

What is Systems Biology?
Where does it come from ?
What are the challenges ahead?

Nicolas Le Novère, EMBL-EBI

What happened to Biology at the end of XXth century?

Annu. Rev. Genomics Hum. Genet. 2001. 2:343-72
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A NEW APPROACH TO DECODING LIFE: Systems Biology

Trey Ideker^{1,2}, Timothy Galitski¹, and Leroy Hood^{1,2,3,4,5}
Institute for Systems Biology¹, Seattle, Washington 98105; Departments of

New Generation Computing, 18(2000)199-216
Ohmsha, Ltd. and Springer-Verlag

invited paper

Perspectives on Systems Biology

Hiroaki KITANO
Sony Computer Science Laboratories, Inc.

**NEW
GENERATION
COMPUTING**
©Ohmsha, Ltd.



Emergence of the notion of system

XVI

XVII

XVIII

XIX

XX

XXI

Global Description of the world

“classical” mechanic, anatomy, physiology

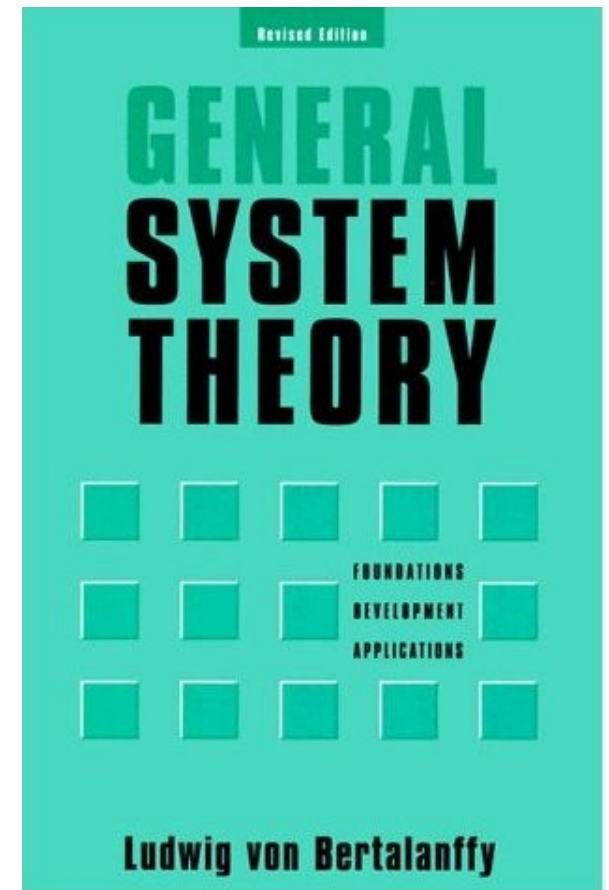
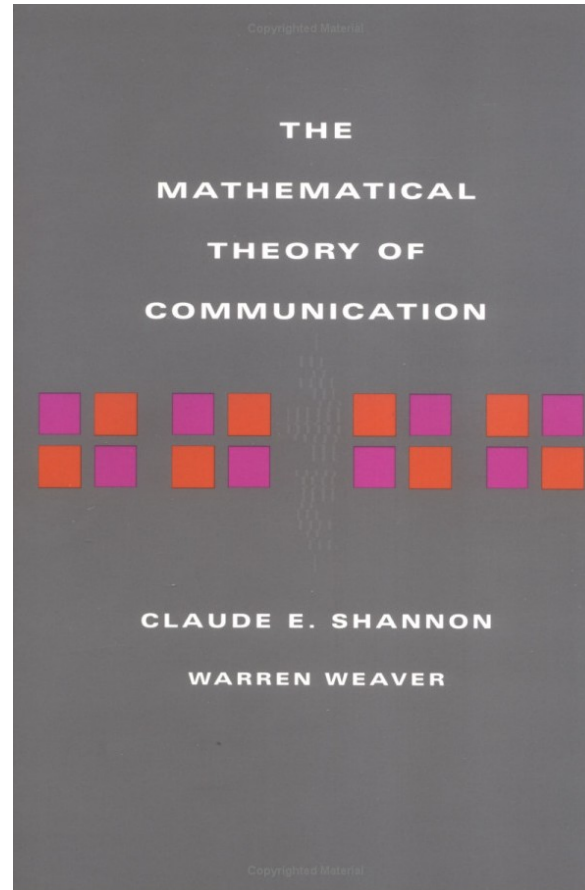
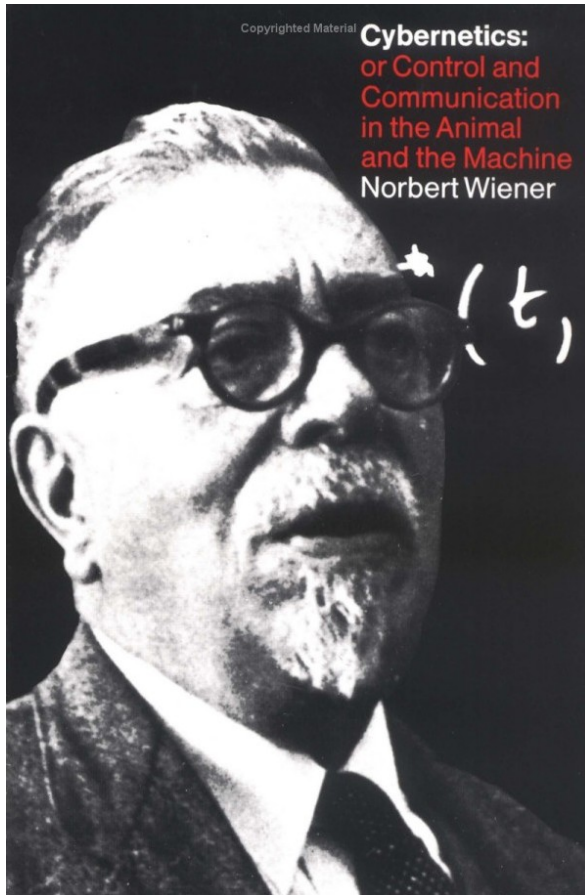
Description of the components of the world

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

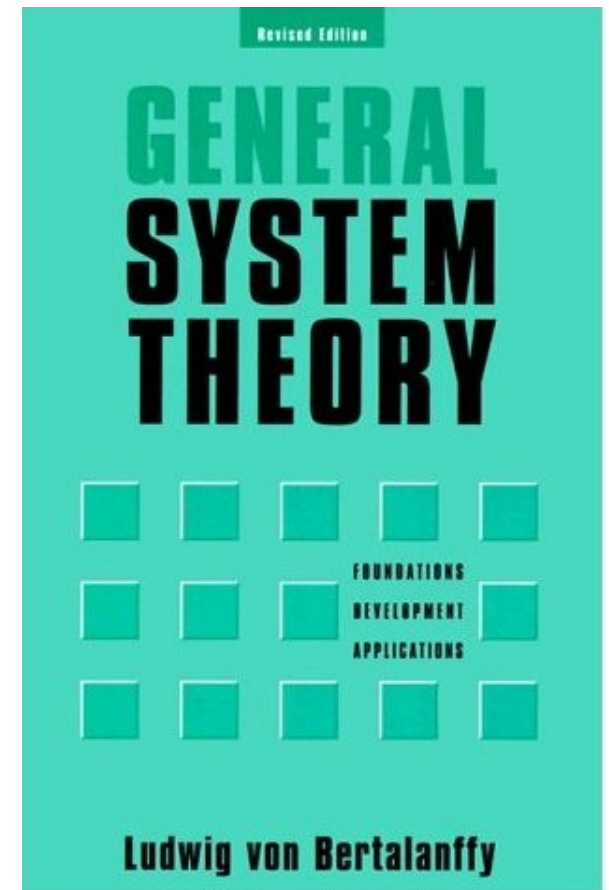
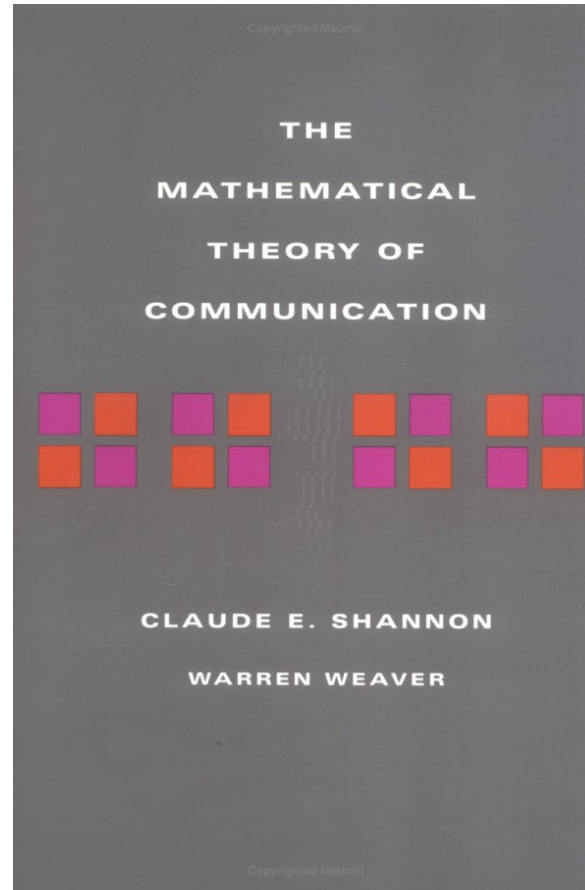
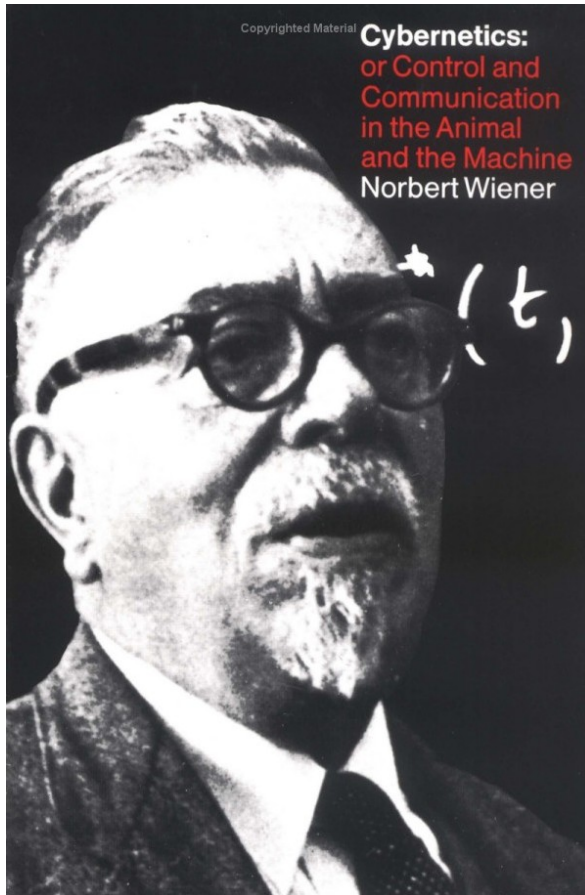
Description of interacting components

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

Systems are formalised mid-XXth

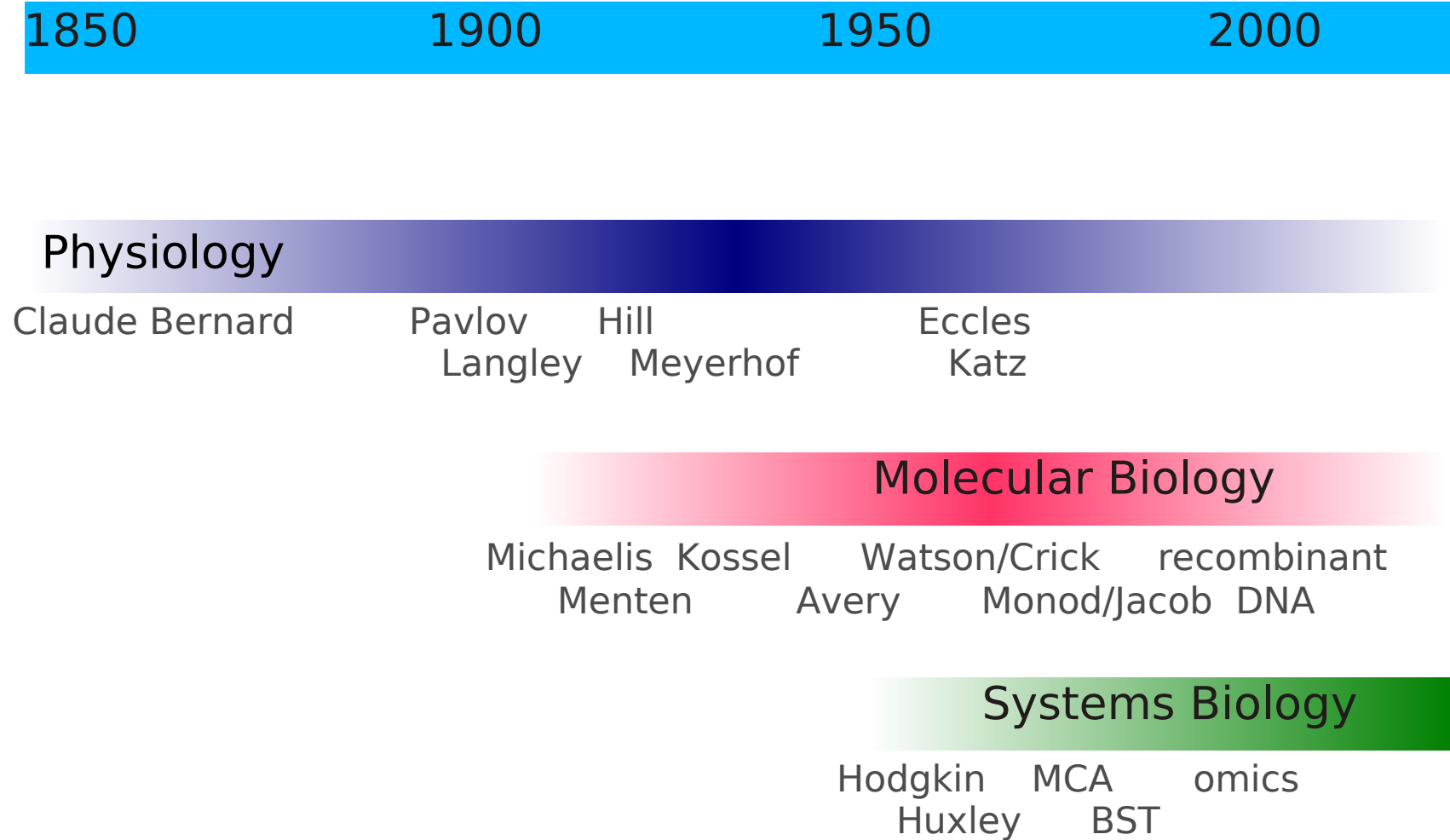


Systems are formalised mid-XXth



"[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 Bertalanffy, 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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(Received 9 November 1951—Revised 15 March 1952)

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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

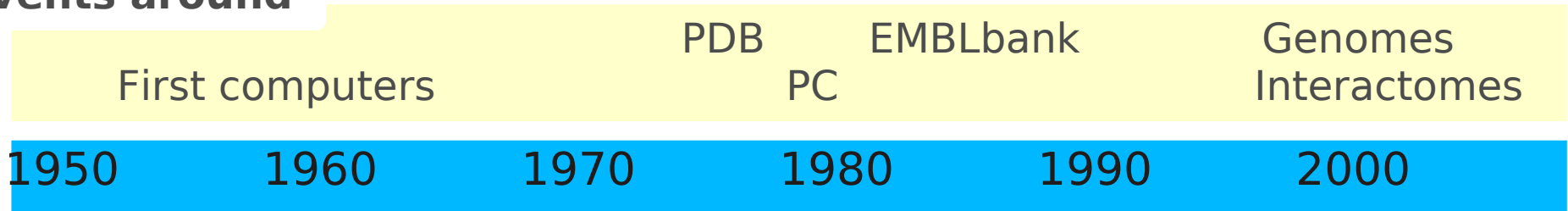
From the Physiological Laboratory, University of Cambridge

(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).

Towards Systems Biology

Events around



Towards Systems Biology

Events around

First computers			PDB	EMBLbank	Genomes
			PC		Interactomes
1950	1960	1970	1980	1990	2000
Hodgkin-Huxley			Goldbeter	Cell Cycle models	
Dennis Noble			Koshland	signalling models	
heart pacemaker			covalent	metabolic models	
			cascades	models of gene reg	
				whole heart	

models

Towards Systems Biology

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models

Rall's cable approximation	complex neurons	simple circuits	Purkinje Neuron	Blue Brain Project
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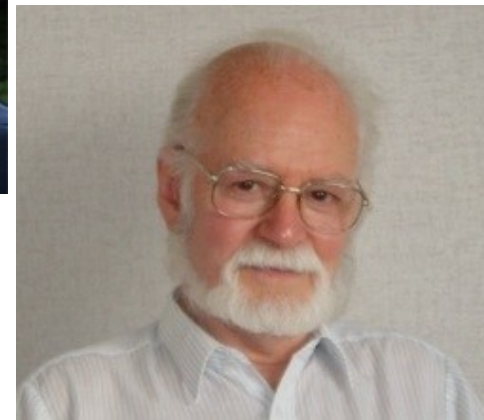
neurobiology

60s and 70s

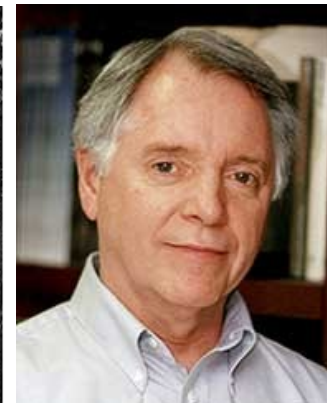
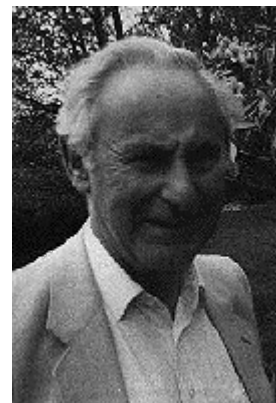
- Mihajlo Mesarovic: 1966 Symposium
“general systems theory and biology



- Stuart Kaufmann,
Rene Thomas: 1969-73
boolean networks for
gene regulation



- Henri Kacser:
Metabolic control analysis,
Michel Savageau:
Biochemical Systems Theory



Towards Systems Biology

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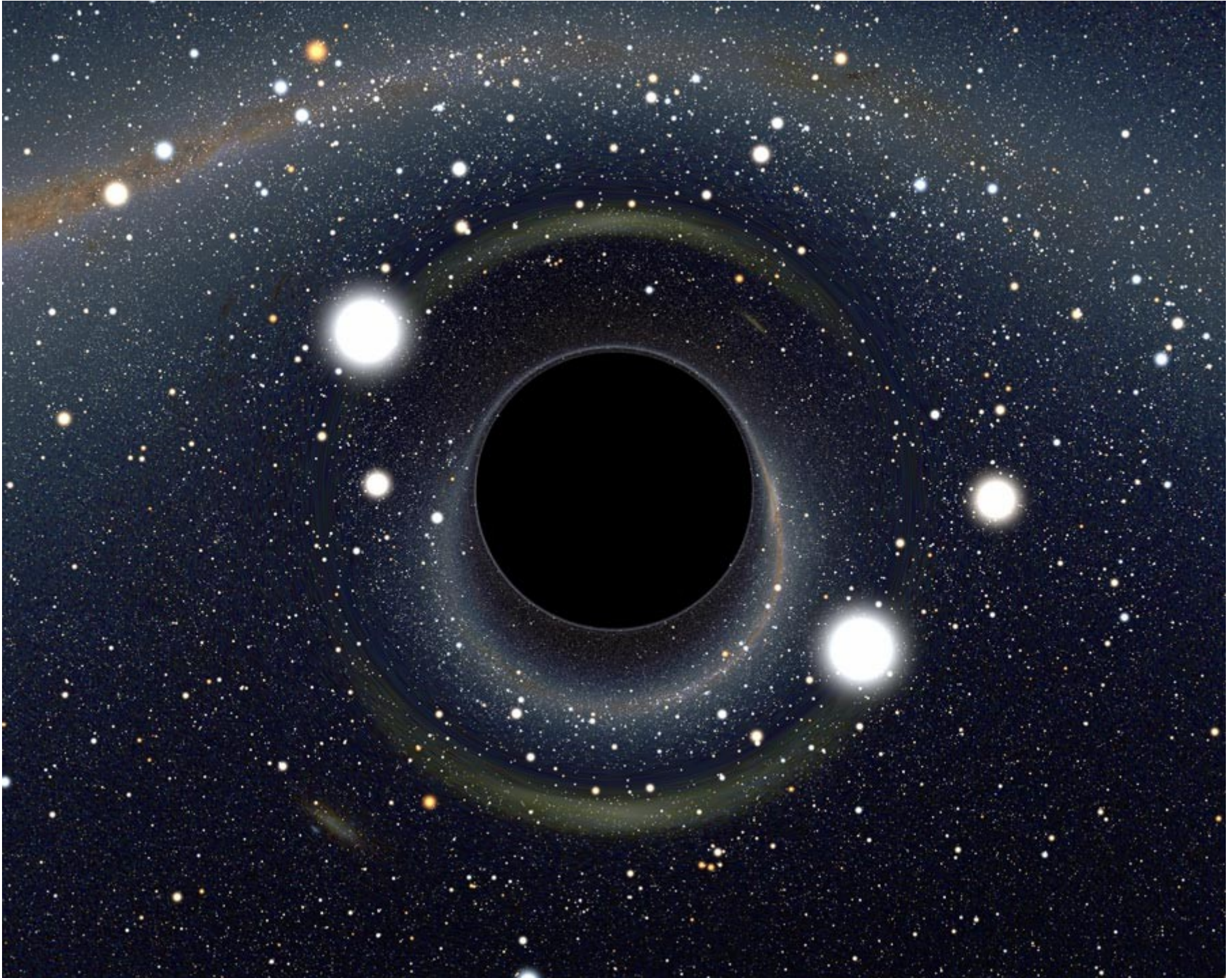
Rall's cable approximation	complex neurons	simple circuits	Purkinje Neuron	Blue Brain Project
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neurobiology

MCA/BST	multi-agent	user-friendly	SBML
	stochastic algorithms	systems	biochemical
			simulators

methods

80s: The reign of Molecular Biology



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
- Structuring 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

Towards Systems Biology

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Barabasi
Repressilator

Towards Systems Biology

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models

Rall's cable approximation	complex neurons	simple circuits	Purkinje Neuron	Blue Brain Project
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neurobiology

MCA/BST	multi-agent	user memory	Synthetic Biology	
stochastic systems	biochemical	simulators		

methods

Network Biology

Barabasi
Repressilator

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

Rise of Systems Biology as a paradigm

1998 1999 2000 2001 2002 2003 2004 2005 2006 2007

Rise of Systems Biology as a paradigm

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ERATO-Kitano

Alliance for Cellular Signaling

SystemsX

HepatoSys

SysBio enters FP6

YSBN

ERASysBio

projects

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Von Dassow

SBML

Klipp

Alon

Choi

Annual Review Science

Kriete

Palsson

publications

Ideker/Hood special issue

Boogerd

"Foundations of Systems Biology"

Kaneko

Szallasi

Grierson

Computational Cell Biology"

IEE Sys Bio

MSB

BMC Sys Bio

Rise of Systems Biology as a paradigm

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Institutes

Tokyo Systems Biology Institute

Seattle Institute for Systems Biology

6 BBSRC centres

BioQuant

Rise of Systems Biology as a paradigm

1998 1999 2000 2001 2002 2003 2004 2005 2006 2007

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Sy

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End of BBSRC
Systems Biology
calls

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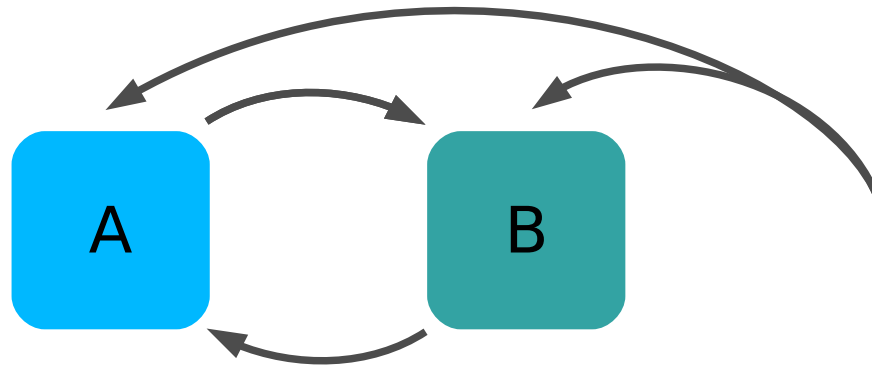
What is Systems Biology?

Molecular and Cellular Biology

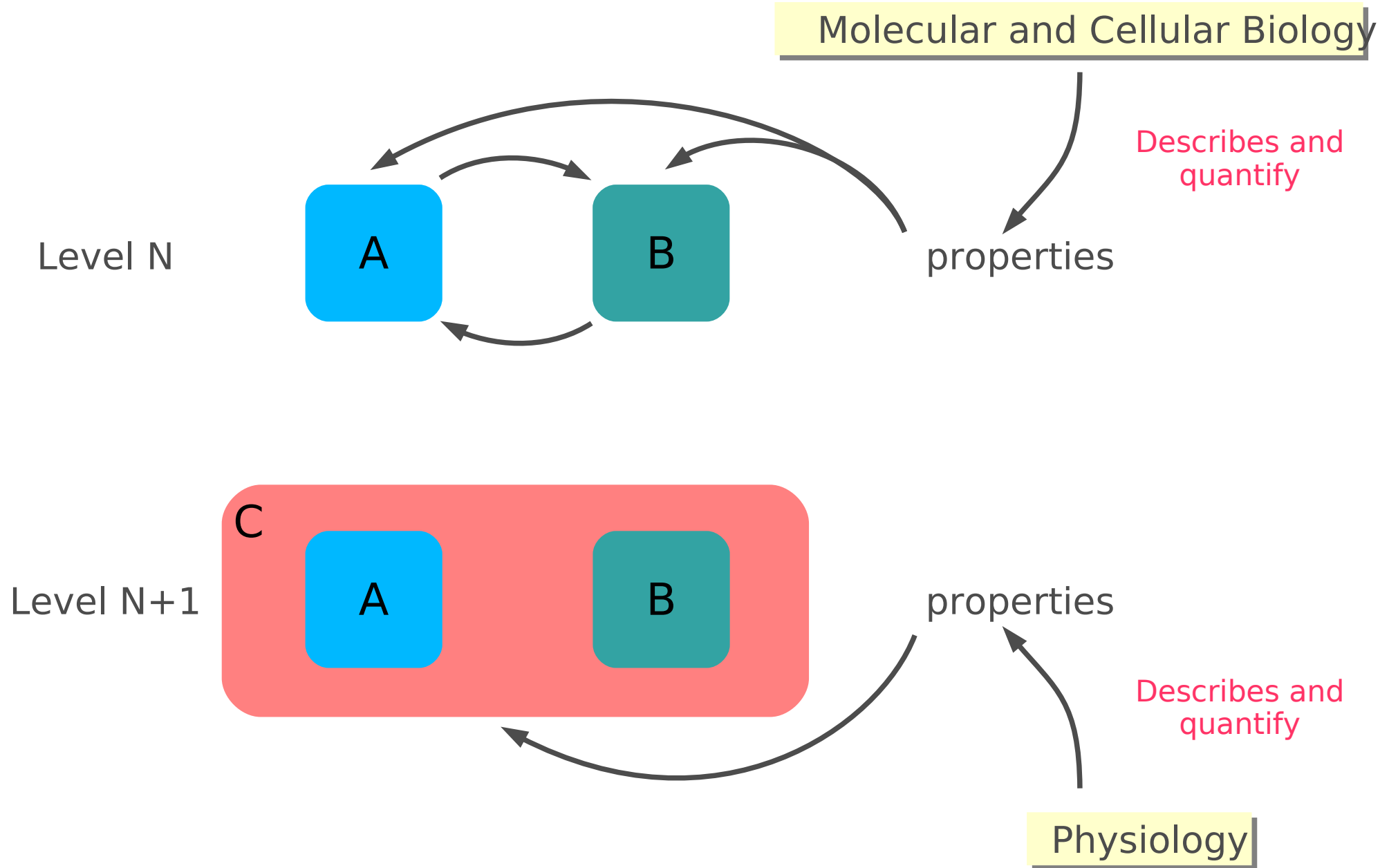
Describes and
quantify

properties

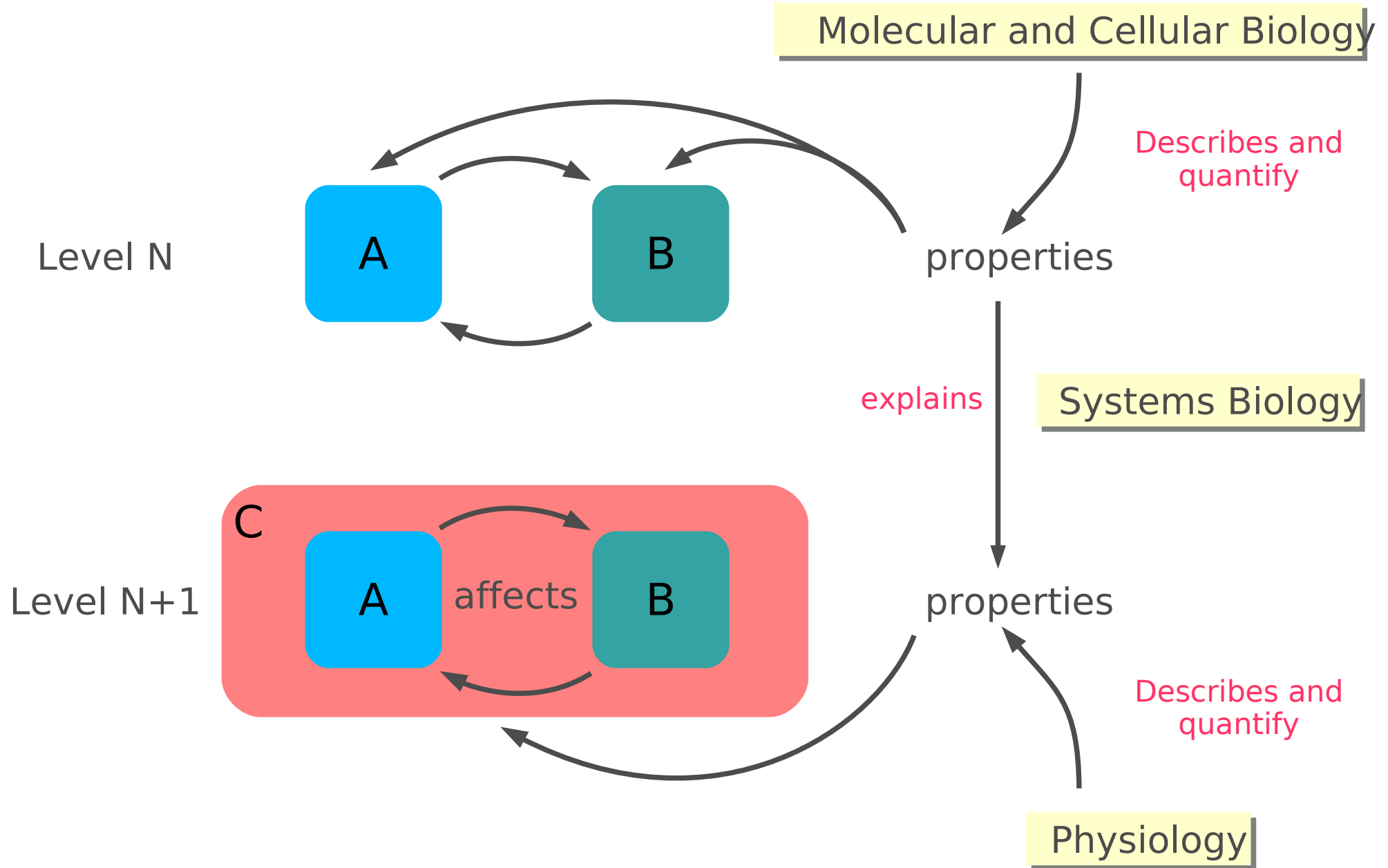
Level N



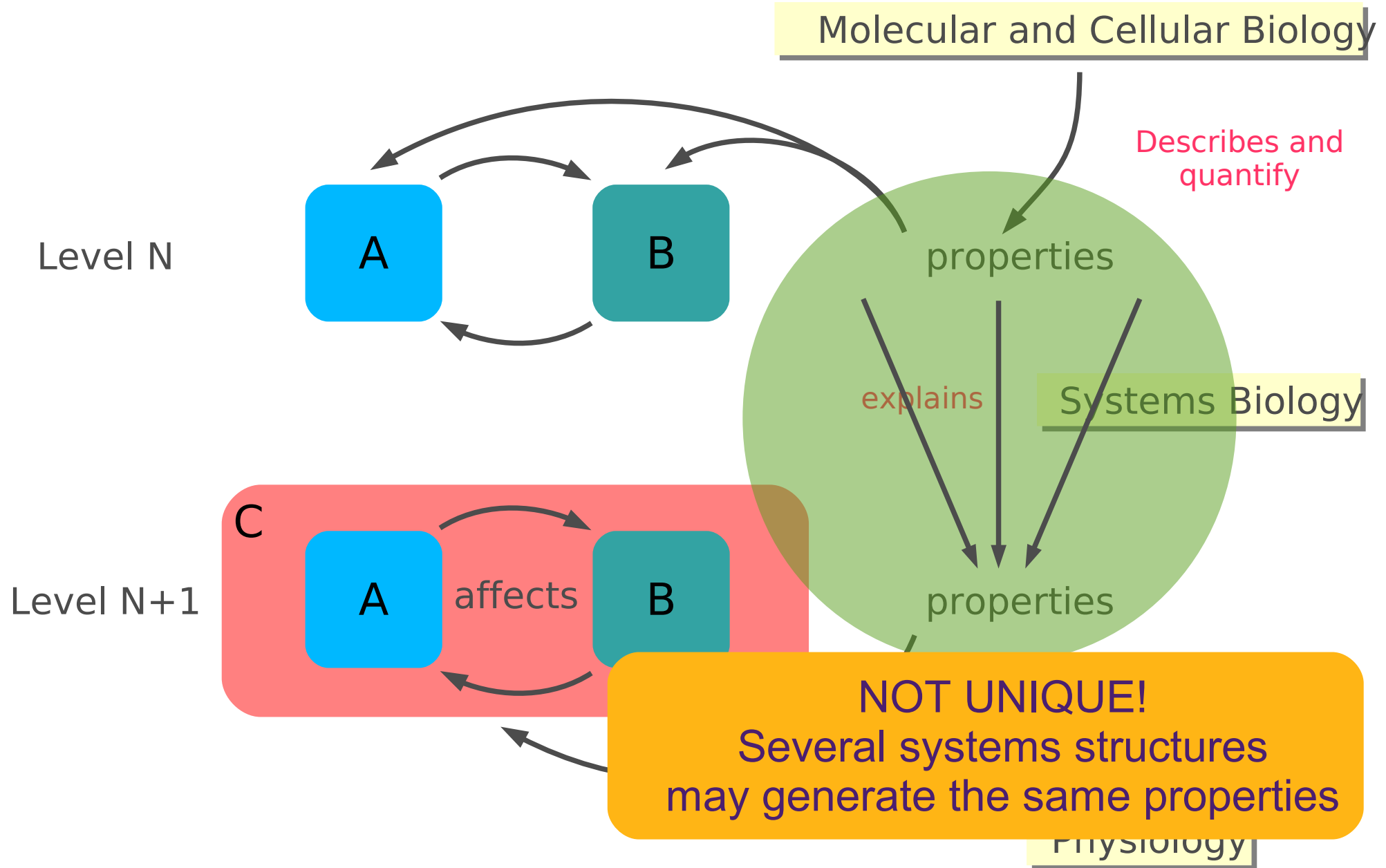
What is Systems Biology?



What is Systems Biology?



What is Systems Biology?



What Systems Biology is not

Purely theoretical: Most systems biologists are actually experimental biologists

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Based on large datasets: in a system of two enzymes, the behaviour of both reactions is different than the ones observed in isolation

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Purely theoretical: Most systems biologists are actually experimental biologists

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Focused on biomolecular systems: systems biology is scale-free, and a biological system can be made up of molecules, cells, organs or individuals

What Systems Biology is not

Purely theoretical: Most systems biologists are actually experimental biologists

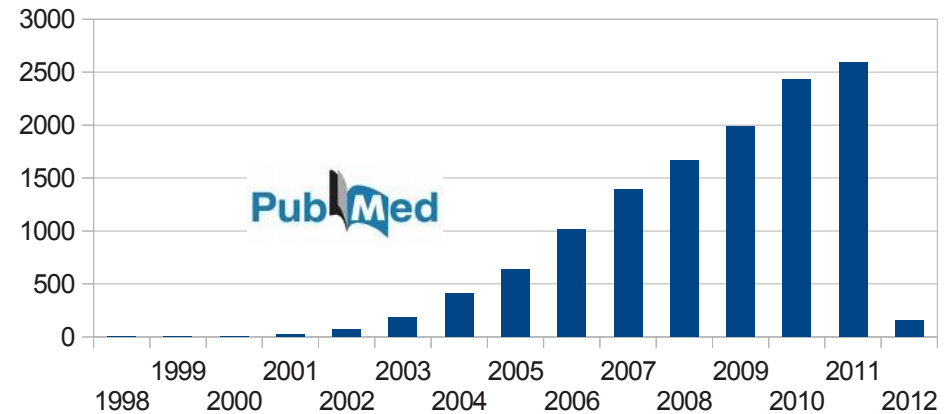
Based on large datasets: in a system of two enzymes, the behaviour of both reactions is different than the ones observed in isolation

Focused on biomolecular systems: systems biology is scale-free, and a biological system can be made up of molecules, cells, organs or individuals

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***

What is Systems Biology?

- First mention of the term: 1928 (L Von Bertalanffy)
- 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

The challenges ahead: Bridging the gaps

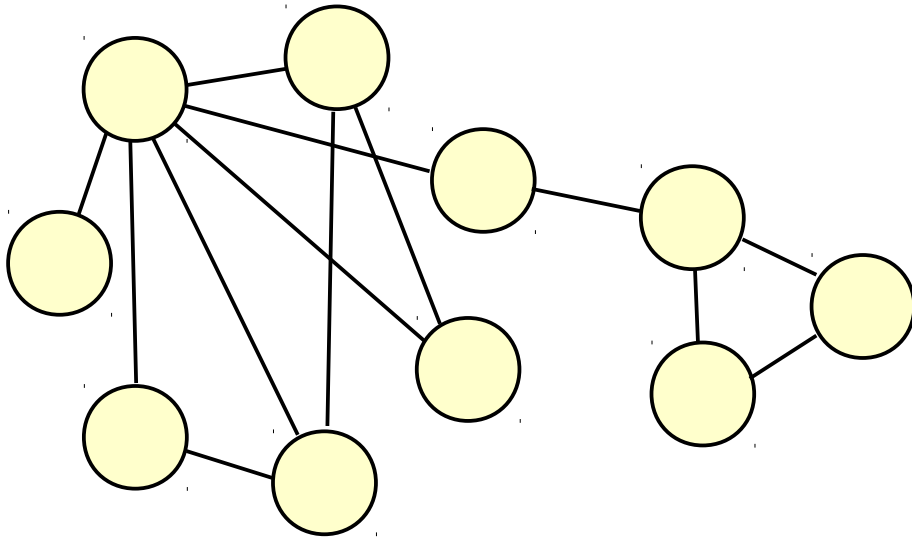
Types of representation

Scales and the mesoscopic gap

Drug discovery models
Vs systems modelling

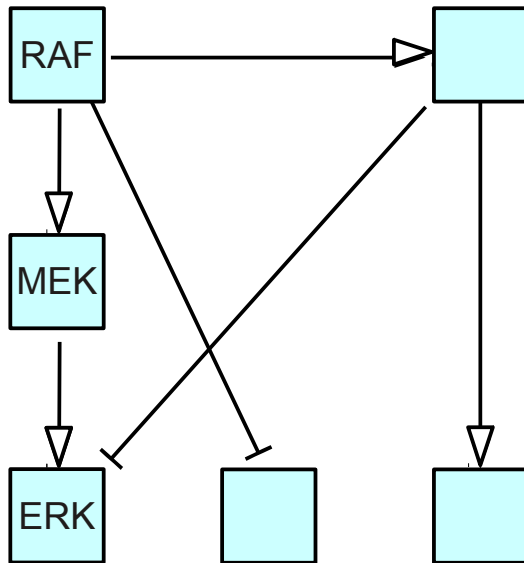
Drug discovery models
Vs “omics” data

Interaction networks



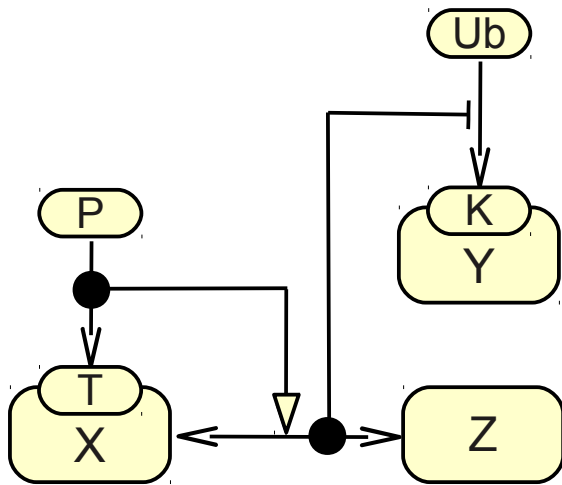
- Non-directional
- Non-sequential
- Non-mechanistic
- Statistical modelling
- Functional genomics
- IntAct, DIP, String

Activity-Flows



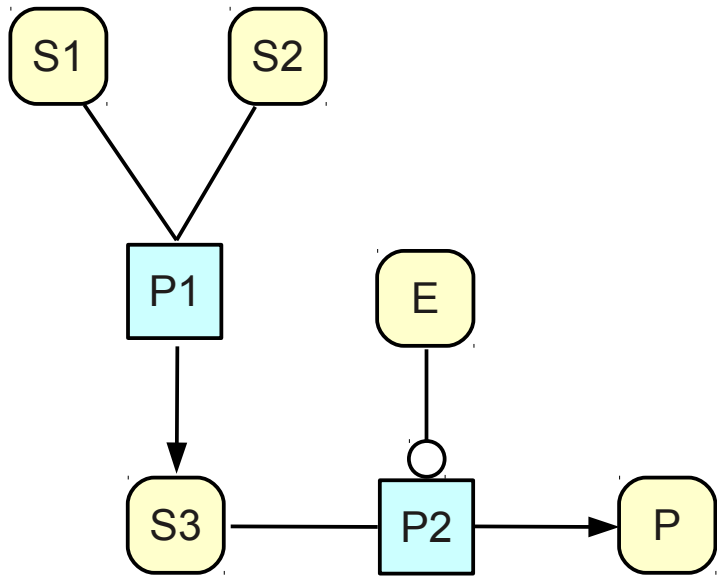
- Directional
- Sequential
- Non-mechanistic
- Logical modelling
- Signalling pathways, gene regulatory networks
- KEGG, STKEs

Entity Relationships

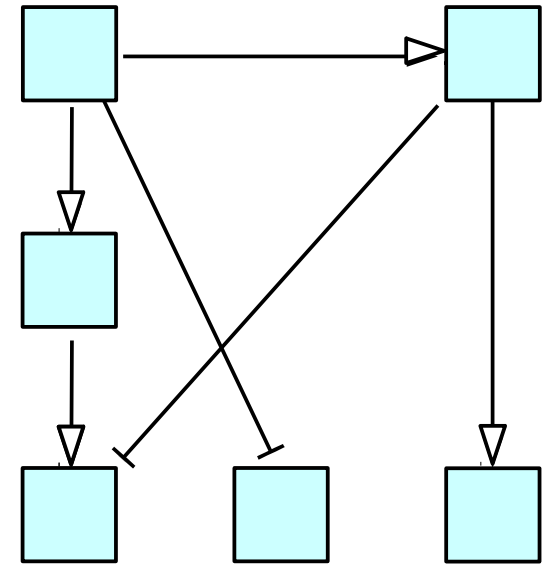
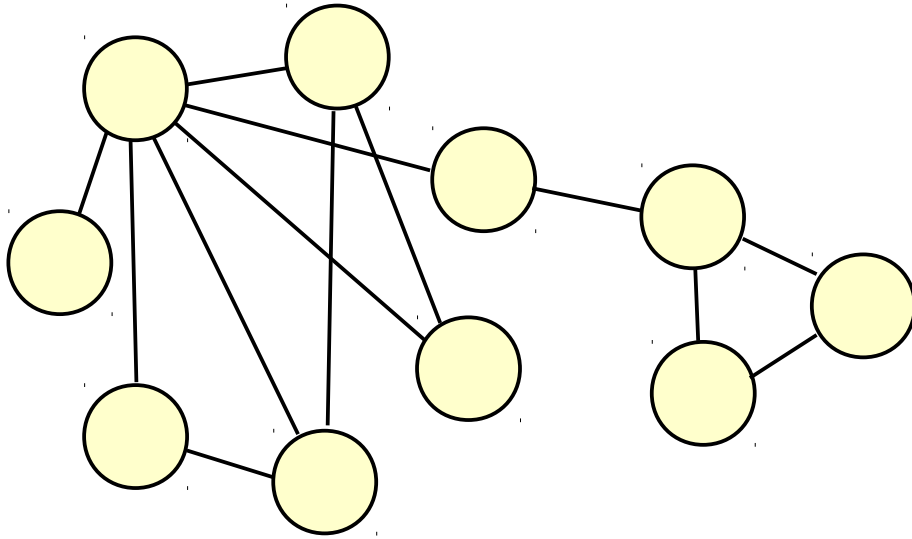


- Directional
- Non-sequential
- Mechanistic
- Independent rules: no explosion
- Rule-based modelling
- Molecular Biology
- MIM

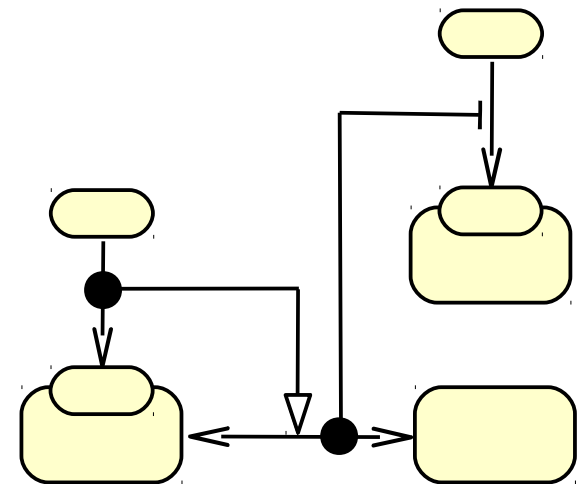
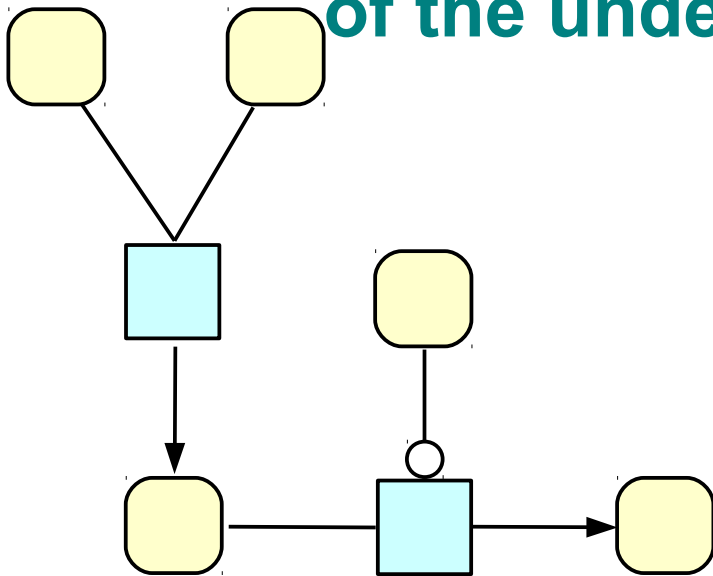
Process Descriptions

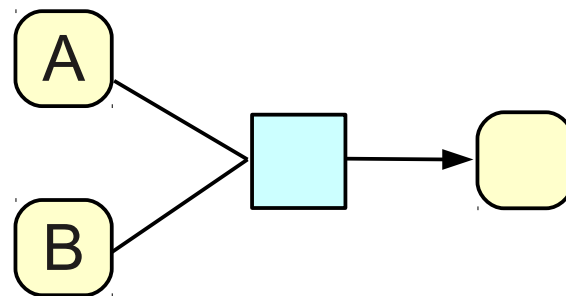
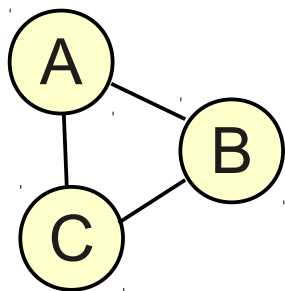


- Directional
- Sequential
- Mechanistic
- Subjected to combinatorial explosion
- **Process modelling**
- **Biochemistry**, Metabolic networks
- KEGG, Reactome

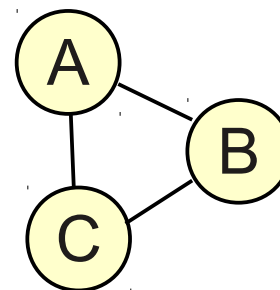
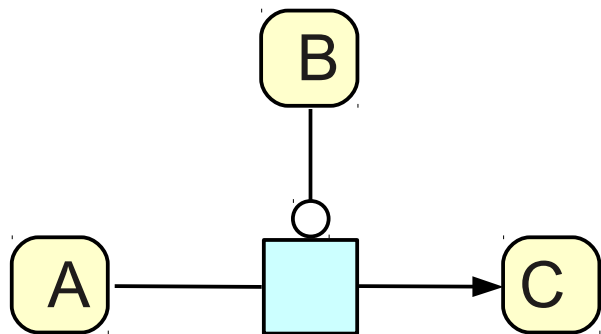


The four views are orthogonal projections of the underlying biological phenomena



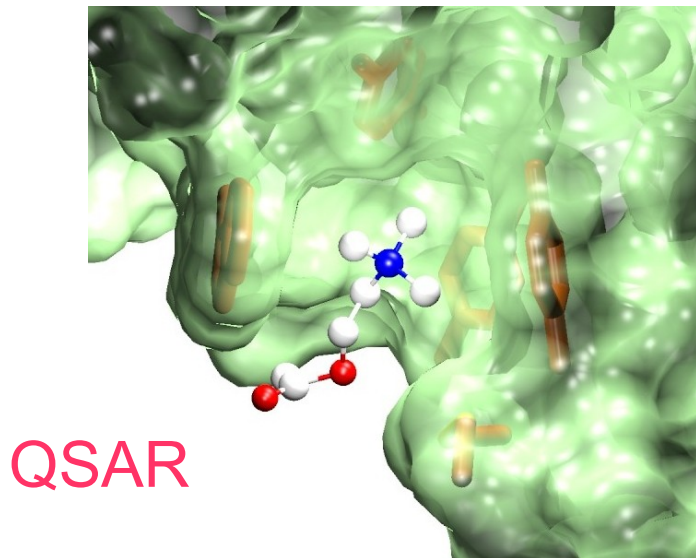


Think scaffolding proteins

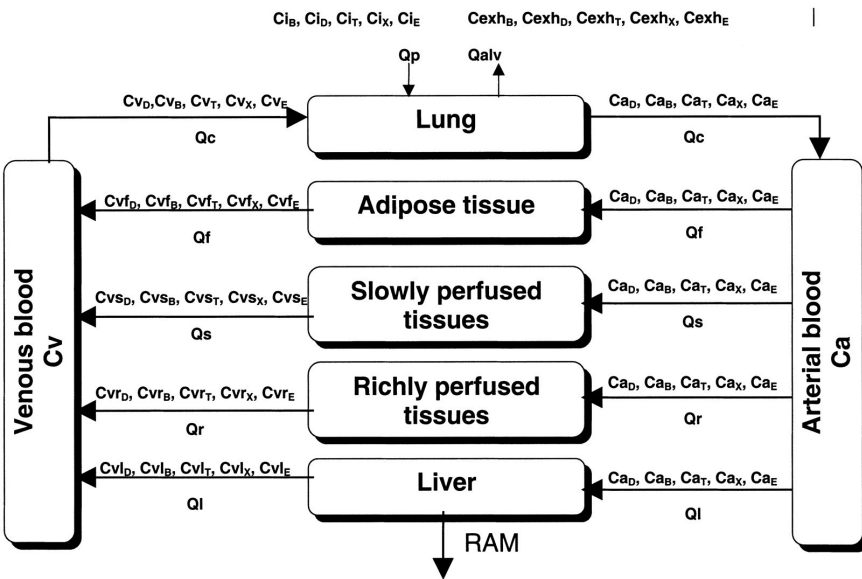
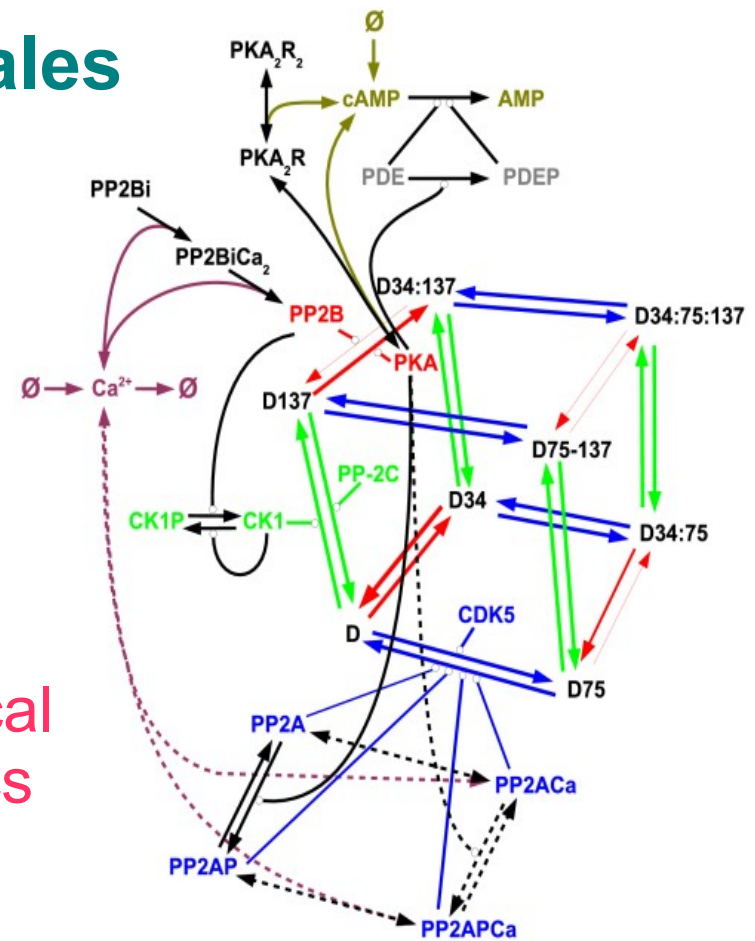


Think phosphorylated signals

The problem of scales



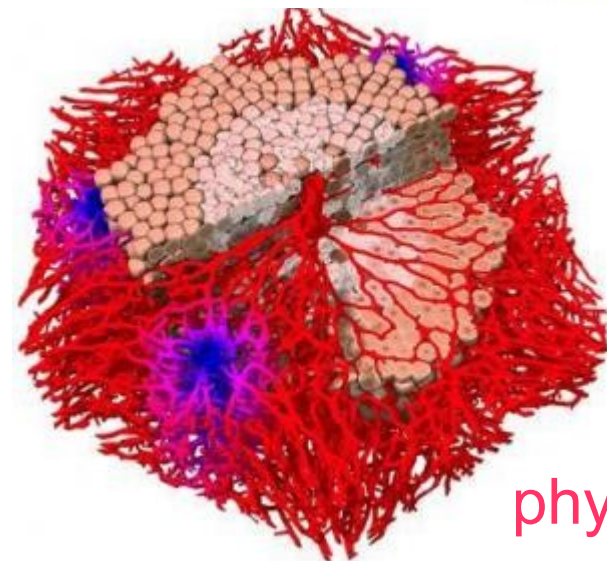
chemical kinetics



$$RAM_D = \frac{V_{max_D} C_{vD}}{K_{mD} \left(1 + \frac{C_{vD}}{K_{iD}} + \frac{C_{vR}}{K_{iR}} + \frac{C_{vL}}{K_{iL}} + \frac{C_{vE}}{K_{iE}} \right) + C_{vD}}$$

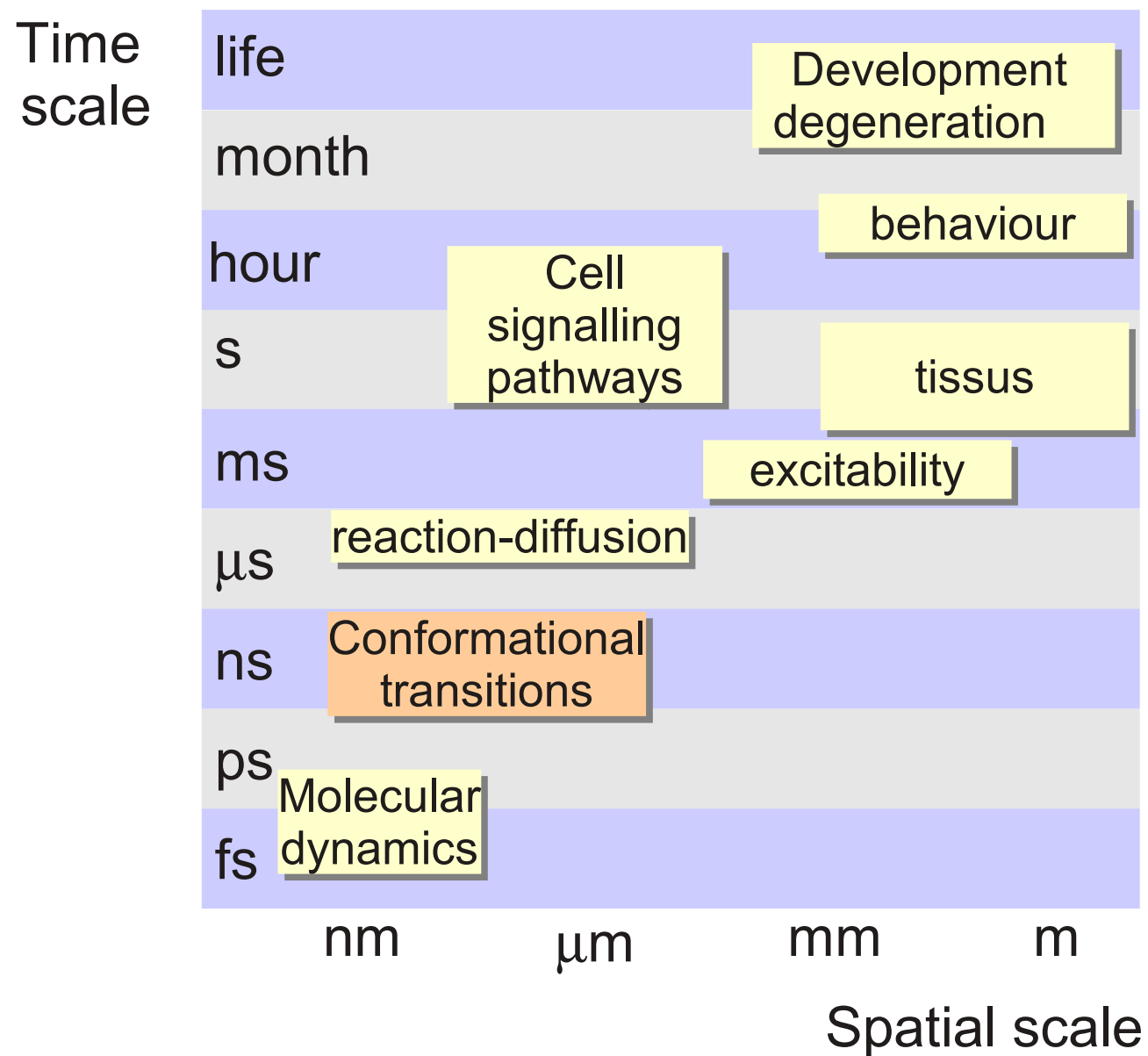
$$RAM_S = \frac{V_{max_S} C_{vS}}{K_{mS} \left(1 + \frac{C_{vD}}{K_{iD}} + \frac{C_{vR}}{K_{iR}} + \frac{C_{vL}}{K_{iL}} + \frac{C_{vE}}{K_{iE}} \right) + C_{vS}}$$

pharmacometrics

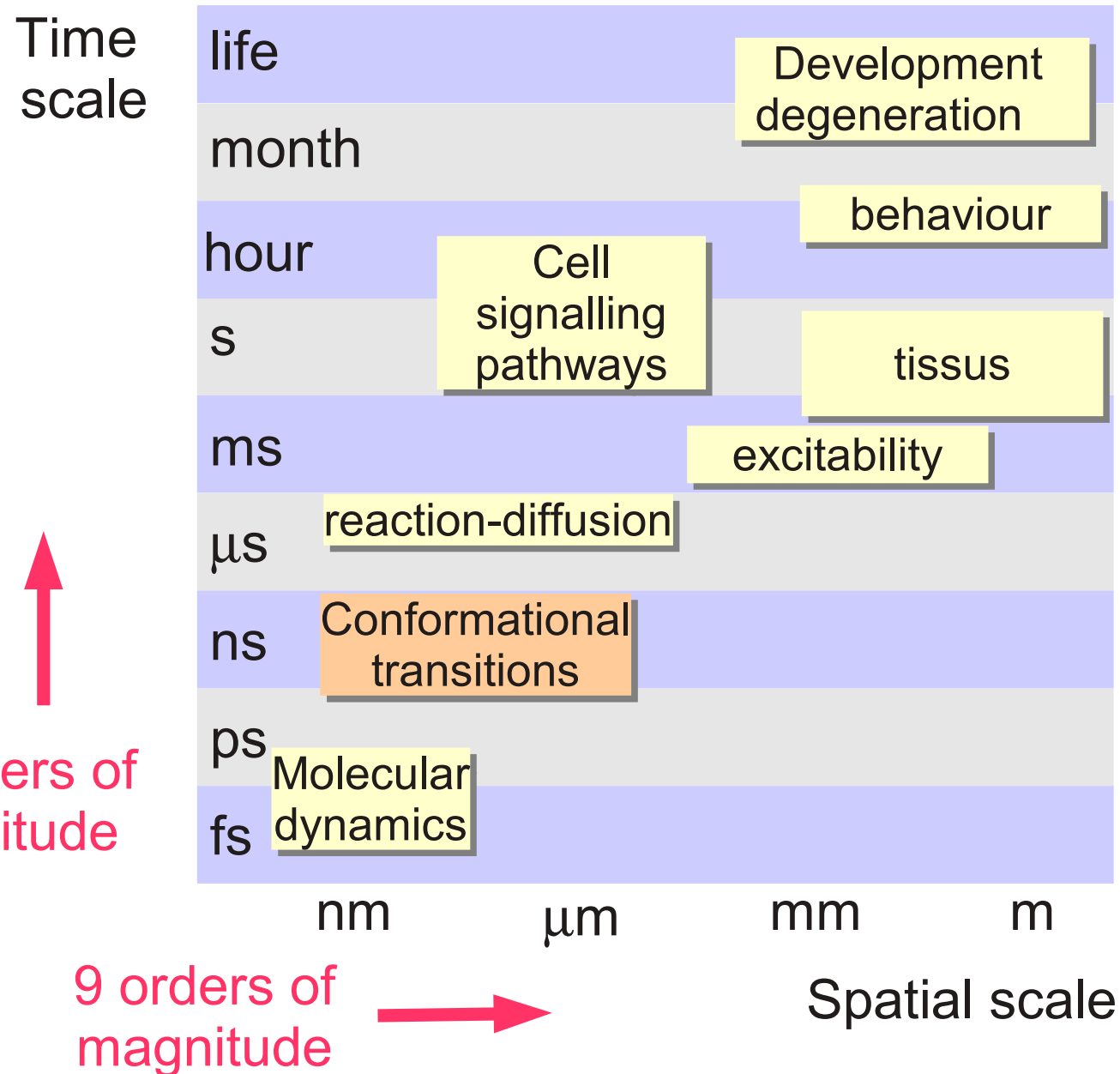


physiology

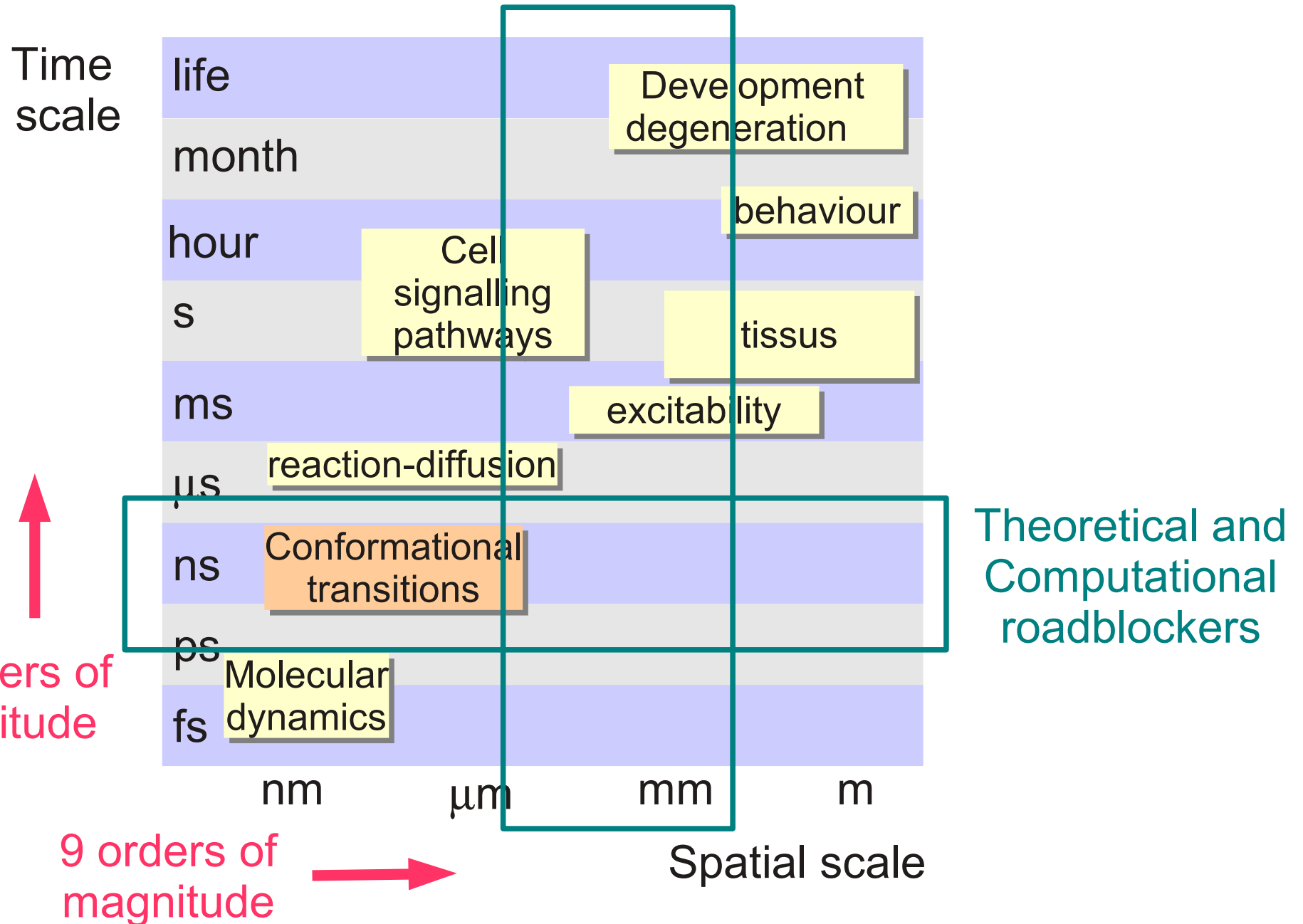
The mesoscopic gap



The mesoscopic gap



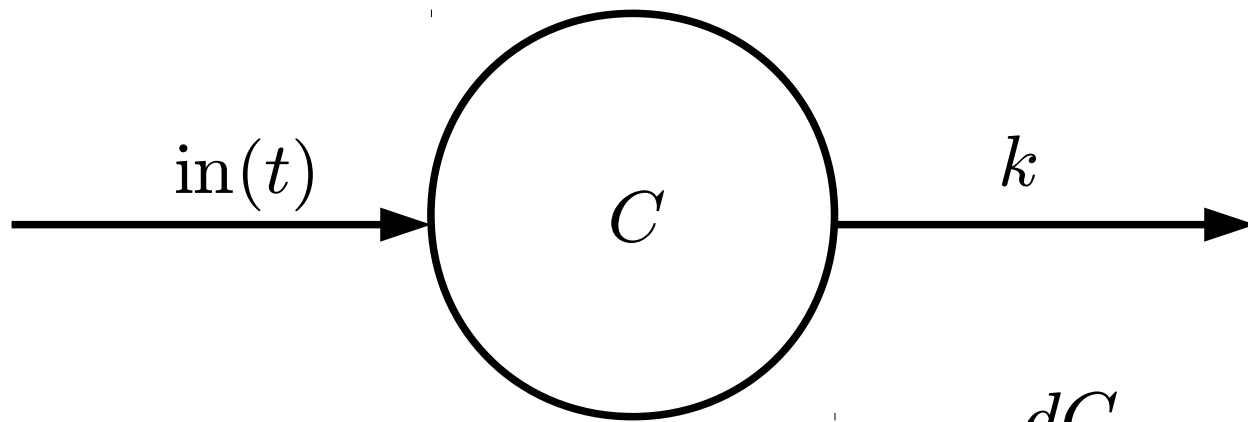
The mesoscopic gap



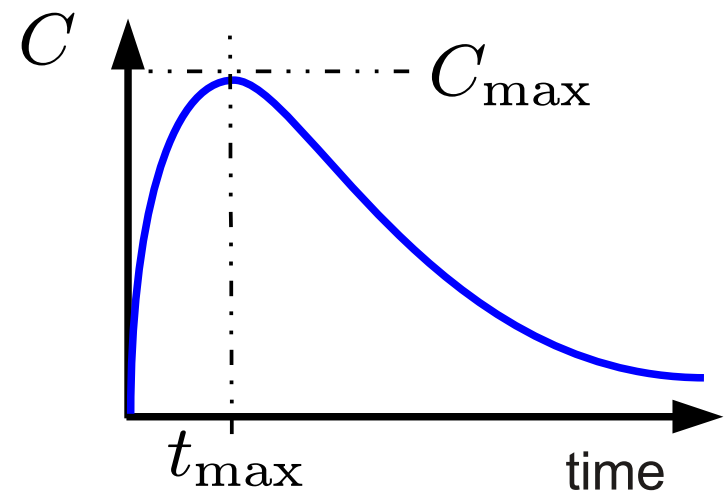
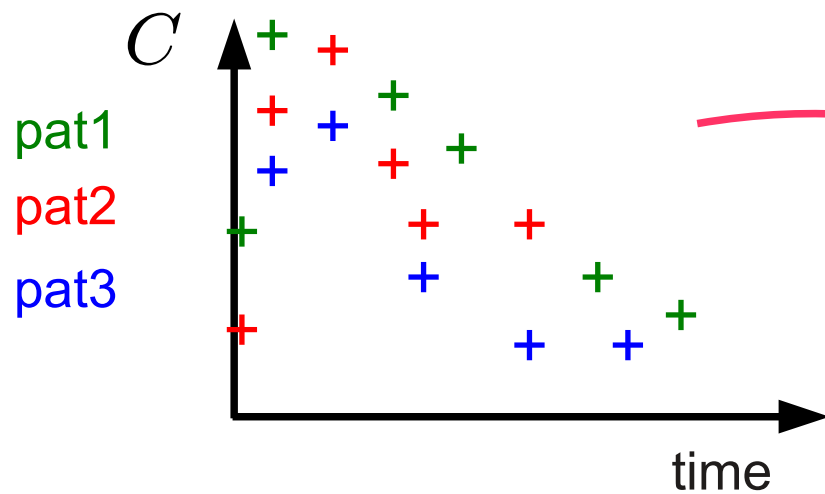
Multi-scale does not mean fine scale plus massive power

- 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 10^{14} more power to simulate E coli during 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.

Drug discovery modelling: pharmacometrics

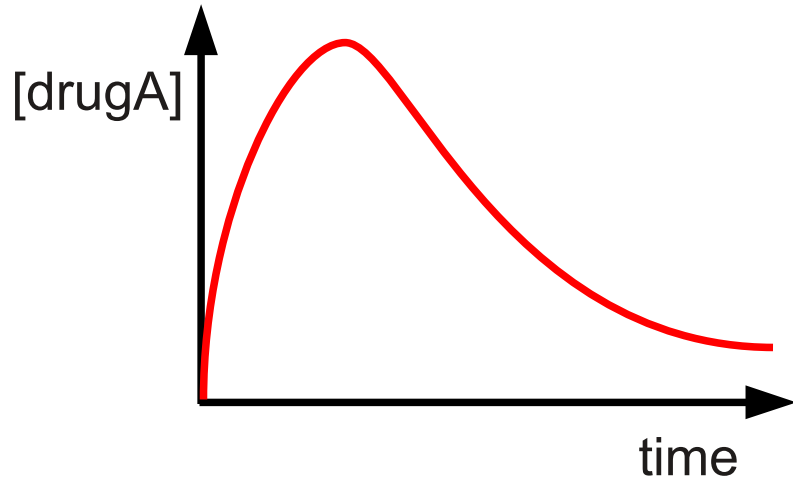


$$\frac{dC}{dt} = \text{in}(t) - k \times C$$

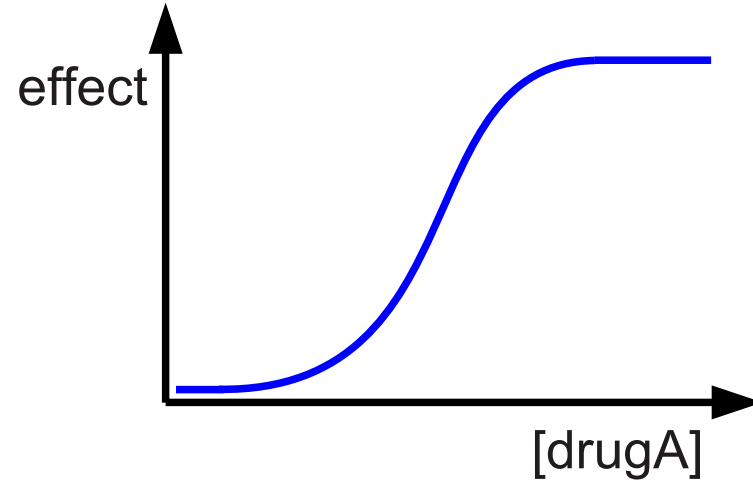


Drug discovery modelling: pharmacometrics

PK

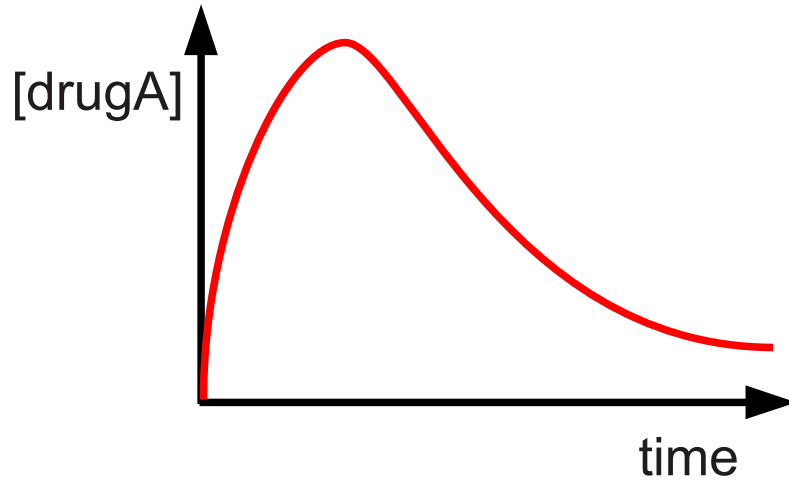


PD

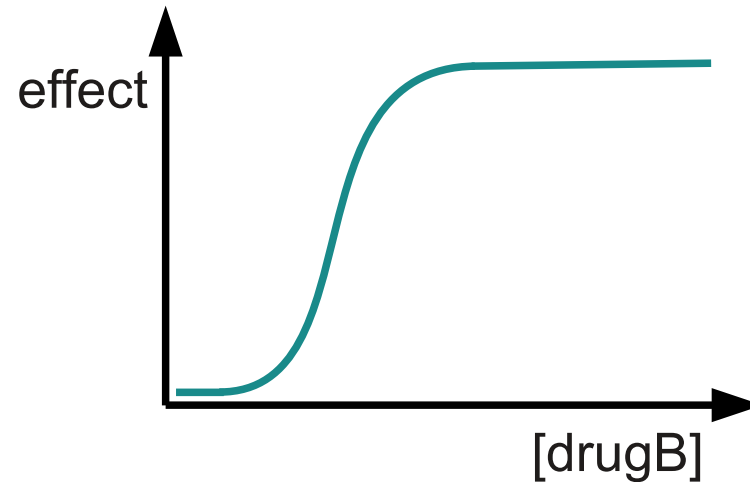
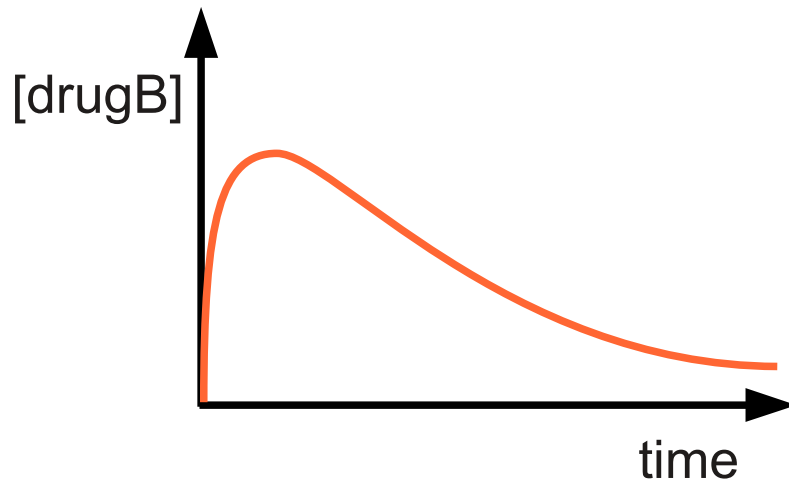
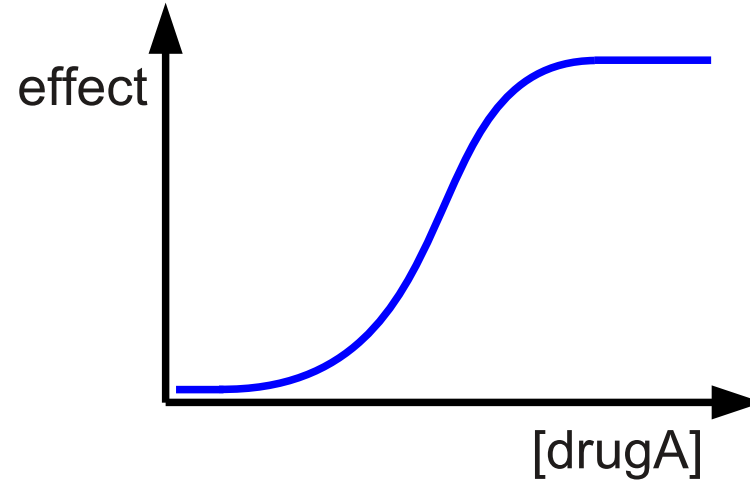


Drug discovery modelling: pharmacometrics

PK

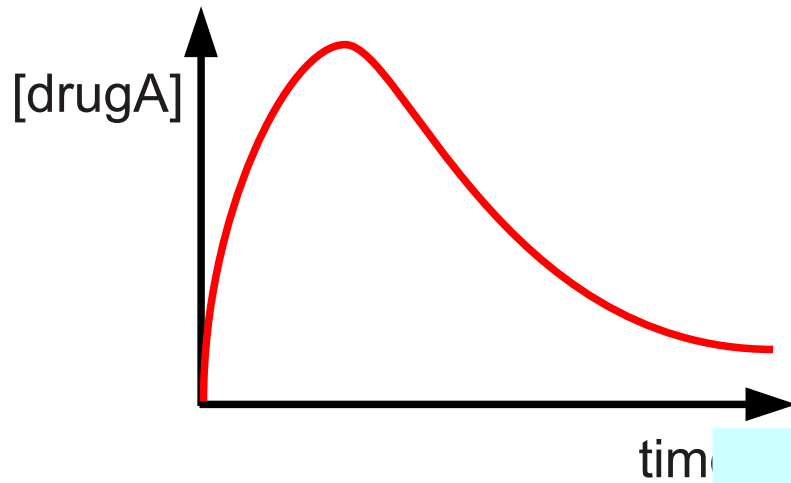


PD

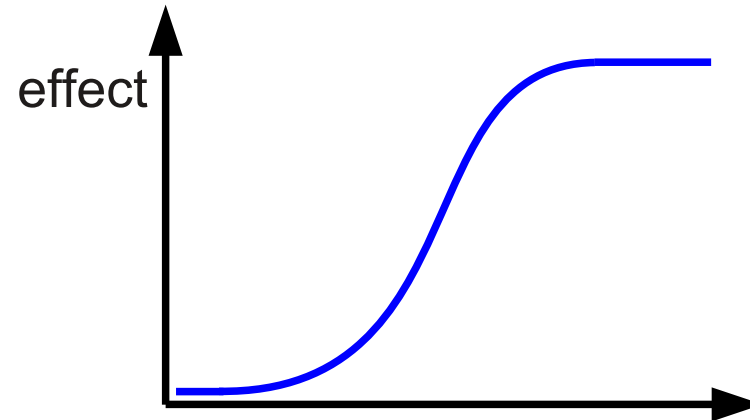


Drug discovery modelling: pharmacometrics

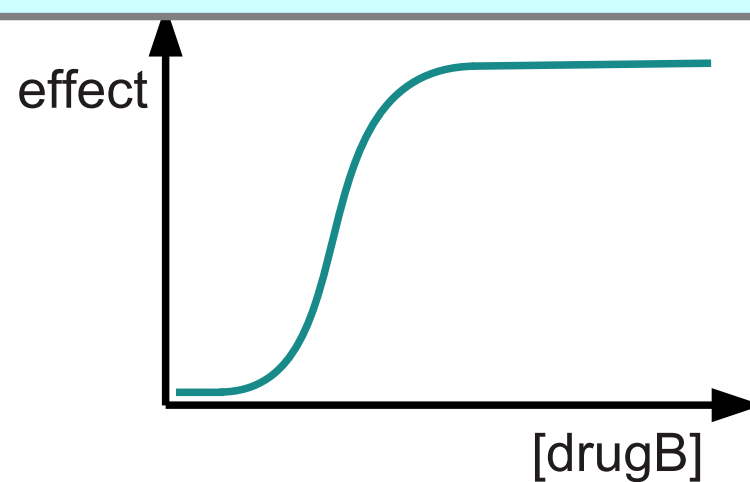
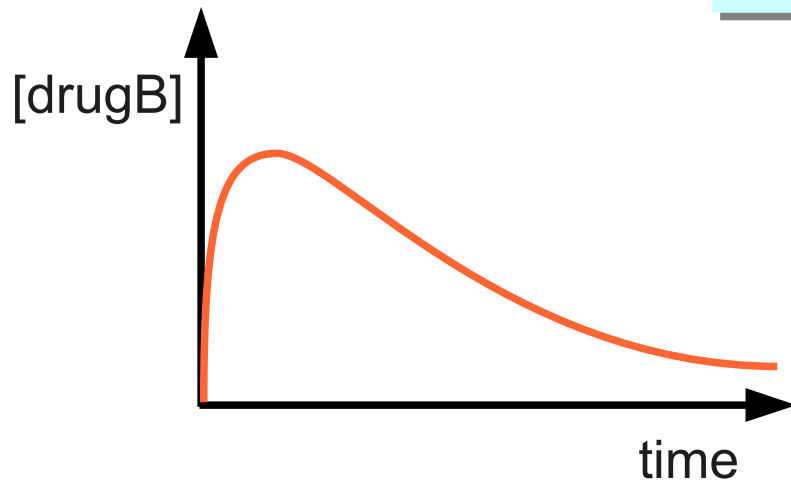
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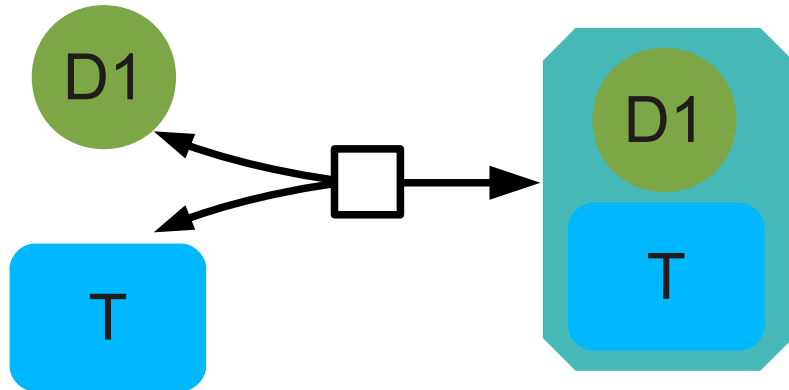
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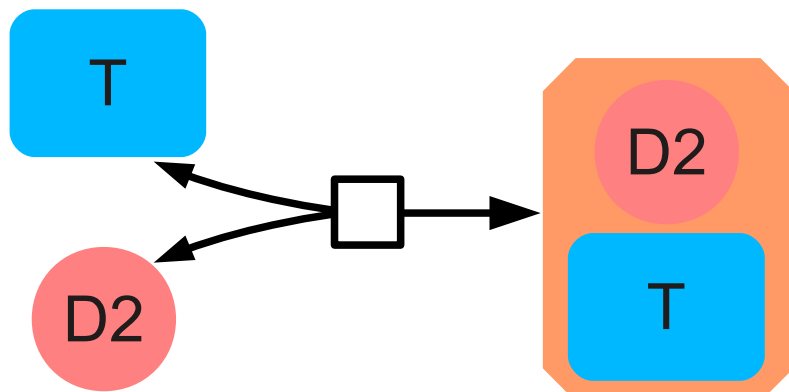
Effect of A+B?



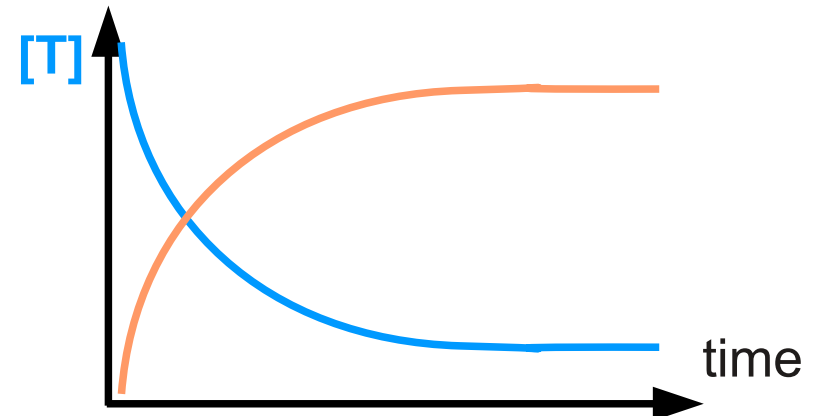
Systems modelling



$$\frac{d[T]}{dt} = -k_1 \times [T] \times [D1]$$

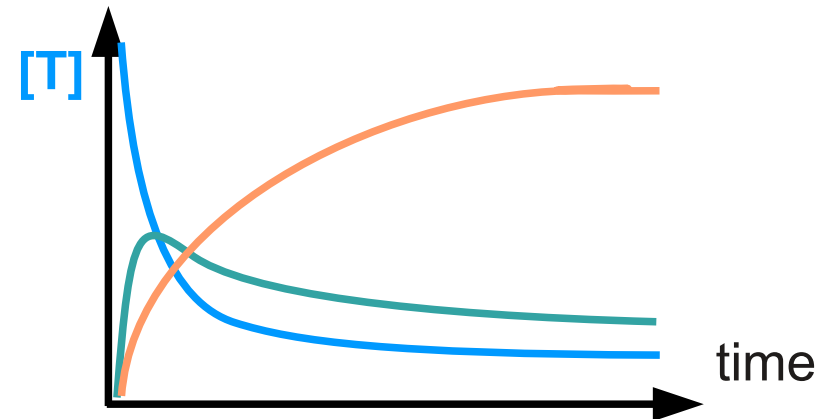
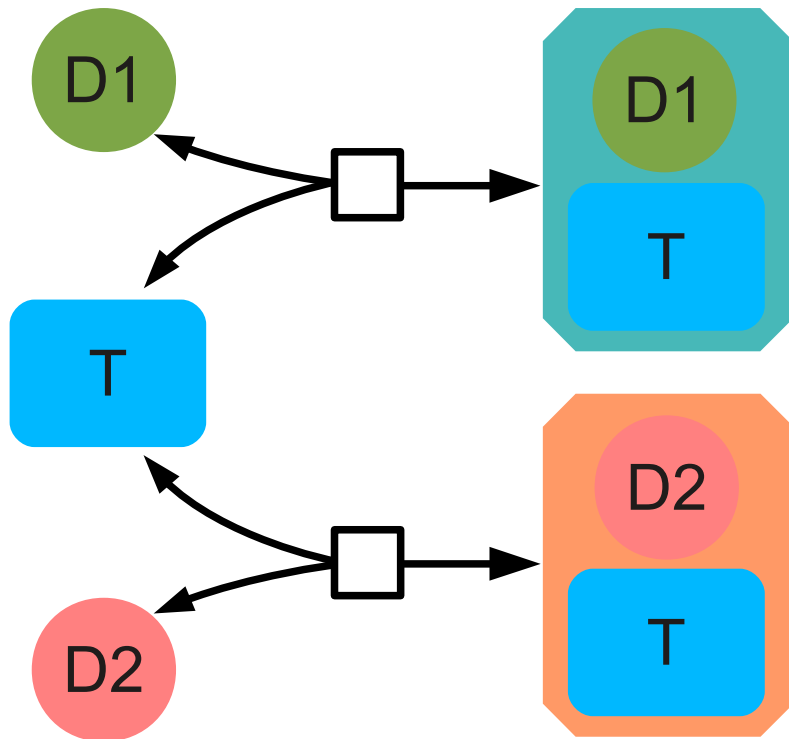


$$\frac{d[T]}{dt} = -k_2 \times [T] \times [D2]$$

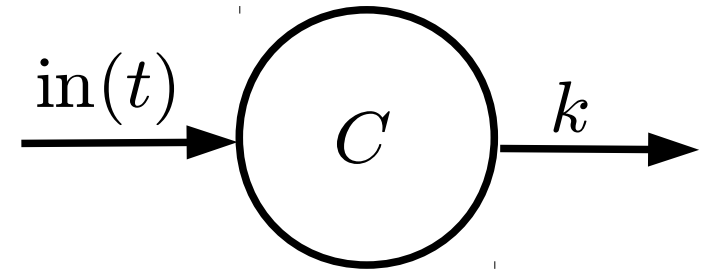
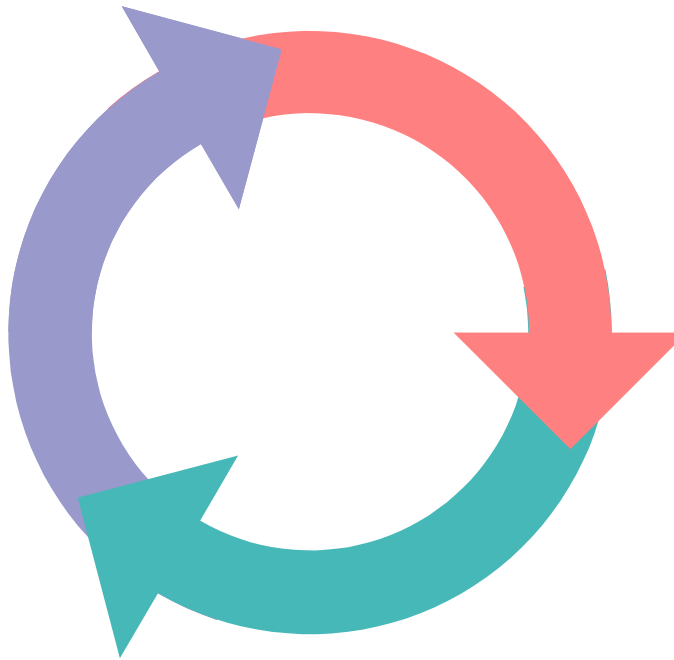
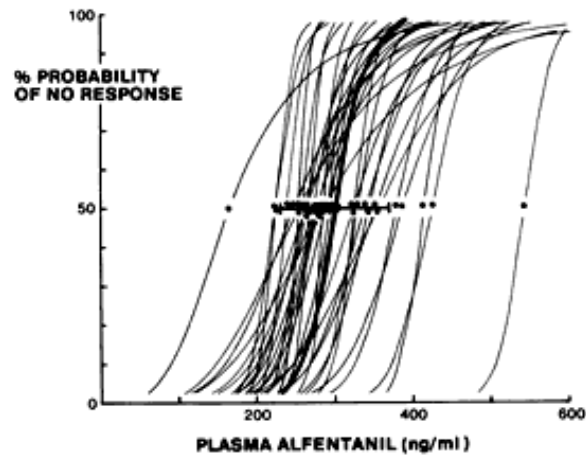
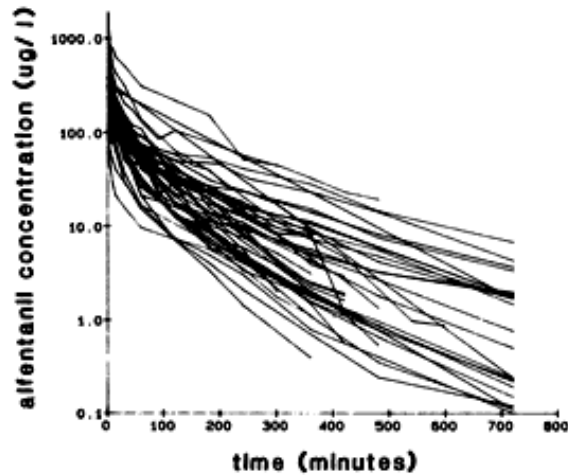


Systems modelling

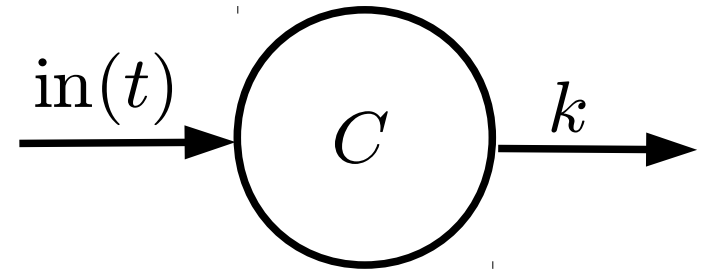
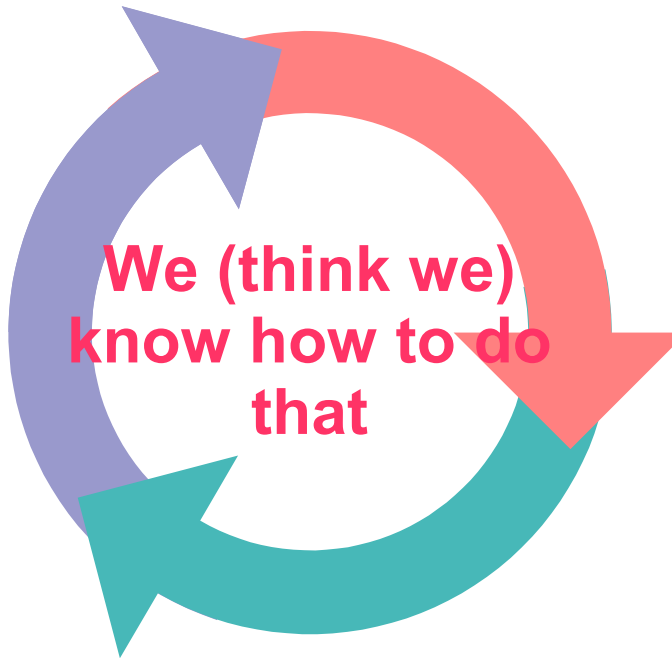
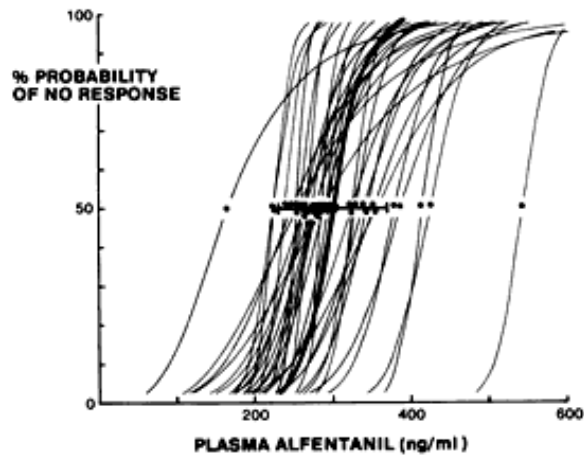
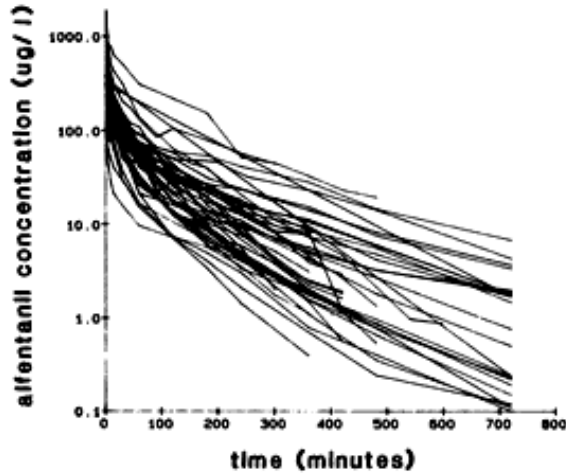
$$\frac{d[T]}{dt} = -k1 \times [T] \times [D1] - k2 \times [T] \times [D2]$$



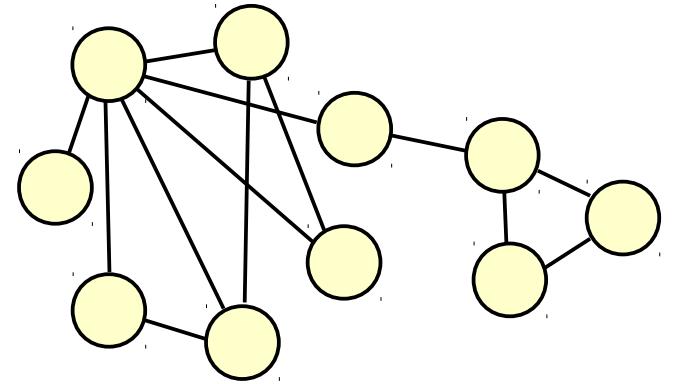
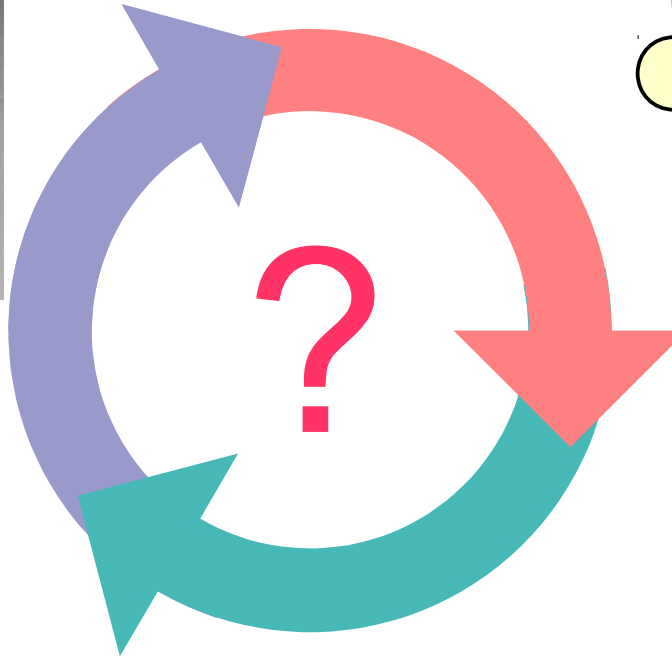
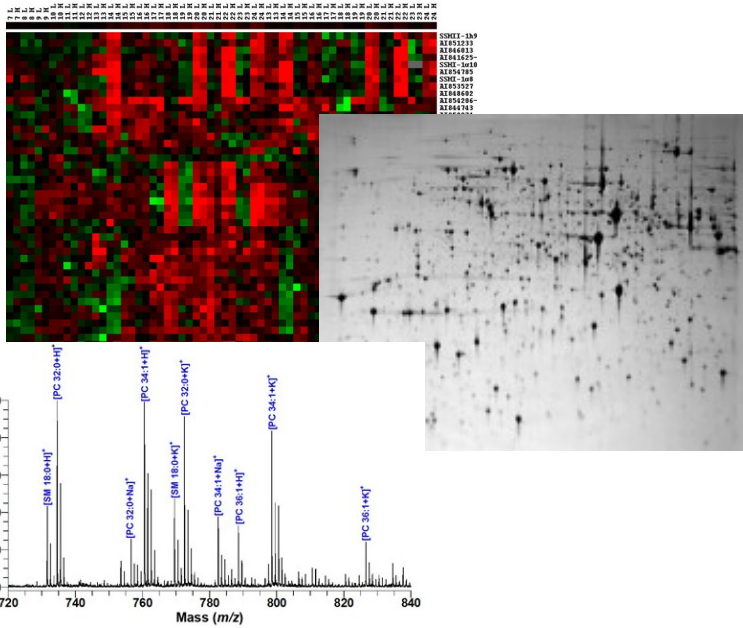
Drug discovery and pharmacometrics models



Drug discovery and pharmacometrics models



Drug discovery and omics



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