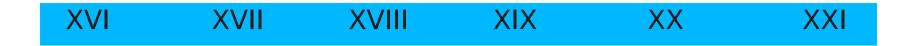
What is Systems Biology? What are the challenges ahead?

Nicolas Le Novère, EMBL-EBI

Emergence of the notion of system



Global Description of the world

"classical" mechanic, anatomy, physiology

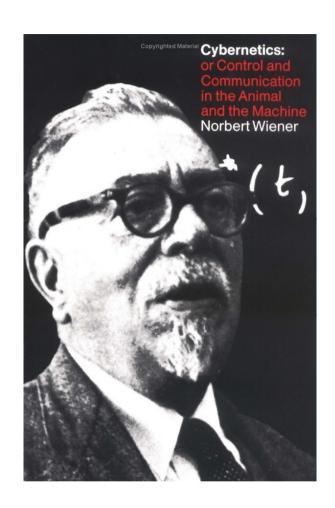
Description of the components of the world

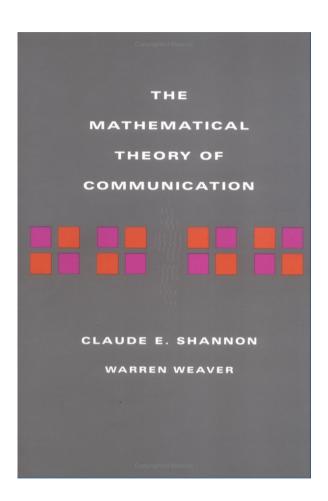
Statistical physics, thermodynamics, quantum mechanic, biochemistry, structural biology, molecular biology

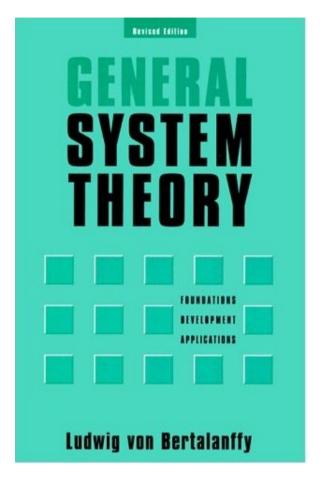
Description of interacting components

Cybernetics, Information theory, telecommunications, automata, multi-agents, Systems Biology

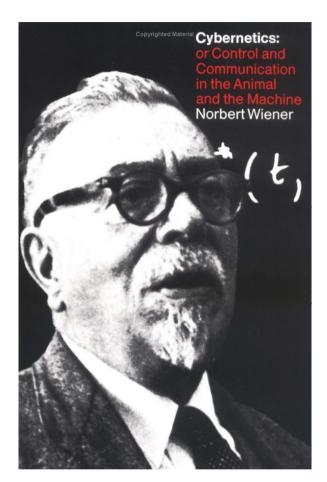
Systems have been formalised for a while

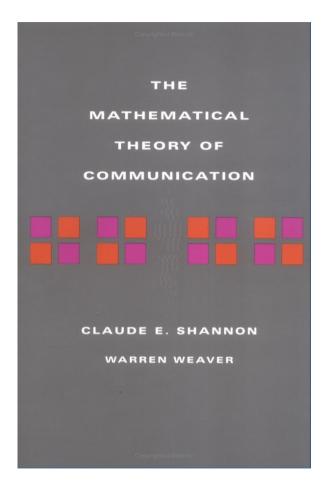


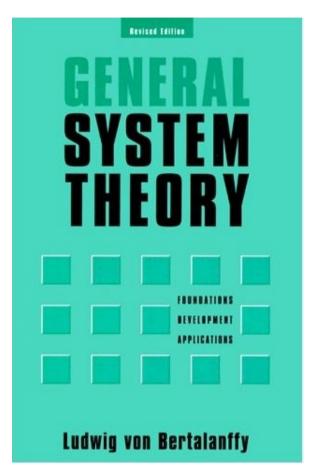




Systems have been formalised for a while



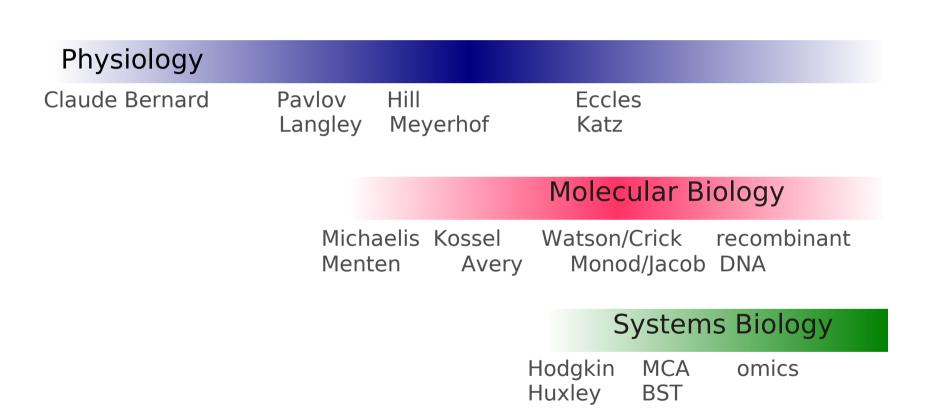




"[A system consists of] a dynamic order of parts and processes standing in mutual interaction. [...] The fundamental task of biology [is] the discovery of the laws of biological systems" Ludwig von Bertalanfy, Kritische Theorie der Formbildung, 1928

The three paradigms of Biology





Computer simulations Vs. mathematical models

[37]

THE CHEMICAL BASIS OF MORPHOGENESIS

By A. M. TURING, F.R.S. University of Manchester

(Received 9 November 1951—Revised 15 March 1952)

It is suggested that a system of chemical substances, called morphogens, reacting together and diffusing through a tissue, is adequate to account for the main phenomena of morphogenesis. Such a system, although it may originally be quite homogeneous, may later develop a pattern or structure due to an instability of the homogeneous equilibrium, which is triggered off by random disturbances. Such reaction-diffusion systems are considered in some detail in the case of an isolated ring of cells, a mathematically convenient, though biologically unusual system. The investigation is chiefly concerned with the onset of instability. It is found that there are six essentially different forms which this may take. In the most interesting form stationary waves appear on the ring. It is suggested that this might account, for instance, for the tentacle patterns on *Hydra* and for whorled leaves. A system of reactions and diffusion on a sphere is also considered. Such a system appears to account for gastrulation. Another reaction system in two

Computer simulations Vs. mathematical models

[37]

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One would like to be able to follow this more general process mathematically also. The difficulties are, however, such that one cannot hope to have any very embracing theory of such processes, beyond the statement of the equations. It might be possible, however, to treat a few particular cases in detail with the aid of a digital computer. This method has the advantage that it is not so necessary to make simplifying assumptions as it is when doing a more theoretical type of analysis.

Birth of Computational Systems Biology

J. Physiol. (1952) 117, 500-544

A QUANTITATIVE DESCRIPTION OF MEMBRANE CURRENT AND ITS APPLICATION TO CONDUCTION AND EXCITATION IN NERVE

By A. L. HODGKIN AND A. F. HUXLEY

From the Physiological Laboratory, University of Cambridge

(Received 10 March 1952)

This article concludes a series of papers concerned with the flow of electric current through the surface membrane of a giant nerve fibre (Hodgkin, Huxley & Katz, 1952; Hodgkin & Huxley, 1952 a-c). Its general object is to discuss the results of the preceding papers (Part I), to put them into mathematical form (Part II) and to show that they will account for conduction and excitation in quantitative terms (Part III).

Events around

First	t computers	PDB	EMBLbank PC		Genomes Interactomes
1950	1960	1970	1980	1990	2000

Events around					
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Ev	ents aro	und					
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Ev	ents ar	ound						
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	models	Rall's cable approximation		plex	simple circuits	Purkinj Neuror		
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							Barabasi Repressila	tor

90s: maturation of the community

- Publication of modelling work in high visibility journals, e.g.:
 - Tyson. modeling the cell-division cycle cdc2 and cyclin interactions. PNAS 1991; McAdams and Shapiro. Circuit simulation of genetic networks. Science 1995; Barkai and Leibler. Robustness in simple biochemical networks. Nature 1997; Neuman et al. Hepatitis C viral dynamics in vivo and the antiviral efficacy of interferon-alpha therapy. Science 1998; Yue et al. Genomic cis-regulatory logic: Experimental and computational analysis of a sea urchin gene. Science 1998; Bray et al. Receptor clustering as a cellular mechanism to control sensitivity. Nature 1998; Bhalla ad Iyengar. Emergent properties of signaling pathways. Science 1998
- Structuration of the community modelling metabolism
- Large-scale modelling and simulation projects
 - E-Cell project 1996; The Virtual Cell 1998
- Availability of high-throughput data on parts and interactions
 - Two-hybrids (1989); microarrays (1995) etc.
- Large-scale funding for wet+dry studies of biological systems
 - Alliance For Cellular Signalling (http://www.afcs.org/). First of the NIH "glue grants". 1998

Formal revival of Systems Biology

- "Modelling" Systems Biology
 - 1998 Hiroaki Kitano founds the Systems Biology Institute in Tokyo
 - First appearance: Kyoda, Kitano. Virtual Drosophila project: Simulation of drosophila leg formation. Genome Informatics Series (1998)
 - Kitano, H. Perspectives on systems biology. New Generation Computing Volume 18, Issue 3, 2000, Pages 199-216
- "Network" Systems Biology
 - First appearance: Leroy Hood. Systems biology: new opportunities arising from genomics, proteomics and beyond. *Experimental Hematology*. Volume 26, Issue 8, 1998, Page 681
 - Schwikowski B, Uetz P, Fields S. A network of protein-protein interactions in yeast. Nat Biotechnol. 2000 Dec;18(12):1257-61.
 - 2000 Leroy Hood founds the Systems Biology Institute in Seattle

1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
T 2 2 (2000	2001	2002	2005	200 1	2005	2000	2007

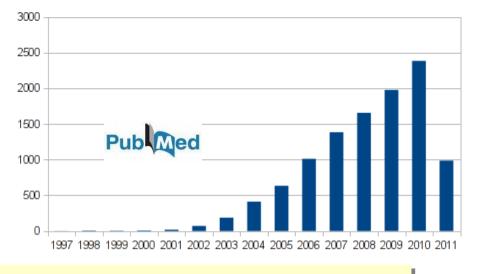
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pro	ojects	SysBio enters FP6 YSBN ERASysBio								
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pro	ojects				YSBN	SysB	io enters E	FP6 RASysBio		
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publi	cations	ľ	Szallas	Boogerd asi Grierson						
Computational Cell Biology" IEE Sys Bio MSB BMC										

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	ERATO-Kitano SystemsX Alliance for Cellular Signaling HenatoSys											
projects HepatoSys SysBio enters FP6 YSBN ERASysBio												
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Tokyo	Tokyo Systems Biology Institute Seattle Institute for Systems Biology 6 BBSRC centres											
Ins	titutes	Seatti	e madicule	BioQua	9 y	6 BBSRC centres						

- First mention of the term:1928 (L Von Bertallanfy)
- Modern revival of the term: 1998 (L Hood, H Kitano)



Systems Biology is the study of the **emerging** properties of a biological system, taking into account all the **necessary** constituents, their **relationships** and their **dynamics**.

Systems-wide analysis (omics)

- Born: 1990s
- Technologies: high-throughput, statistics
- People's background: molecular biologists, mathematicians
- Key lesson: the selection of a phenotype is done at the level of the system, not of the component (gene expression puzzle)

Application of systems-theory

- Born: 1960s
- Technologies: quantitative measurements, modelling
- People's background: biochemists, engineers
- Key lesson: the properties at a certain level are emerging from the dynamic interaction of components at a lower level

Nobel Symposium on Systems Biology (June 2009)

Naama Barkai

Bernard Palsson

Nicolas Le Novère

Jens Nielsen

Johan Elf

networks

Leroy Hood

Marc Vidal

Mike Snyder

Marc Kirschner

Charlie Boone

Ruedi Aebersold

Terence Hwa

Erin O'Shea

Jussi taipale

models

Eric Davidson

Stanislas Leibler Michel Savageau

Lucy Shapiro Roger Brent Hans Westerhoff

Uwe Sauer Francois Nedelec

Jorg Stelling

Edda Klipp Boris Kholodenko

Bela Novak

Jim Ferrell

Hiroaki Kitano

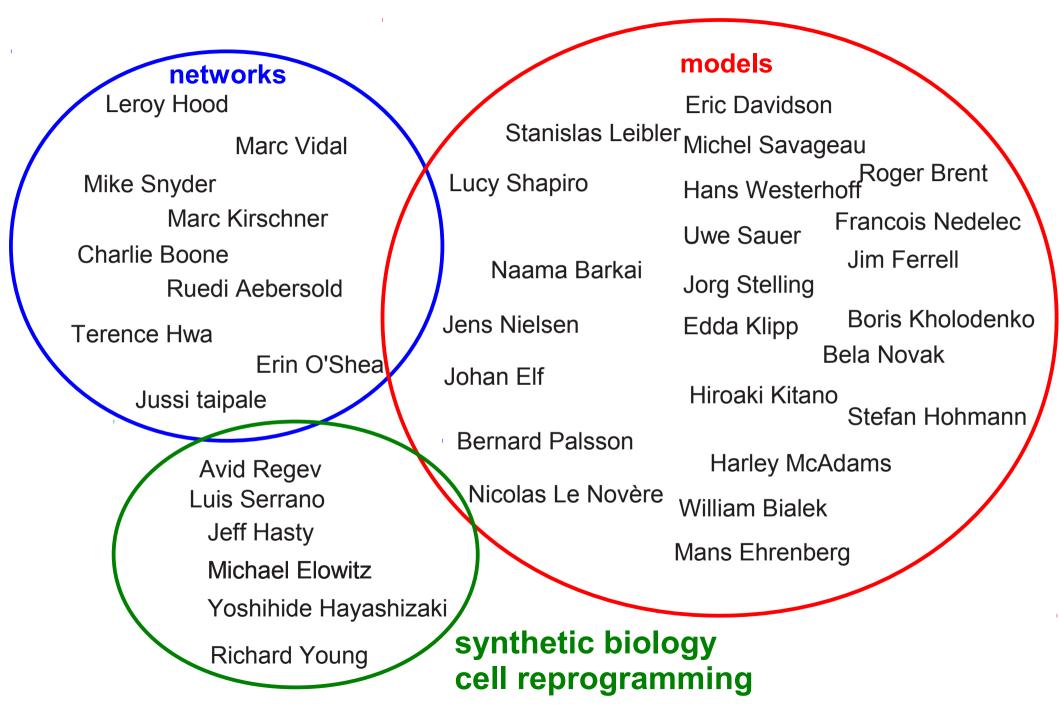
Stefan Hohmann

Harley McAdams

William Bialek

Mans Ehrenberg

Nobel Symposium on Systems Biology (June 2009)



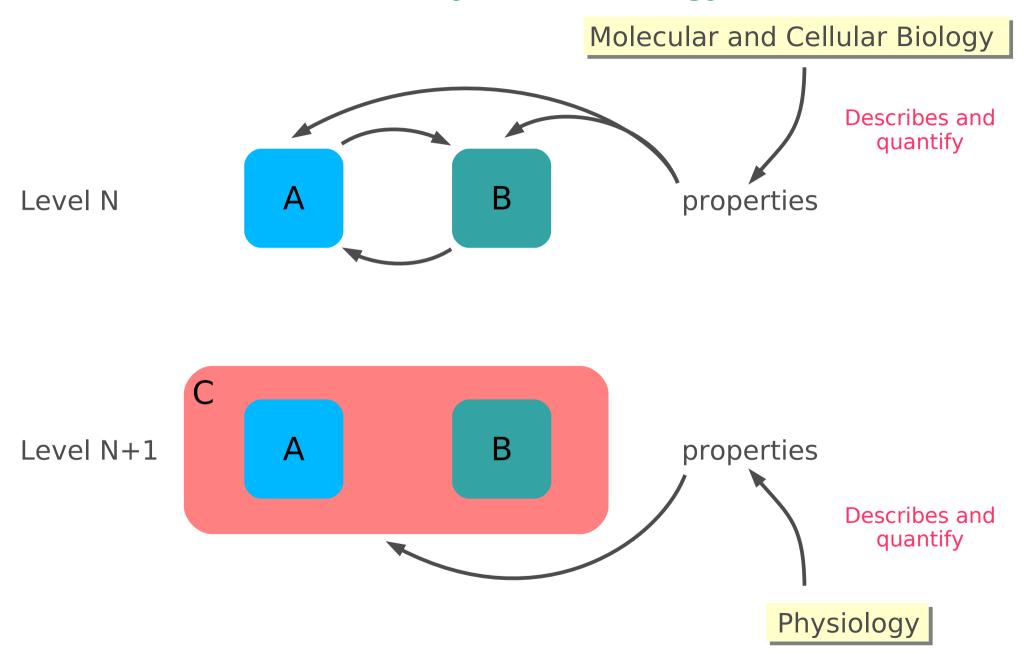
Describes and quantify

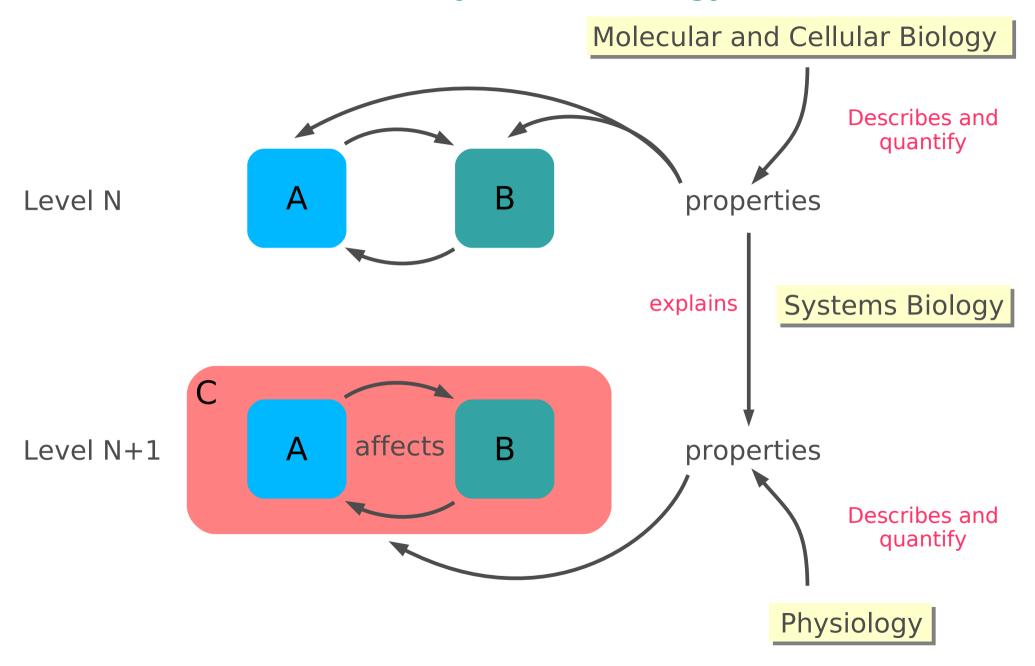
Level N

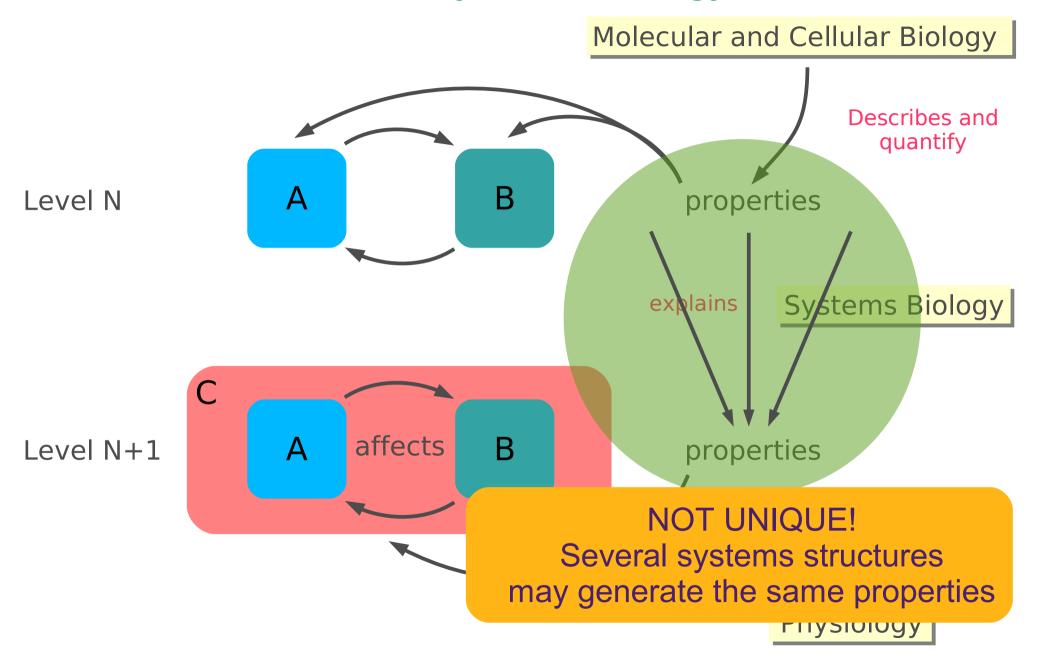
A

B

properties







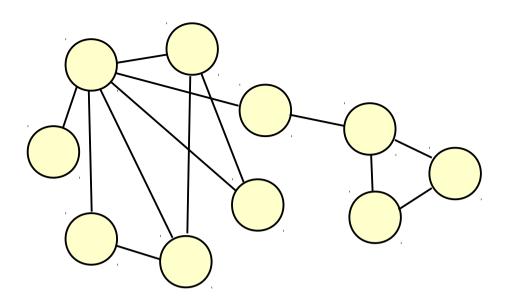
The challenges ahead: Bridging the gaps

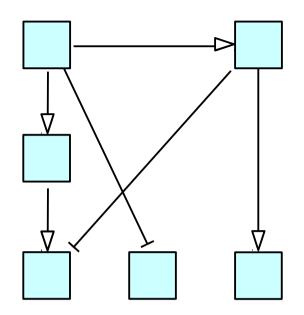
Types of representation

Scales and the mesoscopic gap

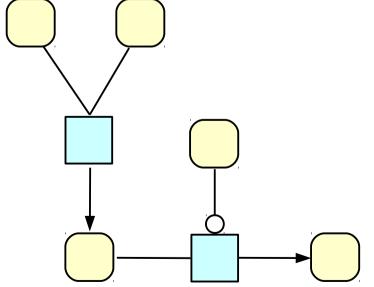
Drug discovery models Vs systems modelling

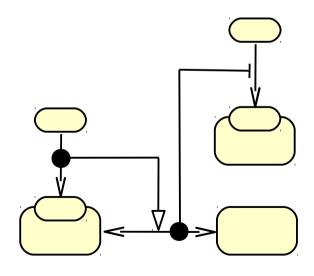
Drug discovery models Vs "omics" data



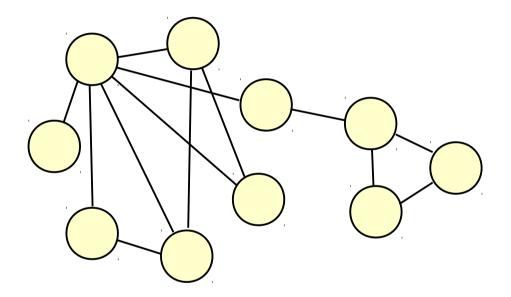


The four views of systems biology



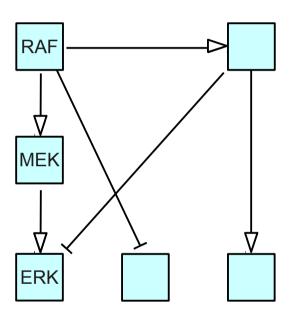


Interaction networks



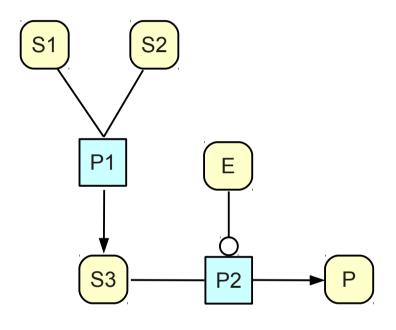
- Non-directional
- Non-sequential
- Non-mechanistic
- Statistical modelling
- Functional genomics
- IntAct, DIP, String

Activity-Flows



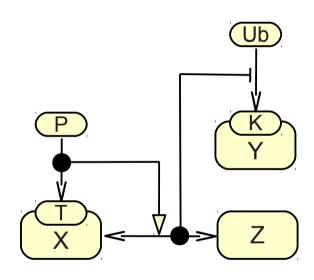
- Directional
- Sequential
- Non-mechanistic
- Logical modelling
- Signalling pathways, gene regulatory networks
- KEGG, STKEs

Process Descriptions

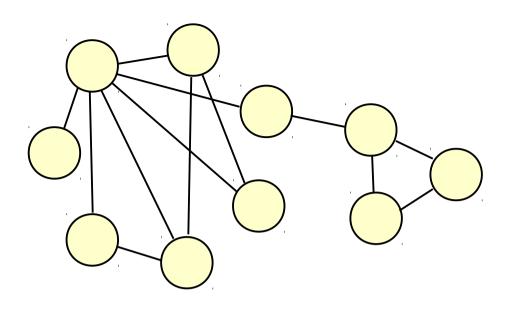


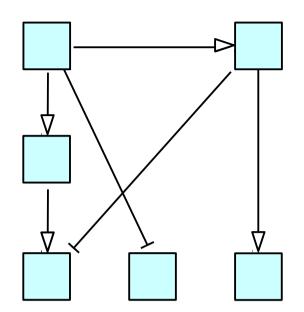
- Directional
- Sequential
- Mechanistic
- Subjected to combinatorial explosion
- Process modelling
- Biochemistry, Metabolic networks
- KEGG, Reactome

Entity Relationships

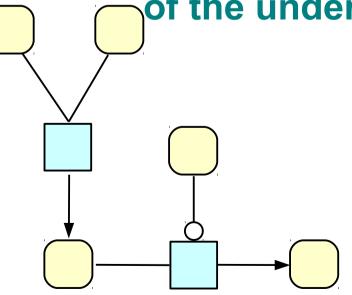


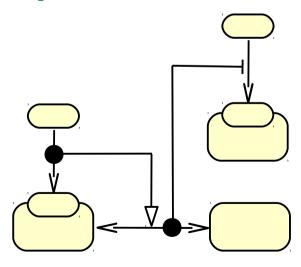
- Directional
- Non-sequential
- Mechanistic
- Independent rules: no explosion
- Rule-based modelling
- Molecular Biology
- MIM

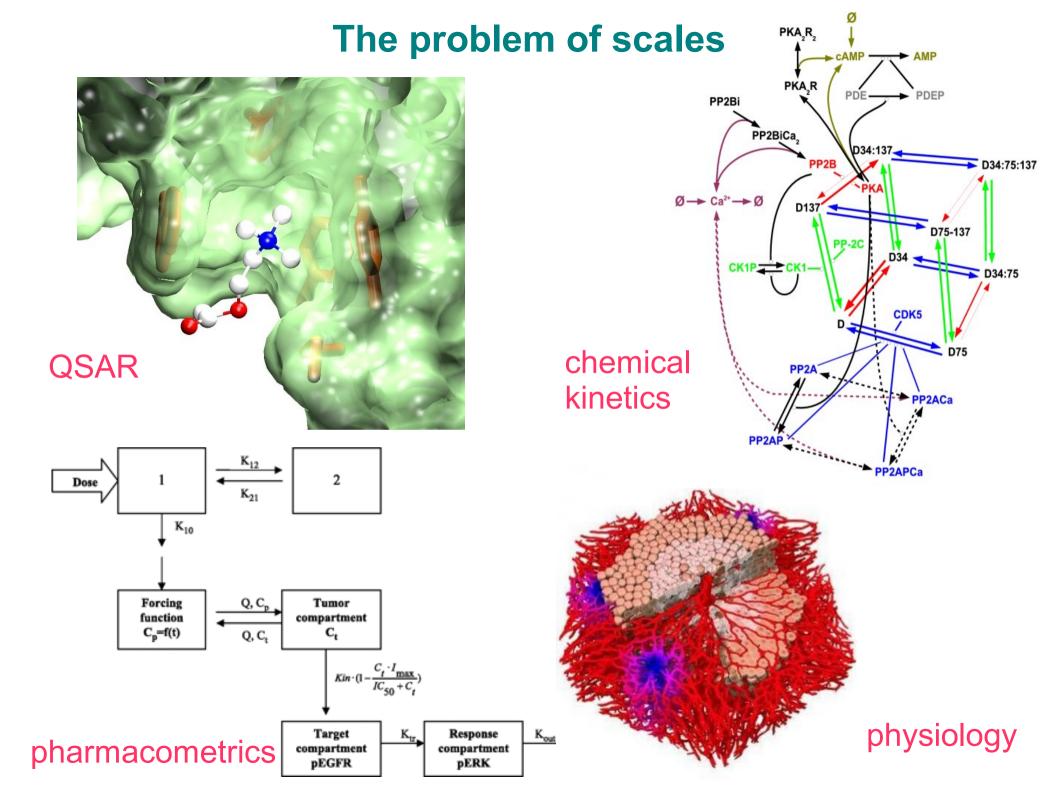




The four views are <u>orthogonal</u> projections of the underlying biological phenomena

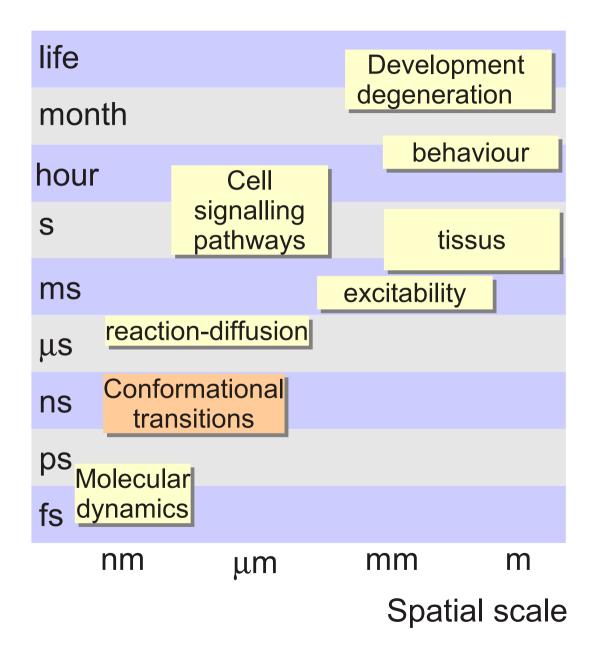




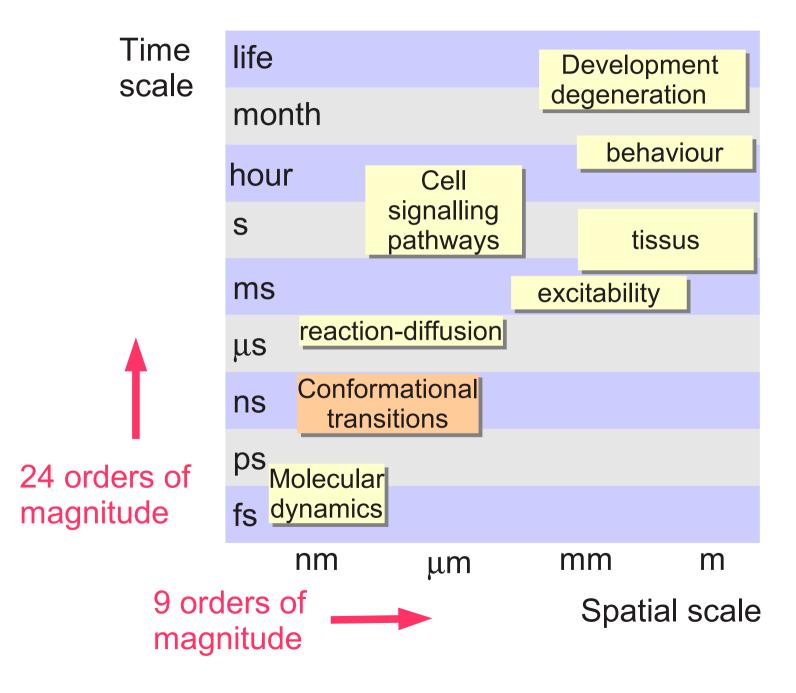


The mesoscopic gap

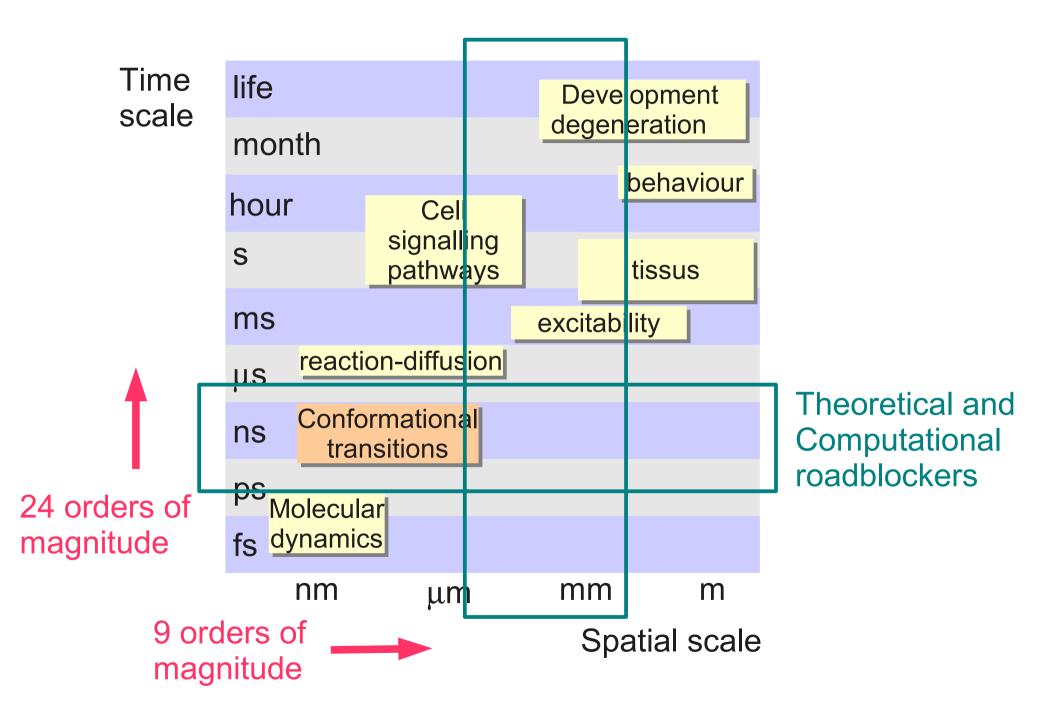
Time scale



The mesoscopic gap

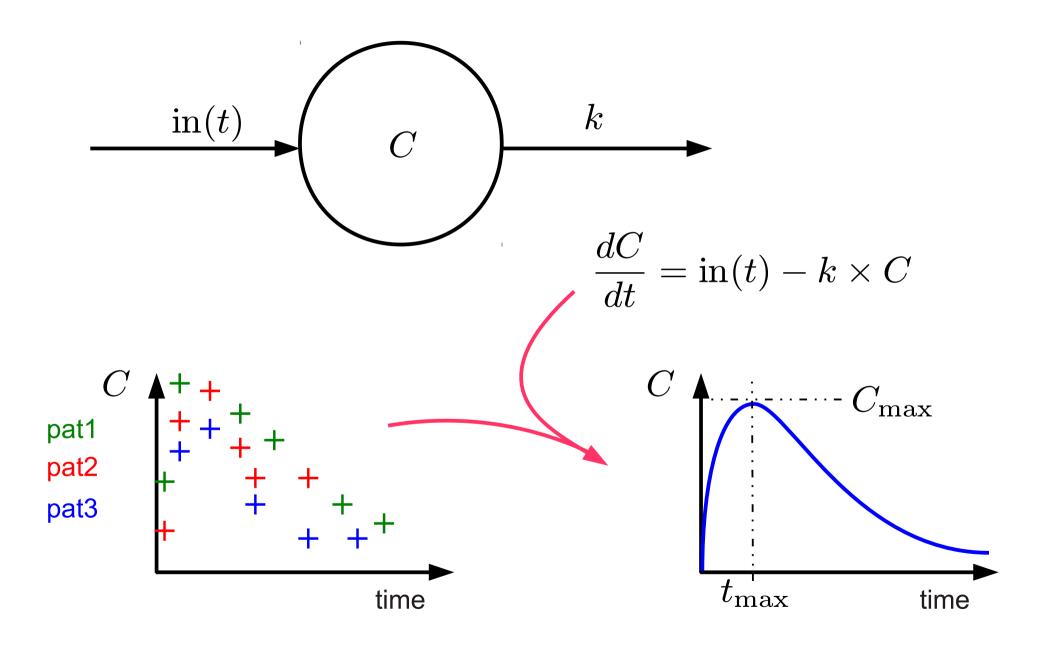


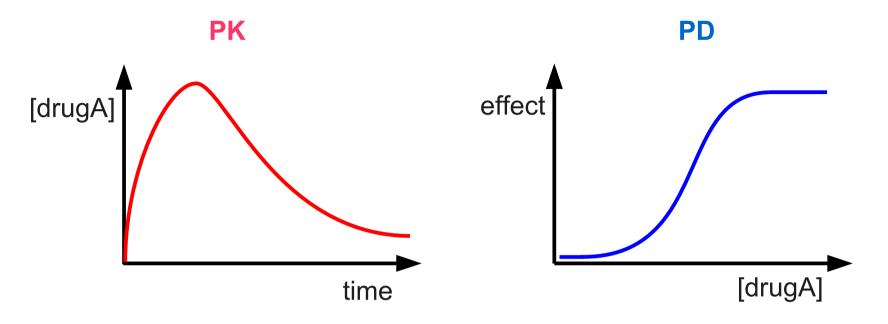
The mesoscopic gap

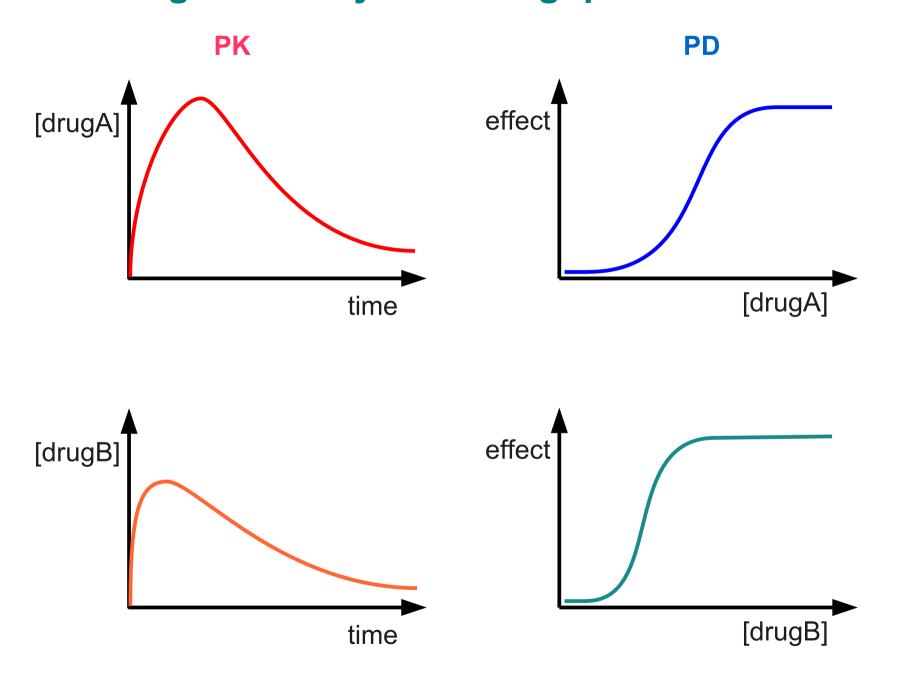


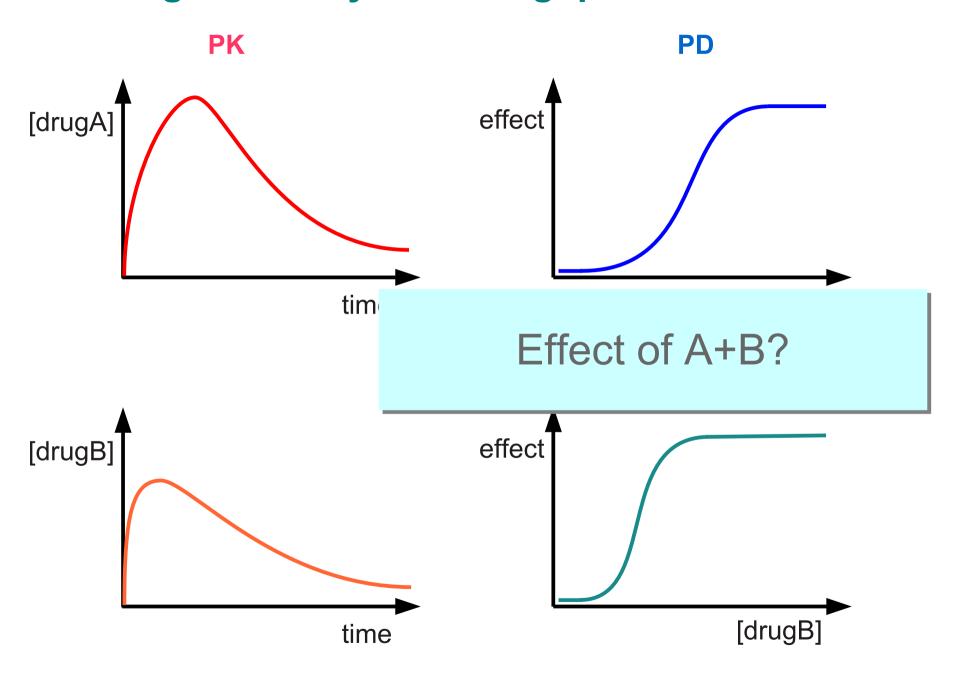
Multi-scale does not mean fine scale plus massive power

- Computational issues
 - In 2008, largest simulations were 1 million atoms for 50 ns (using > 30 years CPU) and 10000 atoms for 0.5 ms.
 - E-coli ~ 1 million million atoms ...
 - We need at least 10¹⁴ more power to simulate E coliduring 1 s
- Theoretical issues
 - Molecular dynamics does not scale linearly with number of interactions
 - We do not know how to simulate mesoscopic phenomena: conformational transitions, secondary structure movements etc.

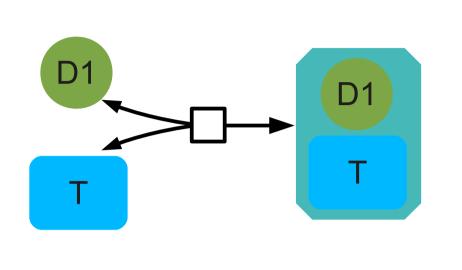


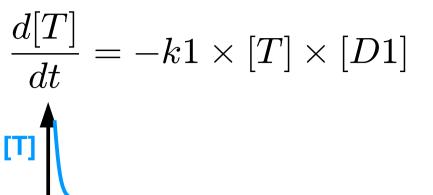


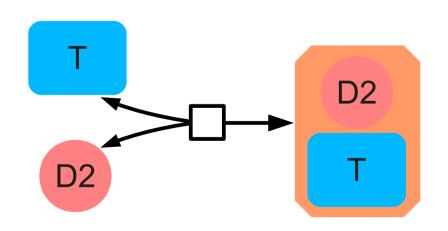


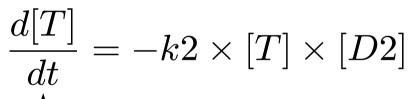


Systems modelling

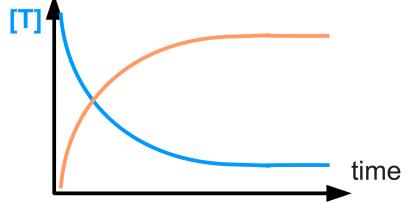






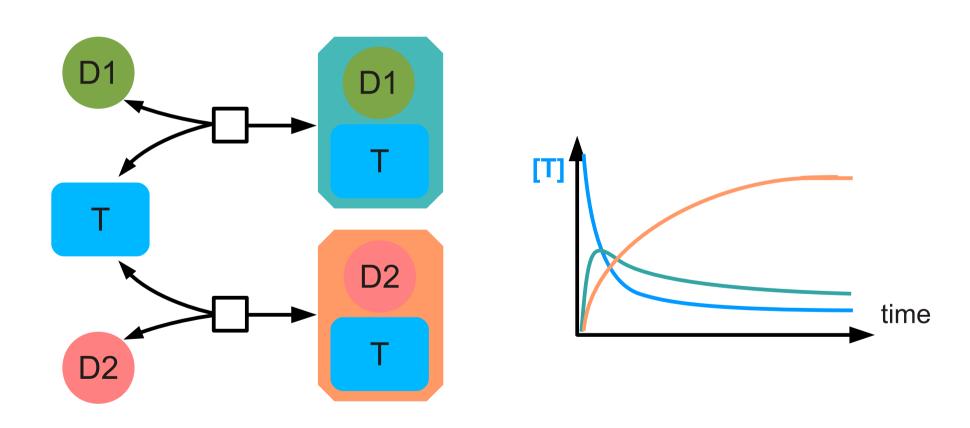


time

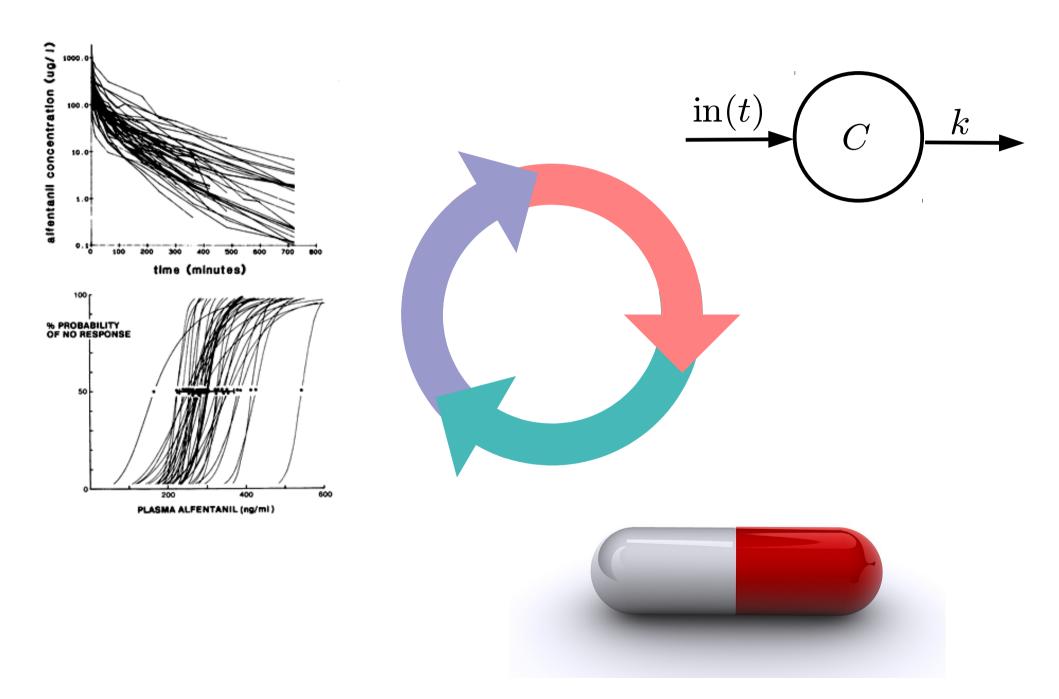


Systems modelling

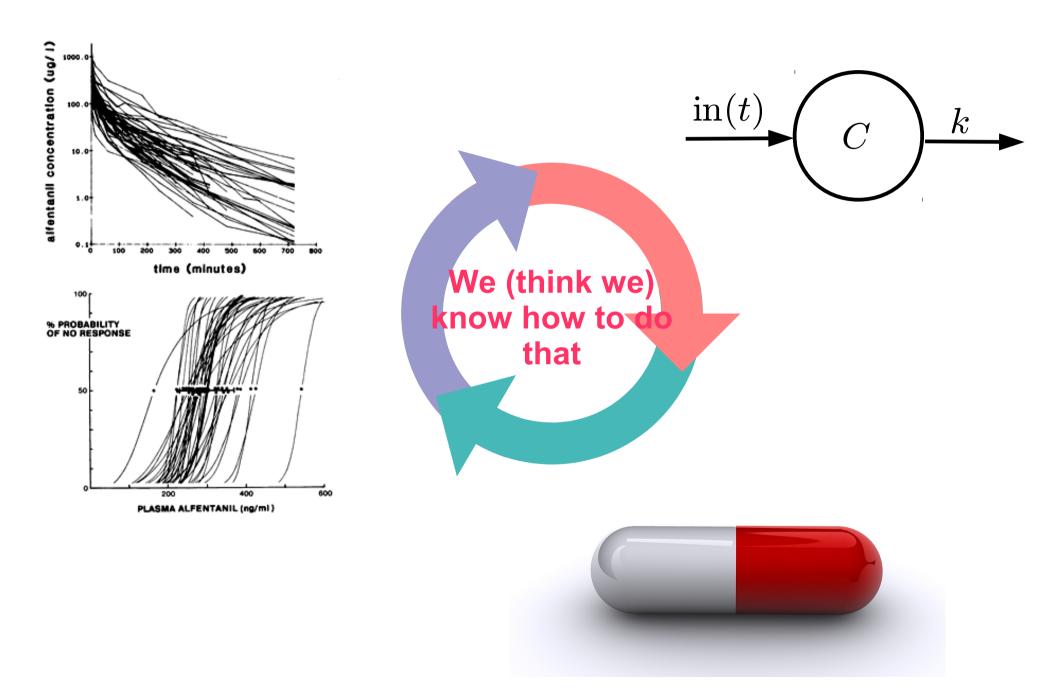
$$\frac{d[T]}{dt} = -k1 \times [T] \times [D1] - k2 \times [T] \times [D2]$$



Drug discovery and pharmacometrics models



Drug discovery and pharmacometrics models



Drug discovery and omics

