

CMACS/AVACS Workshop

Parameter Identification using δ -Decisions for Hybrid Systems in Biology

Bing Liu

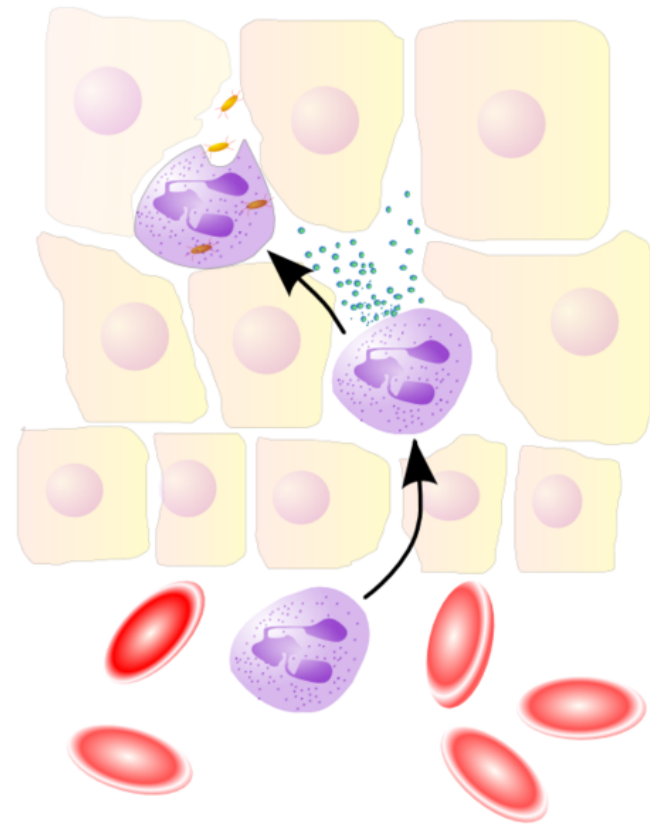
Joint work with

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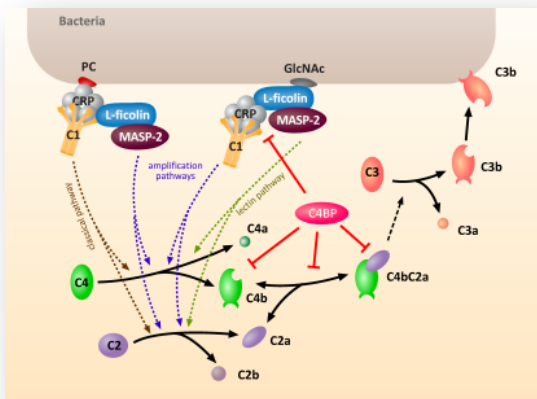
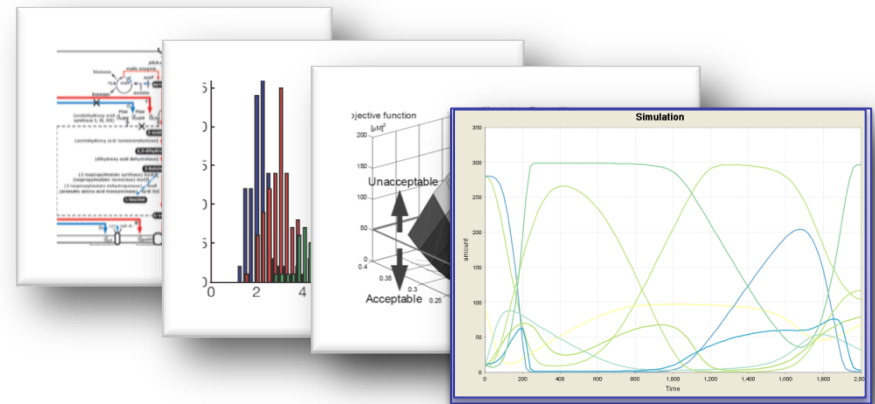
Biological System

The Inner Life of the Cell

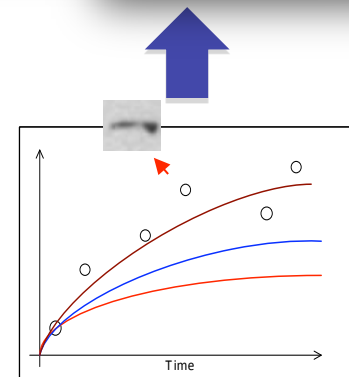


Computational Modeling

- Building a model
 - Structure
 - Calibration (parameter estimation)
 - Validation
- Performing analysis

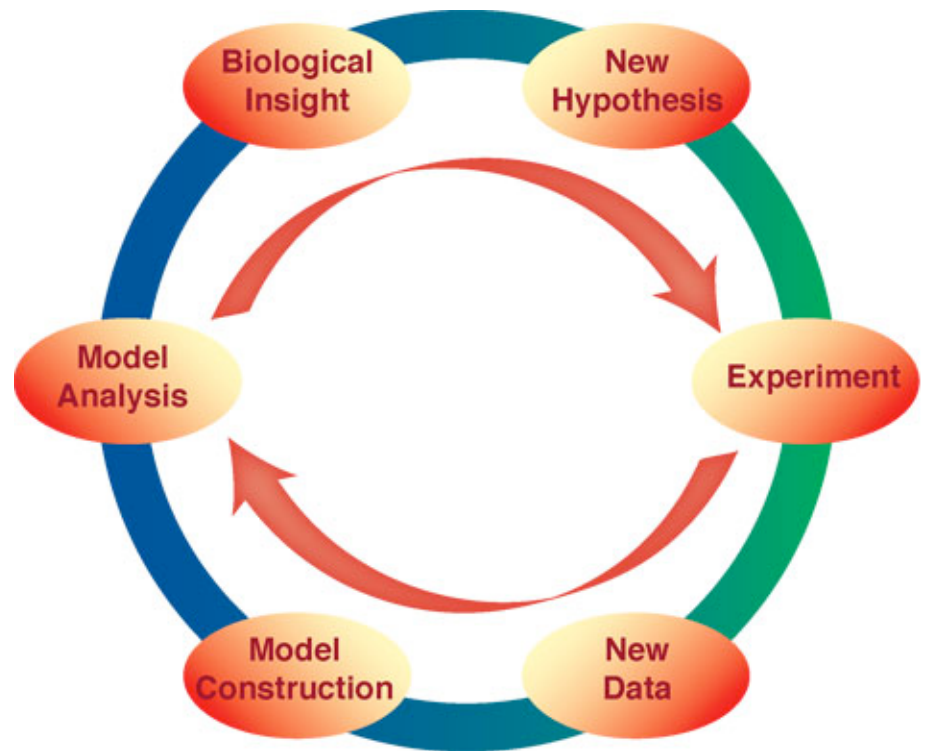


$$\begin{aligned}
 \frac{dc_1}{dt} &= -k_1 \cdot c_1 \cdot c_2 + k_2 \cdot c_3 \\
 \frac{dc_2}{dt} &= -k_1 \cdot c_1 \cdot c_2 + k_2 \cdot c_3 + k_{17} \cdot c_{18} + k_{11} \cdot c_{11} \\
 \frac{dc_3}{dt} &= k_1 \cdot c_1 \cdot c_2 - k_2 \cdot c_3 - k_3 \cdot c_3 \cdot c_4 + k_4 \cdot c_5 \\
 \frac{dc_4}{dt} &= -k_3 \cdot c_3 \cdot c_4 + k_4 \cdot c_5 + k_{11} \cdot c_{11} + k_{20} \cdot c_{21} \\
 \frac{dc_5}{dt} &= k_3 \cdot c_3 \cdot c_4 - k_4 \cdot c_5 - k_5 \cdot c_5 \cdot c_6 + k_6 \cdot c_7 \\
 \frac{dc_6}{dt} &= -k_5 \cdot c_5 \cdot c_6 + k_6 \cdot c_7 + k_{11} \cdot c_{11} + k_{20} \cdot c_{21} \\
 \frac{dc_7}{dt} &= k_5 \cdot c_5 \cdot c_6 - k_6 \cdot c_7 - k_7 \cdot c_7 \cdot c_8 + k_8 \cdot c_9 \\
 \frac{dc_8}{dt} &= -k_7 \cdot c_7 \cdot c_8 + k_8 \cdot c_9 + k_{11} \cdot c_{11} + k_{20} \cdot c_{21} \\
 \frac{dc_9}{dt} &= k_7 \cdot c_7 \cdot c_8 - k_8 \cdot c_9 - k_9 \cdot c_9 \cdot c_{10} + k_{10} \cdot c_{11} \\
 &\quad - k_{15} \cdot c_9 \cdot c_{17} + k_{16} \cdot c_{18}
 \end{aligned}$$



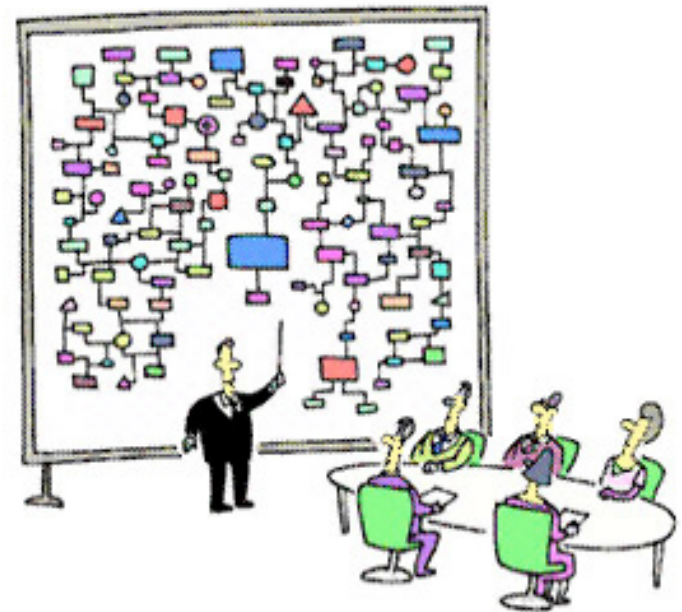
Computational Modeling

- Building a model
 - Structure
 - Calibration
(parameter estimation)
 - Validation
- Performing analysis



Computational Modeling

- Formalisms
 - Differential equations
 - Boolean network
 - Petri nets
 - Rule-based models
 -
- **Multi-mode?**

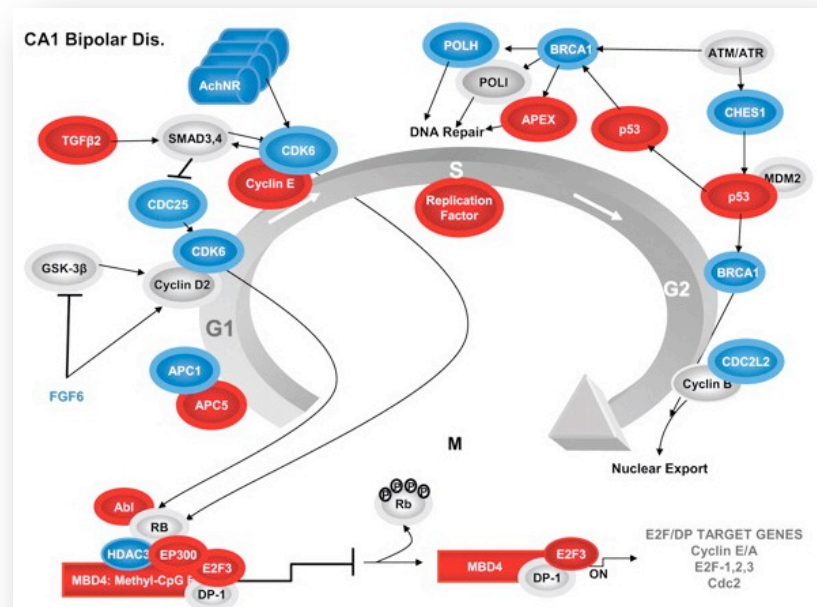
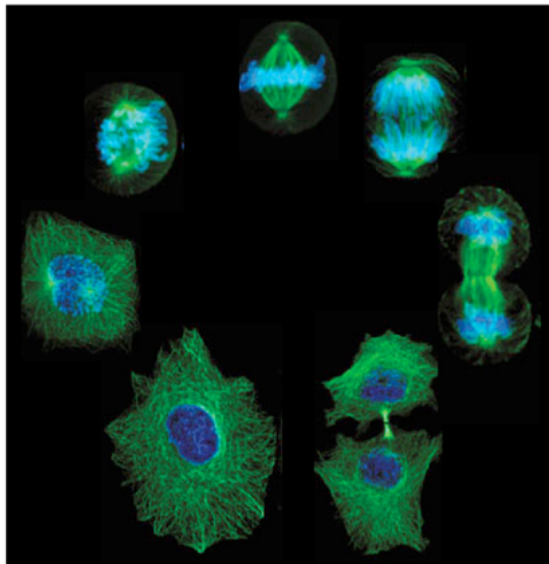


"And that's why we need a computer."

Hybrid Systems

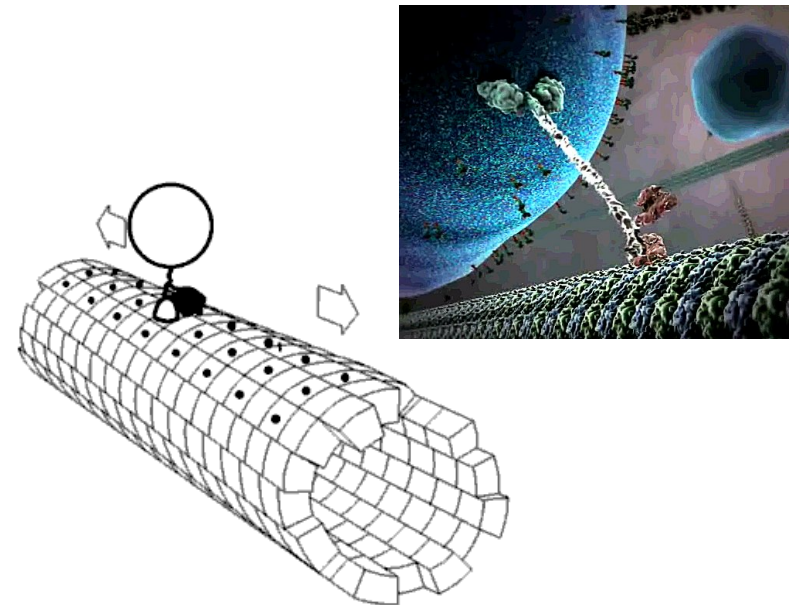
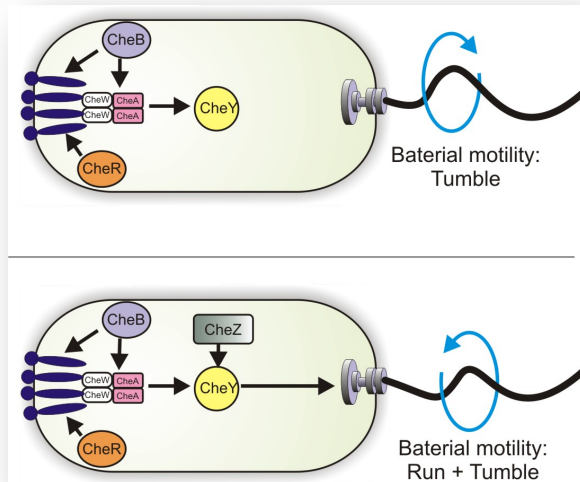
- Activation of different networks at different stages
 - E.g. Cell cycle, Cell differentiation

Cell Cycle



Hybrid Systems

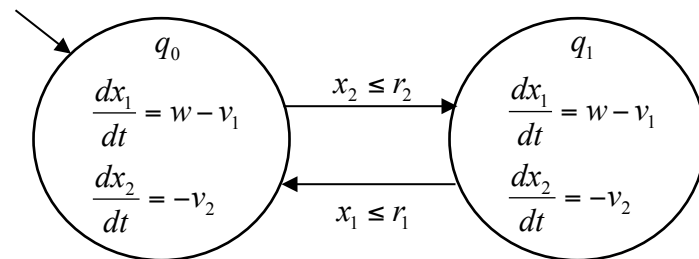
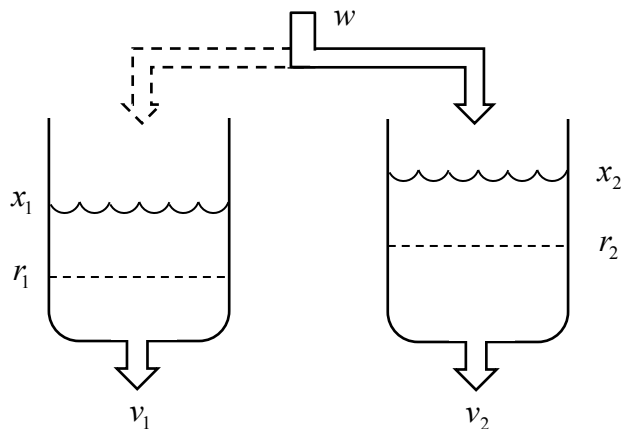
- More examples:
 - *E. coli* chemotaxis, kinesin walking, gene transcription, drug treatment,



Hybrid Systems

- Evolve in a **continuous** way in each mode
- Ruled by **discrete** transitions
- Hybrid automata

$$H = \langle X, Q, \text{flow}, \text{guard}, \text{reset}, \text{inv}, \text{init} \rangle$$



Hybrid Systems

$$H = \langle X, Q, \text{Init}, \text{Flow}, \text{Jump} \rangle$$

- A continuous space $X \subseteq \mathbf{R}^k$ and a finite set of modes Q
- $\text{Init} \subseteq Q \times X$: initial configurations
- Flow : continuous flows
 - Each mode q is equipped with differential equations

$$\frac{d\vec{x}}{dt} = f_q(\vec{x}, t)$$

- Jump : discrete
 - The systems can be switched from q to q' , resetting modes and variables

Hurdles

- How to answer questions such as:
 - Which model structure is better?
 - What conditions may lead to a desired state?
 - How to control the system to avoid bad states?
 -
- **Parameter synthesis** problem
- Analyzing nonlinear hybrid automata is challenging
 - even simple reachability questions can be **undecidable**

Our Approach

- Use **δ -complete decision procedures** to tackle the parameter synthesis problem for nonlinear hybrid models
 - Encode a parameter synthesis problem as a first-order formula over the reals
 - Perform bounded model checking
 - Employ an interval constraints propagation (ICP) based algorithm to identify the resulting parameters

Delta-Decisions

- A decision procedure using numerical techniques (with an error bound δ):
 - φ is false
 - $\varphi^{-\delta}$ is true
- The delta-decision problem is decidable for bounded first-order formulas over arbitrary Type 2 computable functions
 - exp, sin, etc, and Lipschitz-continuous ODEs

δ -Complete Bounded Model Checking

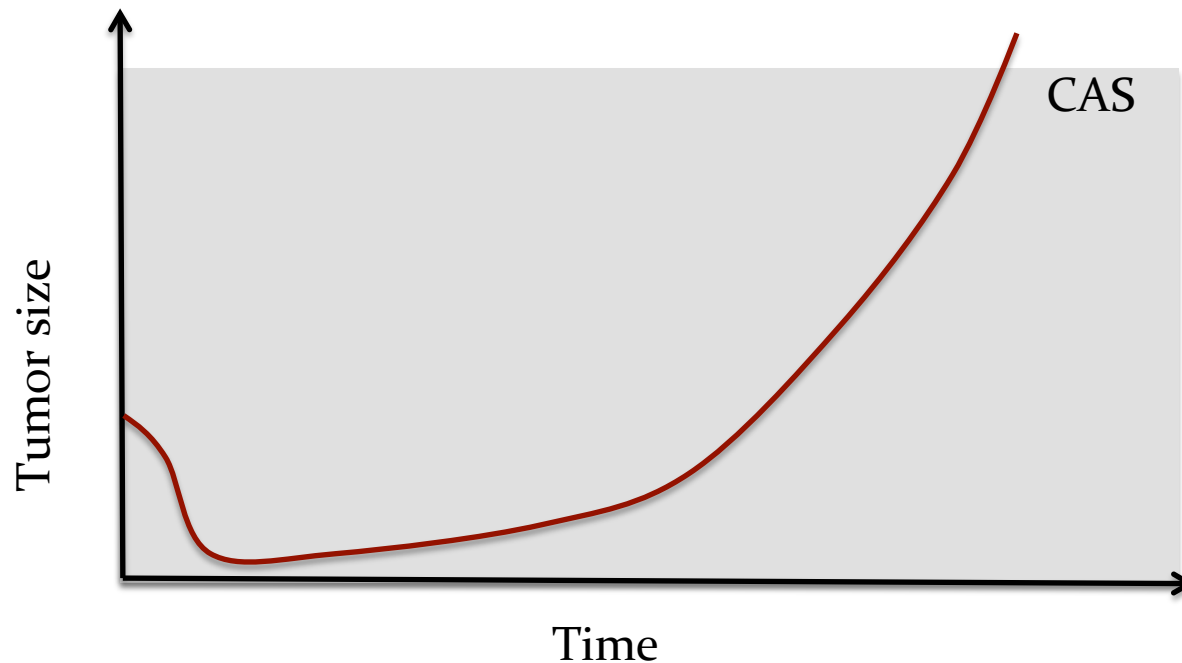
- Practical tools:
 - dReal and dReach
 - DPLL(T), interval arithmetic, constraint solving, reliable integration, etc.

Case Studies - I

- Prostate cancer
 - Second leading cause of cancer-related deaths among men in US
- Hormone therapy
 - Androgen deprivation
 - Continuous androgen suppression (CAS)
 - Intermittent androgen suppression (IAS)

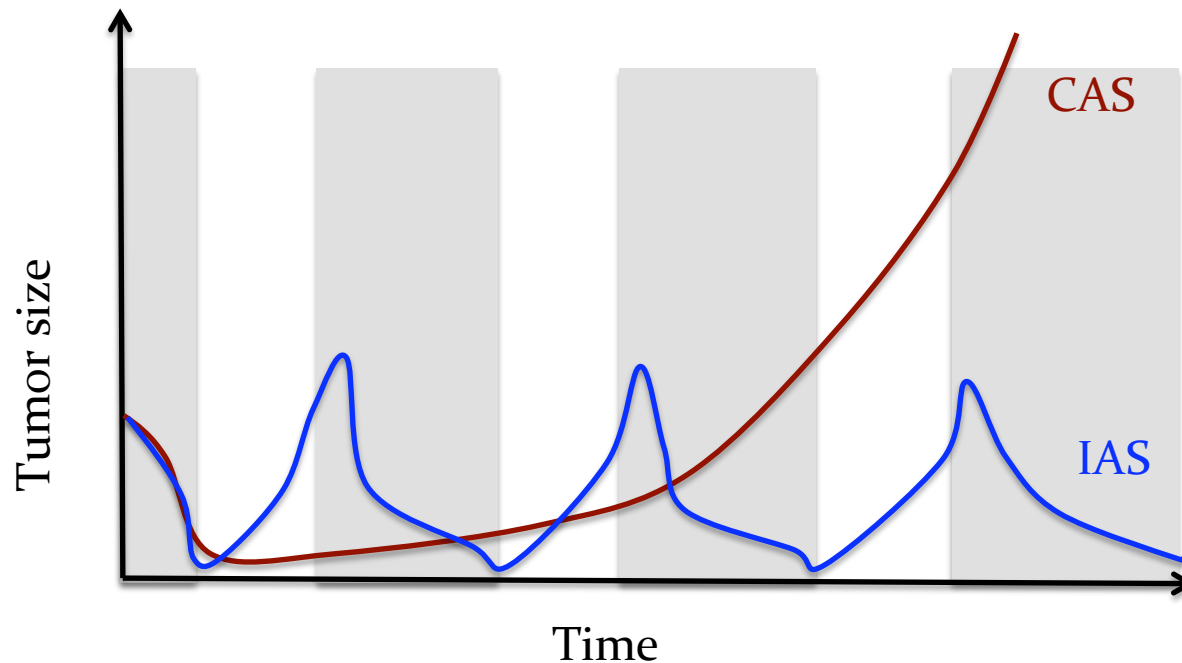
Continuous Androgen Suppression

- Side effects: anemia, osteoporosis, impotence, etc.
- Relapse after a median duration of 18-24 months, due to the proliferation of androgen independent (AI) cancer cells.



Intermittent Androgen Suppression

- Reduce side effects
- May delay the time to relapse
 - Avoid emergence of AI cells



Intermittent Androgen Suppression

- Clinical phase II and III trials confirm its advantage in terms of quality of life and cost
- For time to relapse and cancer-specific survival, its advantage depends on individual patients and the treatment scheme
- How to design a personalized treatment scheme for each individual patient?

Model

- Population of AD cells, AI cells, serum androgen concentration, PSA level (Ideta et al. 2008)

jump_{2→1} :

$$x + y \geq r_1 \wedge \frac{dx}{dt} + \frac{dy}{dt} > 0$$

flow₁ : **Mode 1 (on-treatment)**

$$\frac{dx}{dt} = \left(\alpha_x \left(k_1 + \frac{(1-k_1)z}{z+k_2} \right) - \beta_x \left(k_3 + \frac{(1-k_3)z}{z+k_4} \right) - m_1 \left(1 - \frac{z}{z_0} \right) \right) x$$

$$\frac{dy}{dt} = m_1 \left(1 - \frac{z}{z_0} \right) x + \left(\alpha_y \left(1 - d \frac{z}{z_0} \right) - \beta_y \right) y$$

$$\frac{dz}{dt} = \frac{-z}{\tau}$$

$$\frac{dv}{dt} = \left(\alpha_x \left(k_1 + \frac{(1-k_1)z}{z+k_2} \right) - \beta_x \left(k_3 + \frac{(1-k_3)z}{z+k_4} \right) - m_1 \left(1 - \frac{z}{z_0} \right) \right) x$$

$$+ m_1 \left(1 - \frac{z}{z_0} \right) x + \left(\alpha_y \left(1 - d \frac{z}{z_0} \right) - \beta_y \right) y$$

flow₂ : **Mode 2 (off-treatment)**

$$\frac{dx}{dt} = \left(\alpha_x \left(k_1 + \frac{(1-k_1)z}{z+k_2} \right) - \beta_x \left(k_3 + \frac{(1-k_3)z}{z+k_4} \right) - m_1 \left(1 - \frac{z}{z_0} \right) \right) x$$

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$$\frac{dz}{dt} = \frac{z_0 - z}{\tau}$$

$$\frac{dv}{dt} = \left(\alpha_x \left(k_1 + \frac{(1-k_1)z}{z+k_2} \right) - \beta_x \left(k_3 + \frac{(1-k_3)z}{z+k_4} \right) - m_1 \left(1 - \frac{z}{z_0} \right) \right) x$$

$$+ m_1 \left(1 - \frac{z}{z_0} \right) x + \left(\alpha_y \left(1 - d \frac{z}{z_0} \right) - \beta_y \right) y$$

jump_{1→2} :

$$x + y \leq r_0 \wedge \frac{dx}{dt} + \frac{dy}{dt} < 0$$

Model

- Proliferation, apoptosis, mutation rates
- Treatment thresholds: r_0 and r_1

jump_{2→1} :

$$x + y \geq r_1 \wedge \frac{dx}{dt} + \frac{dy}{dt} > 0$$

flow₁ : **Mode 1 (on-treatment)**

$$\frac{dx}{dt} = \left(\alpha_x \left(k_1 + \frac{(1-k_1)z}{z+k_2} \right) - \beta_x \left(k_3 + \frac{(1-k_3)z}{z+k_4} \right) - m_1 \left(1 - \frac{z}{z_0} \right) \right) x$$

$$\frac{dy}{dt} = m_1 \left(1 - \frac{z}{z_0} \right) x + \left(\alpha_y \left(1 - d \frac{z}{z_0} \right) - \beta_y \right) y$$

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$$\frac{dv}{dt} = \left(\alpha_x \left(k_1 + \frac{(1-k_1)z}{z+k_2} \right) - \beta_x \left(k_3 + \frac{(1-k_3)z}{z+k_4} \right) - m_1 \left(1 - \frac{z}{z_0} \right) \right) x$$

$$+ m_1 \left(1 - \frac{z}{z_0} \right) x + \left(\alpha_y \left(1 - d \frac{z}{z_0} \right) - \beta_y \right) y$$

flow₂ : **Mode 2 (off-treatment)**

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$$+ m_1 \left(1 - \frac{z}{z_0} \right) x + \left(\alpha_y \left(1 - d \frac{z}{z_0} \right) - \beta_y \right) y$$

jump_{1→2} :

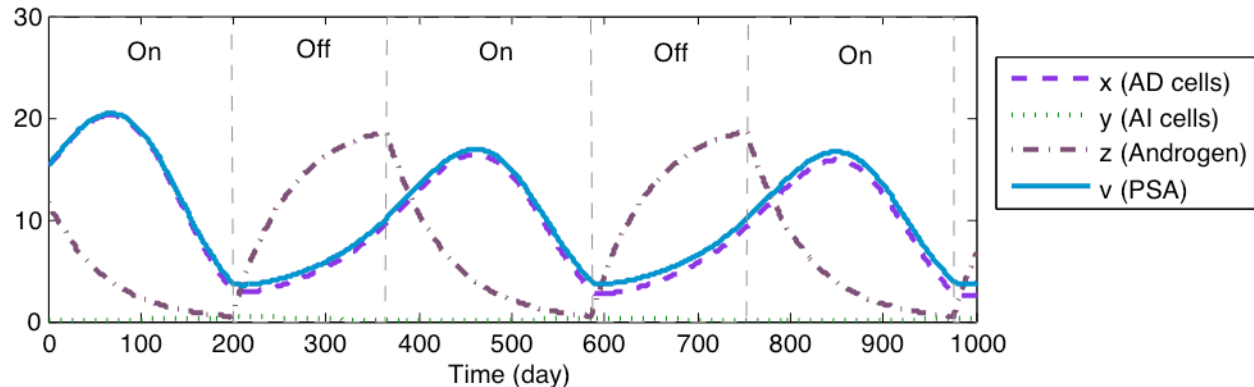
$$x + y \leq r_0 \wedge \frac{dx}{dt} + \frac{dy}{dt} < 0$$

Model Selection

- Hypothesis 1
 - AI cells grow at the constant rate independent of the androgen level
- Hypothesis 2
 - AI cells do not grow when the androgen level is normal
- Hypothesis 3
 - AI cells decrease when the androgen level is normal

Model Selection

- Observation
 - When $r_o = 4$ (ng ml⁻¹) and $r_i = 10$ (ng ml⁻¹), cancer relapse can be avoided within 1000 days
 - Define cancer relapse: PSA level > 30 ng ml⁻¹
- Bounded model checking
 - Property: $900 \leq \tau \leq 1000 \wedge v \leq 30$
 - H₁: unsat
 - H₂: unsat
 - **H₃: sat**

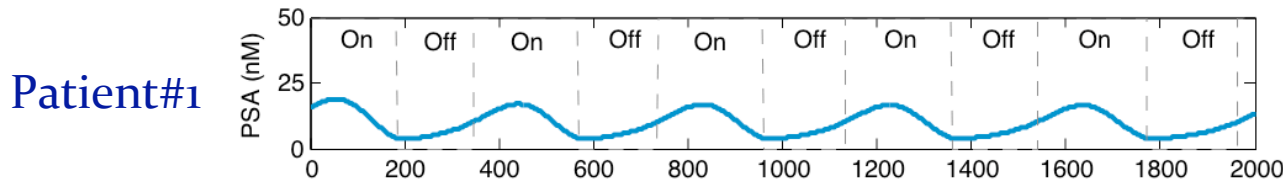


Personalized Therapy Design

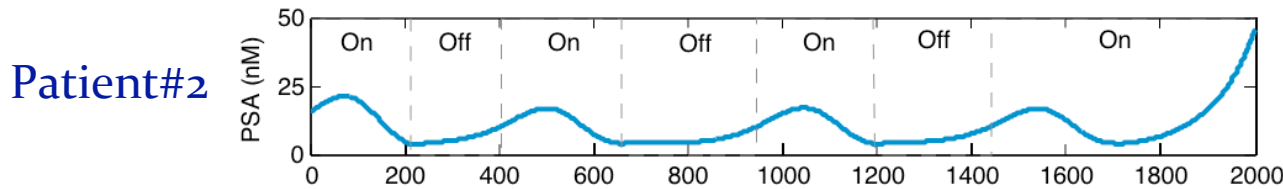
- Personalized parameters
 - α_y - the proliferation rate of AI cells
 - β_y - the apoptosis rate of AI cells
 - m_1 - the mutation rate from AD to AI cells
 - $z(o)$ - the initial androgen level

Personalized Therapy Design

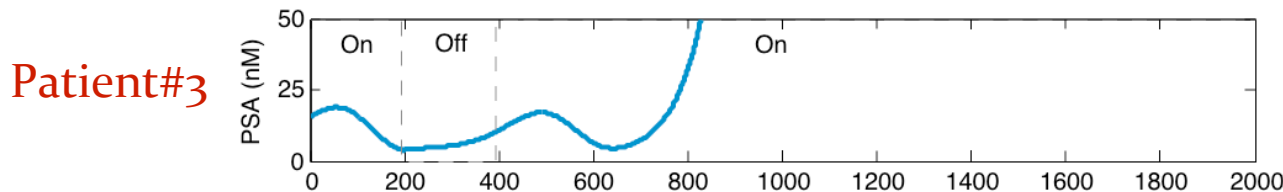
- Different patients may respond differently to the same treatment scheme ($r_o = 4$ and $r_i = 10$)



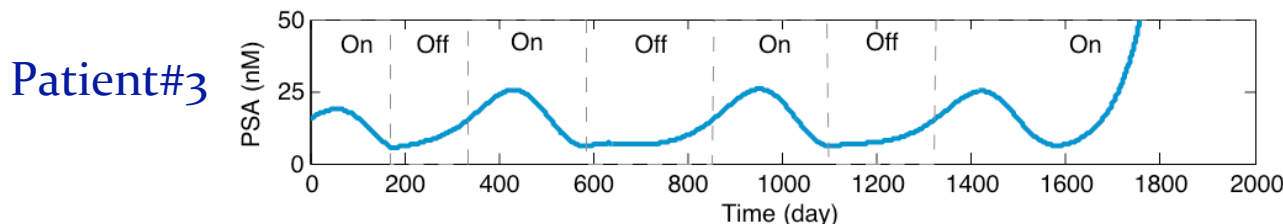
avoided ($r_o = 4$ and $r_i = 10$)



delayed ($r_o = 4$ and $r_i = 10$)



relapse ($r_o = 4$ and $r_i = 10$)



delayed ($r_o = 5$ and $r_i = 16$)

Personalized Therapy Design

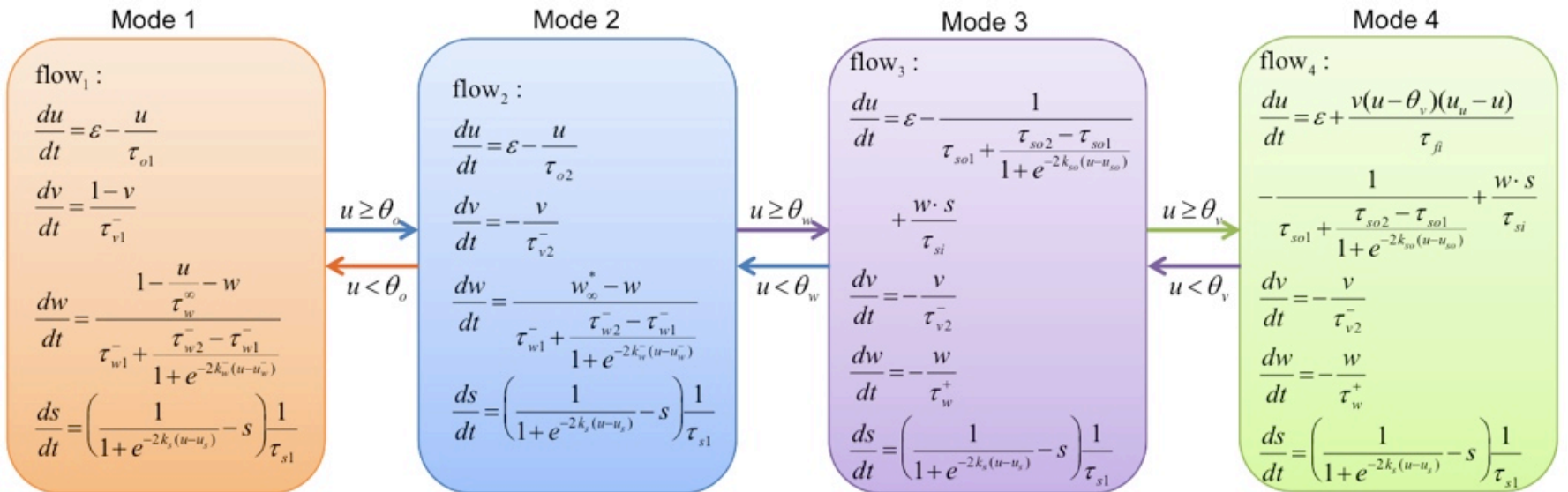
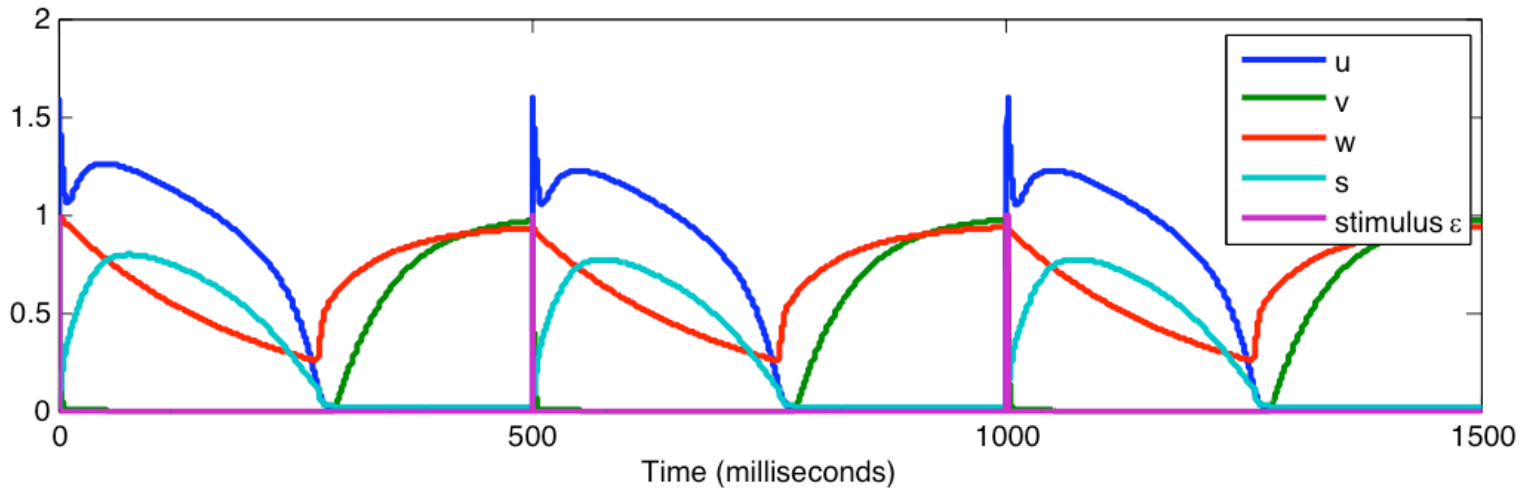
- Apply IAS therapy to a patient for 1-2 cycles and measure PSA time serials
- Estimate personalized parameters by fitting PSA data
- Given r_o in $[0,8)$ and r_i in $[8,15]$, verify if H3 can reach $900 \leq tau \leq 1000 \wedge v \leq 30$ (i.e. no relapse)
 - False: androgen suppression does not work
 - True: feasible values for r_o and r_i will be returned.

Personalized Therapy Design

- Patients dataset:
 - 109 patients
 - Phase II clinical trials (Bruchovsky et al, Cancer, 2007)
- Partial results:

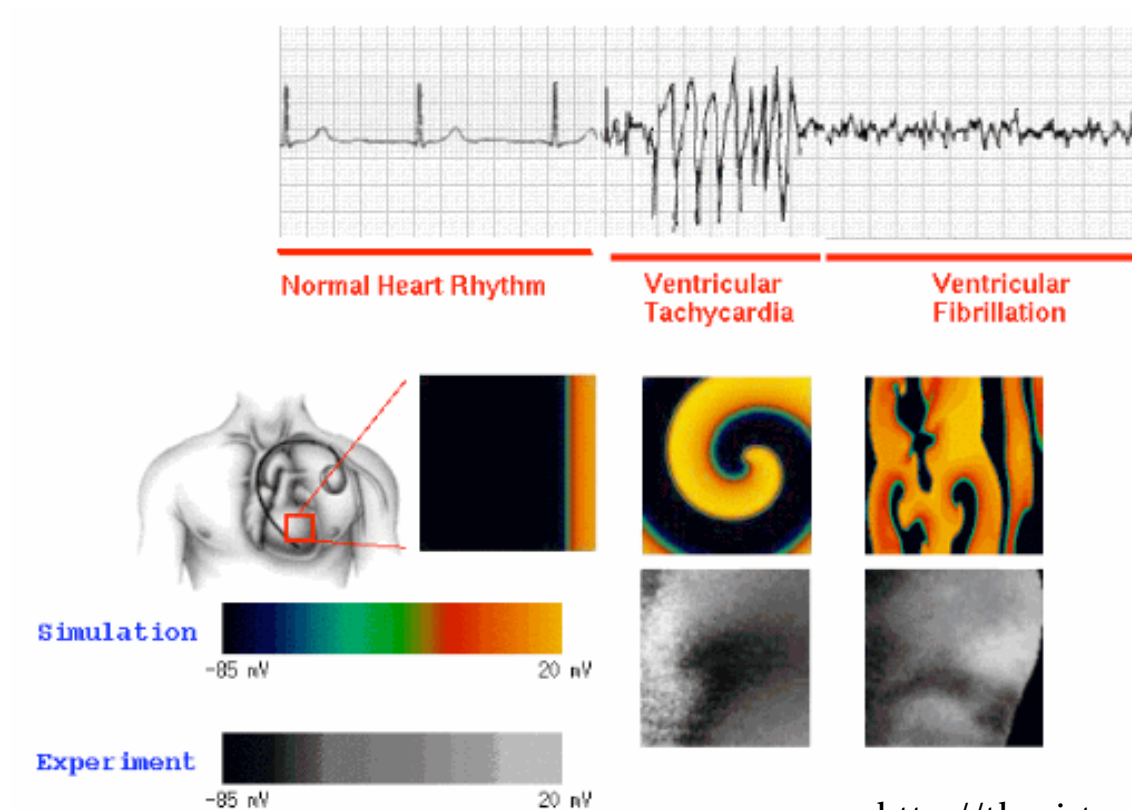
Case Studies - II

- Cardiac cell
 - Minimal Resistor Model (Fenton et al, J Theor Biol, 2008)
 - The electrical activity are governed by opening and closing of ion channels



Cardiac Disorders

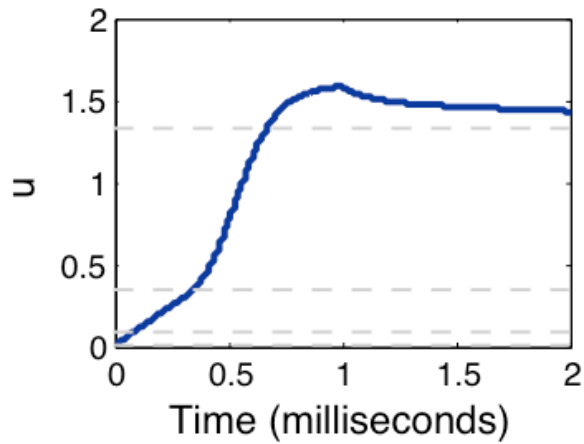
- When the cardiac cell loses its excitability, it will lead to disorders such as ventricular tachycardia and fibrillation



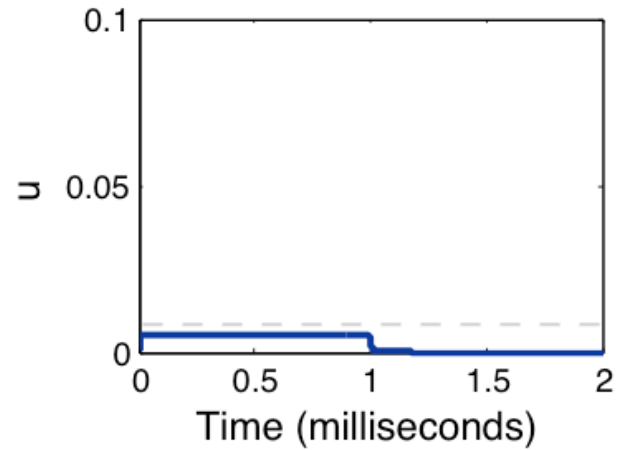
Cardiac Disorders

- When the cardiac cell loses its excitability, it will lead to disorders such as ventricular tachycardia and fibrillation
- Under what circumstances, a cardiac cell will fail to generate a successful AP (i.e. globally $u < \theta_v$)?
 - Related parameter ranges identified by Grosu et al. CAV 2011 (**linear approximation**)
 - We answer this by identifying the ranges for parameters in the **original** nonlinear model

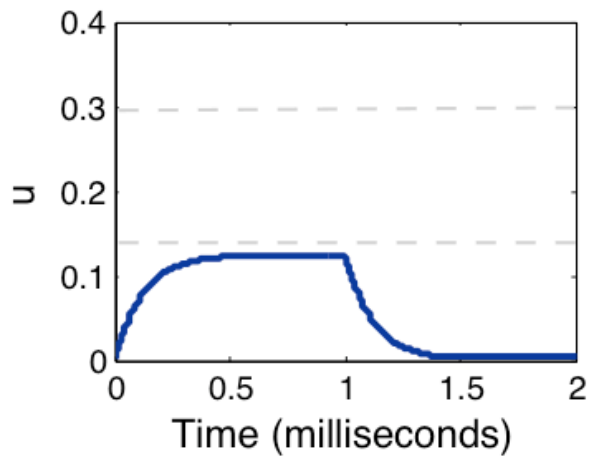
$$\tau_{o1} \in (0, 0.006) \vee \tau_{o2} \in (0, 0.13) \vee 6.2\tau_{o2} + \tau_{o1} \geq 9.9$$



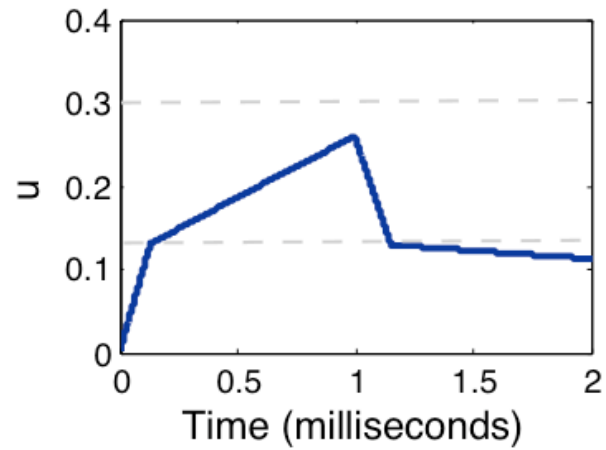
(a)



(b)



(c)



(d)

Summary

- A delta-decision based framework for parameter identification
 - Model selection
 - Therapy optimization
 - Diseased-related conditions identification
- What's next
 - More analysis for cardiac cell model
 - Parameter estimation
 - DNA damage induced cellular senescence