

Computational Systems Neurobiology

Nicolas Le Novère

Computational Neurobiology group

EMBL-EBI, Cambridge, UK

<http://www.ebi.ac.uk/compneur/>



Neurobiology != Neuroscience

- ♦ Computational Neurosciences
 - Modelling and simulation of neural phenomena, that is related to the nervous system.
e.g.: formal neural networks, behavioural models etc.
- ♦ Computational Neurobiology
 - Modelling and simulation of neuronal phenomena, that is related to the neuron.
e.g.: modelling of signalling pathways, of synaptic function etc.

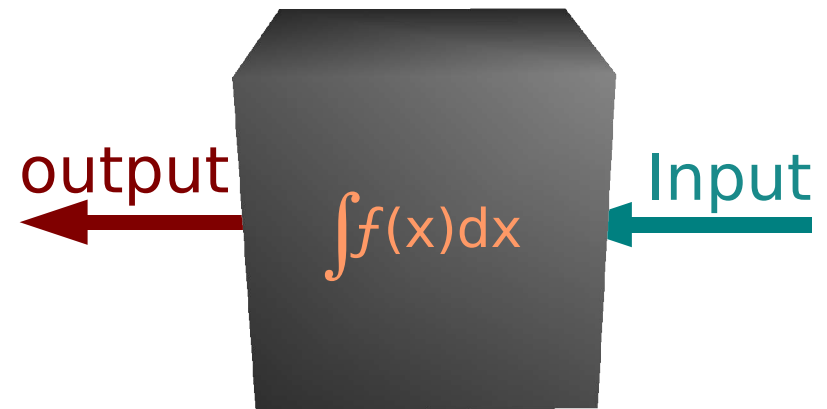
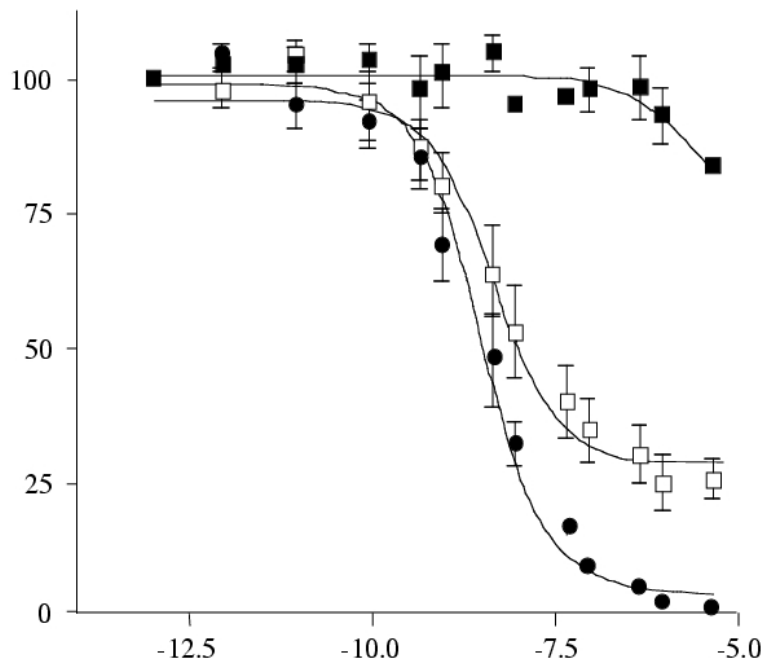
Classical modelling approaches in theoretical biology

(1)-The phenomenology

Snapshot of the system

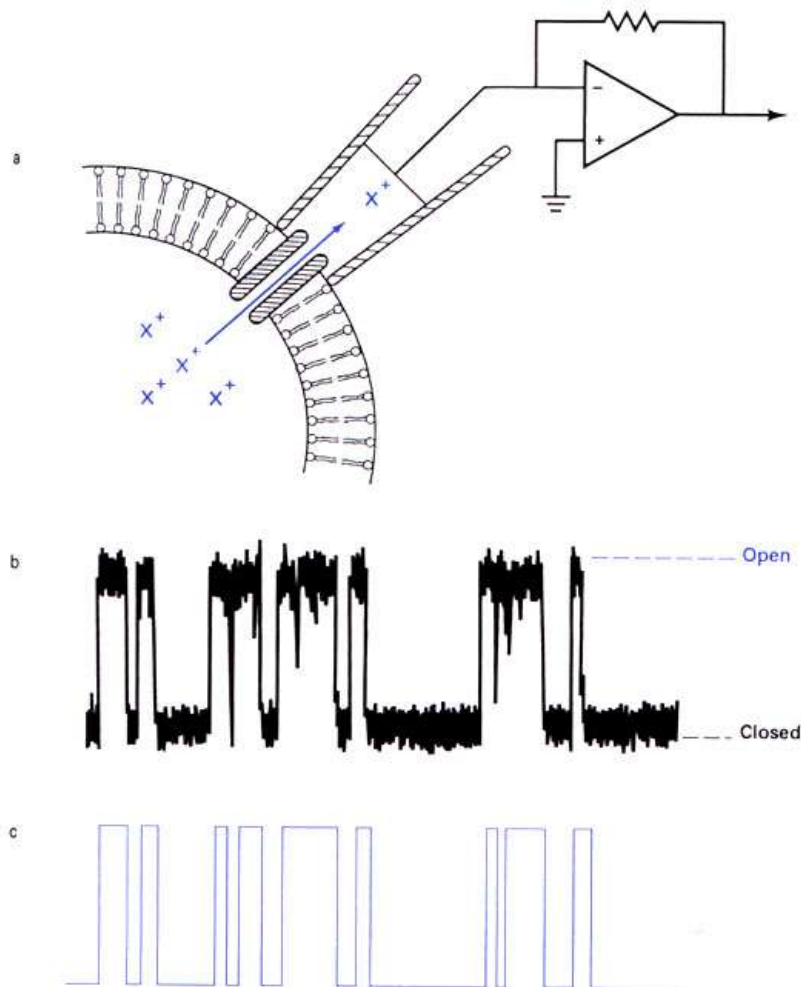
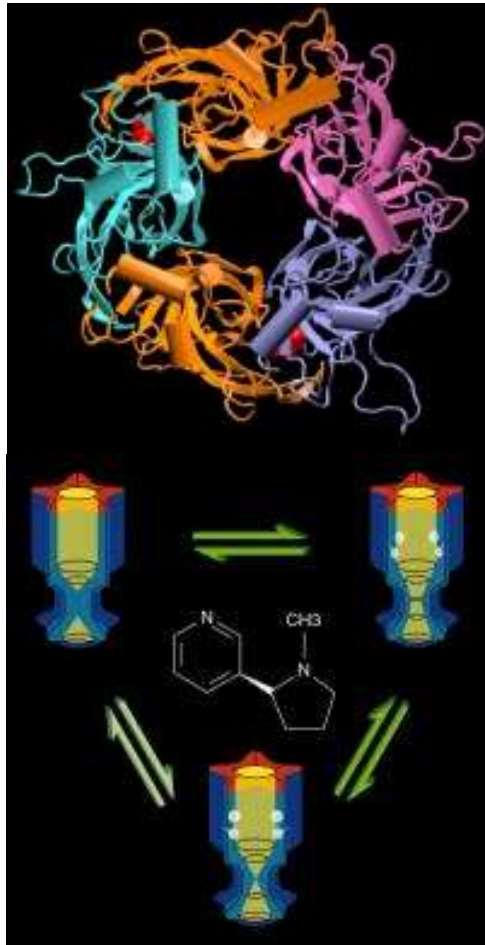
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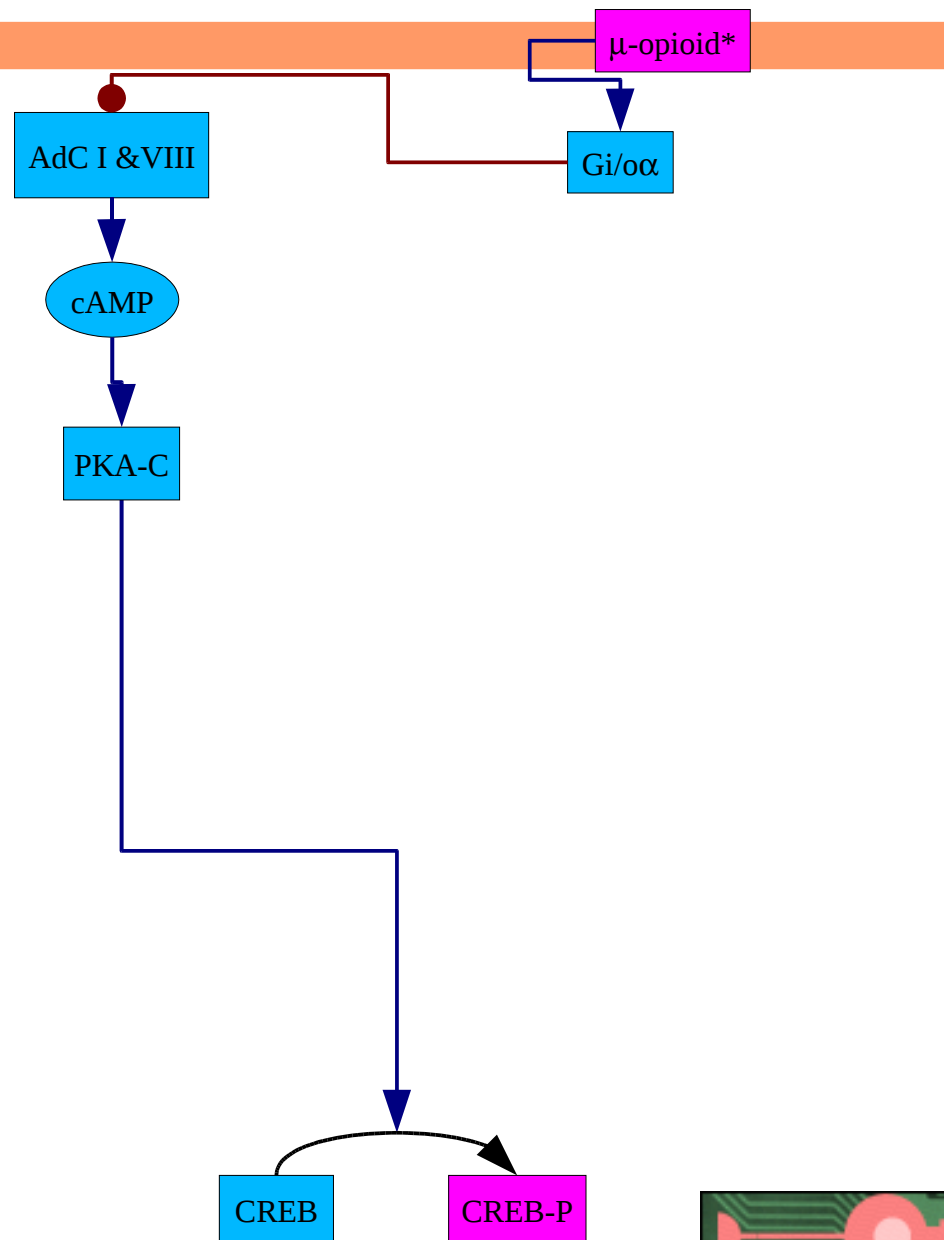
Abstraction

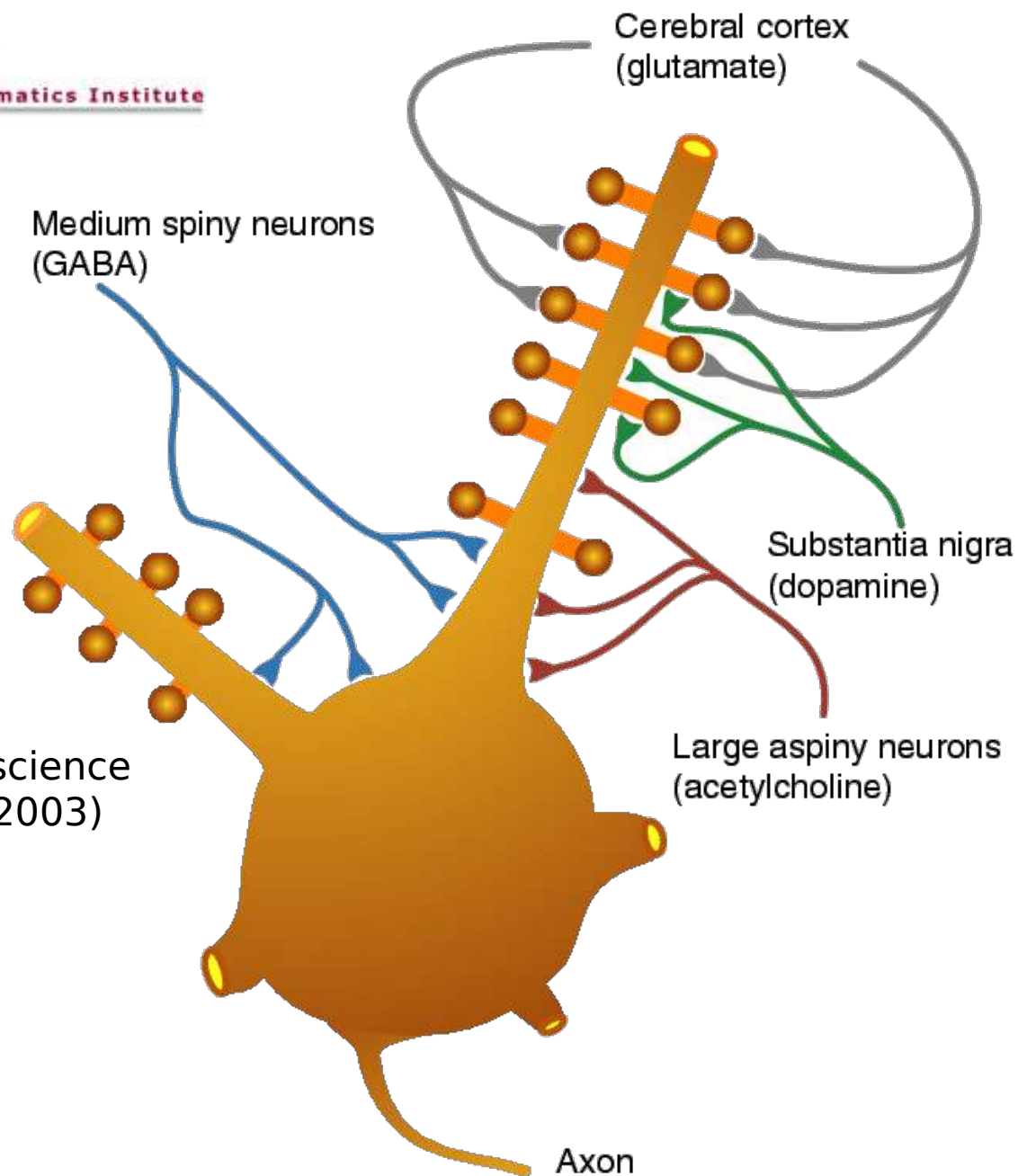


Classical modelling approaches in theoretical biology

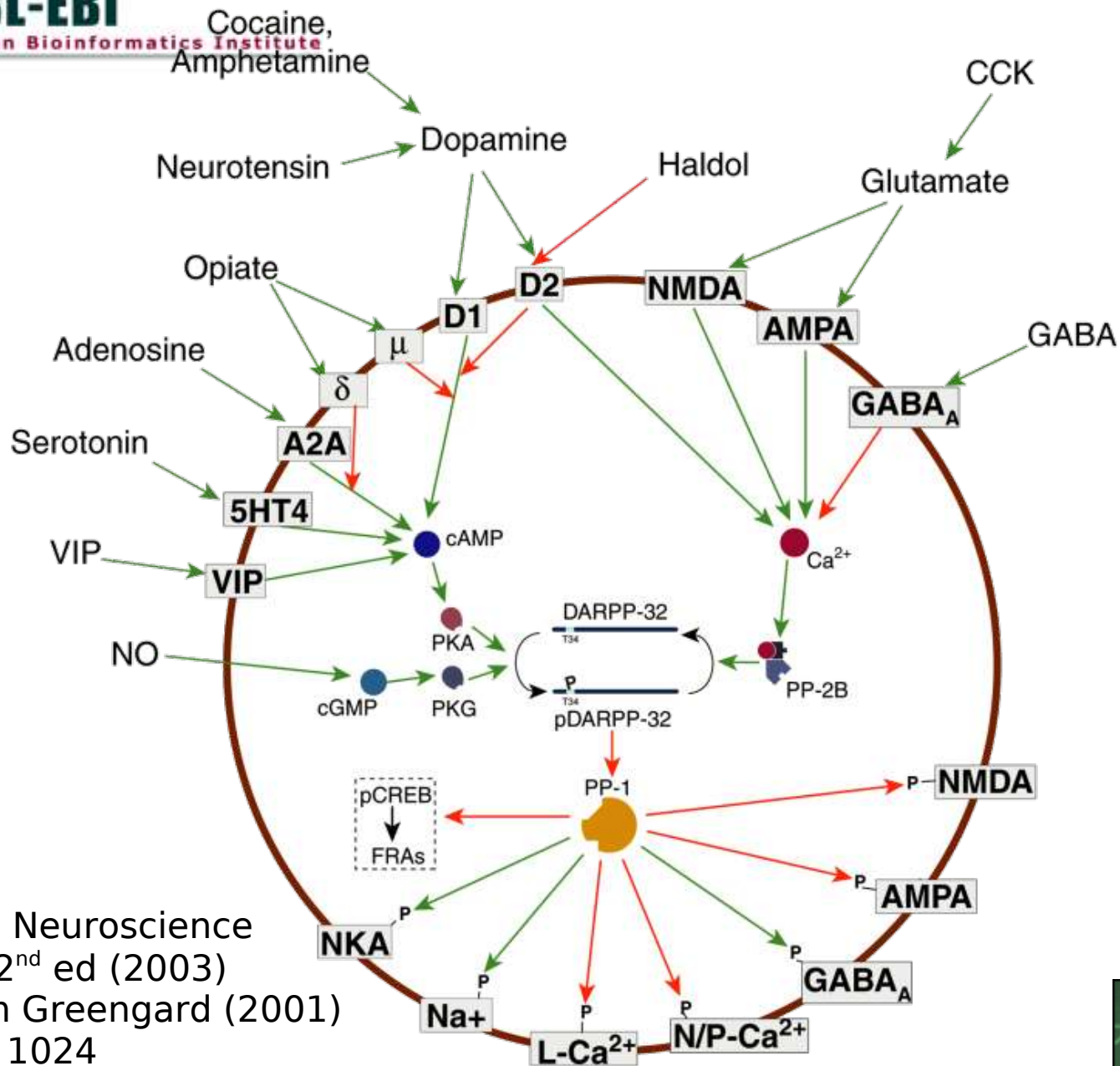
(2)-The reductionism

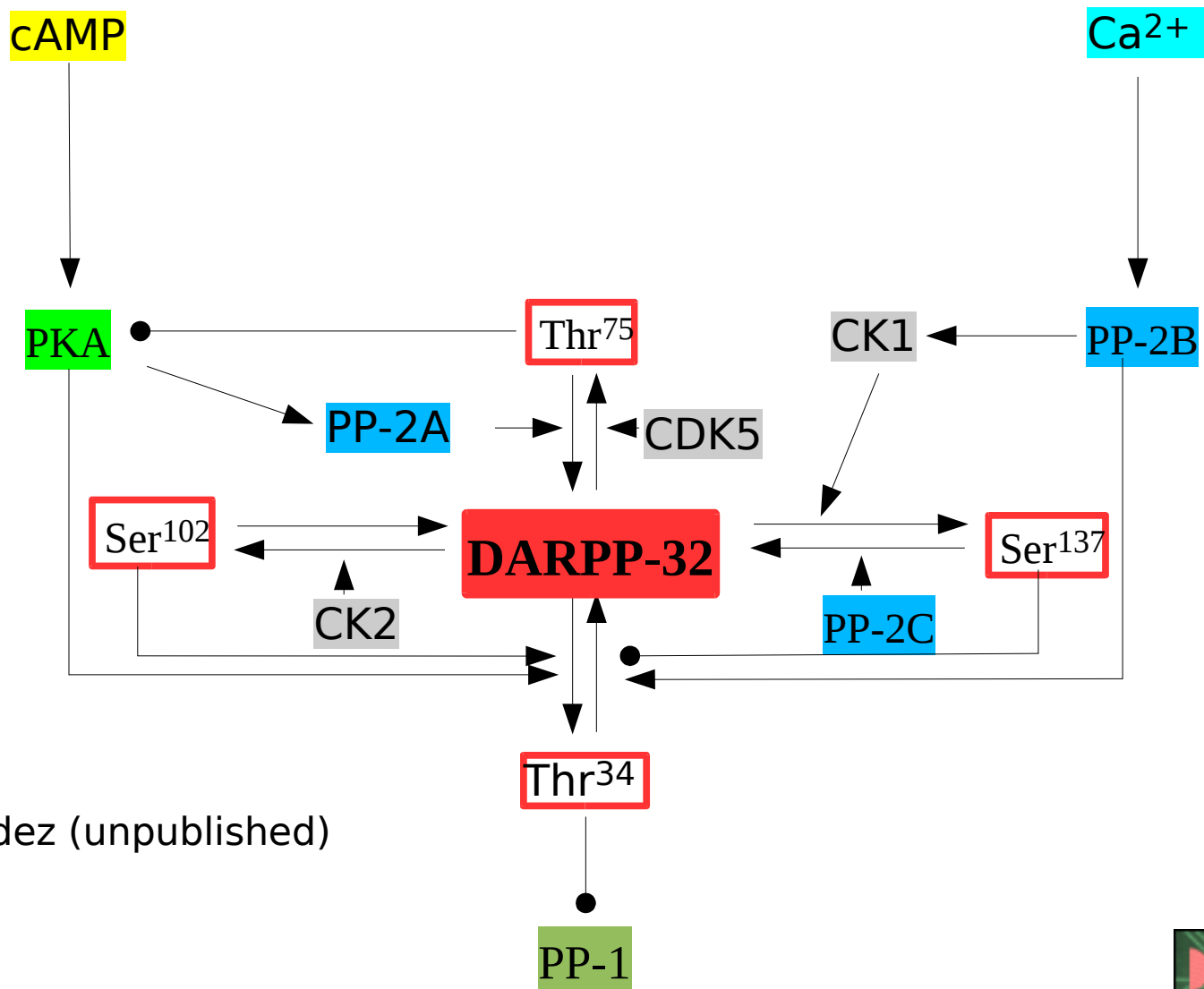






Fundamental Neuroscience
Squire et al. 2nd ed(2003)





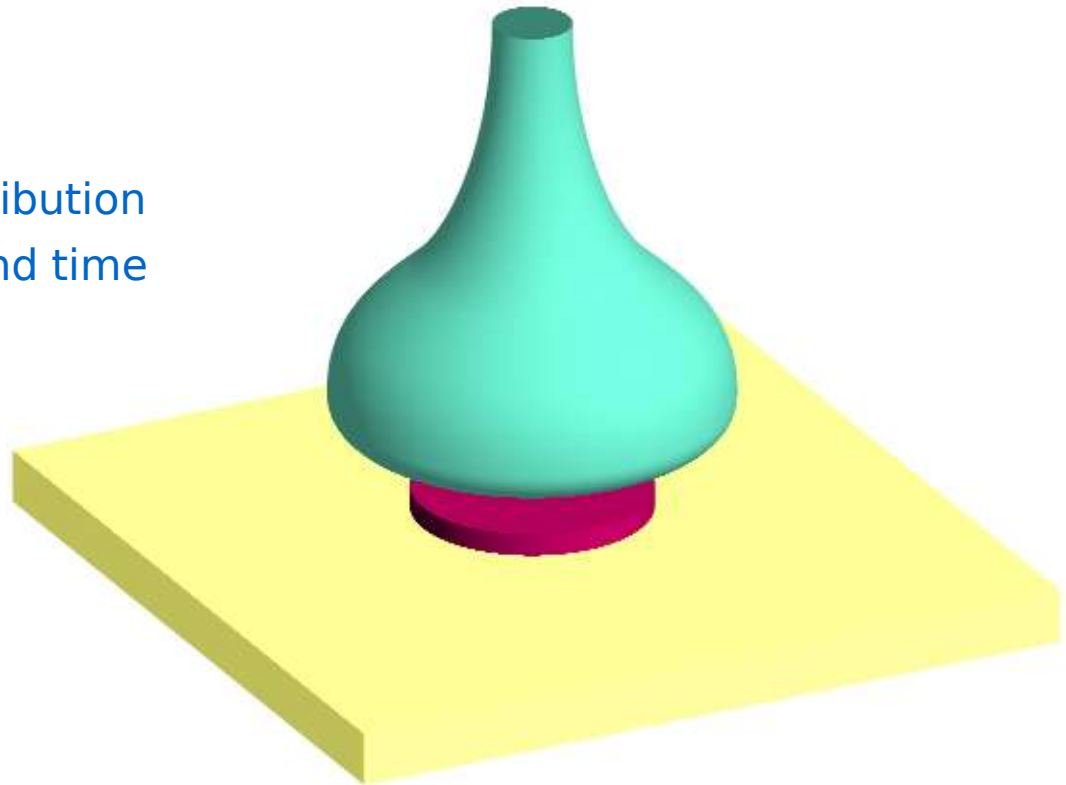
Éric Fernandez (unpublished)

Demo Genesis kinetikit

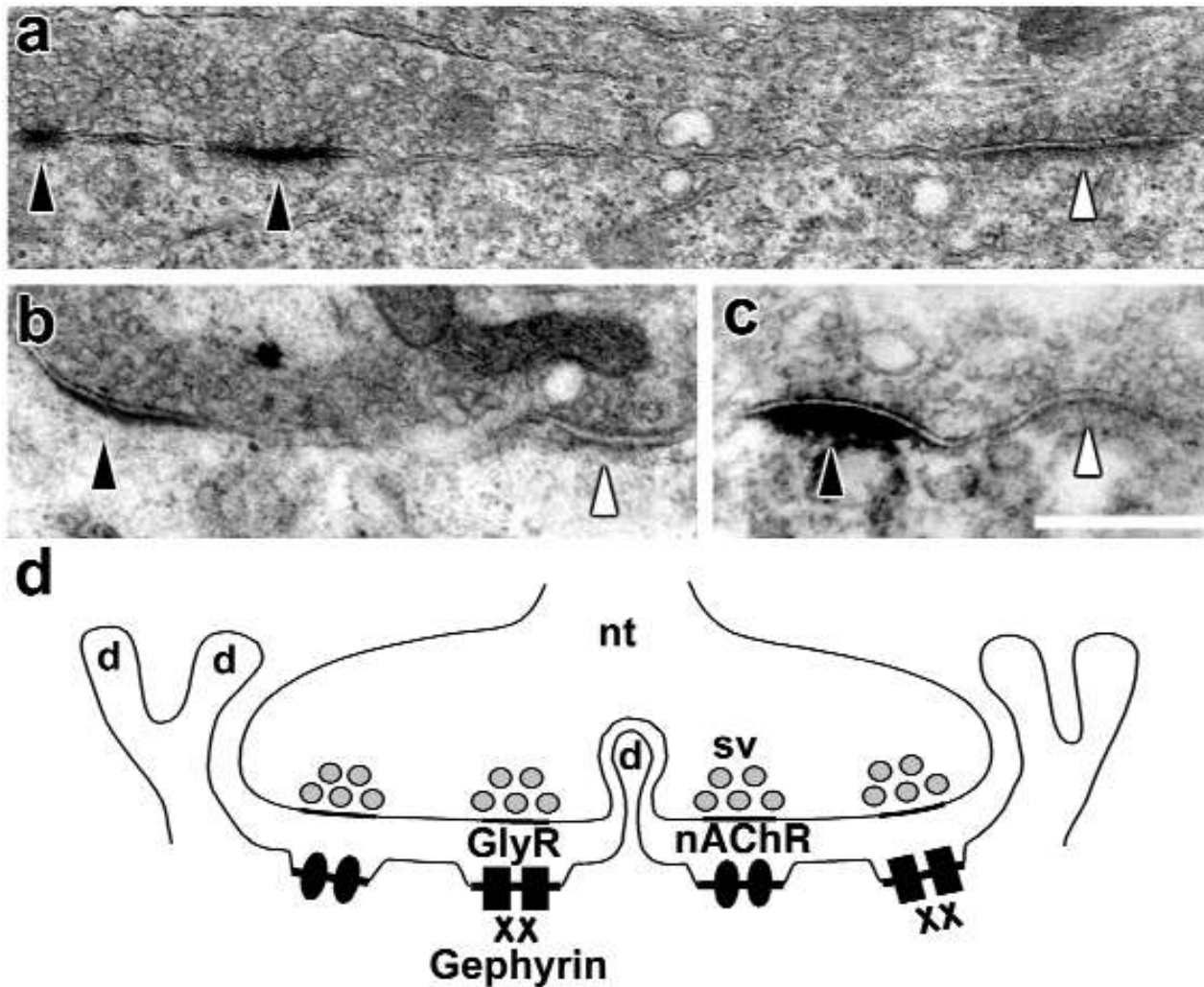
(<http://www.ncbs.res.in/~bhalla/kkit/index.html>)

Classical view of the synapse

- ◆ One transmitter
- ◆ One receptor
- ◆ Homogenous distribution
- ◆ Frozen in space and time



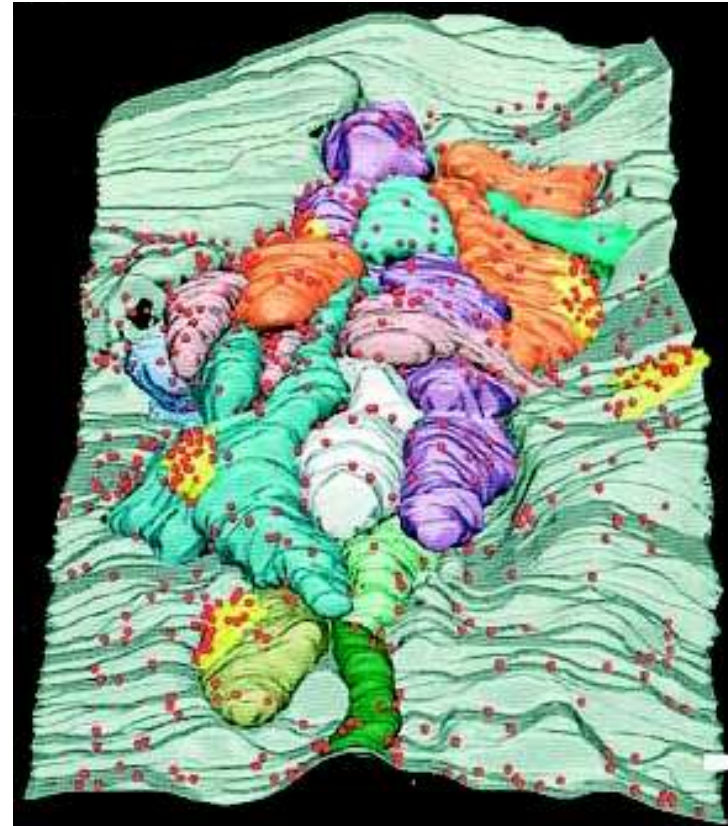
Pharmacological complexity



Tsen et al. (2000) *Nat Neurosci*, 3: 126-132

Structural complexity (1)

Atlas of Ultrastructural Neurocytology
<http://synapses.mcg.edu/atlas/eurosci>



Shoop et al. (2002)
J Neurosci, 22: 748-756

Demo MCell

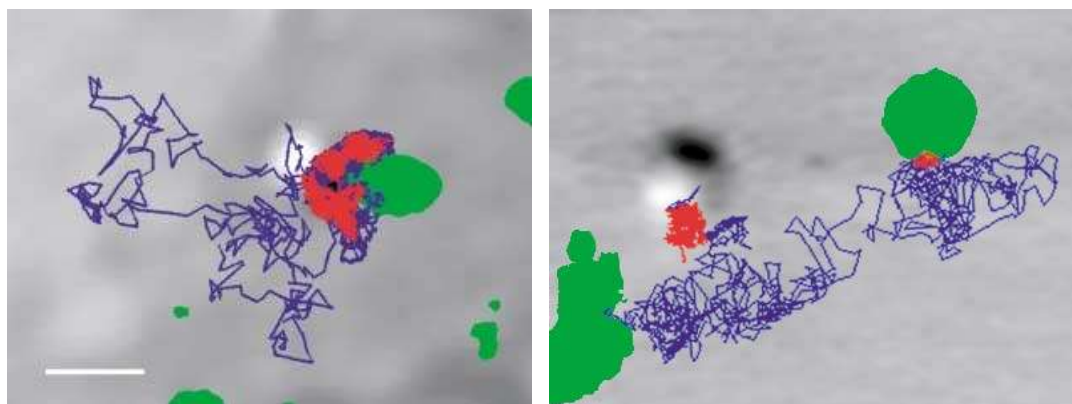
(<http://www.mcell2.cnl.salk.edu/>)



Computational
Neurobiology

Temporal complexity

Barry and Ziff. (2002)
Curr Opin Neurobiol, 12: 279-286

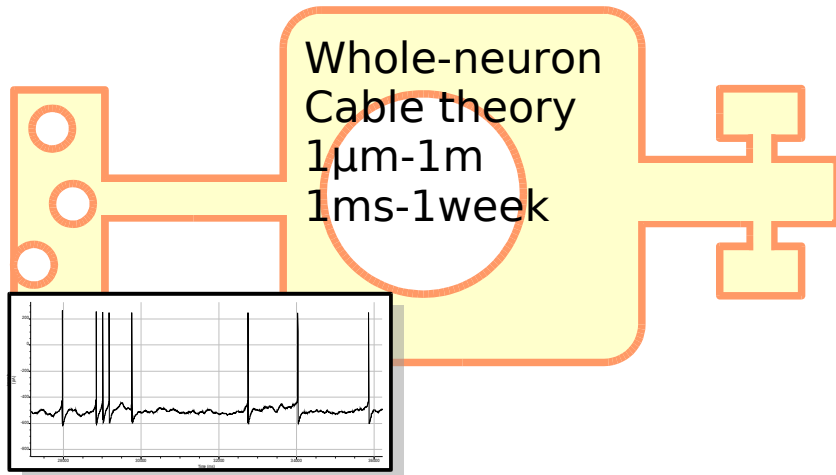


Choquet & Triller (2003)
Nat Rev Neurosci, 4: 251-265

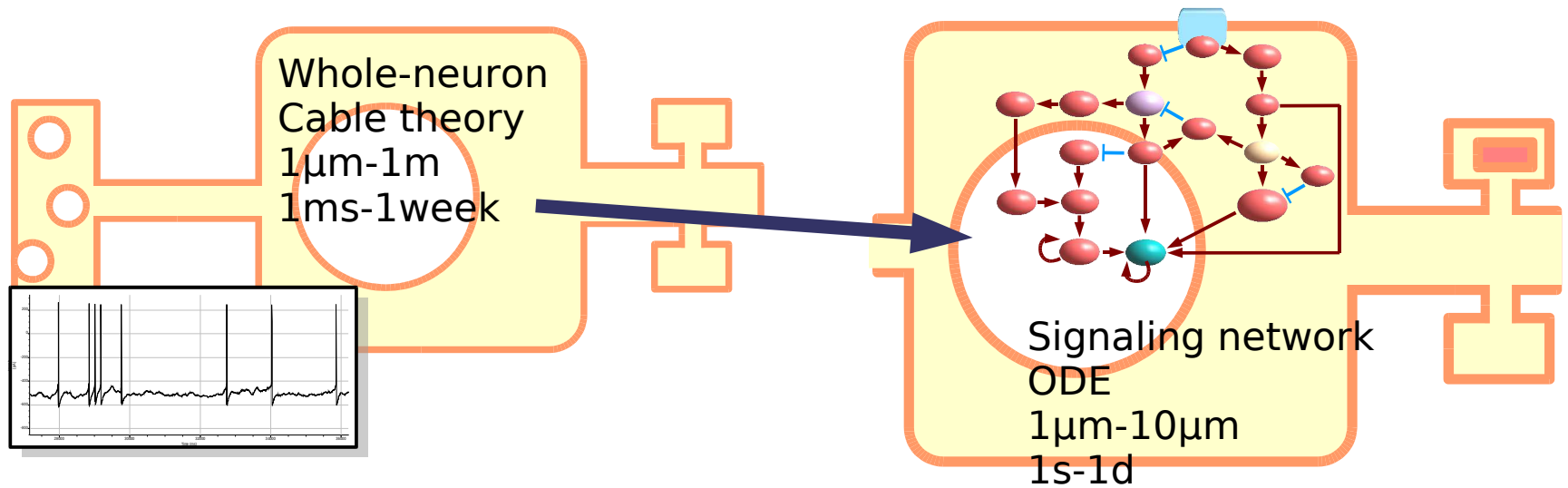
Demo Abstract Protein Simulator

(<http://www.anc.ed.ac.uk/~fwh/protsim/index.php>)

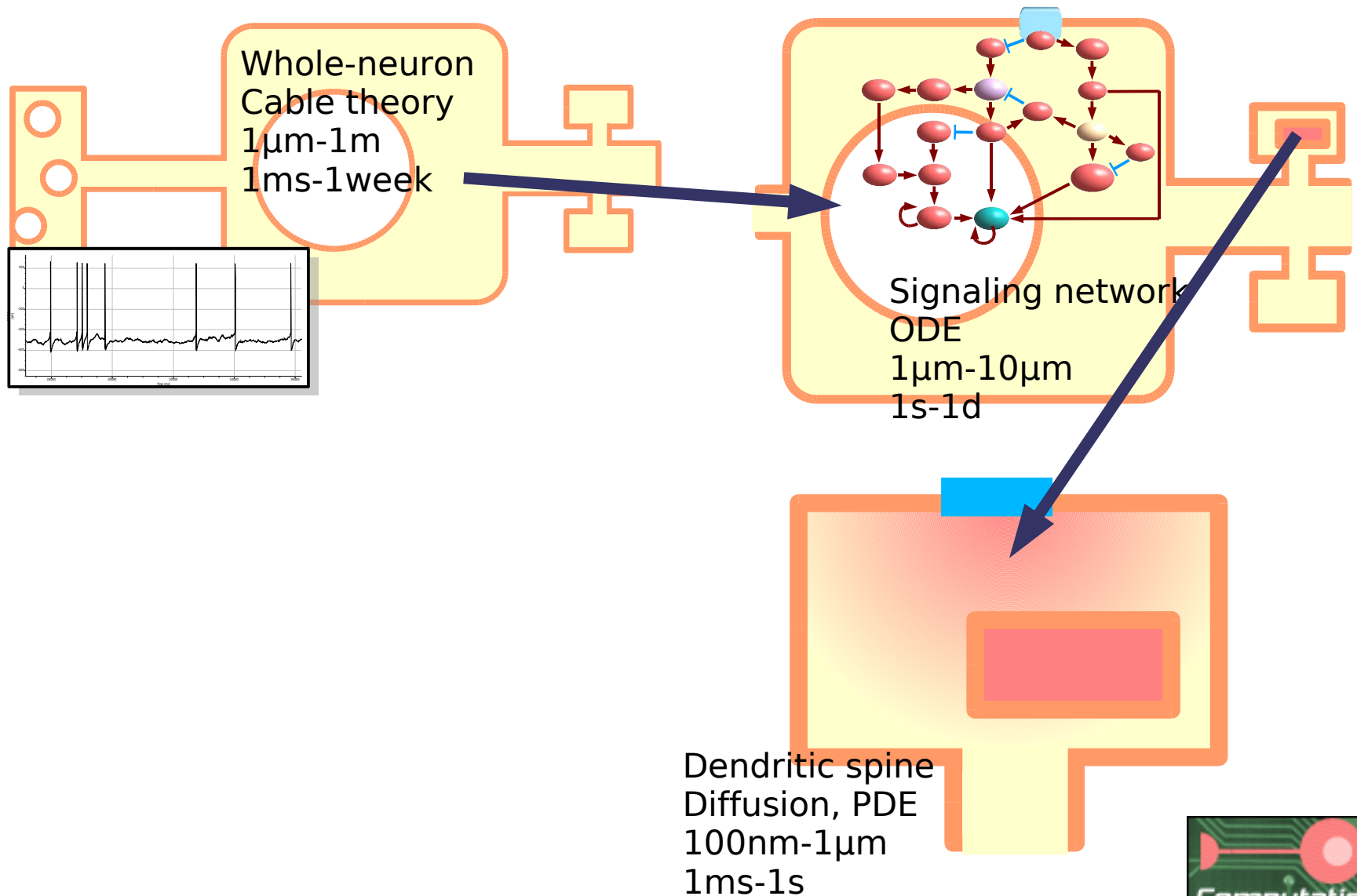
Modular multi-scales multi-algorithms program



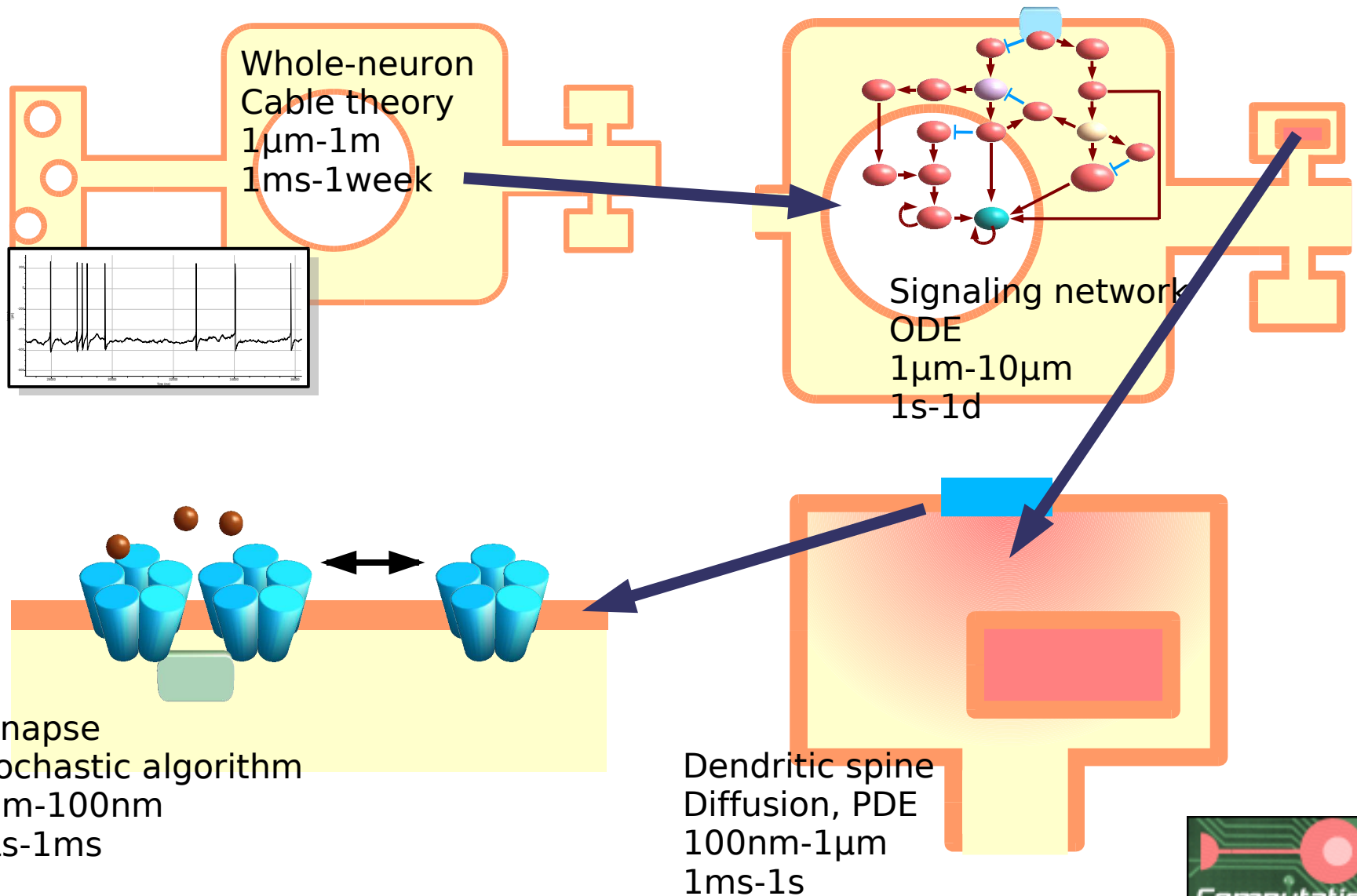
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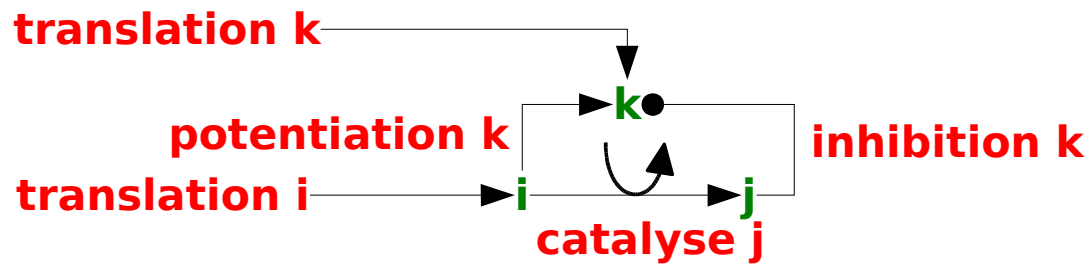


Modular multi-scales multi-algorithms program



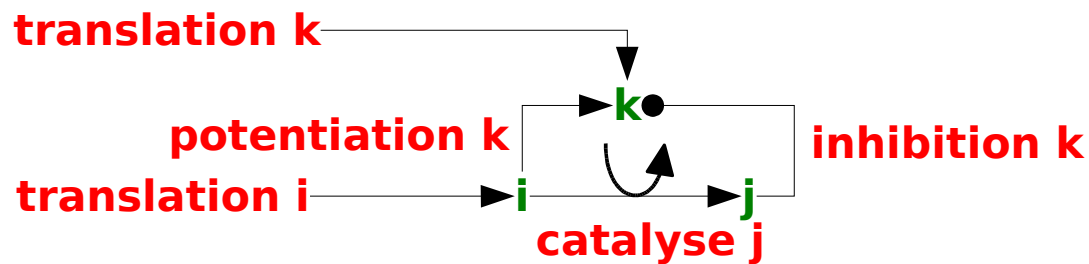
E-Cell System 3 (Kouichi Takahashi)

shared mem, hyper-threading



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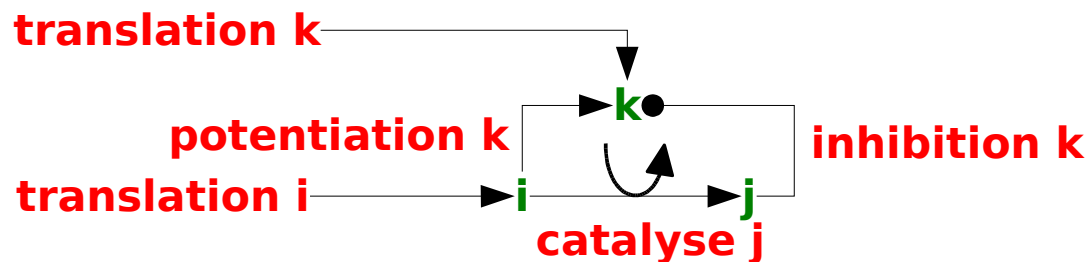
variable *j*

variable *i*

variable *k*

E-Cell System 3 (Kouichi Takahashi)

shared mem, hyper-threading



catalyse j
(ExpressionFluxProcess)

inhibition k
(MassActionFluxProcess)

potentiation k
(MassActionFluxProcess)

translation i
(GillespieProcess)

translation k
(GillespieProcess)

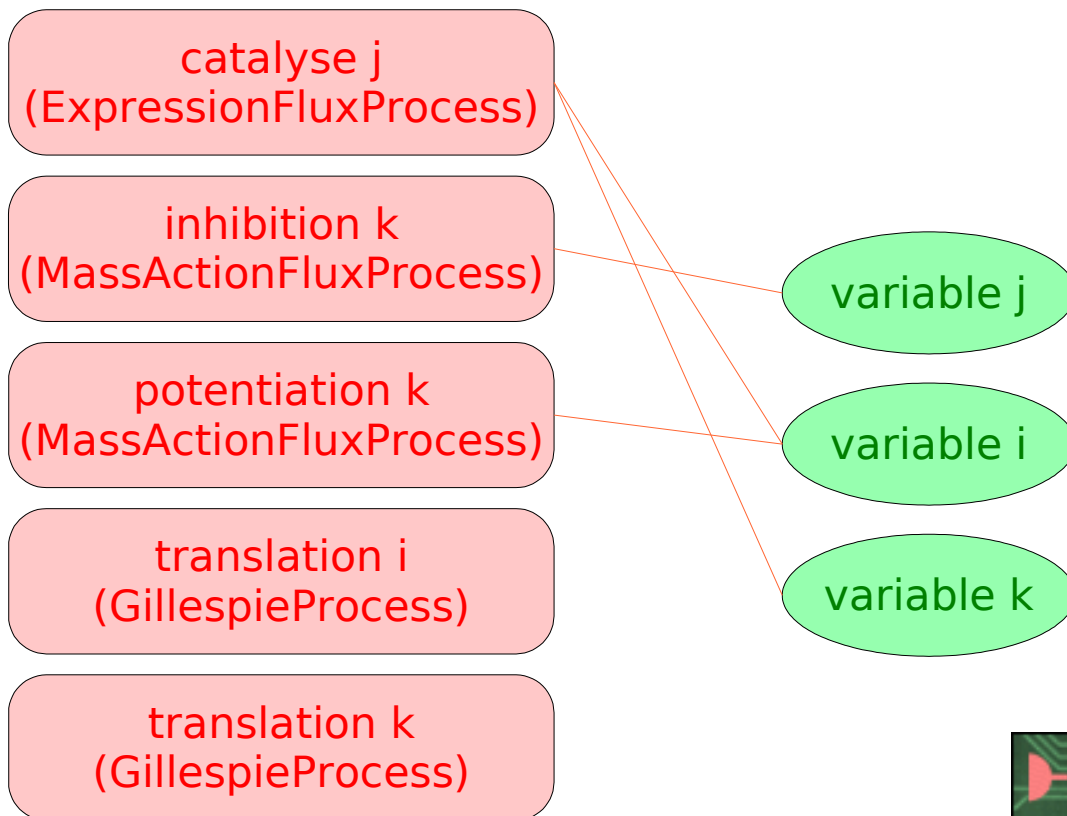
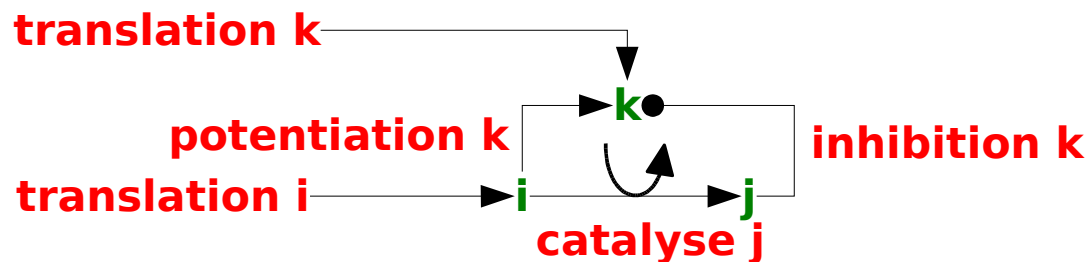
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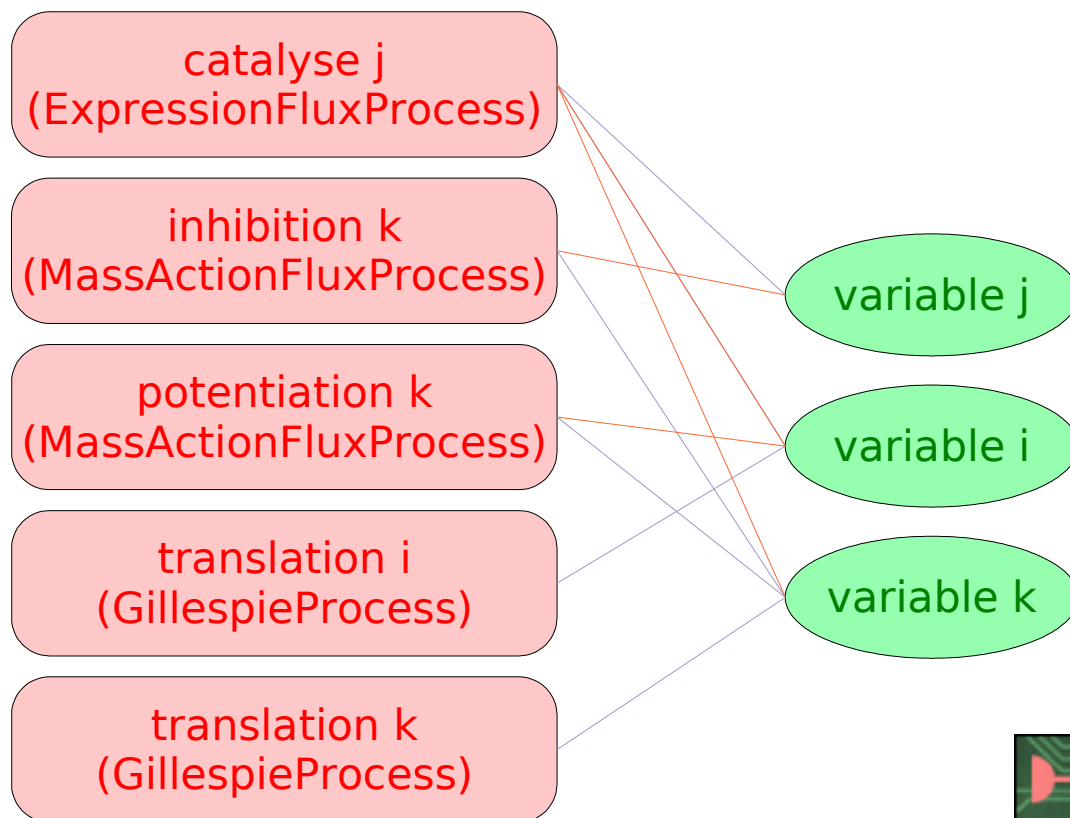
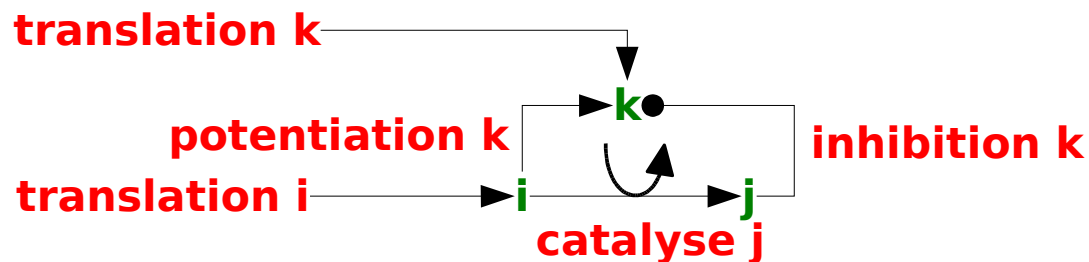
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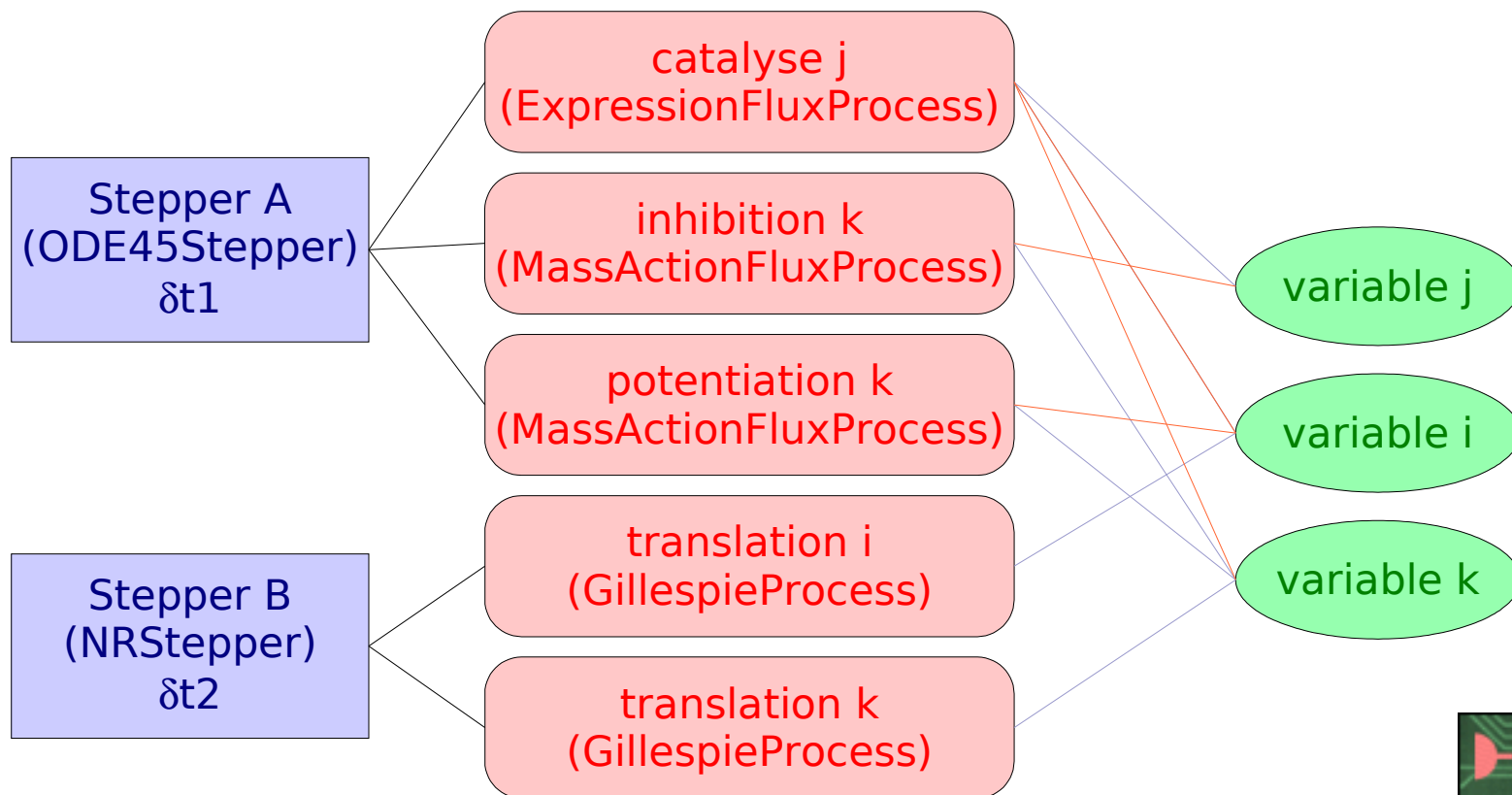
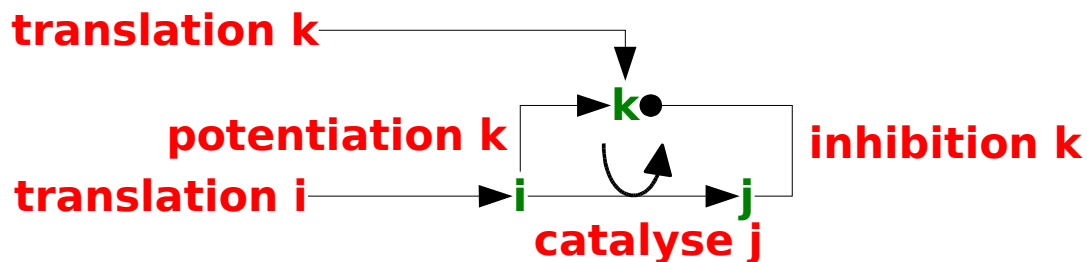
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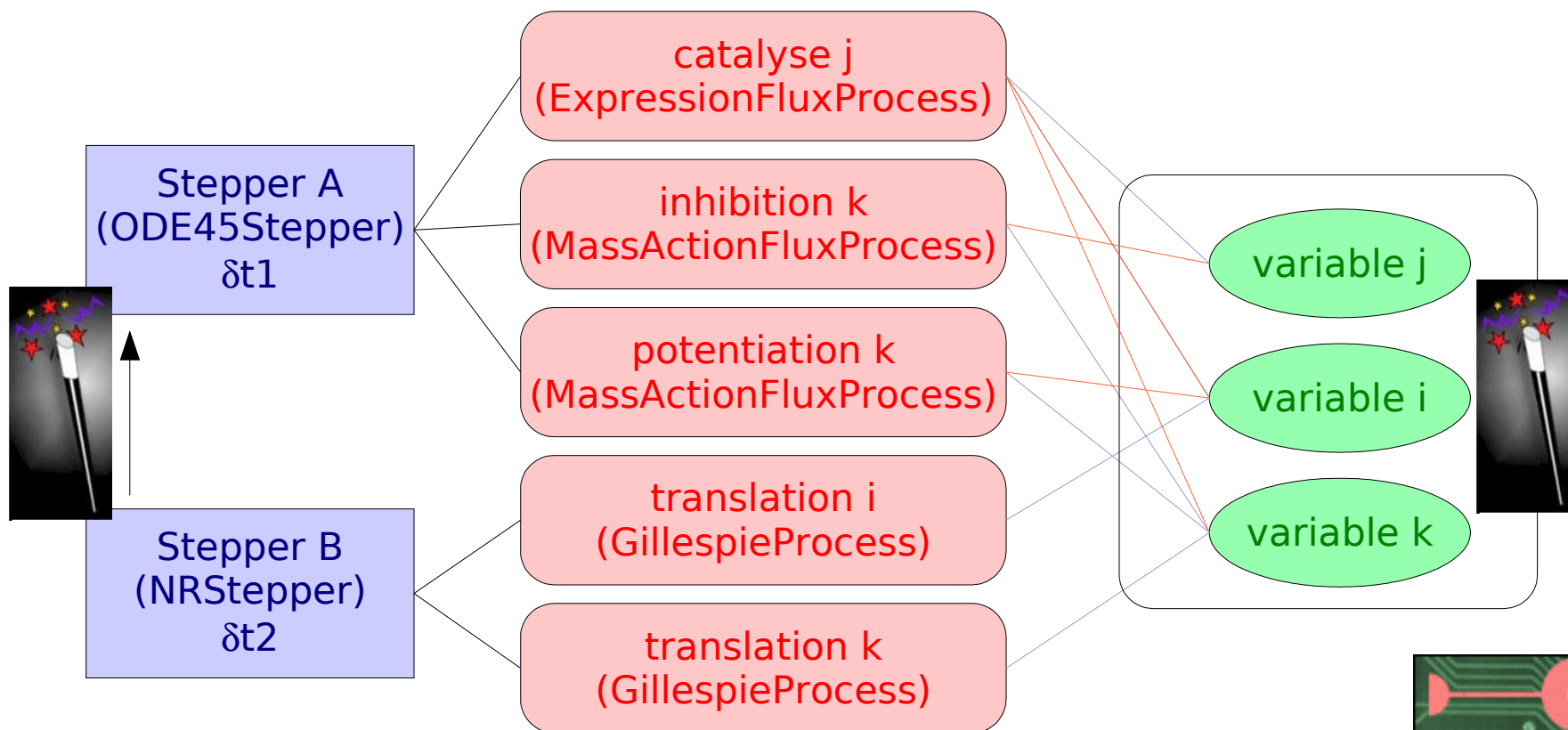
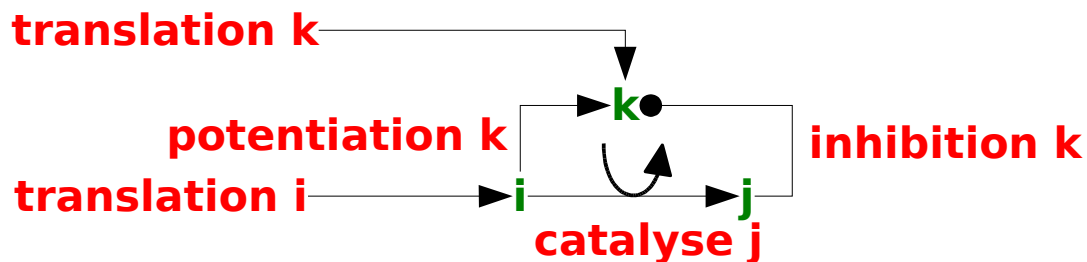
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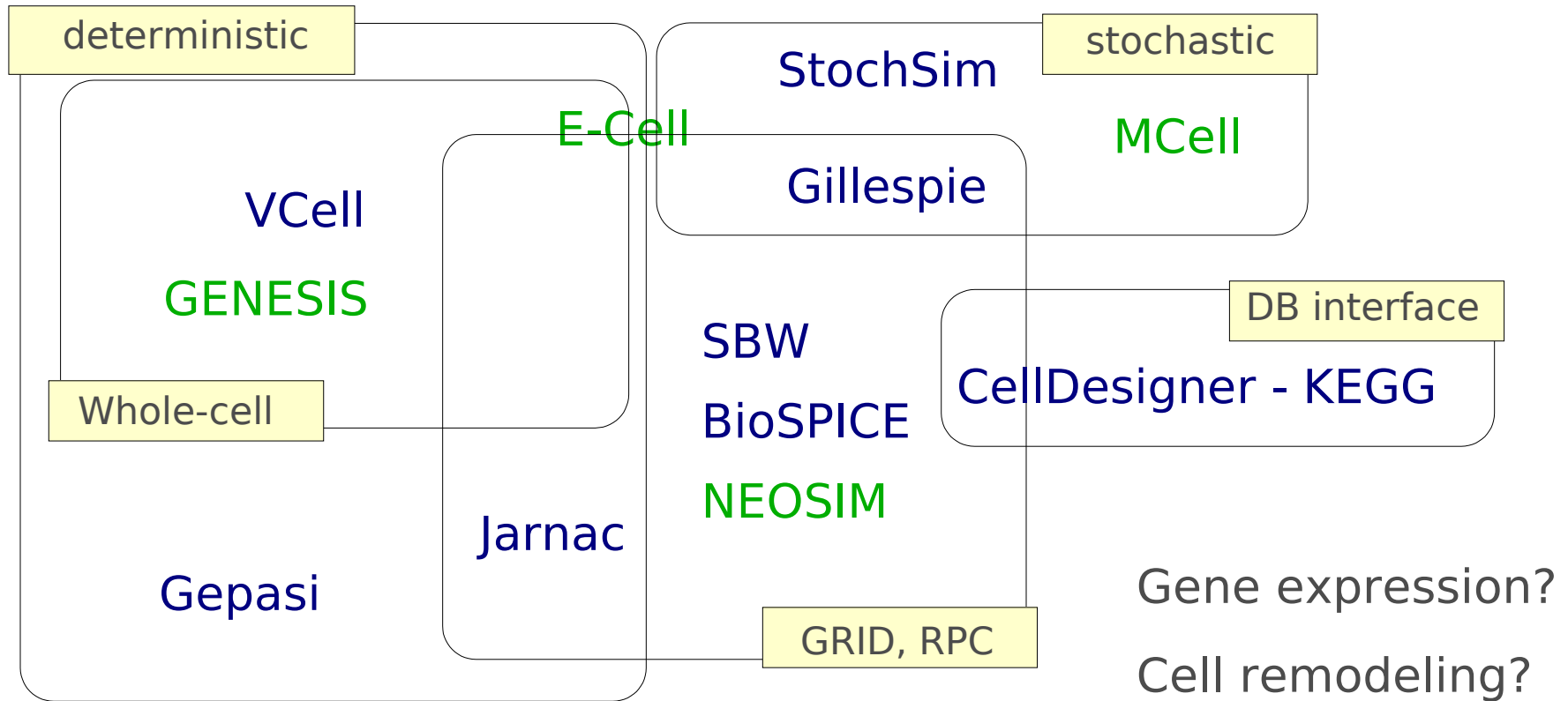
E-Cell System 3 (Kouichi Takahashi)

shared mem, hyper-threading



Existing efforts

used to model neurons



All these programs speak SBML
(Systems Biology Markup Language)



SBML Systems Biology Markup Language

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A Tool-Neutral Exchange Format

The Systems Biology Markup Language (SBML) is a computer-readable format for representing **models of biochemical reaction networks**. SBML is applicable to metabolic networks, cell-signaling pathways, genomic regulatory networks, and many other areas in systems biology.

Internationally Supported and Widely Used

SBML has been evolving since mid-2000 through the efforts of an international group of software developers and users. Today, SBML is **supported by over 50 software systems**, including the following (where '*' indicates SBML support in development):

BALSA	CellDesigner	Gepasi	MathSBML	SClpath
BASIS	Cellerator	Jarnac	Modesto	SigPath
BioCharon	Cellware	JDesigner	MOMA*	SigTran
biocyc2SBML	COPASI	JigCell	Monod	Simpatica
BioGrid	Cytoscape	JSIM	NetBuilder	StochSim
Bio Sketch Pad	DBsolve	JWS*	PathArt	STOCKS
BioSpreadsheet	Dizzy	Karyote*	PathScout	Trelis
BioUML	E-CELL	kegg2sbml	PathwayBuilder	Virtual Cell
BSTLab	ecellJ	Kinsolver*	ProcessDB*	VLX Suite
CADLIVE	ESS	libSBML	SBW	WinSCAMP

A Free and Open Language

Advances in biotechnology are leading to larger, more complex models. The systems biology community needs information standards if models are to be shared, evaluated and developed cooperatively. SBML's widespread adoption **offers many benefits**:

- Enabling the use of multiple tools without rewriting models for each tool
- Enabling models to be shared and published in a form other researchers can use even in a different software environment
- Ensuring the survival of models (and the intellectual effort put into them) beyond the lifetime of the software used to create them

KEGG2SBML 1.0 Released!

(March 28, 2004) The first full version of KEGG2SBML, the KEGG-to-SBML converter, is now available. It supports SBML Level 2, KEGG release 29, LIGAND release 29 and KGML v0.3.

[read more](#)

MathSBML 2.3.0 Released!

(March 15, 2004) The latest version of MathSBML has just been released, and it's chock-full of features. MathSBML now supports virtually every aspect of SBML Level 2.

'sysbio' survey results are in

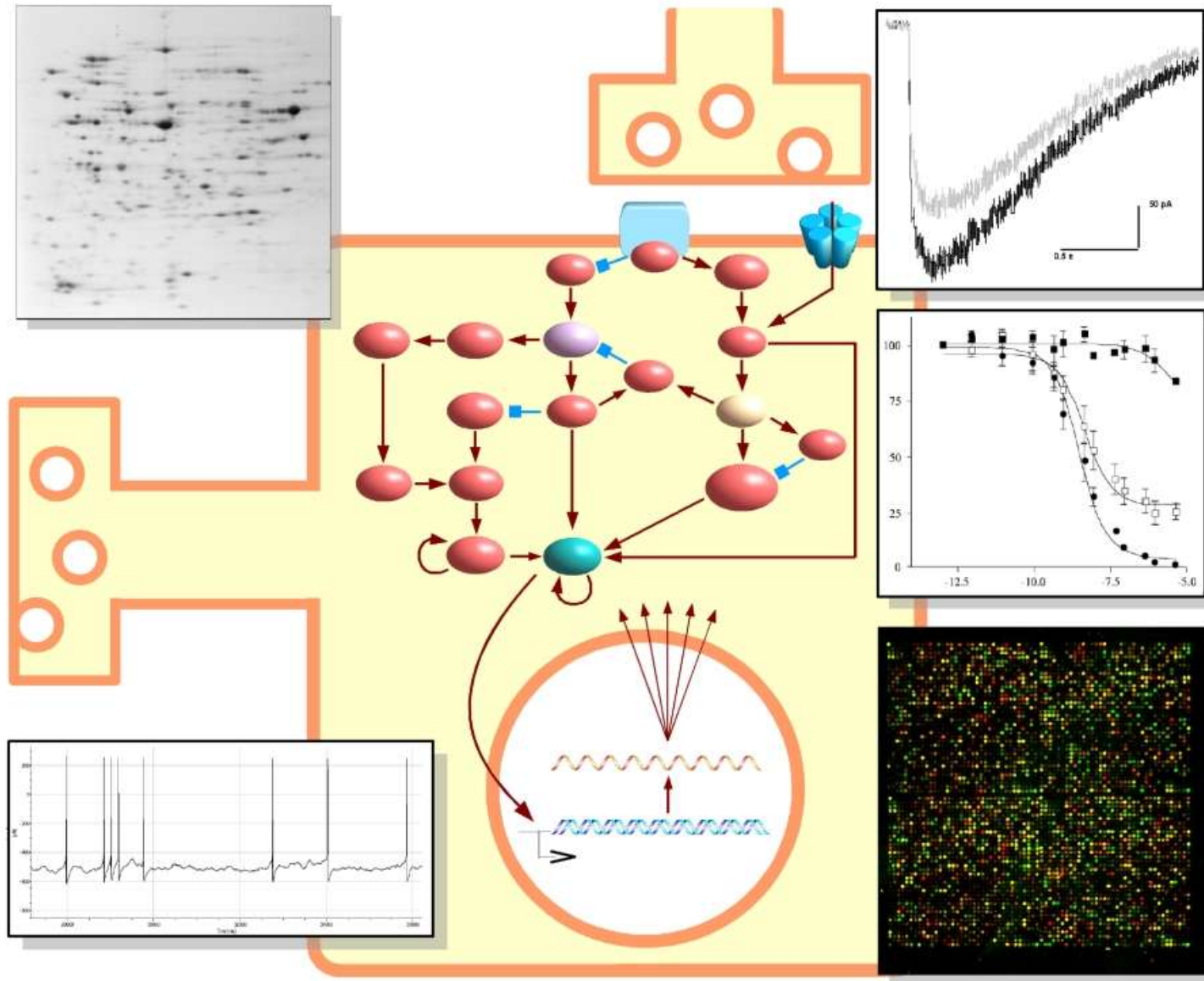
(February 28, 2004) The results are in, and people voted to expand the role of the 'sysbio' mailing list. The changes take effect immediately.

'sysbio' mailing list survey

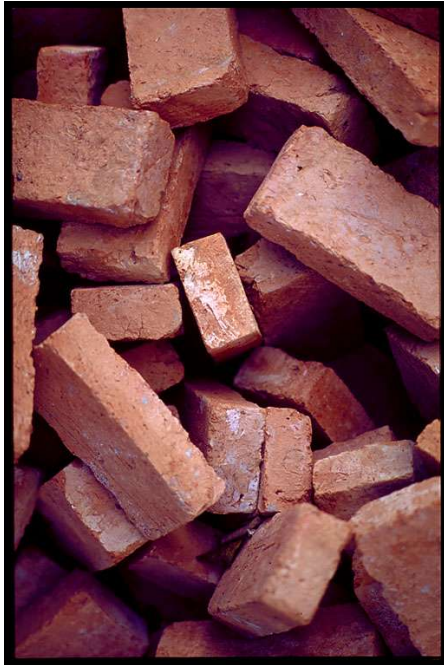
(February 10, 2004) We are running a survey to find out what to do with the 'sysbio@caltech.edu' mailing list. Please visit [the survey page](#) to cast your vote.

[read more](#)

Heterogeneous quantitative data



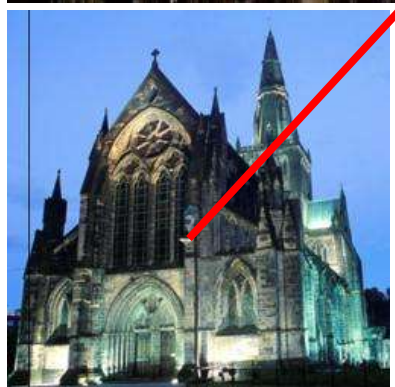
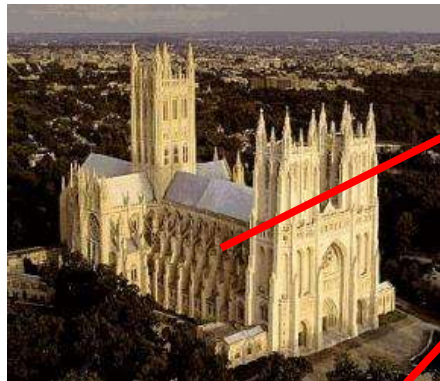
Cellular Neurobiology today



Cellular Neurobiology today



Cellular Neurobiology today

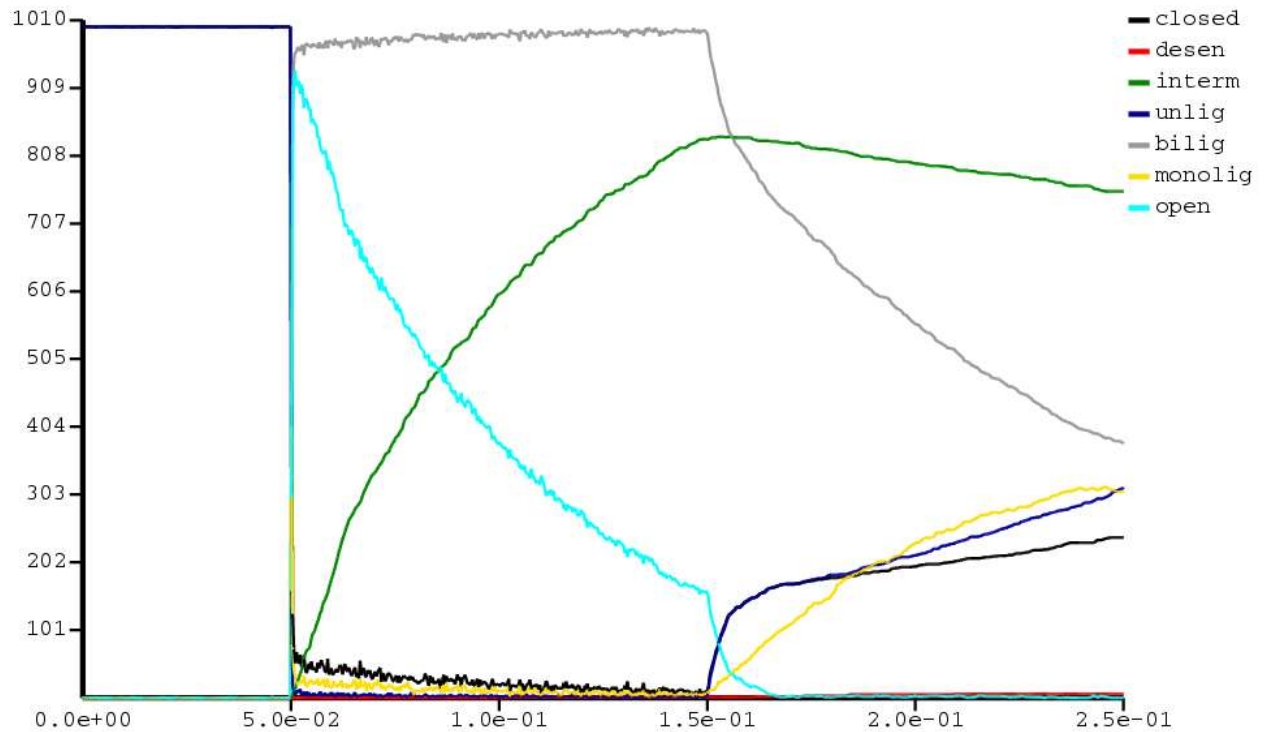


**In Computational Neurobiology
the bottleneck is often the data,
not the tool**



A minimal example: Stochastic simulation of a nicotinic EPSP

- 12 reactants
- 17 reactions
- 36 parameters
- 2 events
- SBML2: 867 lines



Parsing can be an HPC problem ;-)