

Bottoms up! How pointy-headed mathematical biologists approach cell biology and what we could gain from computational biologists

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Mathematical modeling

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Overview

Modeling how
HPV promotes
cervical cancer

Modeling the
integrated
stress response
in cells

Modeling
asthma within
a host

Conclusions

- Models predict how mechanisms or processes at one level create interesting consequences at another level, “emergent properties”

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- “Emergent properties” are behaviors we can’t figure out without assistance

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- Mathematical biologists use models to understand how nonlinear feedbacks create surprises

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- “Emergent properties” are behaviors we can’t figure out without assistance
- Mathematical biologists use models to understand how nonlinear feedbacks create surprises
- In particular, we’ll look out how the details of these feedbacks amplify, filter, and control responses to external challenges



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I'll illustrate this approach with three projects:

- HPV and cancer
- The cellular stress response
- How viruses can trigger asthma

Acknowledgments

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- HPV: Anna Miller, Karl Munger
- Integrated stress response:
Laura Strube, Julie Hollien, Nels Elde
- Asthma Modeling: June-Hyuk Lee, Peter Kim, James Moore

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- Asthma Modeling: June-Hyuk Lee, Peter Kim, James Moore
- Modeling the Dynamics of Life fund
- James S. McDonnell Foundation
- NSF RTG program
- Soonchunhyang University Research Fund



* No computers were mistreated by the use of Microsoft products in creating this talk

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- Most HPV (human papillomavirus) infections clear in under a year
- Some chronic HPV infections induce cervical cancer
- HPV has two genes that hijack cell cycle control
 - E7 leads to aberrant proliferation by interfering with the checkpoint controlled by the famous RB protein (pRB)
 - E6 leads to uncontrolled proliferation by interfering with apoptosis controlled by the even more famous p53 protein

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 - E6 leads to uncontrolled proliferation by interfering with apoptosis controlled by the even more famous p53 protein
- Low risk types lead to warts, high risk types to cancer

Questions for modeling

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- Which aspects of the hijacking control cancer initiation?
- What are the key differences between high and low risk viruses?
- Why is the delay between infection and cancer so long?

The normal cell cycle

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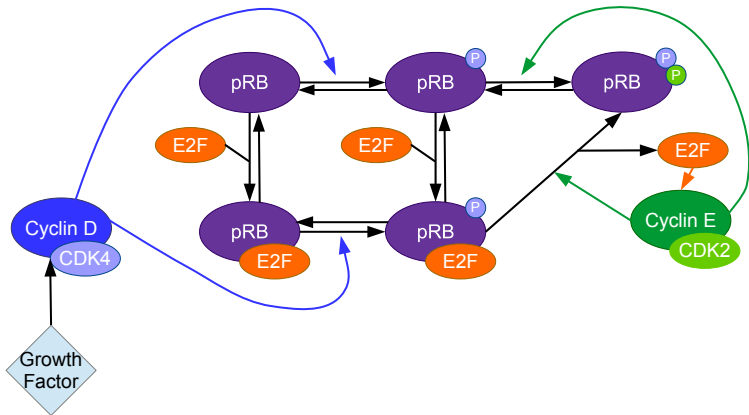
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- Cyclin D initiates the cell cycle
- E2F controls transcription
- pRB sequesters E2F

- Free E2F promotes cyclin E
- Cyclin E initiates positive feedback

The behavior of the basic model

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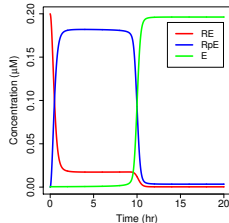
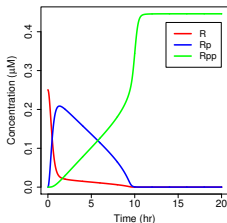
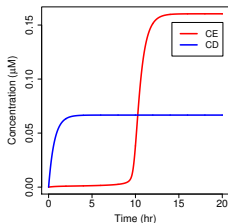
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System of 8 differential equations.



The key output is whether and when the positive feedback kicks in.

The model with the E7 protein from HPV

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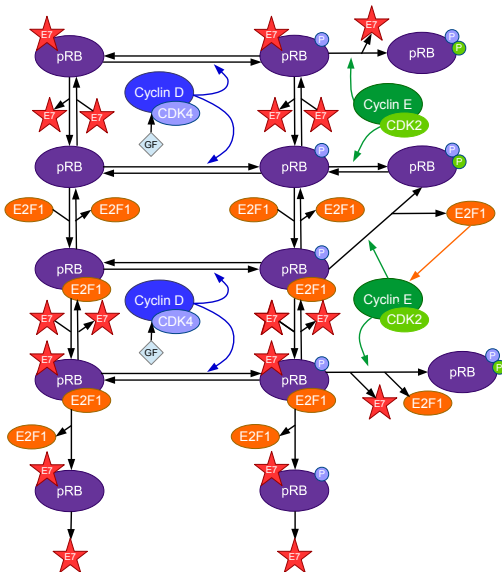
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- E7 binds pRB and releases E2F
- High risk E7 also degrades pRB.

E7 accelerates cell division

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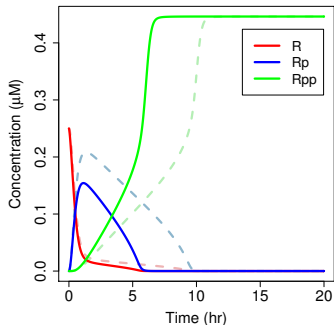
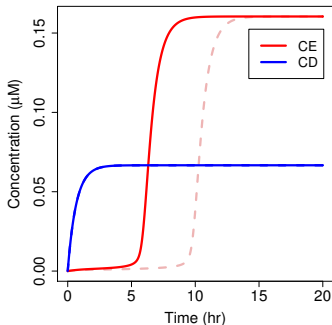
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Solid lines are infected cells, dashed lines uninfected.



E7 reduces dependence on growth factor

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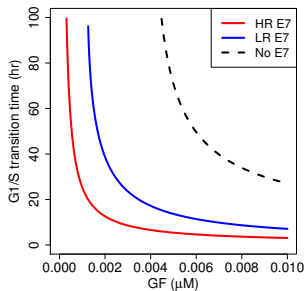
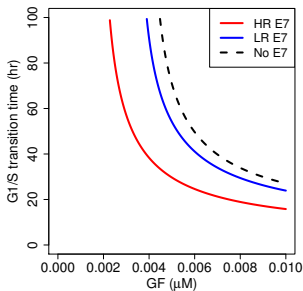
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Effects of a low (left) or high (right) concentration of high risk (HR) or low risk (LR) E7.



What have we learned and what next?

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- This is a complex analog device

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- This is a complex analog device
- Getting the feedbacks right is essential

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- The model provides a foundation for extending to other cell types

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Conclusions

- This is a complex analog device
- Getting the feedbacks right is essential
- The model provides a foundation for extending to other cell types
- And for predicting the slow and relatively rare progression to cervical cancer

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Cells got problems.

- Need oxygen

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Cells got problems.

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- Need amino acids

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- Need oxygen
- Need amino acids
- Attacked by viruses

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Cells got problems.

- Need oxygen
- Need amino acids
- Attacked by viruses
- Can't fold all of those proteins

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- Can't fold all of those proteins

Cells have specialized detectors that initiate a pathway to reduce production of most proteins by sequestering the eukaryotic initiation factor $eIF2\alpha$, but somehow upregulate specific stress response proteins that eventually reverse the process.

State diagram of the stress response

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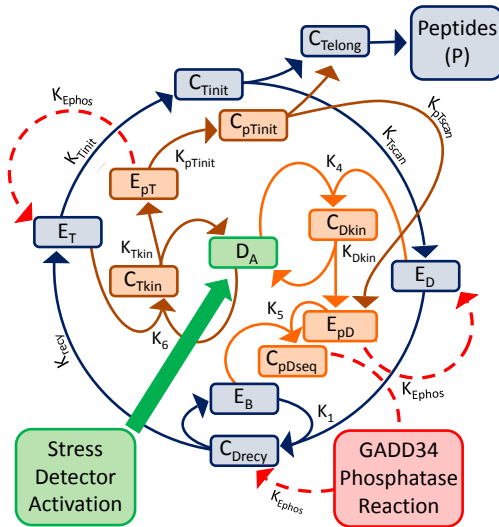
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ATF4 dynamics

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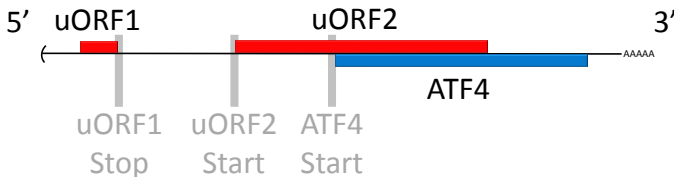
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ATF4 is a transcription factor that should be upregulated when other proteins are downregulated.



Uses a nifty system that turns on when $eIF2\alpha$ is at an intermediate level.

Main result

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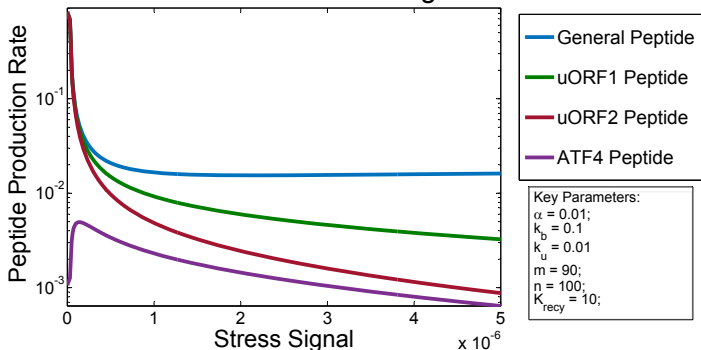
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Equilibrium Peptide Production Rates as a Function of Stress Signal



What have we learned and what next?

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- System uses a complex set of feedbacks, including an unusual mRNA structure, to control protein production

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- System uses a complex set of feedbacks, including an unusual mRNA structure, to control protein production
- Turning off always starts simultaneously with turning on
- The details are crucial for understanding whether a cell will recover or fail
- The details also indicate the points of weakness that viruses can and do exploit

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First, some background on viruses

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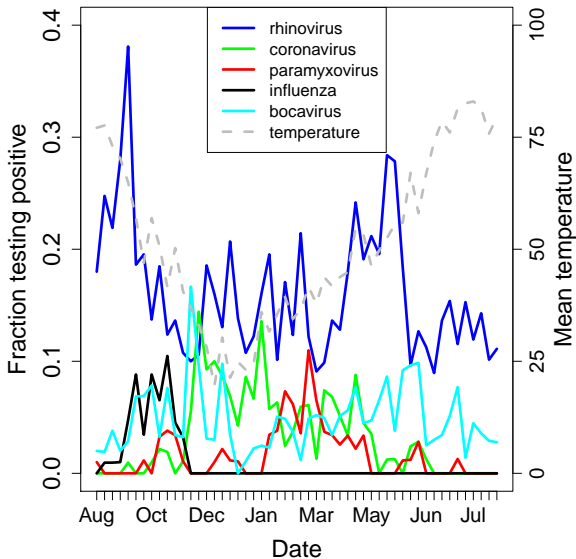
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Rhinovirus is more than a nuisance

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- Severe early infections predispose children to develop asthma many years later
- Infections are a chief trigger of asthma exacerbations
- Infections severe in those with asthma

Early infections and later asthma

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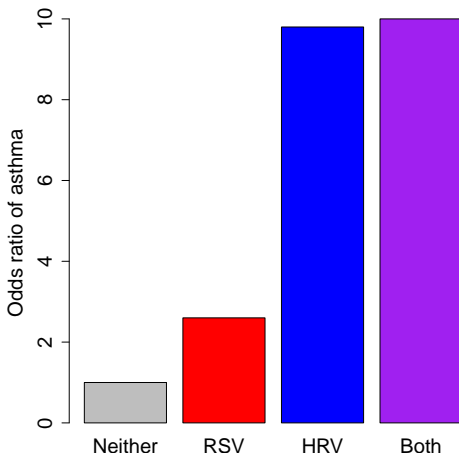
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Most evidence indicates that severe viral infections cause later asthma rather than merely being markers of susceptibility

Jackson, 2008

How might rhinovirus promote asthma?

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- Viruses infect epithelial cells

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- Viruses infect epithelial cells
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- This promotes “alternative activation” of macrophages (cells that act as the custodians of the body)

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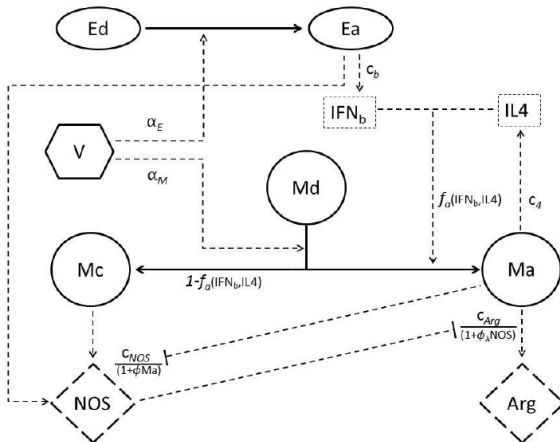
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- Viruses infect epithelial cells
- Cells scream (chemically) with interferon
- This promotes “alternative activation” of macrophages (cells that act as the custodians of the body)
- Alternative activated macrophages release IL-4 (a chemical signal associated with asthma)
- IL-4 promotes allergic response and airway remodeling

The state diagram

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What the model looks like

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Differential equations for epithelial cells (E_d), interferon (F), dormant and alternatively activated macrophages (M_d and M_a), IL4, and some other stuff that didn't fit on the slide.

$$\frac{dE_d}{dt} = -\alpha_E V E_d + \gamma_E E_a - \delta_{Ed}(E_d - E_{d0})$$

$$\frac{dF}{dt} = c_b E_a - \delta_F(F - F_0)$$

$$\frac{dM_d}{dt} = -\alpha_M V M_d - \delta_{Md}(M_d - M_{d0})$$

$$\frac{dM_a}{dt} = f_a \alpha_M V M_d - \delta_{Ma} M_a$$

$$\frac{dIL4}{dt} = c_4 M_a - \delta_{IL4}(IL4 - IL4_0)$$

Behavior of model

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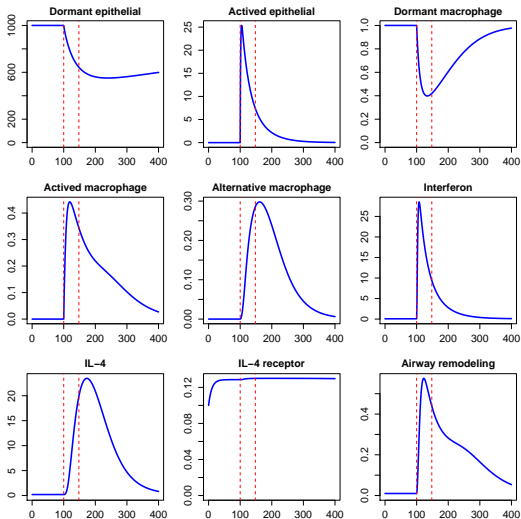
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Effects of infection severity

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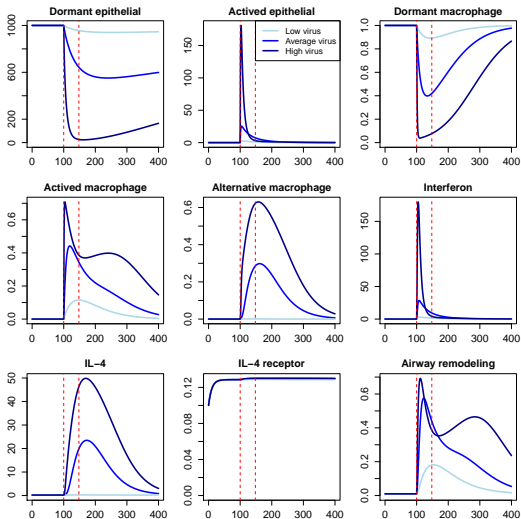
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Effects of interferon production

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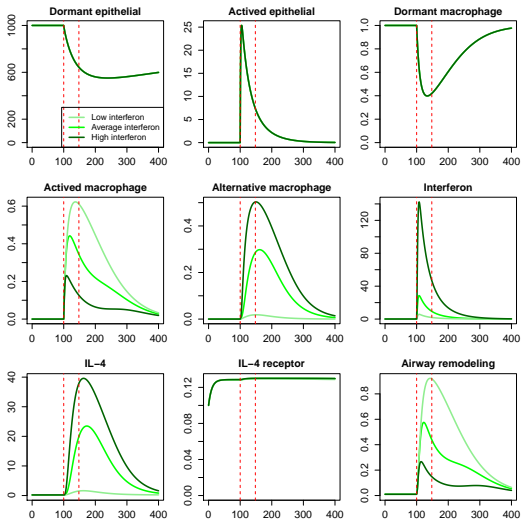
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- Propose ways to measure the irreversible changes

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- Propose ways to measure the irreversible changes
- Model repeated infections and downstream immune system effects

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- Propose ways to measure the irreversible changes
- Model repeated infections and downstream immune system effects
- Connect with the full complexity of how asthma is initiated

Pathways to asthma

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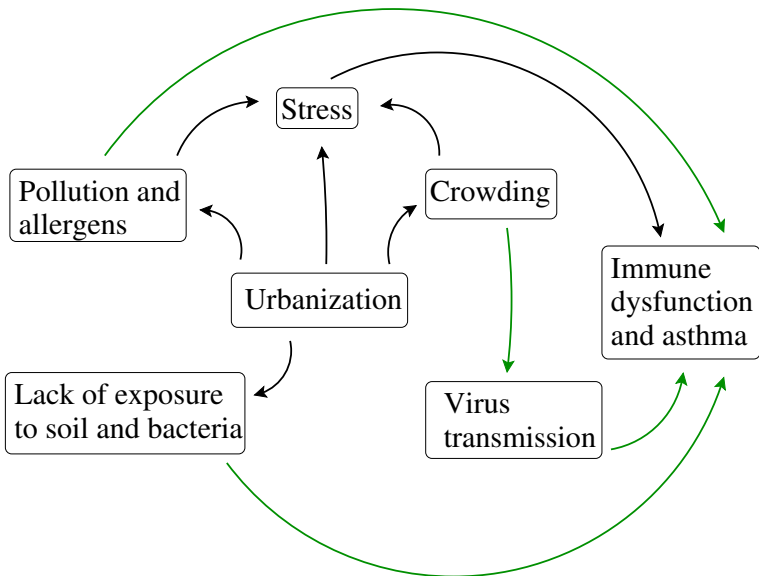
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The strengths and weaknesses of this approach

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- Clear description of assumptions and predictions

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- Clear description of assumptions and predictions
- Close to the way biologists think

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- Proposes specific experiments

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- Proposes specific experiments
- But...

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- Clear description of assumptions and predictions
- Close to the way biologists think
- Proposes specific experiments
- But...
- Estimating the parameters is a nightmare

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- **The old bad version:** You tell me about your system for 20 minutes and I'll get back to you

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- **The old bad version:** You tell me about your system for 20 minutes and I'll get back to you
- **The new good version:** We work closely together to develop a model to answer questions and pose new questions
- **What we fear:** Big Data and Computational Biology will answer all the questions and put us out of business

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Conclusions

- **The old bad version:** You tell me about your system for 20 minutes and I'll get back to you
- **The new good version:** We work closely together to develop a model to answer questions and pose new questions
- **What we fear:** Big Data and Computational Biology will answer all the questions and put us out of business
- **What we hope:** Big Data and Computational Biology will establish the interactions, feedbacks and parameters efficiently, and we can establish new collaborations to deeply understand the dynamics