Inverse Methods in Systems Biology

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Cells are complex systems



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Cells are complex systems



In the face of continuously changing environments and its state, cells need to respond appropriately:

Cells are complex systems



- In the face of continuously changing environments and its state, cells need to respond appropriately:
- inputs: nutrients, repellants, heat shock, DNA damage, ...
- responses: movement, growth, protein production, death

 Complex networks of genes and pathways are involved in mediating the various inputs to the appropriate responses



Signal transduction network: Hanahan and Weinberg, Cell (2000)

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Forward Problems

• Consider ODE models: $\dot{y}(t) = f(y(t),q)$

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Forward Problems

- Consider ODE models: $\dot{y}(t) = f(y(t),q)$
- The Forward analysis may include:
 - numerical integration for a set of given parameters
 - sensitivity analysis
 - bifurcation analysis

reactions $\rightarrow \frac{dy}{dt} = f(y,q) \rightarrow \{y(t), \text{ bifurcations}\}$



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In Inverse Problems, one looks for the causes of observed and desired effects

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Parameter identification from time-course data

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- Parameter identification from time-course data
- Inverse bifurcation: infer model mechanisms that can achieve the desired bifurcation behaviors
 - maximize the parameter domain for oscillations
 - place bifurcation points at the desired locations

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 - solutions may not exist or unique
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- Inverse problems are typically *ill-posed*:
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- To numerically tackle inverse problems, regularization strategies are needed

Forward operator equation:

$$F(q) = y$$

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Inverse problem: determining q from y

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- While stabilizing ill-posed problems, regularization brings bias to the solution
- For biological problems, usually want to find solutions that are *sparse*, i.e., having as few non-zero entries as possible: Ockam's razor

Sparsity-Promoting Regularization

► As the regularization term, consider smoothed functionals $\mathbb{R}^n \to \mathbb{R}$: $l_{p,\varepsilon}(q) = \sum_i (q_i^2 + \varepsilon)^{p/2}$

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- ► Convex only within the box $\{q : |q_i| < \sqrt{\varepsilon}, 0 < i \le n\}$
- Recent applications of sparse solutions using non-convex penalty:
 - Exact reconstruction of sparse signals via nonconvex minimization, R. Chartrand (2007)
 - Compressive sensing using l₁ re-weighting, E. Candes, S. P. Boyd, M. Wakin *et al.* (2007)
 - Log-det heuristic for matrix rank minimization with applications to Hankel and Euclidean distance matrices, M. Fazel, H. Hindi and S. P Boyd (2003)



M. Swat, A. Kel, H. Herzel, Bioinformatics (2004)

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Which of the interactions play important roles in controlling the geometry of the bifurcation diagram?

Map various bifurcation phenotypes to parameter sets

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- Consider the following 3 modes of transformations of the nominal bifurcation diagram:



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 Inverse bifurcation problem: from conditions on bifurcation diagrams, infer the governing mechanisms

Inverse Bifurcation: effect of sparsity-promiting penalty



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Inverse Bifurcation: effect of sparsity-promiting penalty



Table: Result of hierarchical algorithm with $p = 0.1, \varepsilon = 10^{-4}$

Modification Case	Level $j = 1$	Level $j = 2$	Level $j = 3$
Elongating SN ₁ nose	$k_n \downarrow 14.3\%$	<u>k₃₄</u> ↑ 31.7%	$\phi_{\text{AP-1}} \downarrow 20.9\%$
	P •	$K_{m2} \uparrow 6.4\%$	¢ _{E2F1} ↑ 7.3%
Moving $SN_{1,2}$ to right	K_{m4} \uparrow 269.3%	<i>J</i> ₁₁ ↑ 191.7%	$k_2 \downarrow 39.9\%$
- , -		$k_p \uparrow 17.3\%$	¢_{E2F1} ↓ 11.7%
			$K_{m2} \downarrow 10.3\%$
Decreasing bistabiliy	<i>J</i> ₁₁ ↑ 128.5%	$k_1 \uparrow 169.1\%$	$k_2 \downarrow 43.7\%$
	$k_p \uparrow 33.8\%$	$K_{m2} \downarrow 21.7\%$	$\phi_{E2F1} \downarrow 28.3\%$
	*	$J_{12} \downarrow 20.1\%$	

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Inverse Bifurcation: identified module

$$\frac{d}{dt}[pRB] = k_1 \frac{[E2F1]}{K_{m1} + [E2F1]} \frac{J_{11}}{J_{11} + [pRB]} \frac{J_{61}}{J_{61} + [pRB_p]} \\ - k_{16}[pRB][CycD_a] + k_{61}[pRB_p] - \phi_{pRB}[pRB], \\ \frac{d}{dt}[E2F1] = k_p + k_2 \frac{a^2 + [E2F1]^2}{K_{m2}^2 + [E2F1]^2} \frac{J_{12}}{J_{12} + [pRB]} \frac{J_{62}}{J_{62} + [pRB_p]} \\ - \phi_{E2F1}[E2F1]$$



$$\frac{d}{dt}[CycD_i] = -k_{34}[CycD_i]\frac{[CycD_a]}{K_{m4} + [CycD_a]} + \cdots$$
$$\frac{d}{dt}[CycD_a] = k_{34}[CycD_i]\frac{[CycD_a]}{K_{m4} + [CycD_a]} + \cdots$$

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 Circadian rhythm underlies the 24 hr activity cycle of many organisms

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- Endogenous oscillator entrainable by 24 hr light-dark cycles

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- Circadian rhythm underlies the 24 hr activity cycle of many organisms
- Endogenous oscillator entrainable by 24 hr light-dark cycles
- Circadian model for Arabidopsis thaliana proposed by Locke et al, Molecular Systems Biology (2005)



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$$cLc'[t] = -r1 cLc[t] - \frac{mt cuclt}{kt+clc[t]} + p1 cLm[t] + r2 cLn[t]$$

$$cLm'[t] = -\frac{mt cuclt}{kt+cln[t]} + \frac{n1 cxn[t]^{k}}{p1 + cxn[t]^{k}} + q1 cPn[t] LD[t, dayLength]$$

$$cLn'[t] = r1 cLc[t] + r2 cLn[t] - \frac{m3 cuclt}{kt+cuclt}]$$

$$cPn'[t] = -\frac{mt cuclt}{kt+cuclt}] + p5 (1 - LD[t, dayLength]) - q3 cPn[t] LD[t, dayLength]$$

$$cTc'[t] = -r3 cTc[t] + p2 cTm[t] + r4 cTn[t] - \frac{cTc[t] (mt+m5 (1-LD[t, dayLength]))}{kt+cTn[t]}$$

$$cTn'[t] = -\frac{mt cuclt}{kt+cTn[t]} + \frac{g3^{c} na cun[t]^{k}}{(g3^{c} + cun[t]^{c})} (g2^{k} + vn(t]^{k})$$

$$cTn'[t] = r3 cTc[t] - r4 cTn[t] - \frac{cTn(t) (mt+m5 (1-LD[t, dayLength]))}{kt+cTn[t]}$$

$$cTn'[t] = r3 cTc[t] - r4 cTn[t] - \frac{cTn(t) (mt+m5 (1-LD[t, dayLength]))}{kt+cTn[t]}$$

$$cXc'[t] = -r5 cXc[t] - \frac{m10 cxc(t)}{kt+cTn[t]} + p3 cXm[t] + r6 cXn[t]$$

$$cXn'[t] = \frac{n3 cTn[t]^{4}}{g4^{4} + cTn[t]^{4}} - \frac{m3 cxn[t]}{kt+cTn[t]}$$

$$cYc'[t] = -r7 cYc[t] - r6 cXn[t] - \frac{m10 cxc(t)}{kt+cTn[t]} + p4 cYm[t] + r8 cYn[t]$$

$$cYc'[t] = -r7 cYc[t] - \frac{m13 cvc(t)}{kt+cvc(t)} + p4 cYm[t] + r6 cYn[t]$$

$$cYn'[t] = r7 cYc[t] - r8 cYn[t] - \frac{m14 cvn[t]}{kt+cvc(t)} - \frac{m14 cvn[t]}{gt^{4} + cun[t]^{4}}$$

ODE system

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 Simulation of model with nominal parameters under 12 hr light-dark cycle



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Evidence suggests GIGANTEA could be gene Y



Phase misfit with experimental data

J. CW Locke et al., Molecular Systems Biology (2005)

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Inverse problem: vary parameters so that Y mRNA peaks at ZT7 rather than ZT11

• The peak time \hat{t} for the level of Y mRNA, satisfies

$$\dot{y}(t) = f(y,q) f_{YmRNA}(y(\hat{t}),q) = 0$$

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Goal: obtain a solution that peaks at time î* by varying as few parameters from the published values, q*, as possible

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$$\dot{y}(t) = f(y,q) f_{YmRNA}(y(\hat{t}),q) = 0$$

- Goal: obtain a solution that peaks at time î^{*} by varying as few parameters from the published values, q^{*}, as possible
- Minimization of the objective:

$$\|\hat{t}(q) - \hat{t}^*\|^2 + \mu l_{p,\varepsilon}(q - q^*) \to \min_q$$

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Y mRNA solution profile for the original parameter set



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Y mRNA solution profile for the identified parameter set



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- Y mRNA solution profile for the identified parameter set
- 1 out of 54 parameters is identified



 Identified parameter: g6, Hill-constant in repression of gene Y by LHY

$$\begin{array}{l} {\rm cLc}'[t] = -r1 \, {\rm cLc}[t] - \frac{\pi z \, {\rm cc}[t]}{k^{2} + {\rm cLc}[t]} + p1 \, {\rm cLm}[t] + r2 \, {\rm cLn}[t] \\ {\rm cLm}'[t] = -\frac{\pi 1 \, {\rm cLm}[t]}{k^{2} + {\rm cLm}[t]^{2}} + q1 \, {\rm cPn}[t] \, {\rm LD}[t, \, {\rm dayLength}] \\ {\rm cLn}'[t] = r1 \, {\rm cLc}[t] - r2 \, {\rm cLn}[t] - \frac{\pi z \, {\rm cLn}[t]}{k^{2} + {\rm cLn}[t]} \\ {\rm cPn}'[t] = -\frac{\pi 15 \, {\rm cPn}[t]}{k^{13} + {\rm cPn}[t]} + p5 \, (1 - {\rm LD}[t, \, {\rm dayLength}]) - q3 \, {\rm cPn}[t] \, {\rm LD}[t, \, {\rm dayLength}] \\ {\rm cTc}'[t] = -\pi 3 \, {\rm cTc}[t] + p2 \, {\rm cTm}[t] + r4 \, {\rm cTn}[t] - \frac{{\rm cTc}[t] \, (\pi 6 + \pi 5 \, (1 - {\rm LD}[t, \, {\rm dayLength}]))}{k^{5} + {\rm cTc}[t]} \\ {\rm cTn}'[t] = -\frac{\pi 4 \, {\rm cTn}[t]}{k^{4} + {\rm cTn}[t]} + \frac{g3^{2} \, n2 \, {\rm cYn}[t]^{k}}{(g3^{2} + {\rm ctn}[t]^{2}) \, (g4^{k} + {\rm cYn}[t]^{k})} \\ {\rm cTn}'[t] = \pi 3 \, {\rm cTc}[t] - r4 \, {\rm cTn}[t] - \frac{{\rm cTn}[t] \, (\pi 8 + \pi 7 \, (1 - {\rm LD}[t, \, {\rm dayLength}]))}{k^{5} + {\rm cTn}[t]} \\ {\rm cTn}'[t] = \pi 3 \, {\rm cTc}[t] - r4 \, {\rm cTn}[t] - \frac{{\rm cTn}[t] \, (\pi 8 + \pi 7 \, (1 - {\rm LD}[t, \, {\rm dayLength}]))}{k^{5} + {\rm cTn}[t]} \\ {\rm cXc}'[t] = -r5 \, {\rm cXc}[t] - \frac{\pi 10 \, {\rm cxo}(t)}{k^{2} + {\rm cXn}[t]} + p3 \, {\rm cXn}[t] + r6 \, {\rm cXn}[t] \\ {\rm cXn}'[t] = \frac{n^{3} \, {\rm cTn}[t]^{d}}{g4^{4} + {\rm cTn}[t]} - \frac{m1 \, {\rm cxn}[t]}{k^{3} + {\rm cXn}[t]} \\ {\rm cXn}'[t] = r7 \, {\rm cXc}[t] - \pi 3 \, {\rm cXn}[t] - \frac{\pi 11 \, {\rm cXn}[t]}{k^{1} + {\rm cYn}[t]} \\ {\rm cYn}'[t] = -r7 \, {\rm cYc}[t] - \frac{\pi 13 \, {\rm cvn}[t]}{k^{1} + {\rm cvn}[t]} + p4 \, {\rm cYn}[t] + r6 \, {\rm cYn}[t] \\ {\rm cYn}'[t] = -\frac{\pi 12 \, {\rm cvm}[t]}{k^{10} + {\rm cvn}[t]} + \frac{\left(q^{2} \, {\rm con}[t] \, {\rm LD}[t, {\rm dayLength}] + \frac{q5^{6} \, {\rm cxn} \, {\rm LD}[t, {\rm dayLength}]}{g5^{6} \, {\rm crat}[t]^{6}} \\ {\rm cYn}'[t] = r7 \, {\rm cYc}[t] - r6 \, {\rm cyn}[t] \, {\rm cTn}[t] - \frac{\pi 11 \, {\rm cxn}[t]}{k^{12} + {\rm cyn}[t]} \\ \end{array} \end{array}$$

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We have seen inverse bifurcation problems inferring the underlying mechanisms controlling the qualitative aspects of dynamics

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- One may also wish to probe the possibility of different classes of behaviors; e.g., transition of a bistable switch to an oscillator

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- We have seen inverse bifurcation problems inferring the underlying mechanisms controlling the qualitative aspects of dynamics
- One may also wish to probe the possibility of different classes of behaviors; e.g., transition of a bistable switch to an oscillator
- Infer mechanisms governing the spectrum of the dynamical system: inverse eigenvalue problems

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► For the dynamical system $\dot{y}(t) = f(y,q)$, many bifurcations of equilibrium correspond to various conditions on eigenvalues of $\frac{df(y,q)}{dy}$

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- Inverse eigenvalue problems: identify the possible model mechanisms bringing about the desired change in the spectrum



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- Hybrid solution algorithm:
 - Lift-and-Project (LP)

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Least square formulations with sparsity regularization:

$$\begin{array}{rcl} \mathsf{LP} & : & J(q) = \|A(q) - A_{\mathrm{proj}}\|_{\mathscr{F}}^2 + \mu l_{p,\varepsilon}(q - q^*) \\ \mathsf{QN} & : & J(q) = \sum_i |\lambda_i(q) - \lambda_i^d|^2 + \mu l_{p,\varepsilon}(q - q^*) \end{array}$$

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Consider a model for GATA transcription factors

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- Scenario: duplication of a gene $A \rightarrow A1$, A2



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Subsequent loss of the activating domain



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Subsequent loss of the activating domain



Can oscillations emerge via a few additional mutations?

Evolutionary scenario



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Evolutionary scenario



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Evolutionary scenario



Identified reactions:



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 Many inverse problems arise from the modelling and analysis of biological systems

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- Many inverse problems arise from the modelling and analysis of biological systems
 - inverse bifurcation problems: reverse engineering, matching model to data

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- Many inverse problems arise from the modelling and analysis of biological systems
 - inverse bifurcation problems: reverse engineering, matching model to data
 - inverse eigenvalue problems: model-building, exploration of possible behaviors
- Sparsity-promoting regularization can be effective in drawing useful insights from biological models

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Collaborators

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