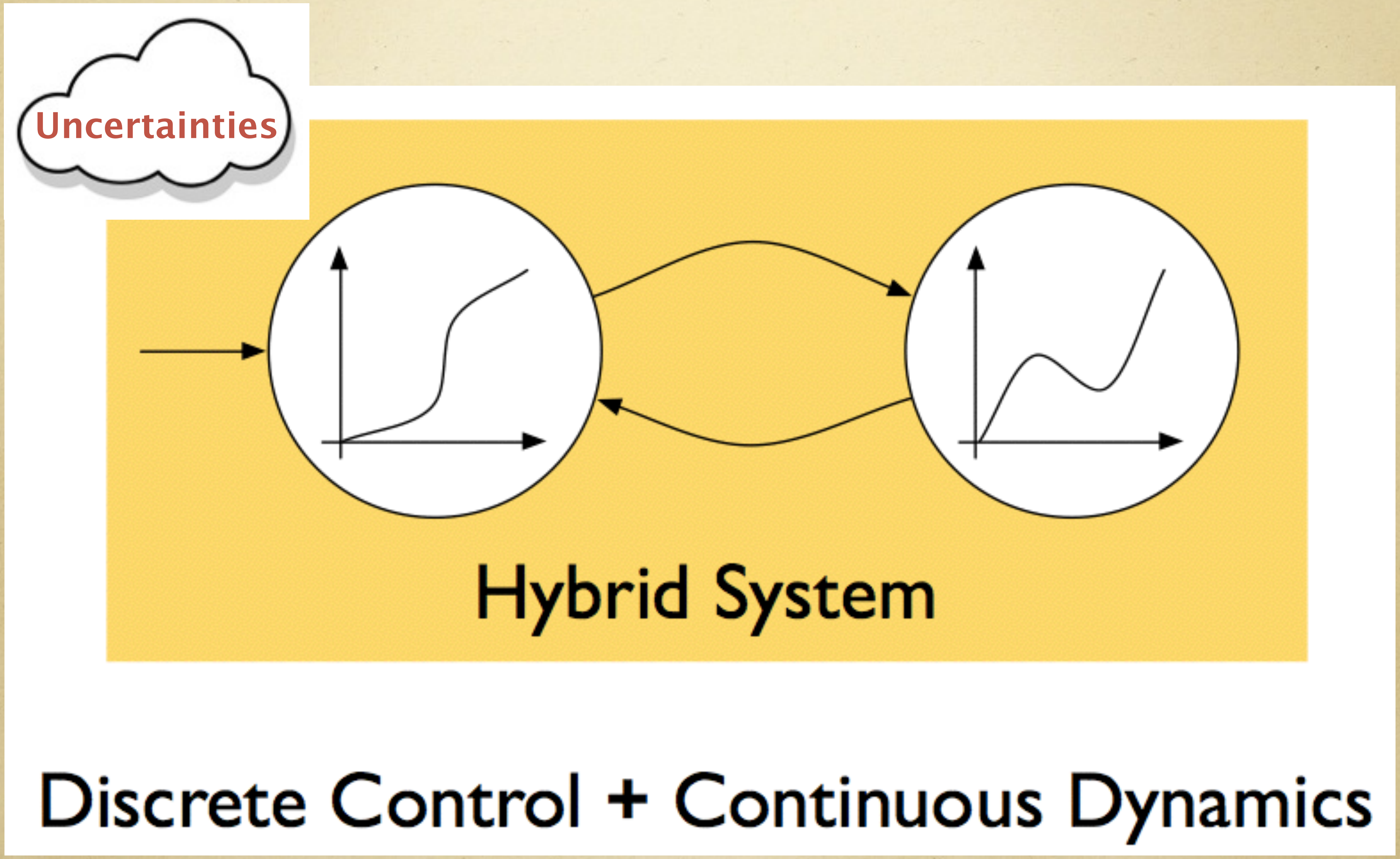

Discrete
Continuous
Stochastic



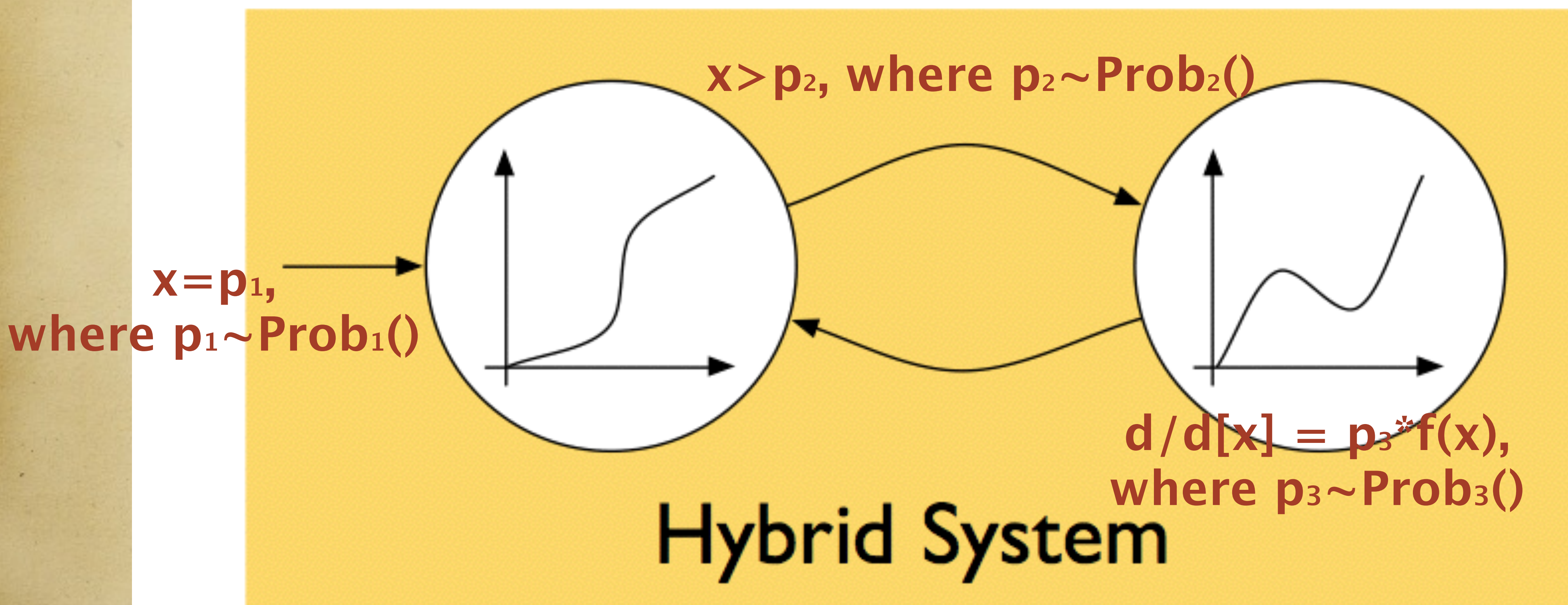



# Stochastic Hybrid Systems

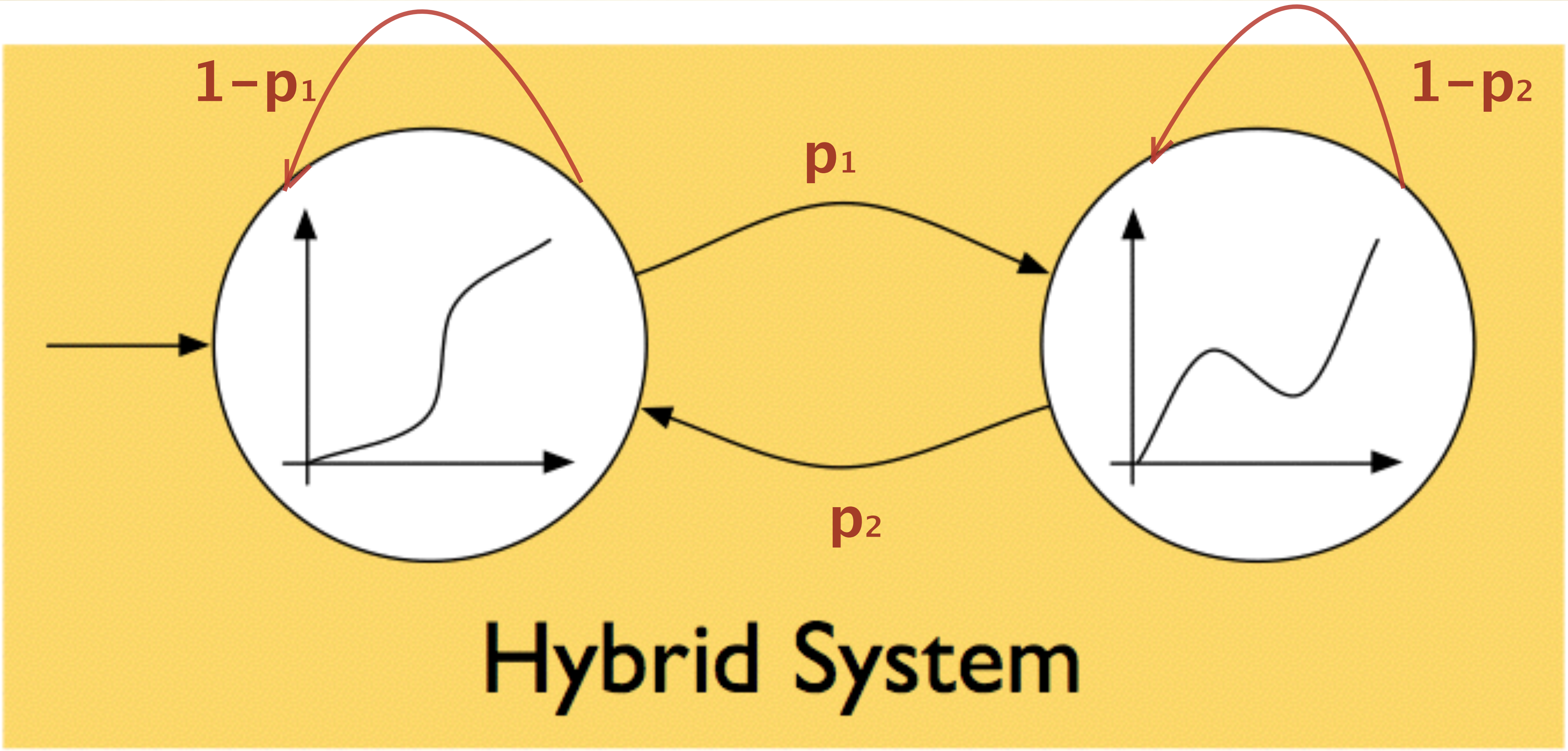


# Stochastic Hybrid Systems




**Hybrid System with Parametric Uncertainty**

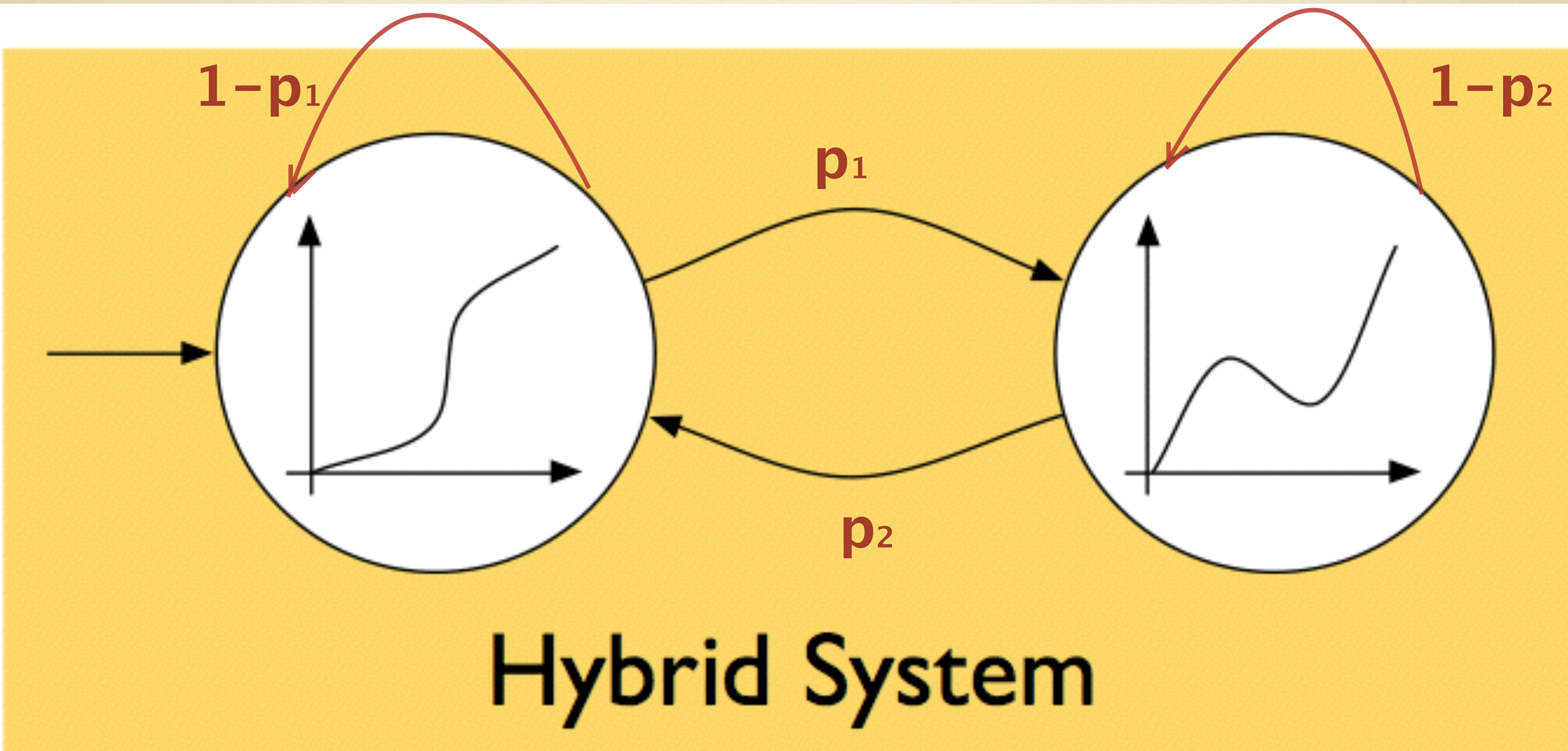
# Stochastic Hybrid Systems




**$p_1$ and $p_2$ are discrete random variables:**

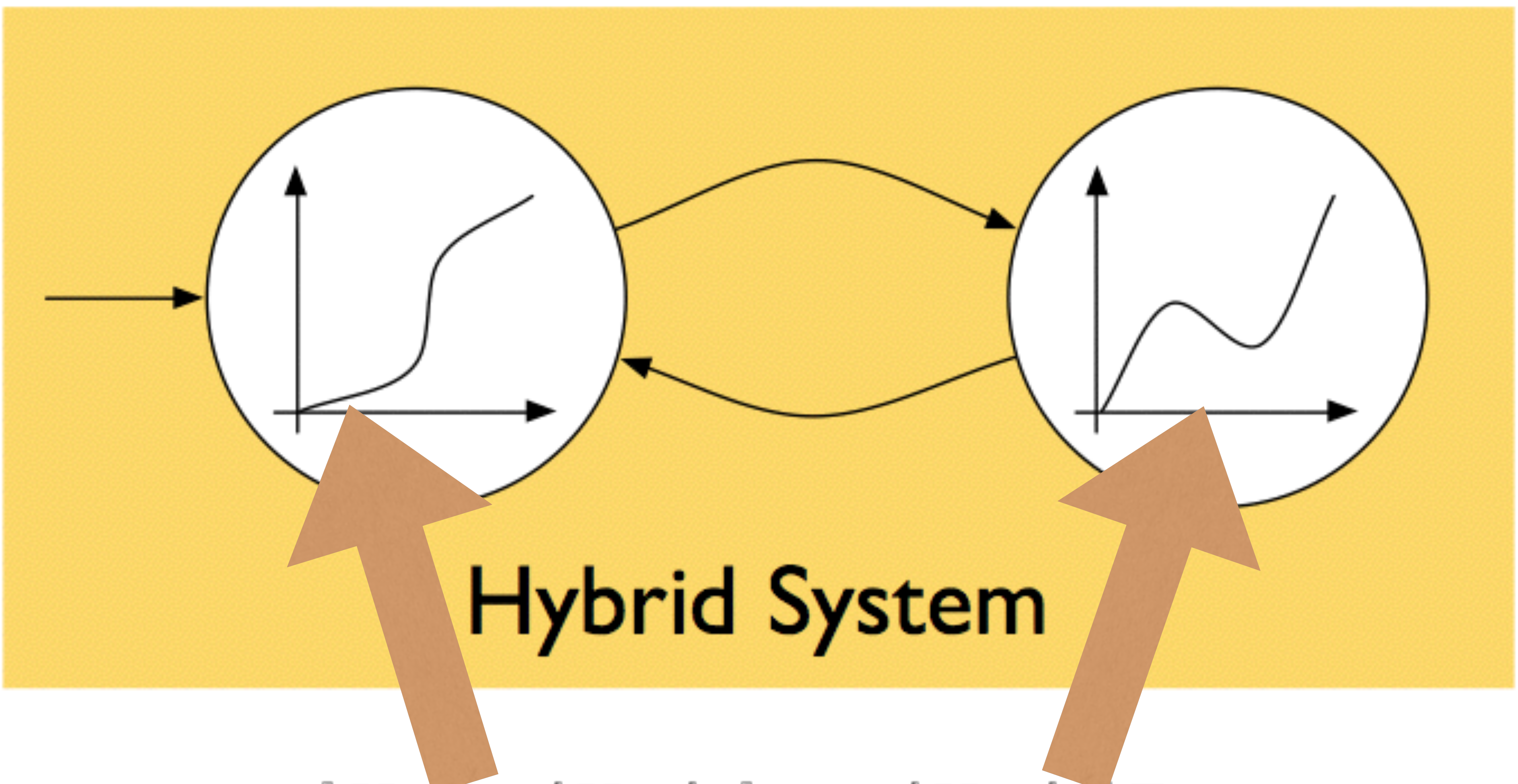
**Probabilistic Hybrid Automata**

# Stochastic Hybrid Systems



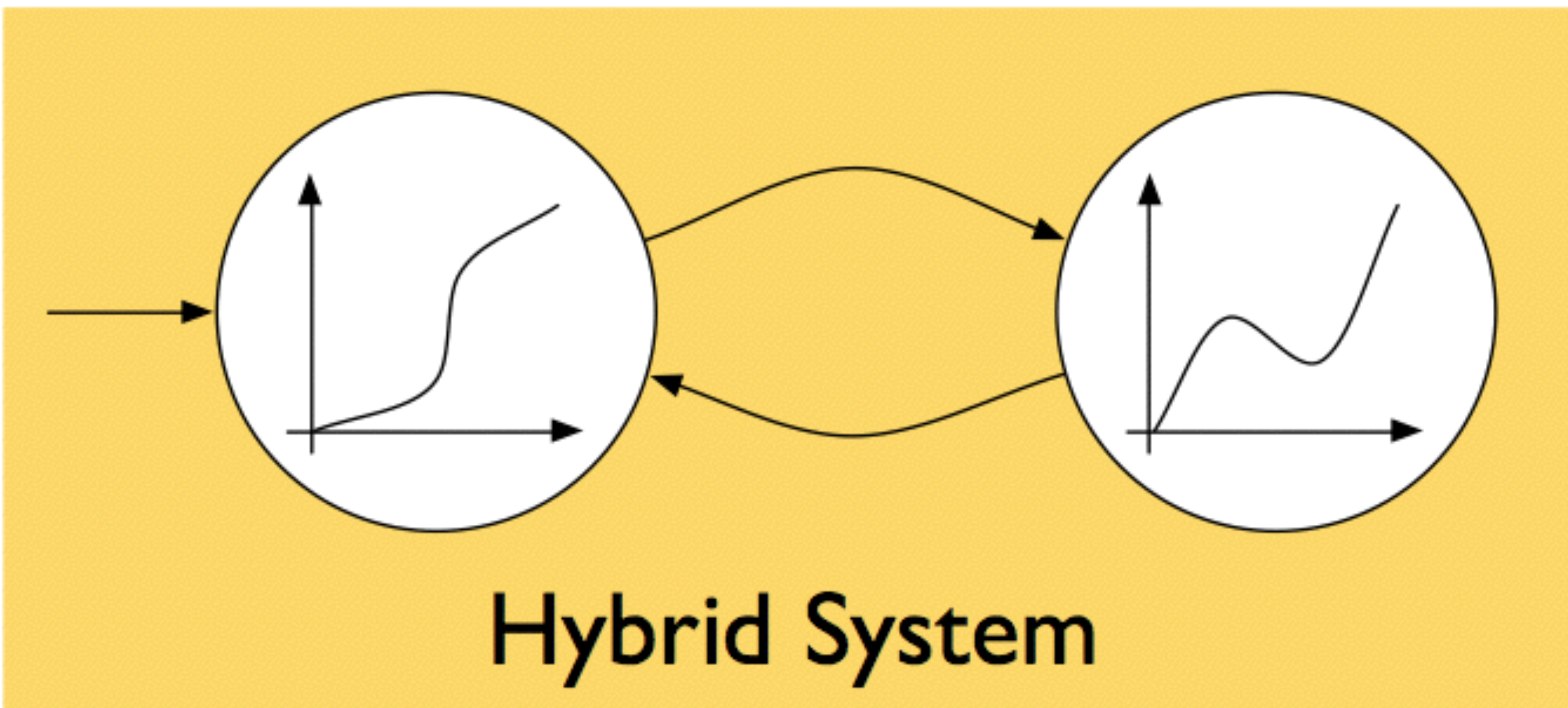

**When continuous distributions are also allowed: Stochastic Hybrid Automata**

# Stochastic Hybrid Systems




$$dX_t = \mu(X_t, t)\,dt + \sigma(X_t, t)\,dB_t,$$

# Stochastic Hybrid Systems




**When all above modifications have been applied:**

**General Stochastic Hybrid Systems**

# **SReach** considers ...

**Definition 1 ($\mathbf{HA}_p$).** *A hybrid automaton with parametric uncertainty is a tuple* $H_p = \langle (Q, E),\ V,\ RV,\ \mathsf{Init},\ \mathsf{Flow}, \mathsf{Inv},\ \mathsf{Jump},\ \Sigma \rangle$, *where*

- *The vertices* $Q = \{q_1, \cdots, q_m\}$ *is a finite set of discrete modes, and edges in* $E$ *are control switches.*
- $V = \{v_1, \cdots, v_n\}$ *denotes a finite set of real-valued system variables. We write* $\dot{V}$ *to represent the first derivatives of variables during the continuous change, and write* $V'$ *to denote values of variables at the conclusion of the discrete change.*
- $RV = \{w_1, \cdots, w_k\}$ *is a finite set of independent random variables, where the distribution of* $w_i$ *is denoted by* $P_i$.
- Init, Flow, *and* Inv *are labeling functions over* $Q$. *For each mode* $q \in Q$, *the initial condition* $Init(q)$ *and invariant condition* $Inv(q)$ *are predicates whose free variables are from* $V \cup RV$, *and the flow condition* $Flow(q)$ *is a predicate whose free variables are from* $V \cup \dot{V} \cup RV$.
- Jump *is a transition labeling function that assigns to each transition* $e \in E$ *a predicate whose free variables are from* $V \cup V' \cup RV$.
- $\Sigma$ *is a finite set of events, and an edge labeling function* $event : E \to \Sigma$ *assigns to each control switch an event.*

# **SReach** considers …

**Definition 2 (PHA$_r$).** *A probabilistic hybrid automaton with additional randomness $H_r$ consists of $Q$, $E$, $V$, $RV$,* Init, Flow, Inv, *$\Sigma$ as in Definition 1, and $Cmds$, which is a finite set of probabilistic guarded commands of the form:*
$g \rightarrow p_1 : u_1 + \cdots + p_m : u_m$,
*where $g$ is a predicate representing a transition guard with free variables from $V$, $p_i$ is the transition probability for the ith probabilistic choice which can be expressed by an equation involving random variable(s) in $RV$ and the $p_i$'s satisfy $\sum_{i=1}^{m} p_i = 1$, and $u_i$ is the corresponding transition updating function for the ith probabilistic choice, whose free variables are from $V \cup V' \cup RV$.*

$x \geq 5 \rightarrow p_1 : (x' = \sin(x)) + (1 - p_1) : (x' = p_x)$,

$p_1 \sim U(0.2,0.9)$, and $p_x \sim B(0.85)$

# **SReach** can handle…

**Definition 3.** *The probabilistic bounded k step $\delta$-reachability for a $HA_p$ $H_p$ is to compute the probability that $H_p$ reaches the target region $T$ in $k$ steps. Given the set of independent random variables $\mathbf{r}$, $Pr(\mathbf{r})$ a probability measure over $\mathbf{r}$, and $\Omega$ the sample space of $\mathbf{r}$, the reachability probability is $\int_{\Omega} I_T(\mathbf{r})dPr(\mathbf{r})$, where $I_T(\mathbf{r})$ is the indicator function which is 1 if $H_p$ with $\mathbf{r}$ reaches $T$ in $k$ steps.*

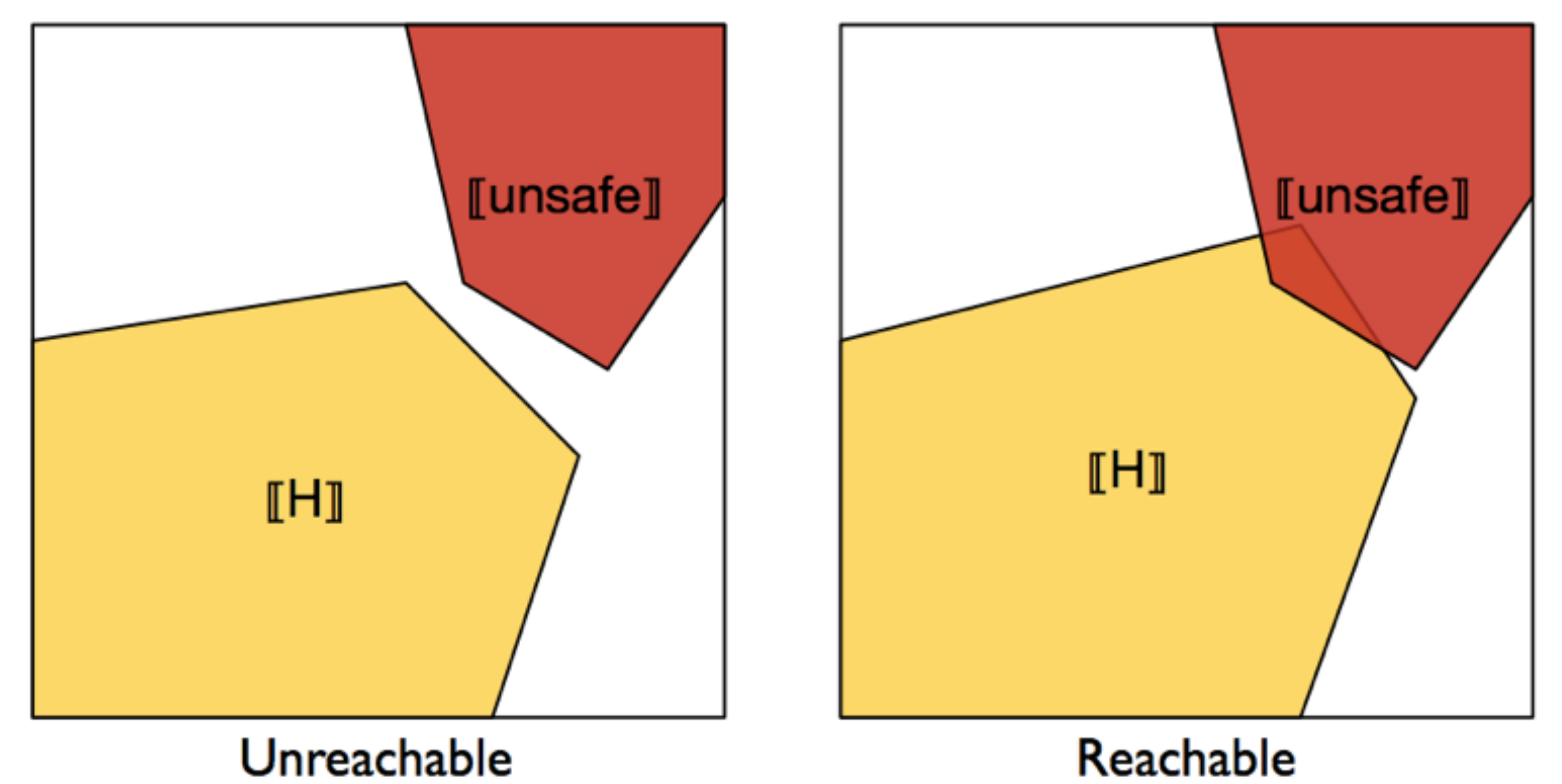
**Definition 4.** *For a $PHA_r$ $H_r$, the probabilistic bounded k step $\delta$-reachability estimated by SReach is the maximal probability that $H_r$ reaches the target region $T$ in $k$ steps: $max_{\sigma \in E} Pr^k_{H_r,\sigma,T}(i)$, where $E$ is the set of possible executions of $H$ starting from the initial state $i$, and $\sigma$ is an execution in the set $E$.*

# **SReach**'s algorithm

- δ-complete bounded reachability analysis technique (dReal/dReach) + statistical testing techniques
- advance the reasoning power of SMT-based bounded model checking to probabilistic models
- the full non-determinism and nonlinear dynamics of models will be considered
- the coverage of simulation will be increased
- the zero-crossing problem can be avoided
- controllable error bounds on the estimated probabilities

# Reachability Analysis of Hybrid Systems

- Can a hybrid system H run into a goal region of its state space?

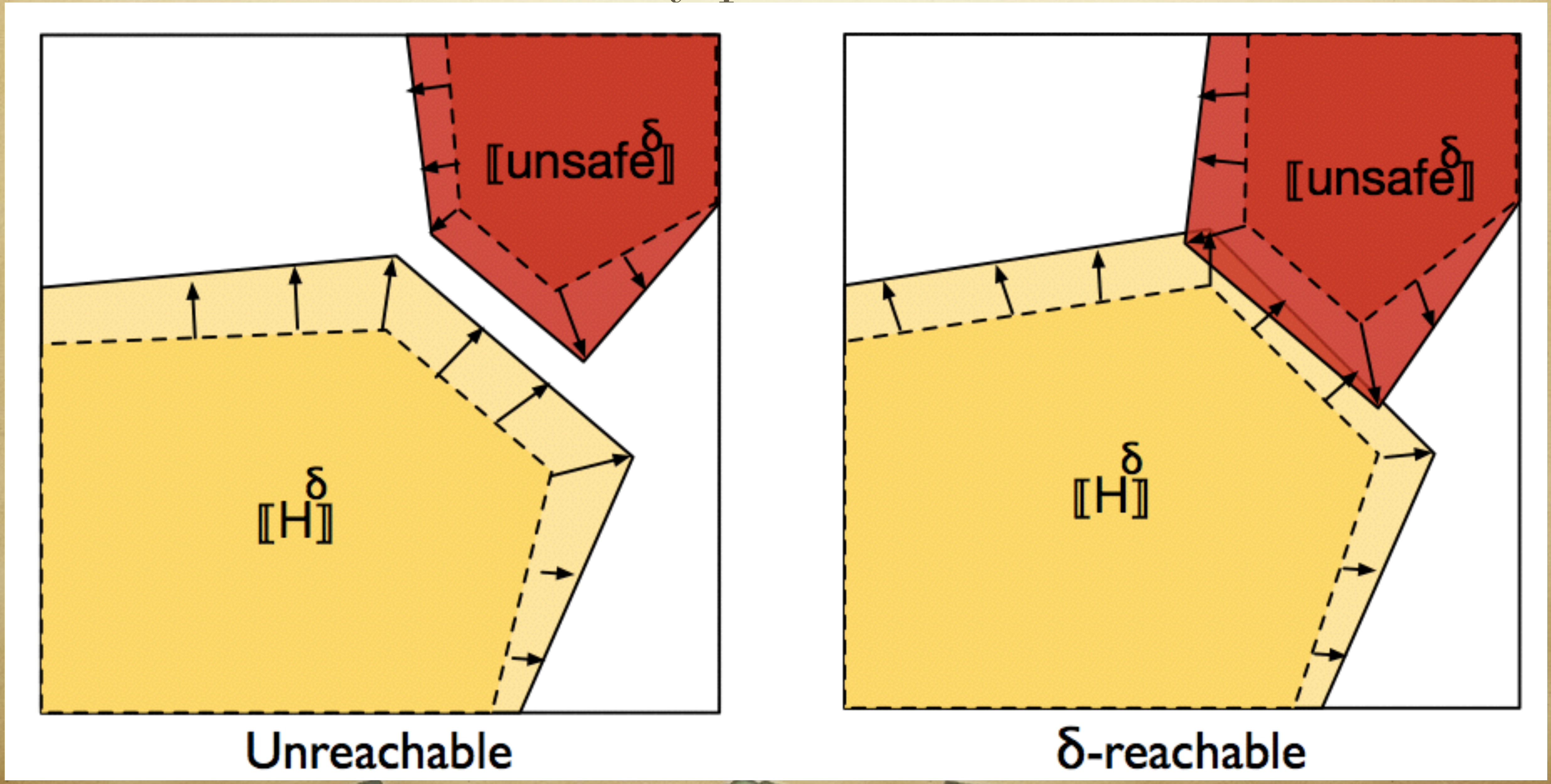


# Bounded Reachability Analysis of Hybrid Systems

- The standard bounded reachability problems for simple hybrid systems are **undecidable**.
  - 1. Give up
  - 2. Don't give Up
    - A. Find a decidable fragment and solve it
    - B. Use approximation

# δ-Reachability Analysis of Hybrid Systems

- Given $\delta \in Q^+$, $[\![H^\delta]\!]$ and $[\![Goal^\delta]\!]$ over-approximate $[\![H]\!]$ and $[\![Goal]\!]$ respectively.
- So, the δ-reachability problem asks



# δ-Reachability Analysis of Hybrid Systems

- **Decidable** for a wide range of nonlinear hybrid systems: polynomials, log, exp, trigonometric functions, ODEs …
- Reasonable complexity bound (PSPACE-complete)
- When it says
  - Unreachable – the answer is **sound**
  - δ-Reachable – may lead to an infeasible counterexample,
    you may try a smaller δ and possibly get rid of it

# SReach's algorithm

**Algorithm 1** SReach

```
function SREACH(MP, ST, δ, k)
    if MP is a HA_p then
        MP ← EncRM_1(MP)                    ▷ encode uncertain system parameters
    else                                    ▷ otherwise a PHA_r
        MP ← EncRM_2(MP)  ▷ encode probabilistic jumps and extra randomness
    end if
    Succ, N ← 0                             ▷ number of δ-sat samples and total samples
    Assgn ← ∅                ▷ record unique sampling assignments and dReach results
    RV ← ExtractRV(MP)                      ▷ get the RVs from the probabilistic model
    repeat in parallel
        S_i ← Sim(RV)                       ▷ sample the parameters
        if S_i ∈ Assgn.sample then
            Res ← Assgn(S_i).res            ▷ no need to call dReach
        else
            M_i ← Gen(MP, S_i)              ▷ generate a dReach model
            Res ← dReach(M_i, δ, k)         ▷ call dReach to solve k-step δ-reachability
        end if
        if Res = δ-sat then Succ ← Succ + 1
        end if
        N ← N + 1
    until ST.done(Succ, N)                  ▷ perform statistical test
    return ST.output
end function
```

# **SReach** answers …

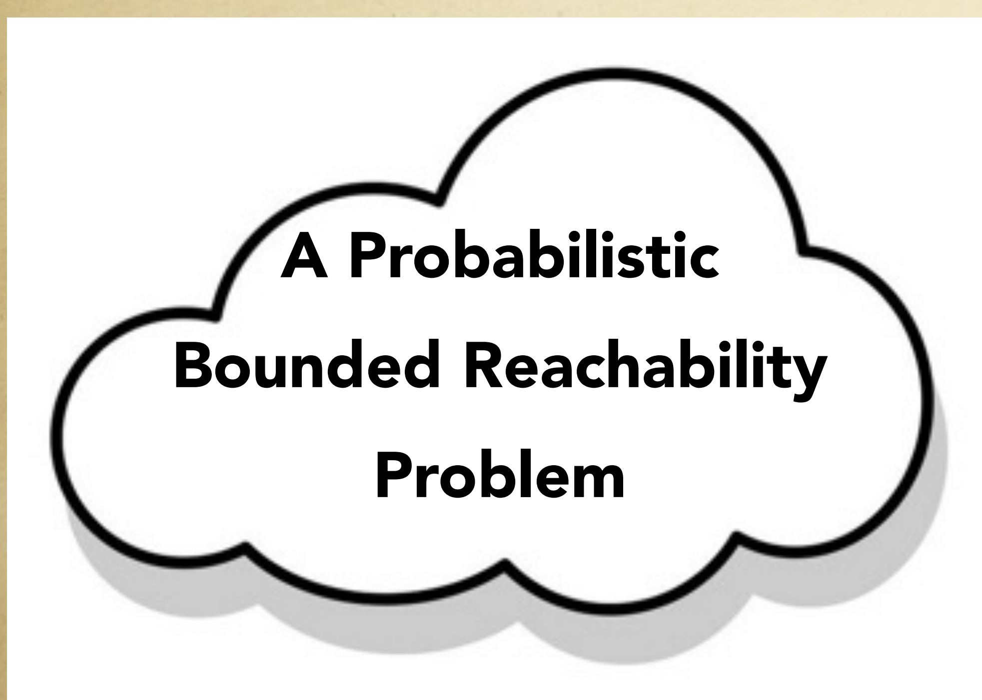
- SReach can answer two types of questions:
  - (1) Does the model satisfy a given reachability property with probability greater than a certain threshold?  hypothesis testing
  - Hypothesis testing methods: Lai's test, Bayes factor test, Bayes factor test with indifference region, and Sequential probability ratio test.

# **SReach** answers …

- SReach can answer two types of questions:
  - (2) What is the probability that the model satisfies a given reachability property? statistical estimation
  - Statistical estimation methods: Chernoff-Hoeffding bound, Bayesian interval estimation with beta prior, and Direct sampling.

# SReach answers …

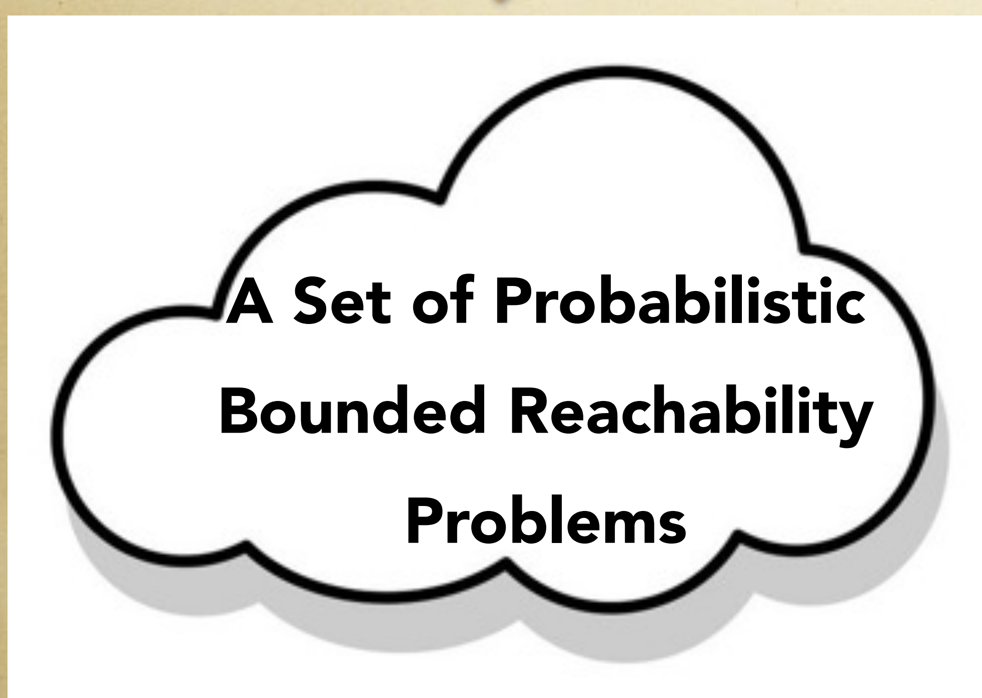
- Parameter Synthesis: How to control the system to reach good states with a desirable probability?




- Does it exist a parameter combination for which the model reaches the given goal region with a desirable probability in bounded steps?
- Considering an assignment of a certain set of system parameters, if a witness is returned, this assignment is potentially a good estimation for those parameters.
- The goal here is to find an assignment with which all the given goal regions with desirable probabilities can be reached in bounded steps.

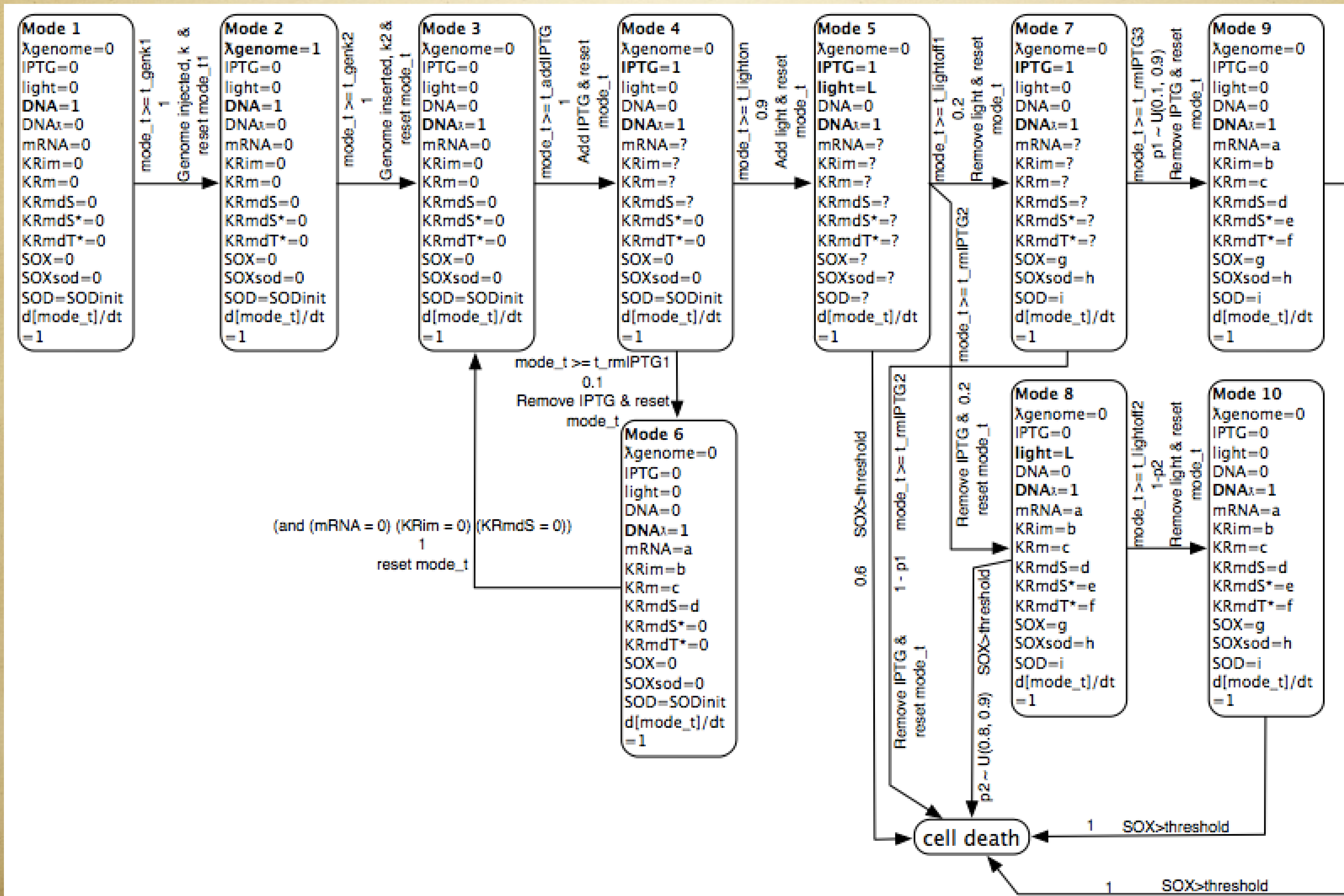
# SReach answers …

- Parametric Sensitivity Analysis: Testing the robustness of the model, Understand the relationships between parameters and the model, etc.



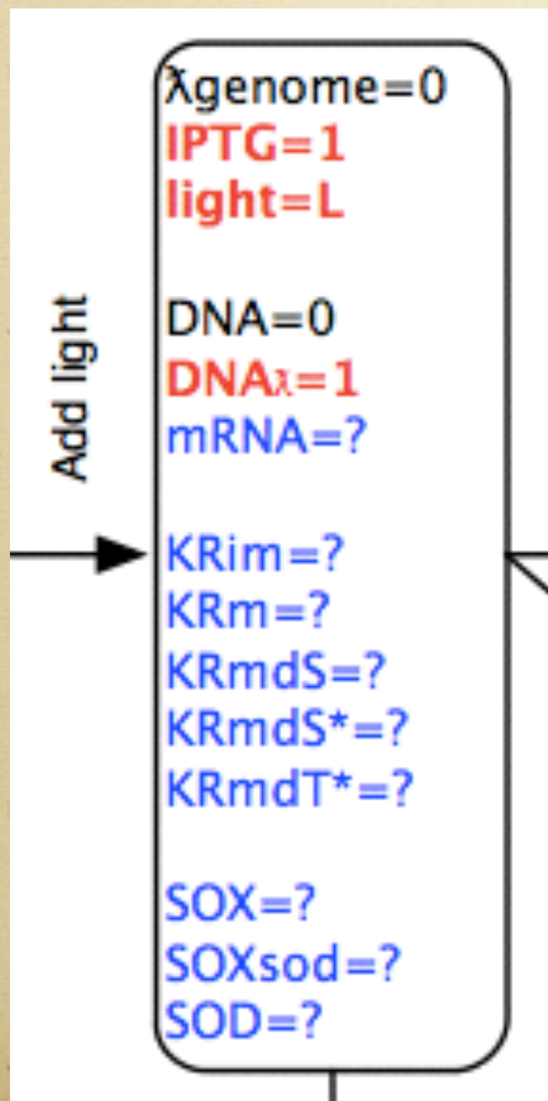

- For different possible values of a certain system parameter, are the results of probabilistic reachability analysis the same?
  - If so, the model is insensitive to this parameter with regard to the given observations.

# Bacteria-killing KillerRed Model



# Bacteria-killing KillerRed Model

$$\begin{aligned}
\frac{d[mRNA]}{dt} &= k_{RNAsyn} \cdot [DNA] - k_{RNAdeg} \cdot [mRNA] \\
\frac{d[KR_{im}]}{dt} &= k_{KR_{im}syn} \cdot [mRNA] - (k_{KR_m} + k_{KR_{im}deg}) \\
&\quad \cdot [KR_{im}] \\
\frac{d[KR_{mdS}]}{dt} &= k_{KR_m} \cdot [KR_{im}] - k_{KR_{mdS}deg} \cdot [KR_{mdS}]
\end{aligned}$$




$$\begin{aligned}
\frac{d[KR_{mdS}]}{dt} &= k_{KR_m} \cdot [KR_{im}] + k_{KR_f} \cdot [KR_{mdS^*}] \\
&\quad + k_{KR_{ic}} \cdot [KR_{mdS^*}] + k_{KR_{nrd}} \cdot [KR_{mdT^*}] \\
&\quad + k_{KR_{SOXd1}} \cdot [KR_{mdT^*}] - k_{KR_{ex}} \cdot [KR_{mdS}] \\
&\quad - k_{KR_{mdS}deg} \cdot [KR_{mdS}] \\
\frac{d[KR_{mdS^*}]}{dt} &= k_{KR_{ex}} \cdot [KR_{mdS}] - k_{KR_f} \cdot [KR_{mdS^*}] \\
&\quad - k_{KR_{ic}} \cdot [KR_{mdS^*}] - k_{KR_{isc}} \cdot [KR_{mdS^*}] \\
&\quad - k_{KR_{mdS^*}deg} \cdot [KR_{mdS^*}] \\
\frac{d[KR_{mdT^*}]}{dt} &= k_{KR_{isc}} \cdot [KR_{mdS^*}] - k_{KR_{nrd}} \cdot [KR_{mdT^*}] \\
&\quad - k_{KR_{SOXd1}} \cdot [KR_{mdT^*}] \\
&\quad - k_{KR_{SOXd2}} \cdot [KR_{mdT^*}] \\
&\quad - k_{KR_{mdT^*}deg} \cdot [KR_{mdT^*}] \\
\frac{d[SOX]}{dt} &= k_{KR_{SOXd1}} \cdot [KR_{mdT^*}] + k_{KR_{SOXd2}} \\
&\quad \cdot [KR_{mdT^*}] - \frac{d[SOX_{sod}]}{dt} \\
\frac{d[SOX_{sod}]}{dt} &= k_{SOD} \cdot V_{maxSOD} \cdot \frac{[SOX]}{K_m + [SOX]}
\end{aligned}$$

# Bacteria-killing KillerRed Model

| $k$ | Est_P | #S_S | #T_S | Avg_T(s) | Tot_T(s) | $k$ | Est_P | #S_S | #T_S | Avg_T(s) | Tot_T(s) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 | 0.544 | 8951 | 16452 | 0.074 | 1219.38 | 8 | 0.004 | 0 | 240 | 0.004 | 0.88 |
| 6 | 0.247 | 3045 | 12336 | 0.969 | 11957.12 | 9 | 0.004 | 0 | 240 | 0.012 | 2.97 |
| 7 | 0.096 | 559 | 5808 | 5.470 | 31770.36 | 10 | 0.004 | 0 | 240 | 0.013 | 3.18 |

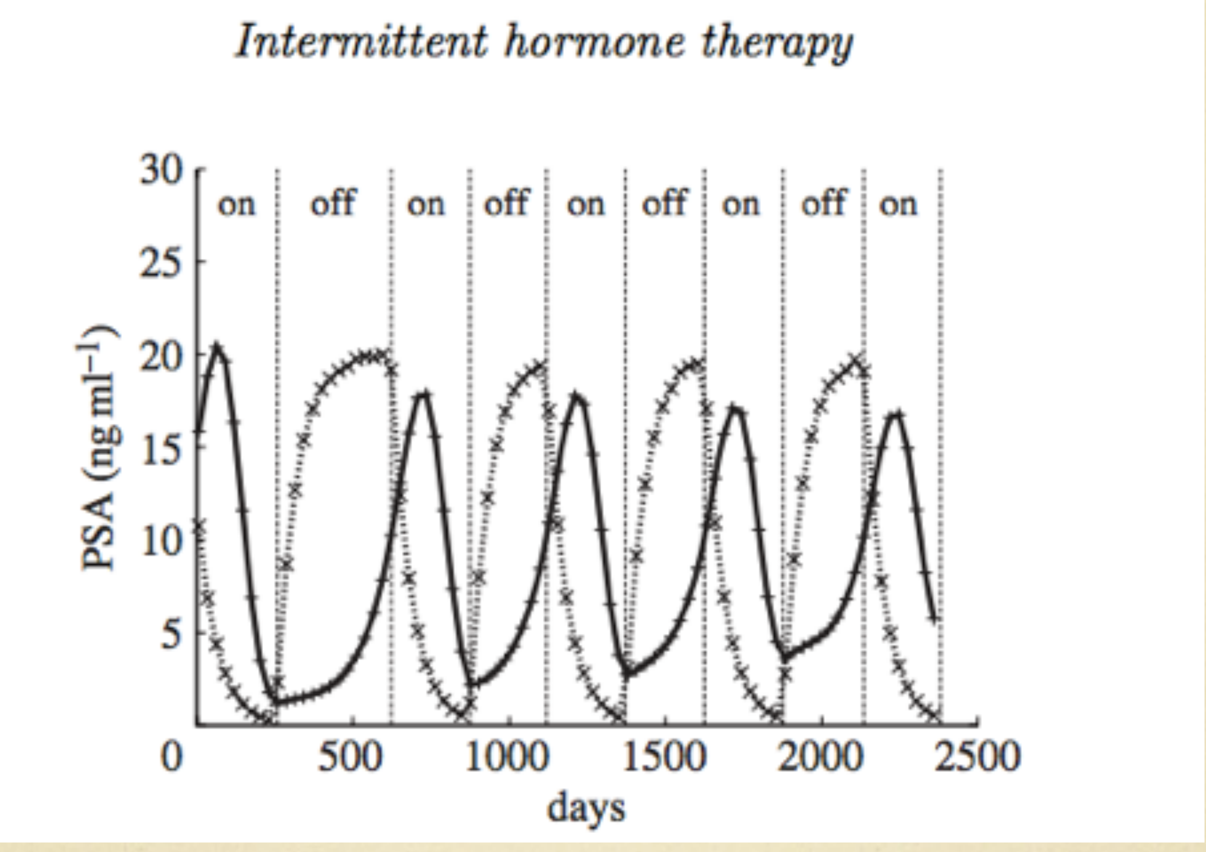
Table 3: Results for the 11-mode killerred model.

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| $t_{lightON}$ (t.u.) | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| $t_{total}$ (t.u.) | 16 | 17.2 | 18.5 | 20 | 21.3 | 22.7 | 23.5 | 24.1 | 25 | 30 |
| $t_{lightOFF_1}$ (t.u.) | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| **killed bacteria cells** | failed | failed | failed | succ | succ | succ | succ | succ | succ | succ |
| $t_{rmIPTG_3}$ (t.u.) | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| **killed bacteria cells** | succ | succ | succ | succ | succ | succ | succ | succ | succ | succ |
| $SOX_{thres}$ (M) | 1e-4 | 2e-4 | 3e-4 | 4e-4 | 5e-4 | 6e-4 | 7e-4 | 8e-4 | 9e-4 | 1e-3 |
| $t_{total}$ (t.u.) | 5.1 | 5.2 | 5.4 | 17 | 19 | 48 | 61 | 71 | 36 | 42 |

Table 4: Formal analysis results for our KillerRed hybrid model

#S_S = number of δ-sat samples, #T_S = total number of samples, Est_P = estimated probability of property, Avg_T(s) = average CPU time of each sample in seconds, and Tot_T(s) = total CPU time for all samples in seconds.

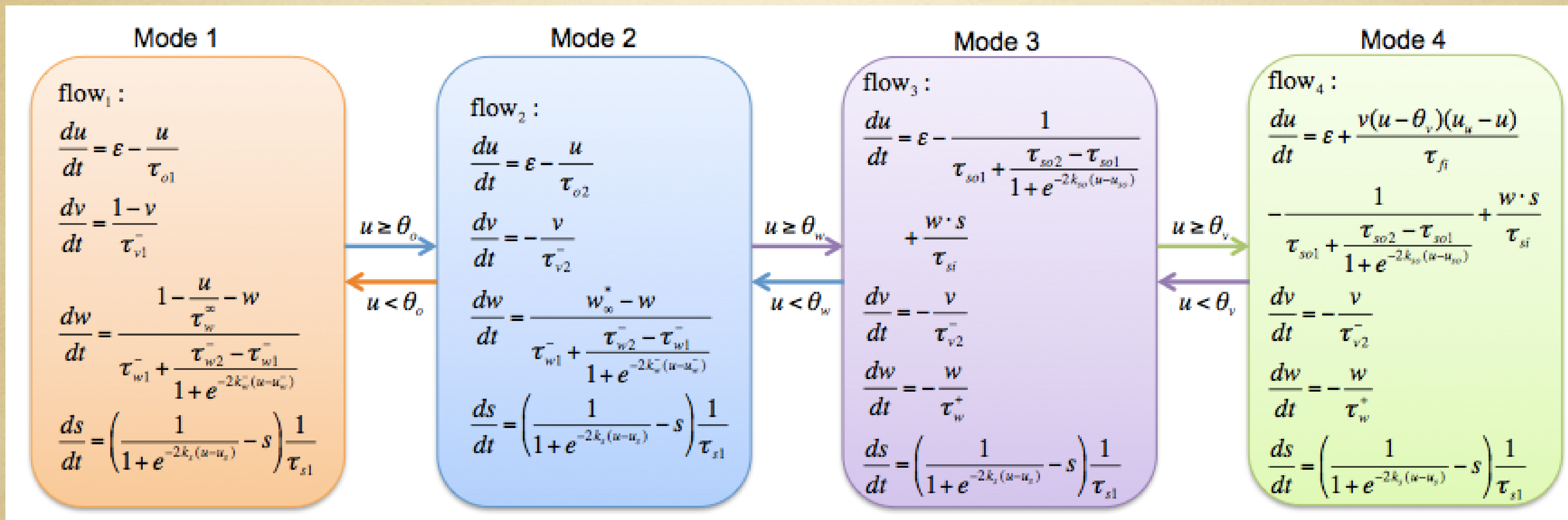
# Prostate Cancer treatment




| Model | #RVs | $r_0$ | $r_1$ | Est_P | #S_S | #T_S | Avg_T(s) | Tot_T(s) |
|---|---|---|---|---|---|---|---|---|
| PCT1 | 6 | 5.0 | 10.0 | 0.496 | 8226 | 16584 | 0.596 | 9892 |
| PCT2 | 6 | 7.0 | 11.0 | 0.994 | 335 | 336 | 54.307 | 18247 |
| PCT3 | 6 | 10.0 | 15.0 | 0.996 | 240 | 240 | 506.5 | 121560 |

Table 2: Results for the 2-mode prostate cancer treatment model ($k = 2$). For each sample generated, *SReach* analyzed systems with 41 variables and 10 ODEs in the unfolded SMT formulae.

# Atrial Fibrillation Model




| Model | #RVs | EPI_TO1 | EPI_TO2 | #S_S | #T_S | Est_P | A_T(s) | T_T(s) |
|---|---|---|---|---|---|---|---|---|
| Cd_to1_s | 1 | U(6.1e-3, 7e-3) | 6 | 240 | 240 | 0.996 | 0.270 | 64.80 |
| Cd_to1_uns | 1 | U(5.5e-3, 5.9e-3) | 6 | 0 | 240 | 0.004 | 0.042 | 10.08 |
| Cd_to2_s | 1 | 400 | U(0.131, 6) | 240 | 240 | 0.996 | 0.231 | 55.36 |
| Cd_to2_uns | 1 | 400 | U(0.1, 0.129) | 0 | 240 | 0.004 | 0.038 | 9.15 |
| Cd_to12_s | 2 | N(400, 1e-4) | N(6, 1e-4) | 240 | 240 | 0.996 | 0.091 | 21.87 |
| Cd_to12_uns | 2 | N(5.5e-3, 10e-6) | N(0.11, 10e-5) | 0 | 240 | 0.004 | 0.037 | 8.90 |

Table 1: Results for the 4-mode atrial fibrillation model ($k = 3$). For each sample generated, *SReach* analyzed systems with 62 variables and 24 ODEs in the unfolded SMT formulae. #RVs = number of random variables in the model, #S_S = number of $\delta$-sat samples, #T_S = total number of samples, Est_P = estimated probability of property, A_T(s) = average CPU time of each sample in seconds, and T_T(s) = total CPU time for all samples in seconds. Note that, we use the same notations in the remaining tables.

# Experimental results

| Benchmark | #Ms | K | #ODEs | #Vs | #RVs | $\delta$ | Est_P | #S_S | #T_S | A_T(s) | T_T(s) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| BBK1 | 1 | 1 | 2 | 14 | 3 | 0.001 | 0.754 | 5372 | 7126 | 0.086 | 612.836 |
| BBK5 | 1 | 5 | 2 | 38 | 3 | 0.001 | 0.059 | 209 | 3628 | 0.253 | 917.884 |
| BBwDv1 | 2 | 2 | 4 | 20 | 4 | 0.001 | 0.208 | 2206 | 10919 | 0.080 | 873.522 |
| BBwDv2K2 | 2 | 2 | 4 | 20 | 3 | 0.001 | 0.845 | 7330 | 8669 | 0.209 | 1811.821 |
| BBwDv2K8 | 2 | 8 | 4 | 56 | 3 | 0.001 | 0.207 | 2259 | 10901 | 0.858 | 9353.058 |
| Tld | 2 | 7 | 2 | 33 | 4 | 0.001 | 0.996 | 227 | 227 | 0.213 | 48.351 |
| Ted | 2 | 7 | 4 | 50 | 4 | 0.001 | 0.996 | 227 | 227 | 12.839 | 2914.448 |
| DTldK3 | 2 | 3 | 4 | 26 | 2 | 0.001 | 0.996 | 227 | 227 | 0.382 | 86.714 |
| DTldK5 | 2 | 5 | 4 | 38 | 2 | 0.001 | 0.161 | 1442 | 8961 | 0.280 | 2509.078 |
| W4mv1 | 4 | 3 | 8 | 26 | 6 | 0.001 | 0.381 | 5953 | 15639 | 0.238 | 3722.082 |
| W4mv2K3 | 4 | 3 | 8 | 26 | 6 | 0.001 | 0.996 | 227 | 227 | 0.673 | 152.771 |
| W4mv2K7 | 4 | 7 | 8 | 50 | 6 | 0.001 | 0.004 | 0 | 227 | 0.120 | 27.240 |
| DWK1 | 2 | 1 | 4 | 14 | 5 | 0.001 | 0.996 | 227 | 227 | 0.171 | 38.817 |
| DWK3 | 2 | 3 | 4 | 26 | 5 | 0.001 | 0.996 | 227 | 227 | 0.215 | 48.806 |
| DWK9 | 2 | 9 | 4 | 62 | 5 | 0.001 | 0.996 | 227 | 227 | 5.144 | 1167.688 |
| Que | 3 | 2 | 3 | 13 | 4 | 0.001 | 0.228 | 2662 | 11677 | 0.095 | 1109.315 |
| 3dOsc | 3 | 2 | 18 | 48 | 2 | 0.001 | 0.996 | 227 | 227 | 8.273 | 1877.969 |
| QuadC | 1 | 0 | 14 | 44 | 6 | 0.001 | 0.996 | 227 | 227 | 825.641 | 187420.507 |
| exPHA01 | 2 | 2 | 4 | 20 | 2 | 0.001 | 0.524 | 345 | 658 | 5.01 | 3295.82 |
| exPHA02 | 2 | 3 | 2 | 17 | 1 | 0.001 | 0.900 | 5361 | 5953 | 0.0004 | 2.35 |
| KRk5 | 6 | 5 | 84 | 194 | 2 | 0.001 | 0.544 | 8946 | 16457 | 0.122 | 2015.64 |
| KRk6 | 8 | 6 | 112 | 224 | 6 | 0.001 | 0.246 | 2032 | 8263 | 1.385 | 11444.22 |
| KRk7 | 10 | 7 | 150 | 271 | 6 | 0.001 | 0.096 | 558 | 5795 | 16.275 | 94311.18 |
| KRk8 | 7 | 8 | 105 | 303 | 6 | 0.001 | 0.004 | 0 | 227 | 0.003 | 0.58 |
| KRk9 | 9 | 9 | 135 | 335 | 6 | 0.001 | 0.004 | 0 | 227 | 0.015 | 3.43 |
| KRk10 | 11 | 10 | 165 | 367 | 6 | 0.001 | 0.004 | 0 | 227 | 0.026 | 5.92 |

Table 5: #Ms = number of modes, K indicates the unfolding steps, #ODEs = number of ODEs in the unfolded formulae, #Vs = number of total variables in the unfolded formulae, #RVs = number of random variables in the model, $\delta$ = precision used in *dReach*.

# Future work

- Apply SReach to real-world models other than biological models
- Stochastic Hybrid Systems with stochastic flows: stochastic differential equations
    - introduce a type of constraints for SDEs, design a theory solver handling this type of constraints, then integrate with dReal solver.

# Thanks!

- https://github.com/dreal/SReach
- Questions?