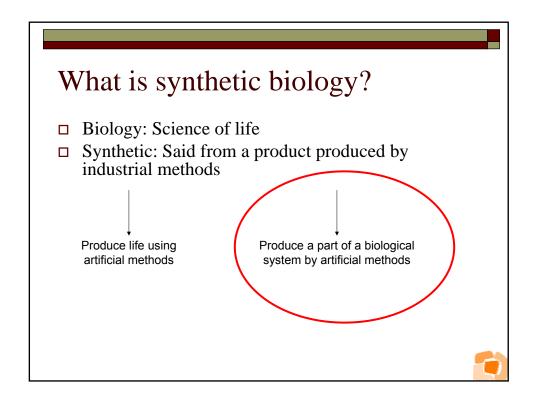
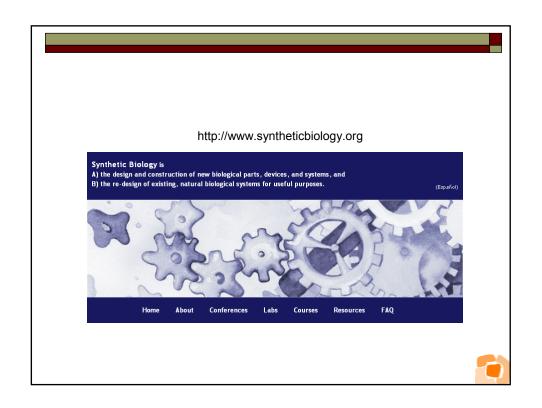


Overview

- □ Introduction
- □ Synthetic biology evolution
- □ Some examples
- □ Biology and engineering. The paradigm of synthetic biology.
- □ Systems biology work
- □ Synthetic gene regulatory systems





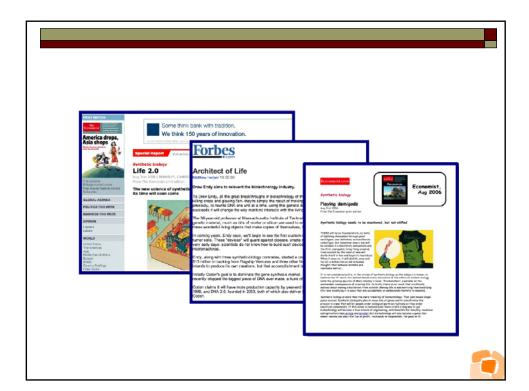


Synthetic Biology History

- □ 1953 –DNA discovery by Watson and Crick
- □ 1961 Discovery of mathematical logic in gene regulation
- □ 1970 First gene synthesized from scratch (alanine tRNA)
- □ 1978 Nobel prize awarded to Werner Arber, Daniel Nathans and Hamilton Smith for the discovery of restriction enzymes
- □ 1978 (Boyer at UCSF) A synthetic version of the human insulin gene was constructed and inserted into the bacterium *E. coli*.
- □ 1980 Kary Mullis invents PCR
- □ 1991 Affymetrix chip-based oligonucleotide synthesis
- □ 2003 Creation of standardized parts libraries at MIT





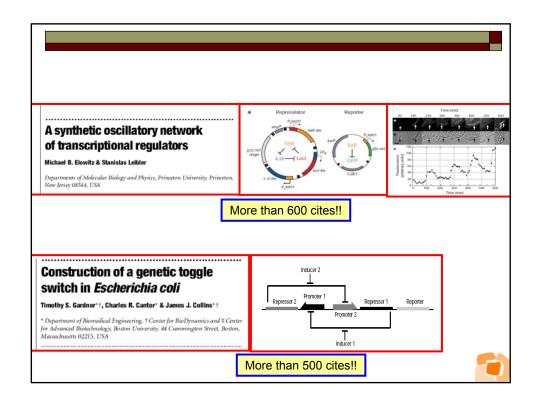




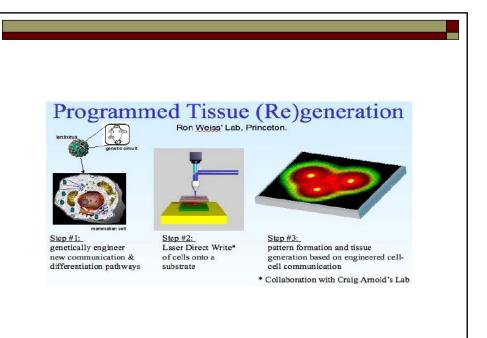


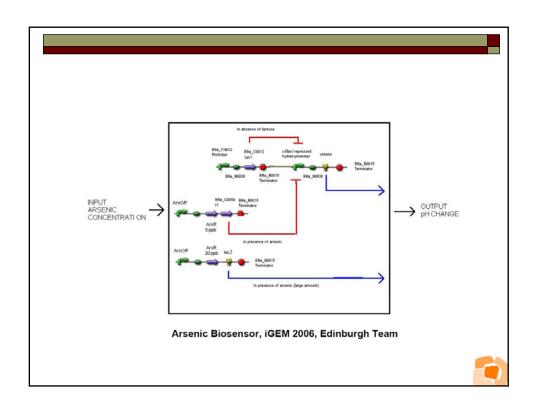


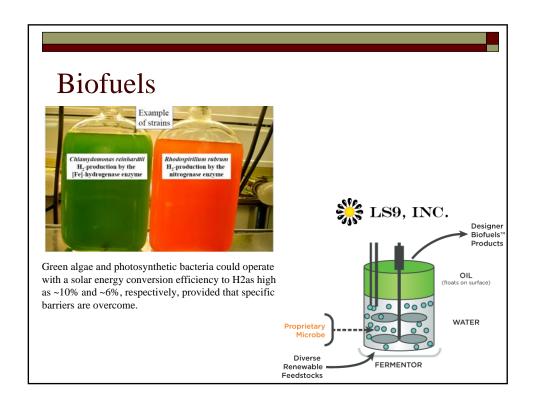


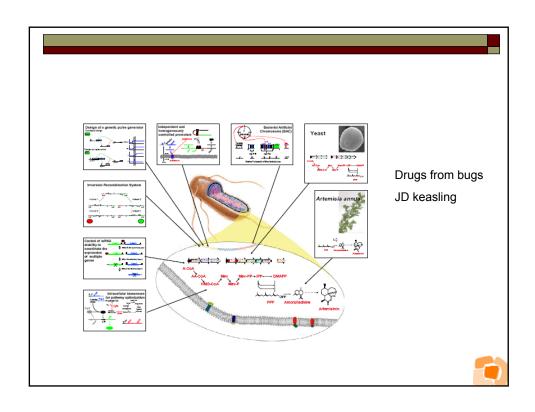


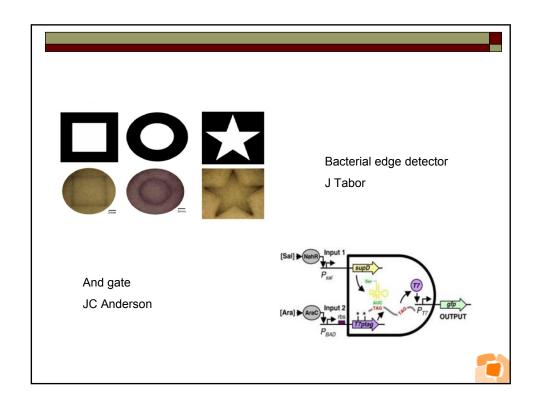


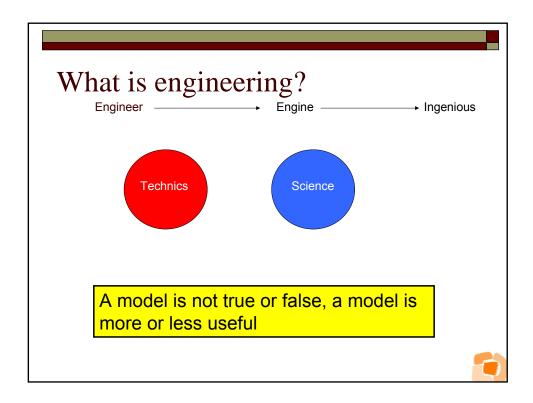


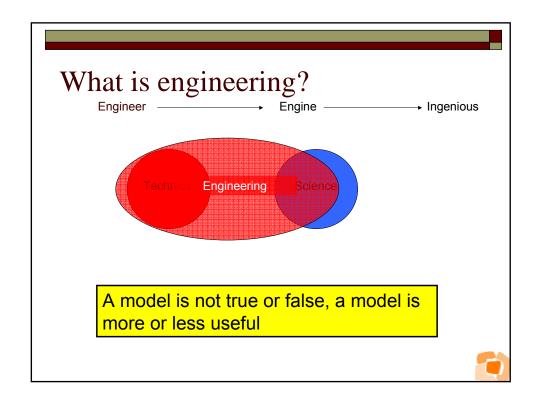


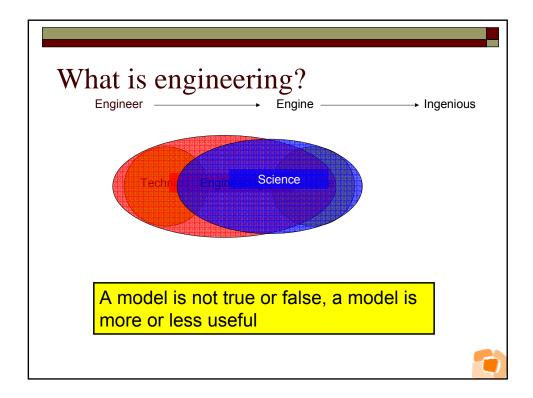


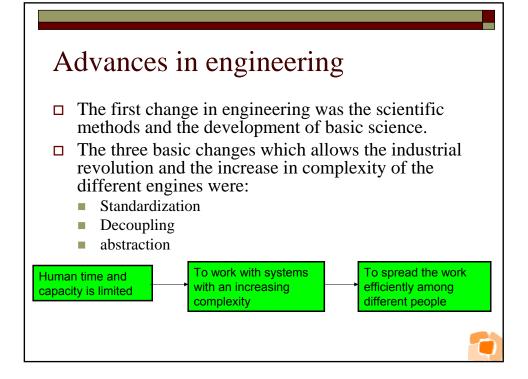


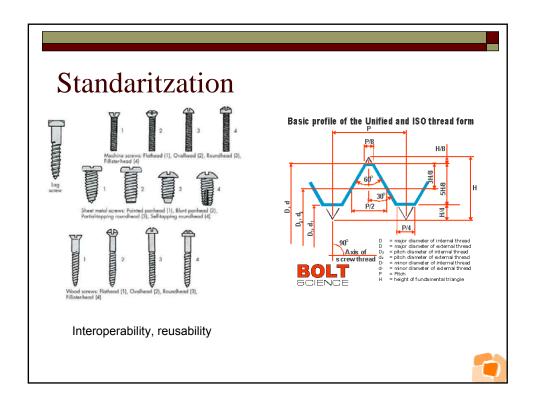












Decoupling

Rules insulating design process from details of fabrication







Abstraction/modularity



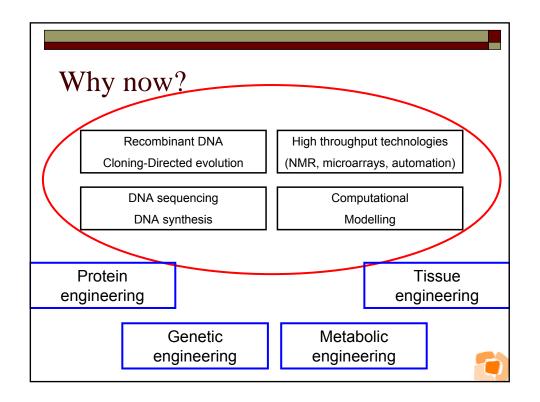


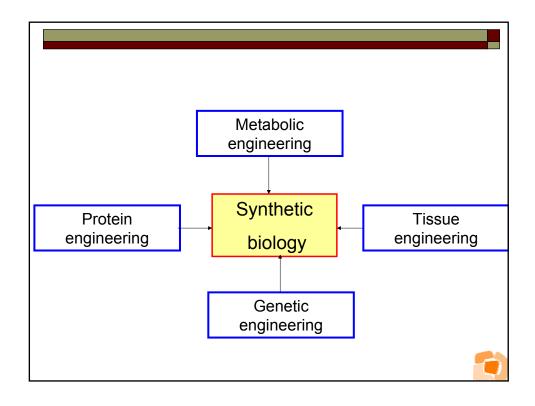


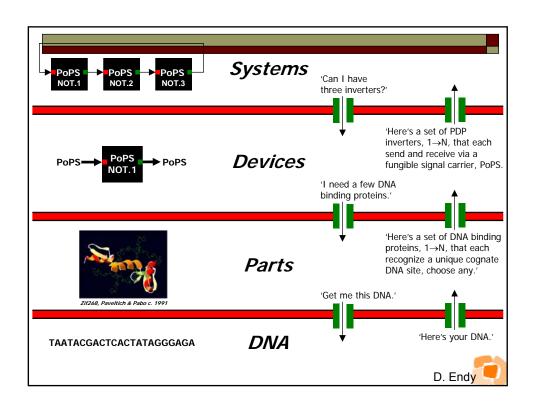
- □ Biology is one of the most complicated machinery that we know
- □ Synthetic biology applies all this procedures to biology.
- ☐ Mechanical Engineering, Electrical Engineering and electronics were all at the stage where they were "too complicated".

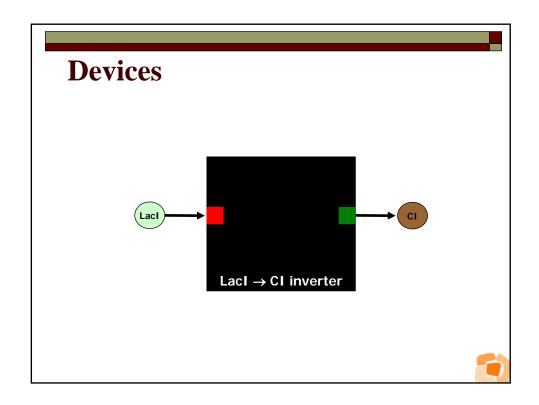


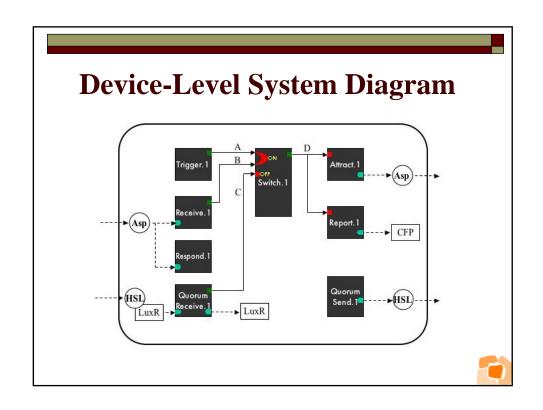


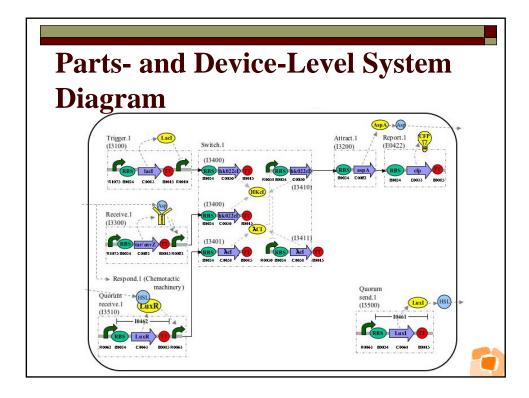










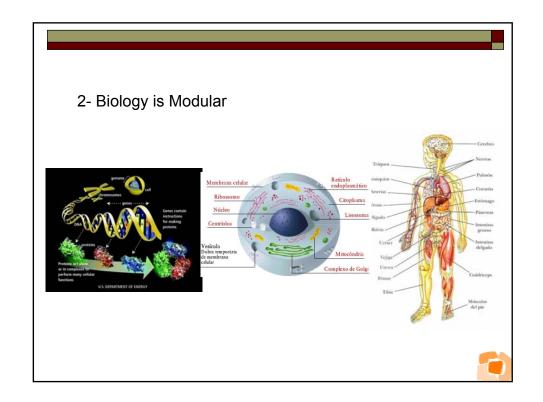


Standariztion

- □ Standard cell host
- □ Standard culture conditions
- □ Standard measurement
- □ Standard functional composition
- □ Standard DNA composition



Can we work in such a way? 1- Biology is hierarchical Cell to organism hierarchy organ systems organs tissues organelles cytoplasm organism to ecosystem hierarchy environment biome community organism

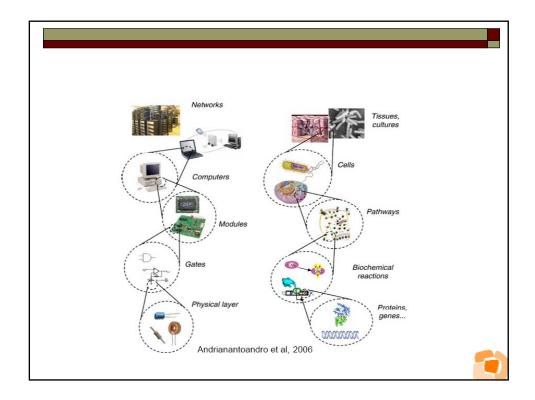




Hierarchy and Modular (recurrent) organization in some standard way allows biology to be understandable and synthetic biology to be possible.

In some way some process of evolution are based on this: adding properties to a system





Applications

- □ Biofuels
- Biomaterials
- □ Biosensors
- □ Drug development
- □ Nanotechnologies.





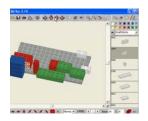
iGEM - The international Genetically Engineered Machine competition



iGEM addresses the question: Can simple biological systems be built from standard, interchangeable parts and operated in living cells? Or is biology simply too complicated to be engineered in this way?

Pure engineering approach







It began in 2003 with several student from MIT trying to play with an oscillator

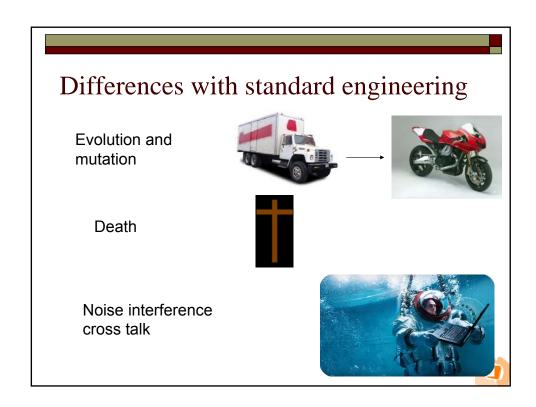


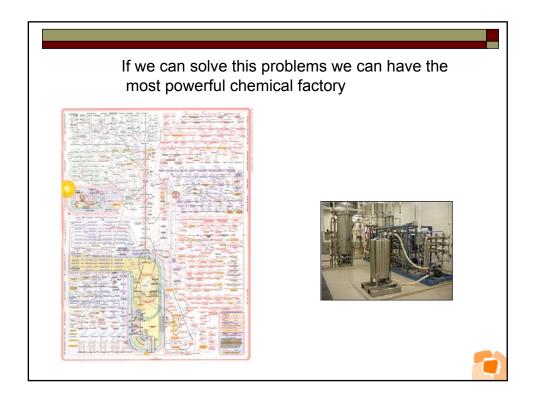
Last year more than 50 teams from universities all over the world participate in that competition



And sometimes they can purely engineer biology

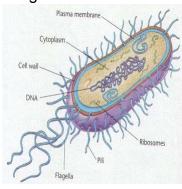






Chassis

All this machinery is going to be inserted in a living organism



Madigan, M.T. Martinko, and J. Parker. 2003. Biology of Microorganisms. Prentice Hall Upper Saddle River, NJ



To insert a system inside an organism could produce an undesired interference between both



Systems Biology

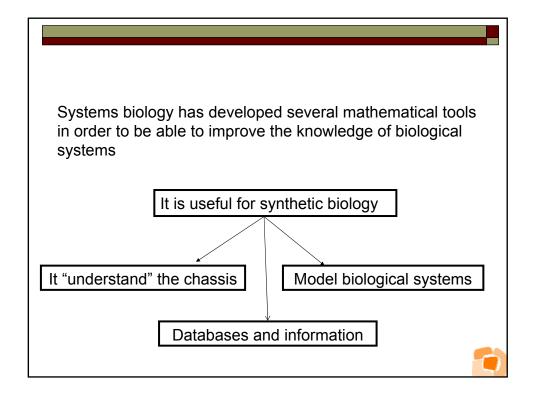
Attempts to describe the living systems as a hole.

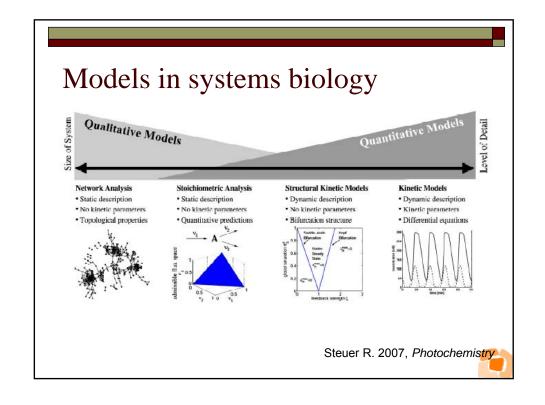
Life not depend only on the expression of a single gen but also in the combination of expressions of different gens.

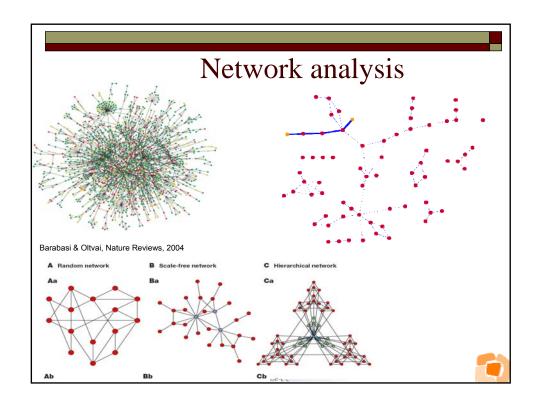
Life is a very complex _ machine

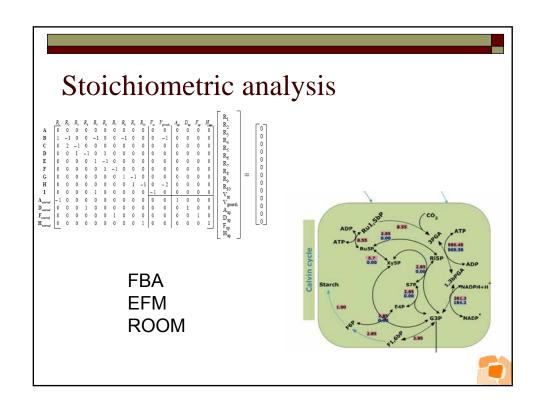
As we increase the complexity of a system it depends more in the protocols of its interactions than on its individual components





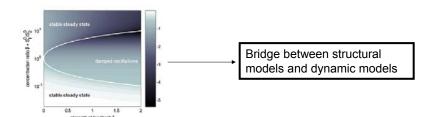






Structural kinetic models

describes the possible dynamics of metabolic systems, as well as the stability and robustness of metabolic states, and concomitantly identifies the relevant interactions and parameters governing the dynamic properties of the system.



Steuer R. 2007, Photochemistry

Kinetic Models

- ☐ They need more parameters than the other approach.
- □ Nowadays it is not possible to use them to describe the whole system, but they could give accurate information of a part of the system.



Kinetic Models

The basic models are based on non linear differential equations.

Hypotesis:

- •The diffusion is not importat (not explicit spatial dependence)
- •The variables are a continuous functions on time (no stochasticity).



Regulatory model

$$\frac{\frac{d Z}{dt}}{1 \frac{\frac{S^n}{K^n}}{K^n}} = Z$$

- •M has a value of 0 or 1
- •K the Hill constant (the value of the signal that yield 50% response)
- •n the Hill coefficient (the slope of the response)
- •Beta is the decay constant of the reporter protein
- •Gamma is the basal gene expresion
- •Alpha sigma dependent gene expresion (gamma=a alpha)



Computer tools

□ A common lenguage has been developed to be able to make the work reusable allowing the comunication between research groups:



http://www.sbml.org



http://www.cellml.org



Functions

- □ **Document and store** the structure of physiological and biochemical reaction networks
- ☐ Store values and math associated with the network dynamics
- □ Do **not** provide commands or instructions for building, simulating, or analyzing networks.
- □ As mozilla is able to read html, there are several programs able to read these languages (mark-up languages).



Example (in SBML)

```
< reaction id="R1" reversible="false" >
    < listOfReactants >
         < speciesReference species="Sout" />
    listOfReactants >
    < istOfProducts >
         < speciesReference species="Sin" />

listOfProducts >

    < kineticLaw >
         <math xmlns=http://www.w3.org/1998/Math/MathML >
                  < ci > v_1 < / ci >
         </ math >
         < listOfParameters >
                  < parameter id="v_1" value="100" />

listOfParameters >

    </ kineticLaw >
</reaction >
```



Characteristics of SBML

- □ Many top-level types, little nesting
 - Units, Compartment, Species, Parameter, Reaction, Rule, Function, Event
- □ Non-modular structure
 - Next SBML 'Level' (3) will introduce modularity
- □ Emphasis on reactions
- □ Some math implicit
 - Explicit rate equations; implicit integration
 - Implicit concentration conversion between compartments
- □ Compartments are physical containers for species
 - Spatial dimensions (volume, surface)

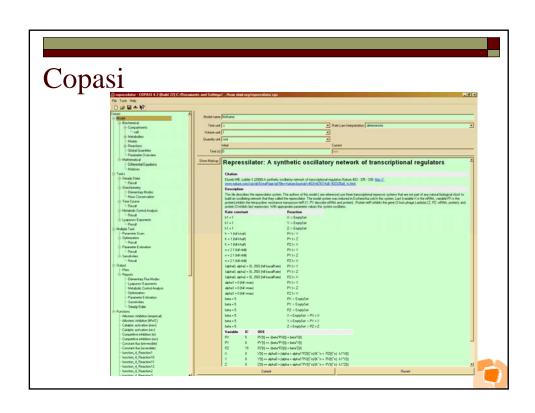


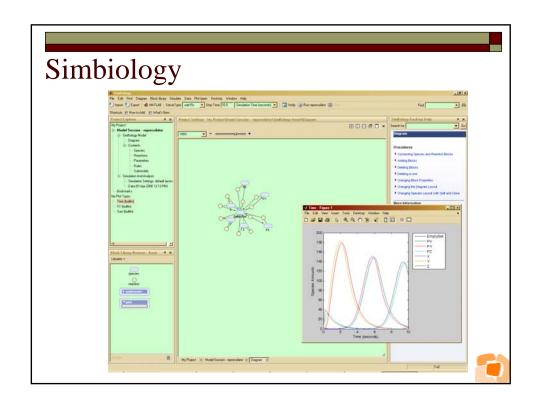
Characteristics of CellML

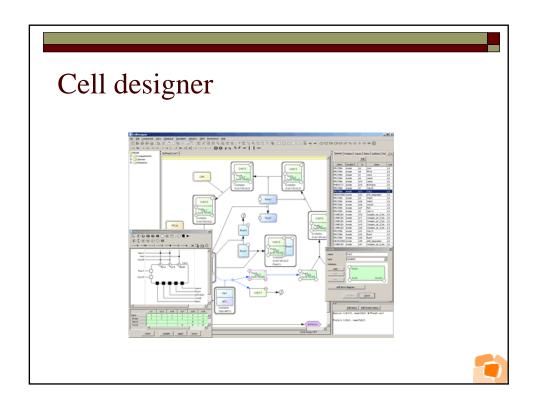
- ☐ Few top-level types, extensive nesting
 - Units, Component, Connection, Group, Import
- □ Highly modular structure
 - Nesting of components in groups
- □ Emphasis on model organization
- □ All math explicit
 - Explicit rate equations; explicit integration
 - Explicit concentration conversion in transport processes
- ☐ Groups may specify physical or conceptual containment
 - No spatial dimensions



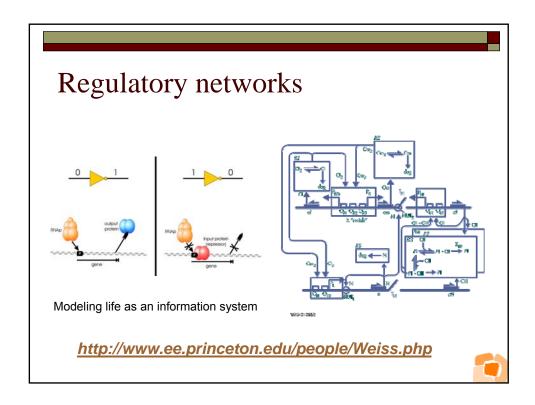


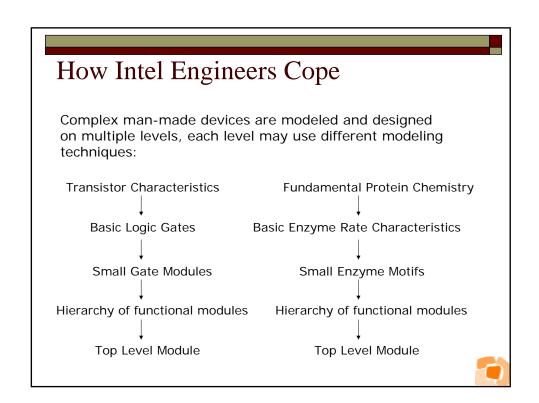


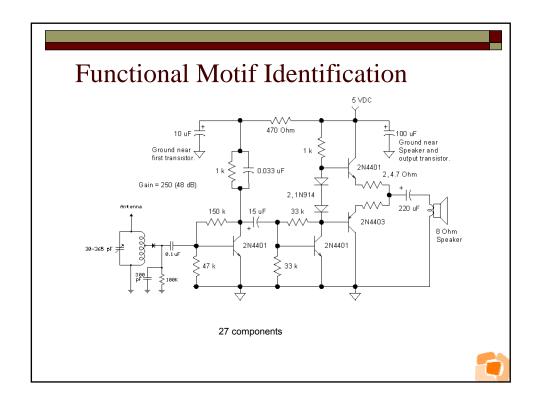


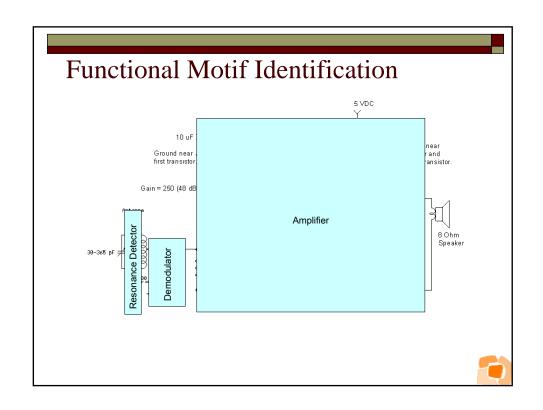


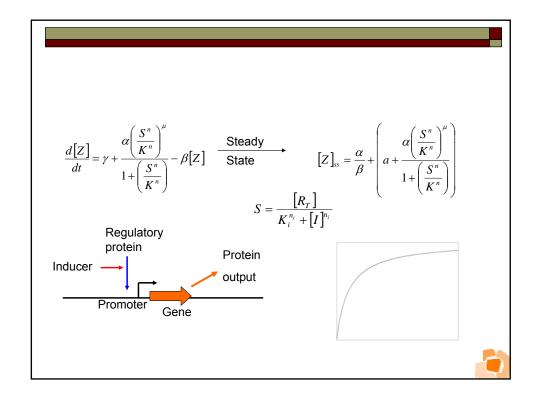








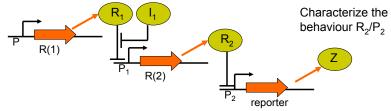




Regulatory protein	Regulated promoters	Inducer
TetR	P_{tet} , P_{LtetO}	tetracycline
LacI	P _{lac} , P _{lacO} , P _{trc}	Lactose, IPTG
cI	$P_L, P_R, P_{RM}, P_{luxOR}$	
LuxR	P _{lux} , P _{luxOR}	AHL







$$\frac{d[R_2]}{dt} = a_1 \alpha_1 + \frac{\alpha_1 \left(\frac{[I_1]^n}{K_1^n} \right)^{\mu}}{1 + \left(\frac{[I_1]^n}{K_1^n} \right)} - \beta_2 [R_2]$$

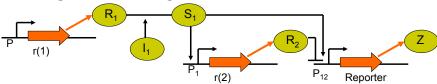
$$= a_1 \alpha_1 + \frac{\alpha_1 \left(\frac{[I_1]^n}{K_1^n} \right)^{\mu}}{1 + \left(\frac{[I_1]^n}{K_1^n} \right)} - \beta_2 [R_2]$$

$$\frac{d[Z]}{dt} = a_2 \alpha_2 + \frac{\alpha_2}{1 + \left(\frac{[R_2]^n}{K_2^n}\right)} - \beta[Z]$$
[Z]

Rosenfeld et al. Science 307 2005



Pulse generating network



$$\frac{d[R_2]}{dt} = \frac{\alpha_1 s^{n_1}}{1 + s^{n_1}} - \beta_2 [R_2] \qquad [R_2]_{ss} = \frac{\alpha_1}{\beta_2} H$$

$$\left[R_2\right]_{ss} = \frac{\alpha_1}{\beta_2}H$$

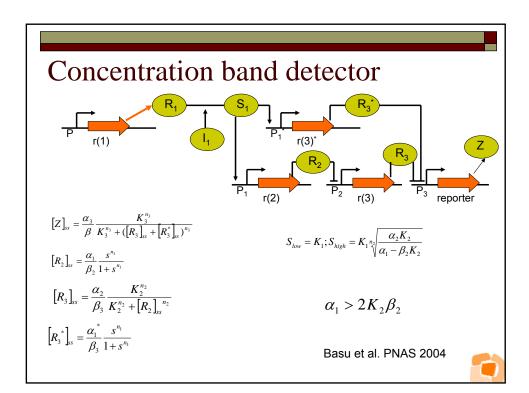
$$H = \frac{s^{n_1}}{1 + s^{n_1}}; s = \frac{S_1}{K_1}$$

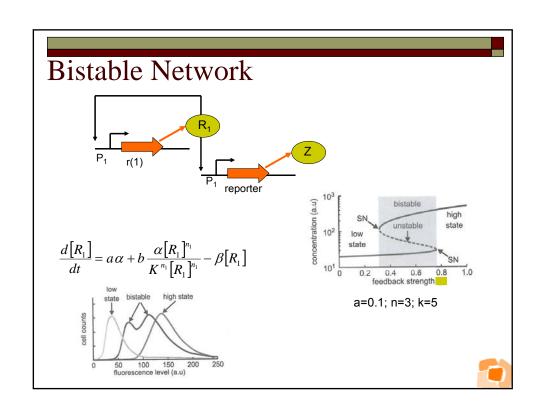
$$\frac{dZ}{dt} = \frac{\alpha_{12}}{1 + \left(\frac{[R_2]}{K_2}\right)^{n_2}} \frac{s^{n_1}}{1 + s^{n_1}} - \beta[Z] \qquad [Z]_{ss} = \frac{\alpha_{12}}{d} \frac{K_2^{n_2} H}{K_2^{n_2} + [R_2]_{ss}^{n_2}}$$

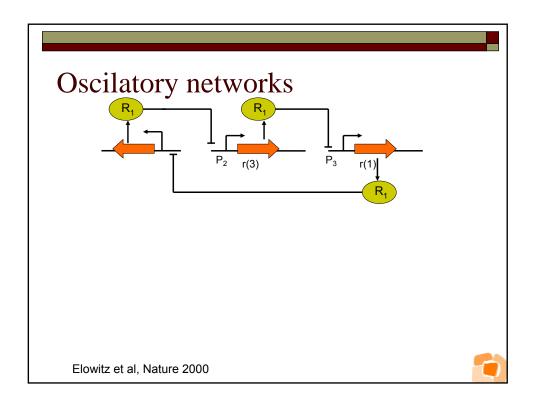
$$[Z]_{ss} = \frac{\alpha_{12}}{d} \frac{K_2^{n_2} H}{K_2^{n_2} + [R_2]_{ss}^{n_2}}$$

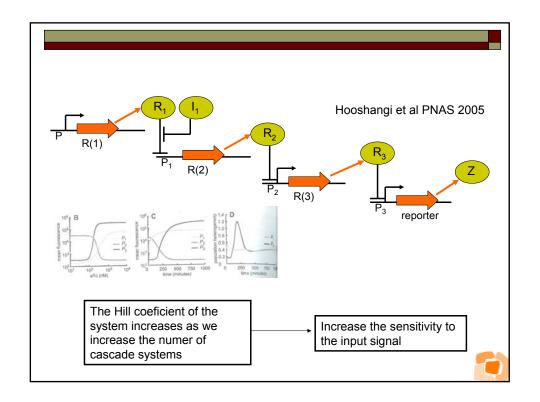
Basu et al. PNAS 2004



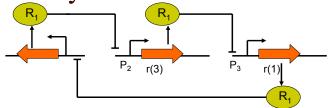












$$\frac{d[M]}{dt} = a\alpha_{tr} + \frac{\alpha_{tr} \left(\frac{S^n}{K^n}\right)^{\mu}}{1 + \frac{S^{\mu}}{K^{\mu}}} - \beta_M[Z]$$

$$\frac{dm_i}{d\tau} = a\kappa + \frac{\kappa}{1 + r_j^n} - m_i$$

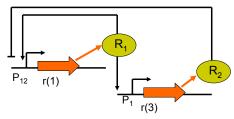
$$\frac{d[Z]}{dt} = \alpha_{tr}[M] - \beta[Z]$$

$$\frac{dr_i}{dt} = \varepsilon (m_i - r_i)$$

Separation of transcription and translation introduces response delays



Robust oscillatory networks



Vilar et al. PNAS 2002

Think about this...



Science

Biological systems are very complex.

Study of simple parts of that systems and increase difficulty gradually.

Engineering

Some of the engineering knowledge is present on simple biological systems.

Be able to design and build simple machines with a desired function.



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