

Toward a Systems Biology of the Neuron

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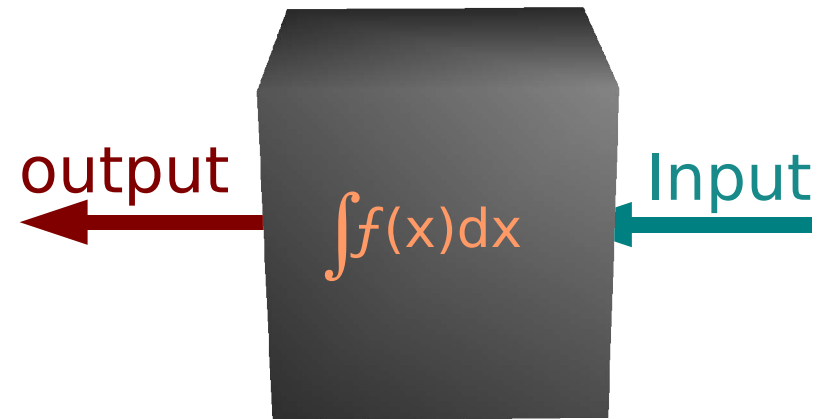
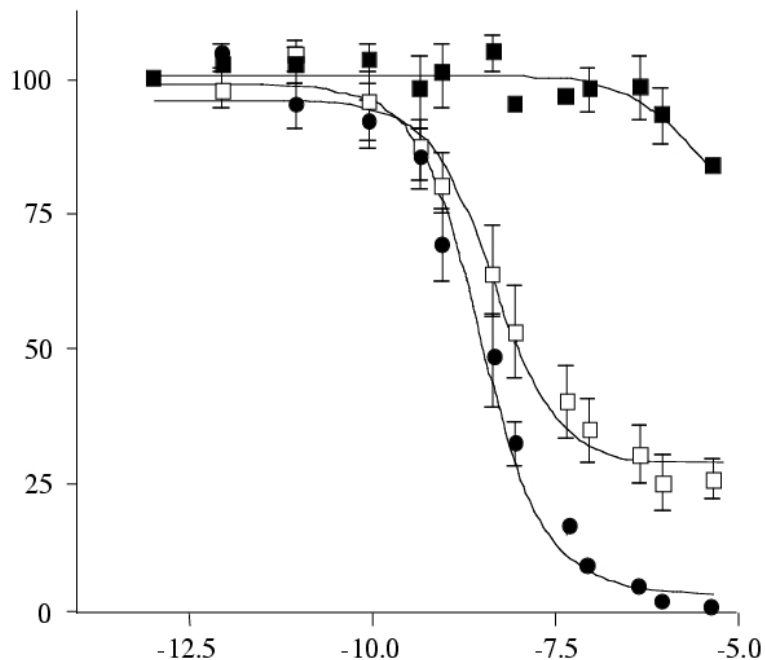
Classical modelling technics

(1)-The phenomenology

Snapshot of the system

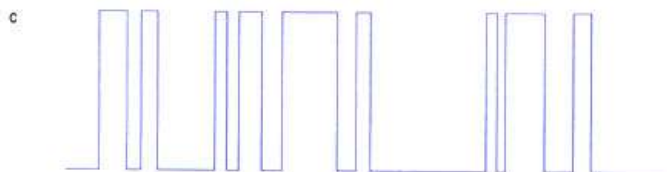
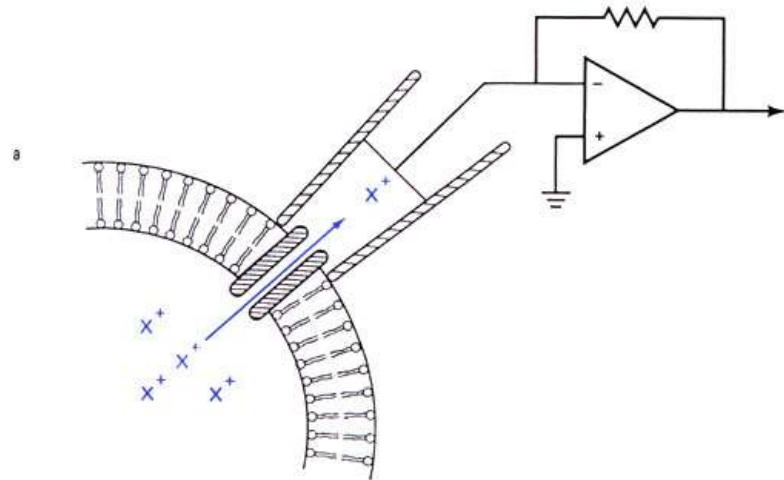
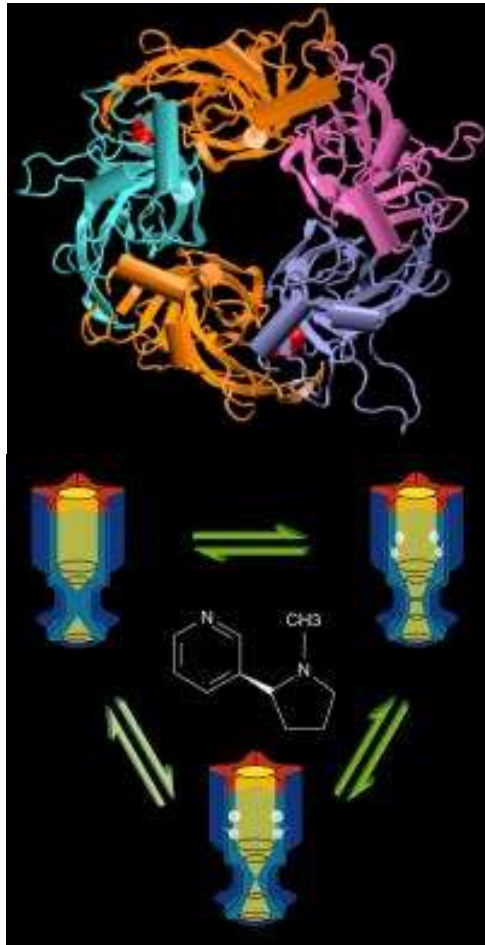
⇒

Abstraction

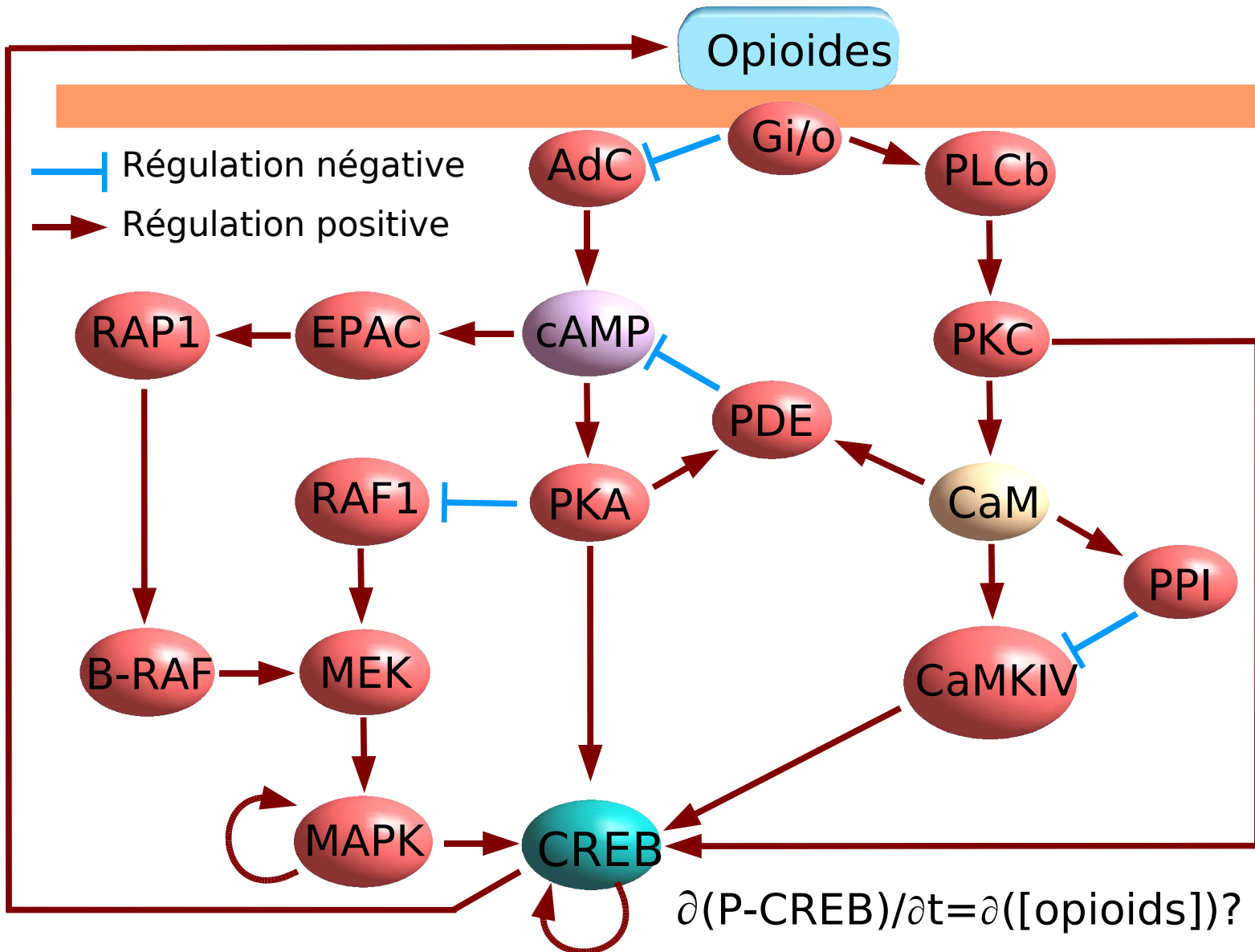


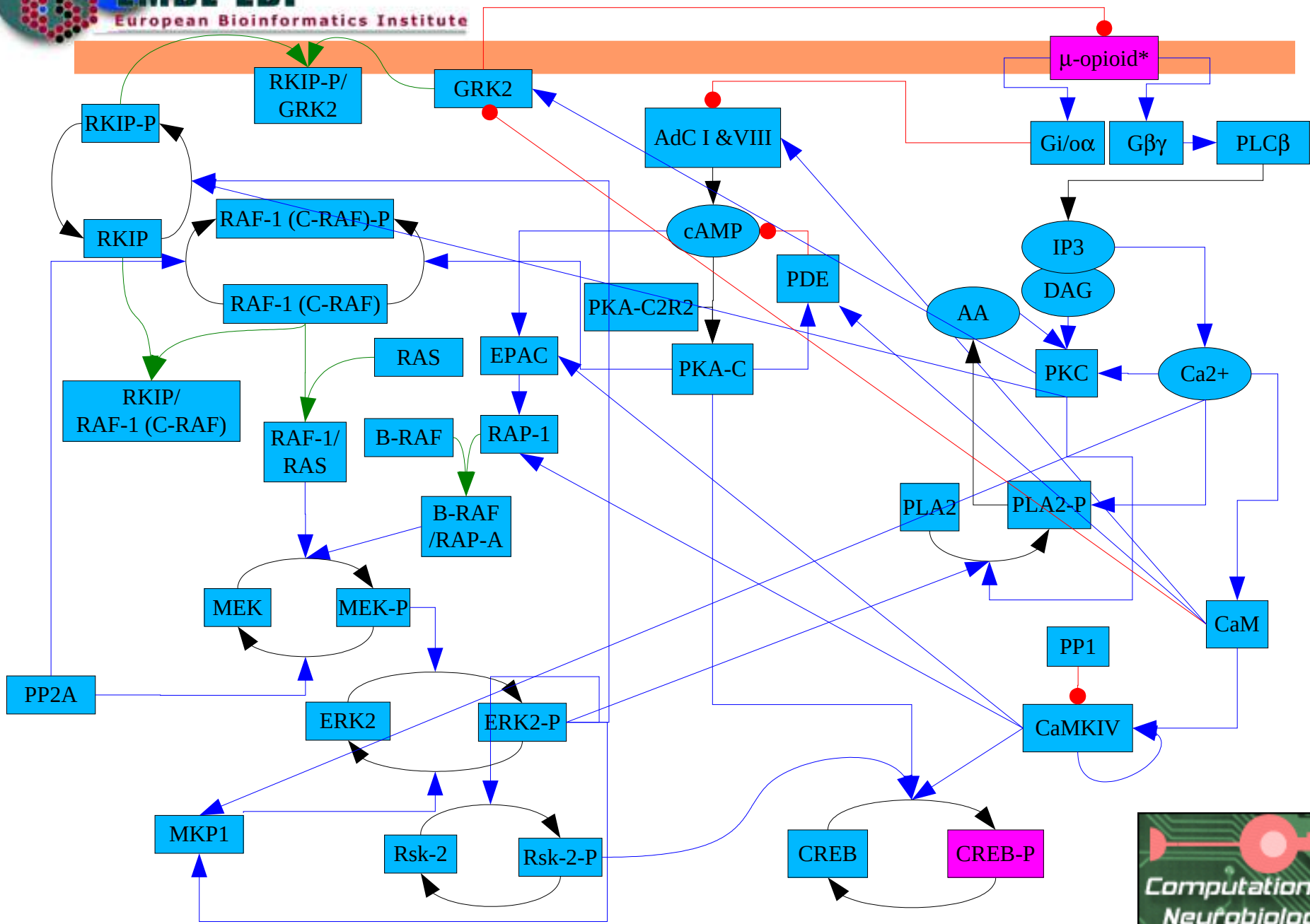
Classical modelling technics

(2)-The reductionism



Emergent properties



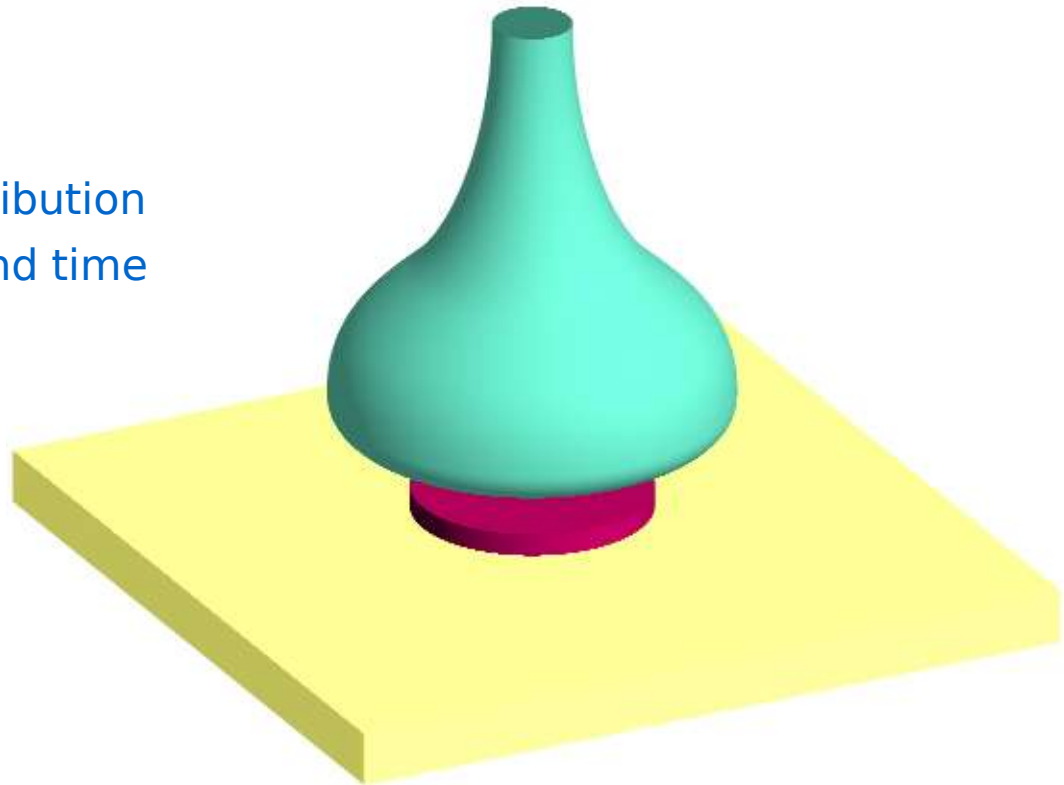


Systems Biology

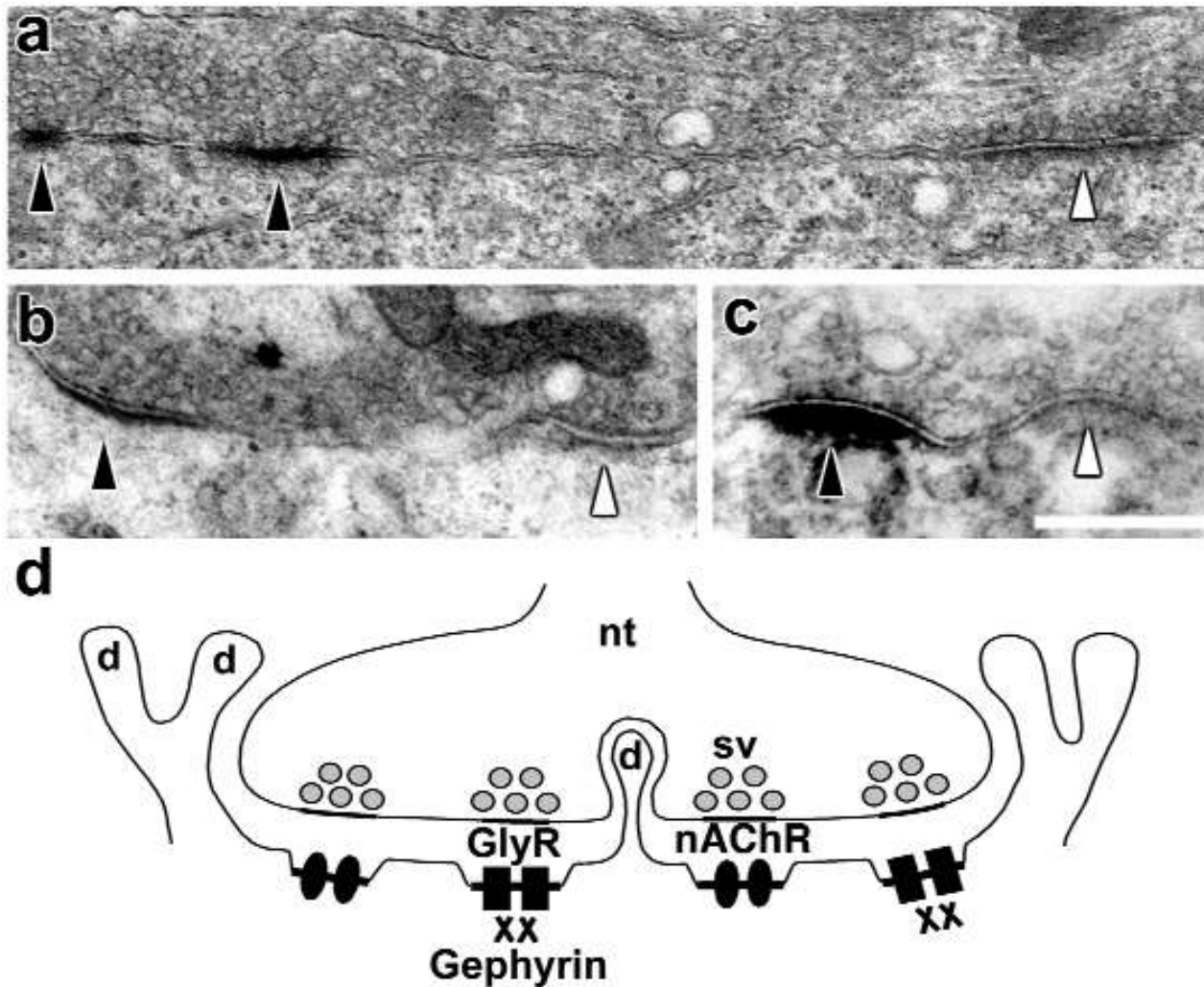
- ◆ Reconstruction of the dynamic systems from the properties of their elementary building blocks
- ◆ Cybernetics properties are conserved across systems (control theory: feedback, feedforward, robustness)
Relationships between building blocks are more important than their elementary properties.
The theoretical treatment is already available
- ◆ Made possible by large-scale data production & improvements of computing power and technics
- ◆ A New Era:
Molecular Biology made Biology understandable
Systems Biology makes Biology predictive

Common (mis)conception of the synapse

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



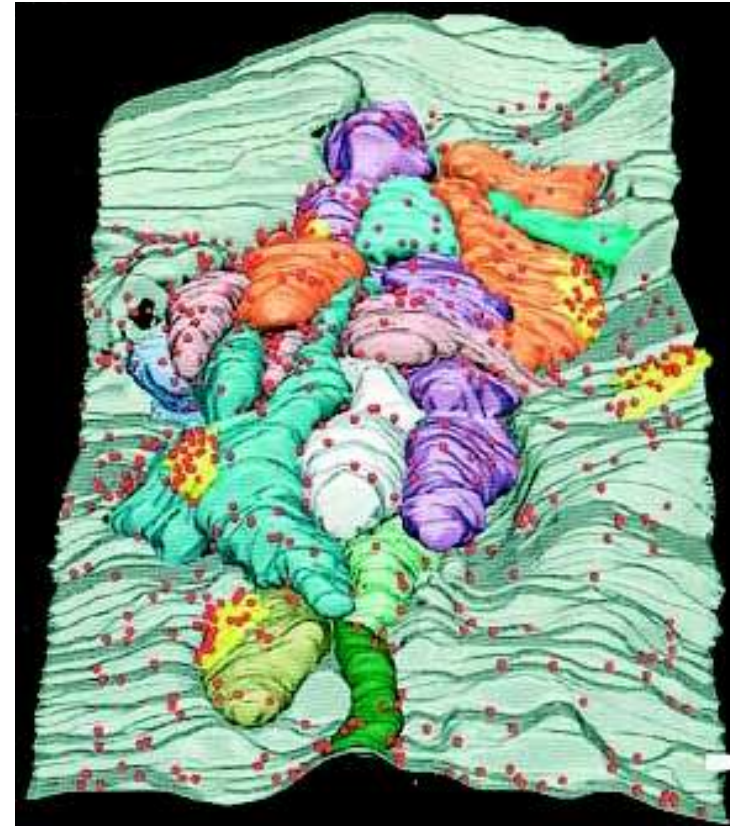
Pharmacological complexity



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

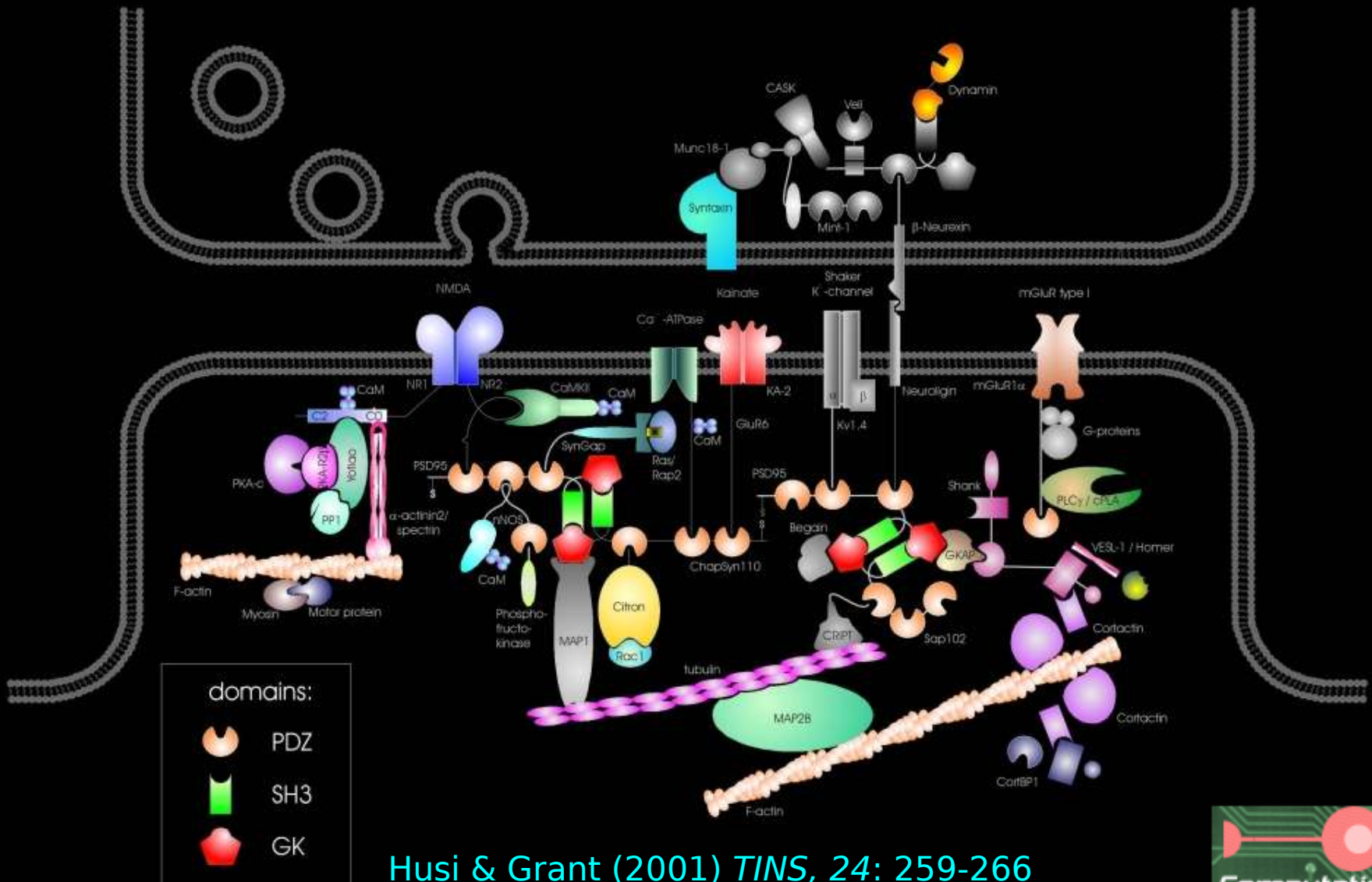
Structural complexity (1)

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



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

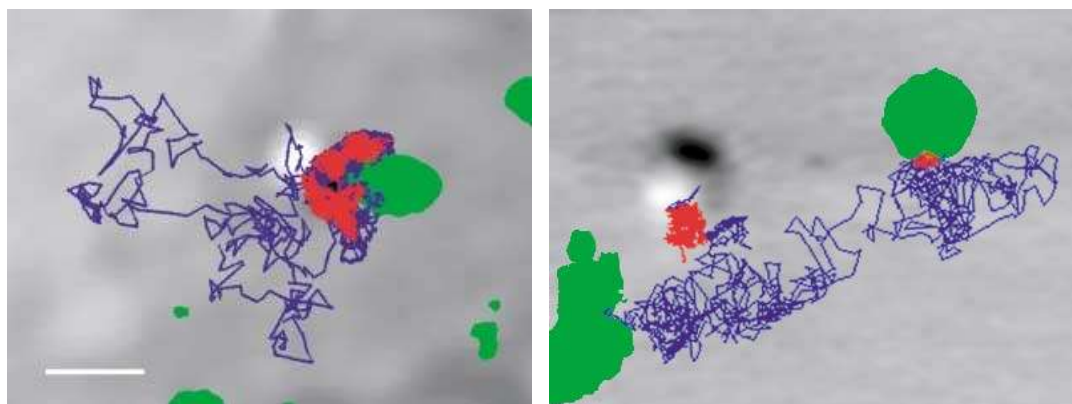
Structural complexity (2)



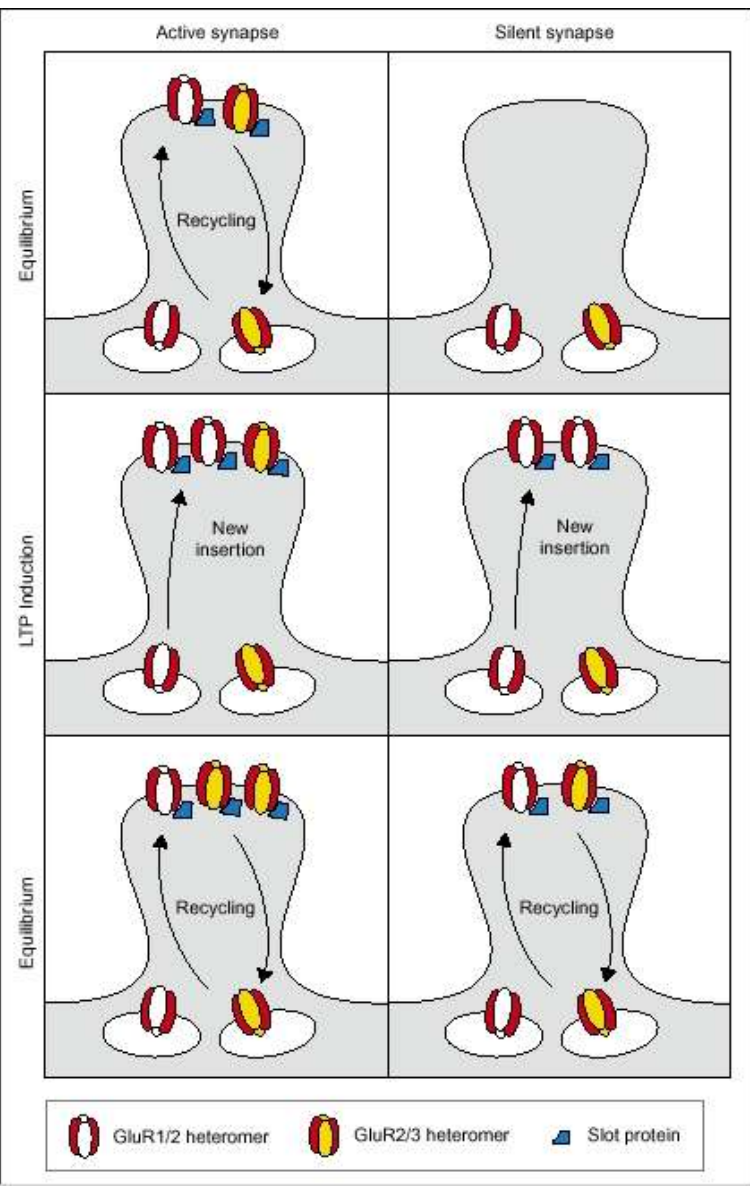
Husi & Grant (2001) *TINS*, 24: 259-266

Temporal complexity

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

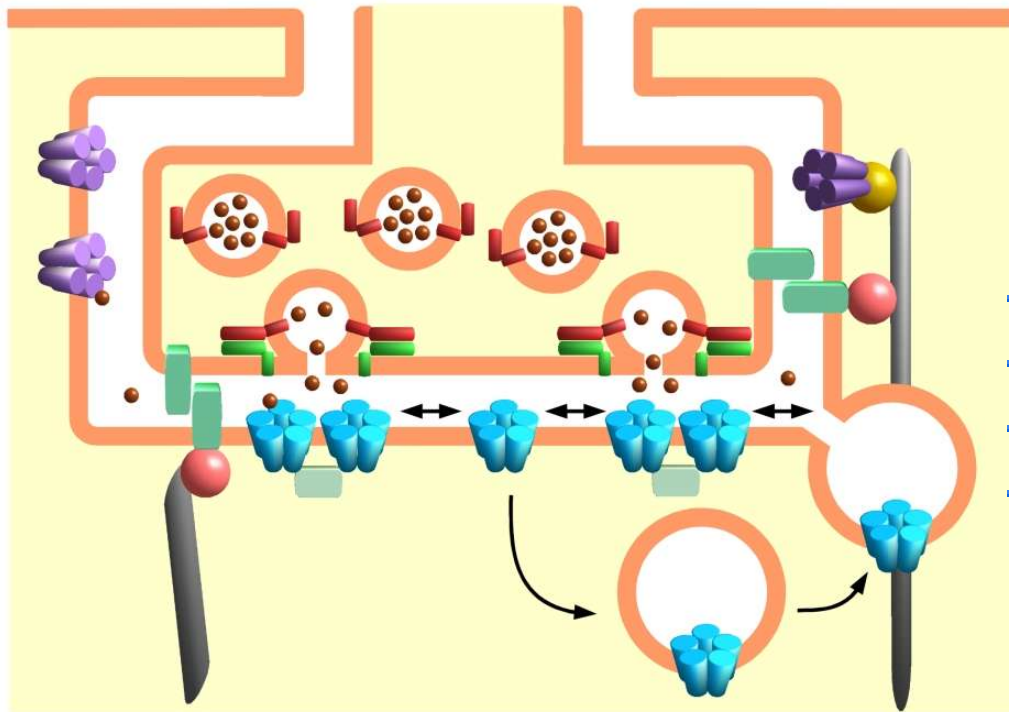
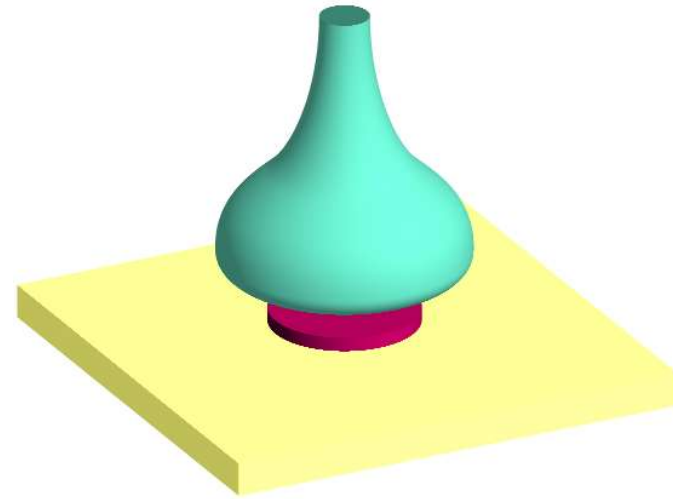


Choquet & Triller (2003)
Nat Rev Neurosci, 4: 251-265



Classical and current views of the synapse

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



- ◆ Several receptors
- ◆ Heterogenous distribution
- ◆ Horizontal and vertical movements
- ◆ Supra-macromolecular assembly

Need a System view?

◆ Signalling pathways exhibits non-linear features

- Interplay between different signalling pathways
 - Presence of feedback and feedforward controls
 - Sensitivity to cell environment
- ⇒ Numerical simulations are mandatory

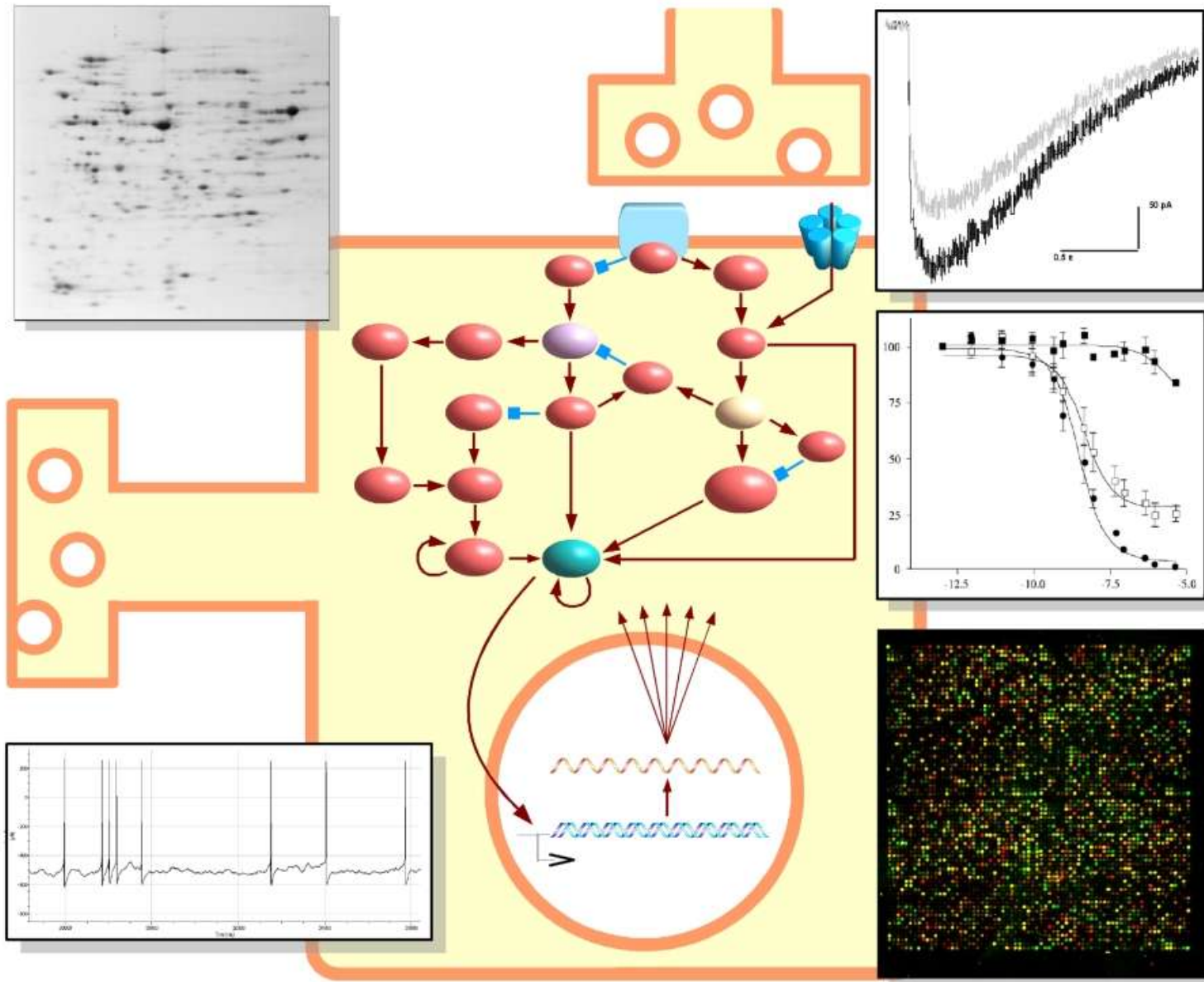
◆ The synaptic millenium revolution

- The synapses can contain several (interacting) types of receptors
 - The spatial organisation of subcellular compartments is important
 - Partners move across the membrane, are inserted and removed
- ⇒ Present models of synaptic transmission are no longer in phase with the current biological knowledge

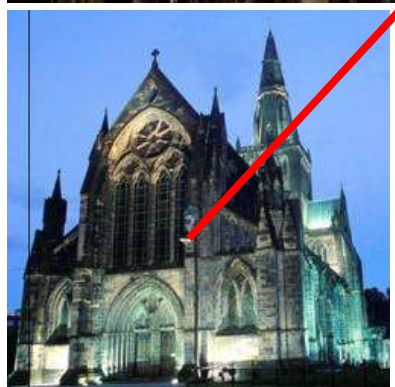
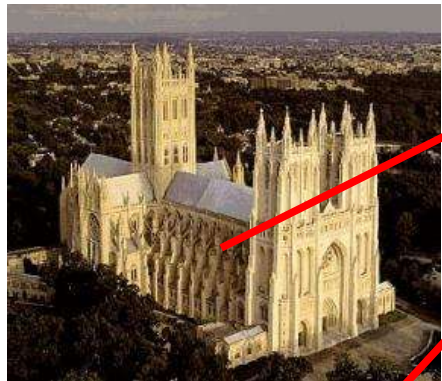
◆ In silico cell pathology

- Realistic modelling of molecular diseases
- Identification of bottlenecks, robust modules, sensitive steps etc.
- Analysis of the effect of pharmacological agents

Heterogeneous quantitative data



Cellular Neurobiology today





DopaNet is supported by:



DopaNet: The Meso-Telencephalic Dopamine Consortium

What is DopaNet?	DopaNet structure
DopaNet members	Open positions
Neuronal ontology	Molecule Pages
How can I help?	Contact

NEW March 2004: The construction of the [Molecule Pages](#), aimed to store detailed functional information about molecules present in DopaNet target cells has been started. Everybody is invited to participate.

June 2003: The construction of an [ontology of the neuronal cell](#) has been started. Everybody is invited to participate.

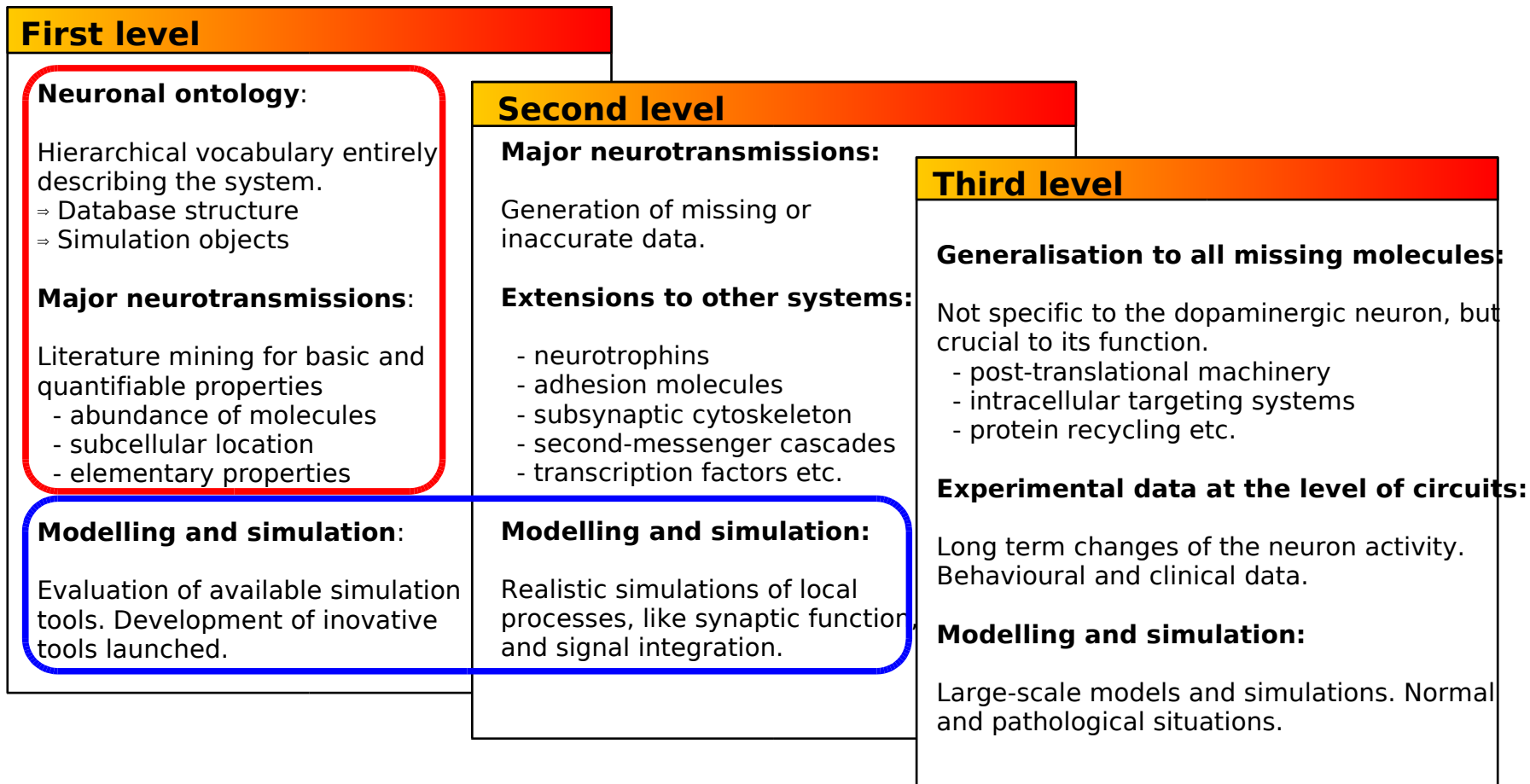
February 2003: The computing infrastructure of DopaNet will be hosted by the [European Bioinformatic Institute \(EBI\)](#), outstation of the [European Molecular Biology Laboratory \(EMBL\)](#).

December 2002: DopaNet is accepted as a network of the [European Science Foundation](#). A grant of 80 000 € is attributed for the period 2003-2005. ([ESF booklet](#))

Nicolas Le Novère

Last modified: Wed Mar 24 14:50:59 GMT 2004

Roadmap



File Edit View Go Bookmarks Tools Window Help

file:///home/nicolas/DopaNet/WWW/dopanet.org/Ontology/dant-ontologyBrows Search

Tree Menu Help

- ① "is a" relationship
- Ⓟ "part of" relationship
- DopaNet_Ontology
 - Ⓟ cellular_component
 - Ⓟ ① cell
 - Ⓟ Ⓟ plasma membrane
 - Ⓟ ① neuron
 - Ⓟ Ⓟ axon
 - Ⓟ Ⓟ axon hillock
 - Ⓟ Ⓟ somato-dendritic compartment
 - Ⓟ Ⓟ perikaryon
 - Ⓟ Ⓟ dendrite
 - Ⓟ Ⓟ dendritic shaft
 - Ⓟ Ⓟ dendritic spine
 - Ⓟ Ⓟ distal dendrite
 - Ⓟ Ⓟ dendritic spine
 - Ⓟ Ⓟ proximal dendrite
 - Ⓟ Ⓟ intermediate dendrite
 - Ⓟ Ⓟ cytoplasm
 - Ⓟ ① extracellular space
 - Ⓟ ① obsolete component
 - Ⓟ ① molecular complex
 - Ⓟ ① molecule
 - Ⓟ Ⓟ molecular_function
 - Ⓟ ① ion channel
 - Ⓟ ① ligand-gated ion channel
 - Ⓟ ① nicotinic acetylcholine-gated receptor
 - Ⓟ ① 5-HT3 receptor
 - Ⓟ ① GABA-A receptor

DA:0000010; dendrite [show tree] [Open node] [Collapse tree]

definition	A protoplasmic process of a nerve cell that receives and integrate signals from other nerve cells, and transmits an impulses to the neuronal cell body.
is a	
part of	DA:0000253
children	DA:0000011 DA:0000256 DA:0000249 DA:0000012 DA:0000247 DA:0000248

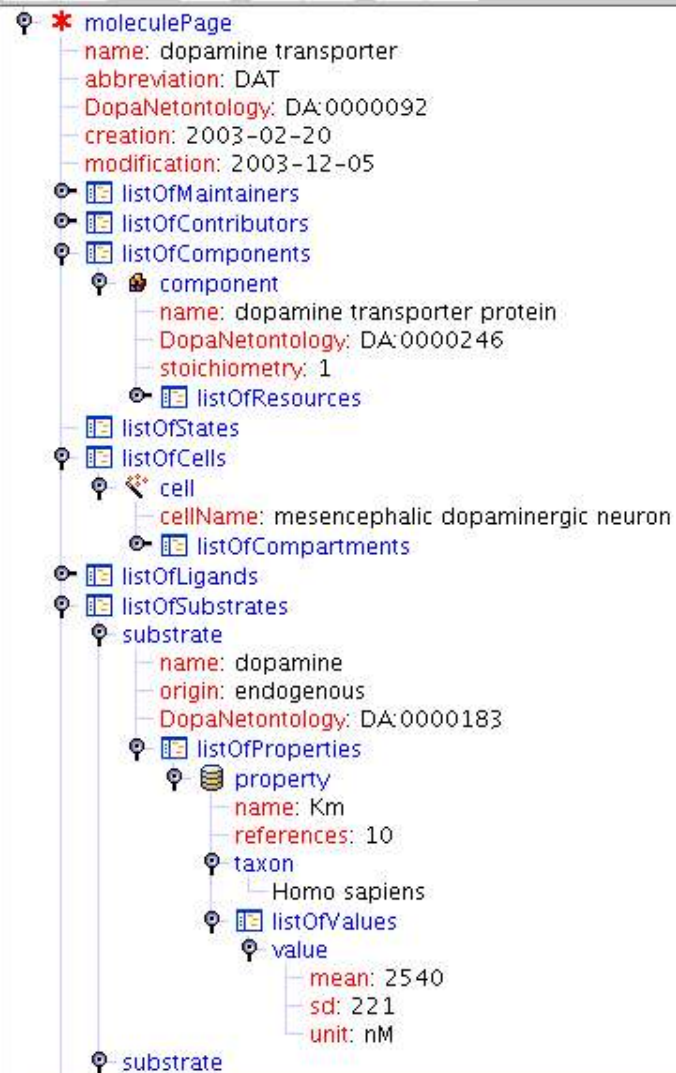
Last modification: Thu Dec 4 19: 11: 29 2003 GMT.

Neuronal ontology

file:///home/nicolas/DopaNet/WWW/dopanet.org/Ontology/Terms/DA0000010.html



/home/nicolas/DopaNet/MolPages/XMLPages/DAT.xml



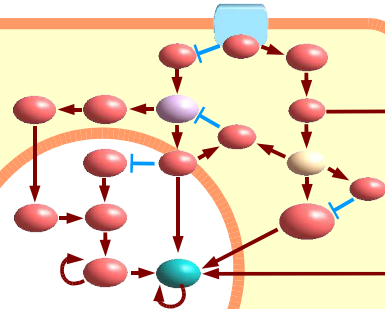
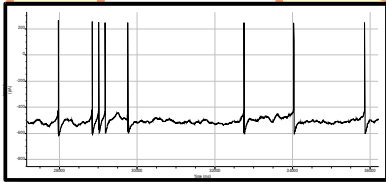
Molecule Pages


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<moleculePage
  DopaNetontology="DA:0000311"
  abbreviation="TGFbR-1" />
<listOfStates>
  <state name="active">
  <state name="inactive">
</listOfStates>
<ListofLigands>
  <ligand
    DopaNetontology="DA:0000279"
    stateligand="TGFbRI_greedy">
    <listOfProperties>
      <property name="Kd" references="7">
        statemolecule="active">
        <listOfValues>
          <value mean="6" sd="2"
            unit="picomole per litre"/>
        </listOfValues>
      </property>
    </listOfProperties>
  </ligand>
</listOfLigands>
<listOfBibitems>
  <bibitem label="7" pmid="12729750">
    Crescenzo et al.
  </bibitem>
</listOfBibitems>
</moleculePage>
```

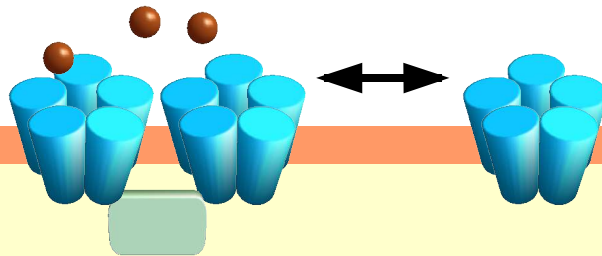
```
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  <state name="TGFbRI_greedy">
</listOfStates>
<listOfLigands>
  <ligand
    DopaNetontology="DA:0000311"
    stateligand="active">
    <listOfProperties>
      <property name="Kd" references="9">
        statemolecule="TGFbRI_greedy">
        <listOfValues>
          <value mean="6" sd="2"
            unit="picomole per litre"/>
        </listOfValues>
      </property>
    </listOfProperties>
  </ligand>
</listOfLigands>
<listOfBibitems>
  <bibitem label="9" pmid="12729750">
    Crescenzo et al.
  </bibitem>
</listOfBibitems>
</moleculePage>
```

Modular multi-scales multi-algorithms program

Whole-neuron
Cable theory
 $1\mu\text{m}-1\text{m}$
 $1\text{ms}-1\text{week}$



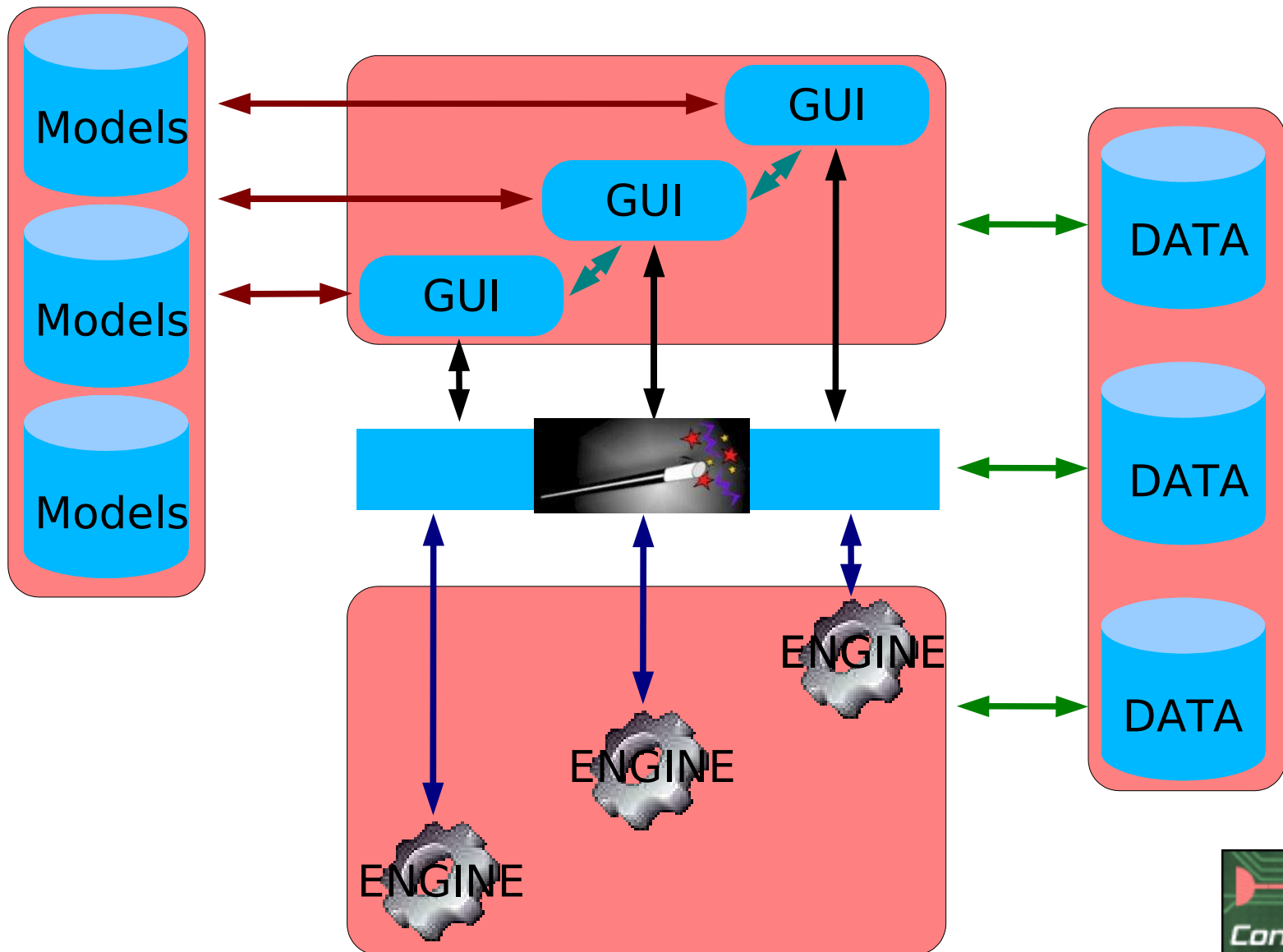
Signaling network
ODE
 $1\mu\text{m}-10\mu\text{m}$
 $1\text{s}-1\text{d}$



Synapse
Stochastic algorithm
 $1\text{nm}-100\text{nm}$
 $1\mu\text{s}-1\text{ms}$

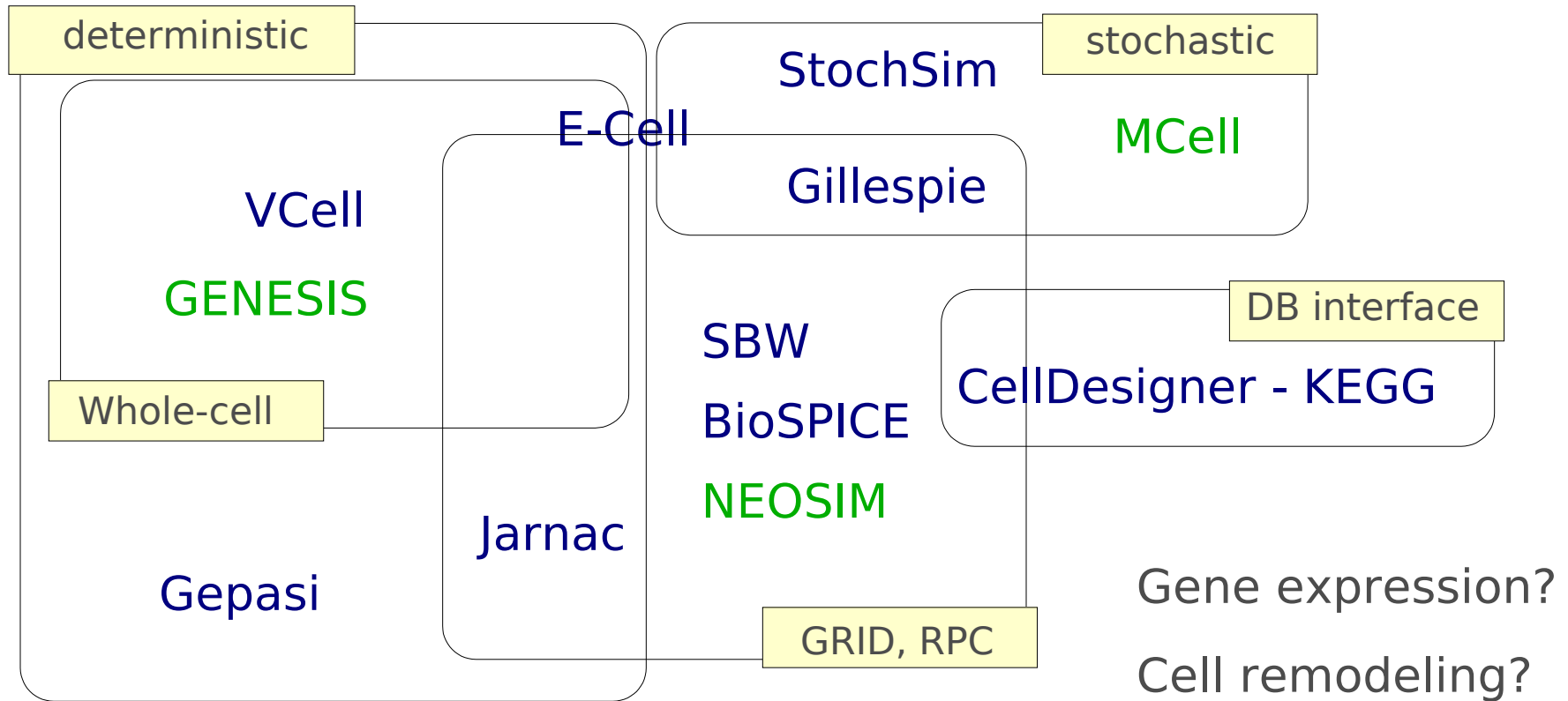
Dendritic spine
Diffusion, PDE
 $100\text{nm}-1\mu\text{m}$
 $1\text{ms}-1\text{s}$

Modular multi-scales multi-algorithms program



Existing efforts

used to model neurons

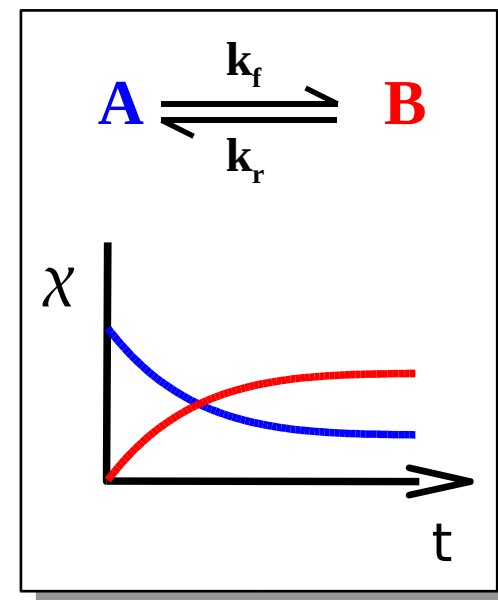


All these programs speak SBML
(Systems Biology Markup Language)



Systems Biology Markup Language

```
<?xml version="1.0" encoding="ISO-8859-1"?>
<sbml xmlns="http://www.sbml.org/sbml/level1" level="1" version="2">
  <model name="Example">
    <listOfReactions>
      <reaction name="_0">
        <kineticLaw formula="(kf * X - kr * Y) * compl">
          <listOfParameters>
            <parameter value="3000" name="kf" />
            <parameter value="1500" name="kr" />
          </listOfParameters>
        </kineticLaw>
        <listOfReactants>
          <speciesReference species="X" />
        </listOfReactants>
        <listOfProducts>
          <speciesReference species="Y" />
        </listOfProducts>
        <notes>
          <body xmlns="http://www.w3.org/1999/xhtml">
            <p>Interconversion between X and Y</p>
          </body>
        </notes>
      </reaction>
    </listOfReactions>
    <listOfSpecies>
      <species units="mole" initialamount="1e-21" compartment="compl" name="X">
        <notes>
          <body xmlns="http://www.w3.org/1999/xhtml">
            <p>the molecule under state X</p>
          </body>
        </notes>
      </species>
      <species units="mole" boundaryCondition="true" initialamount="0" compartment="compl" name="Y">
        <notes>
          <body xmlns="http://www.w3.org/1999/xhtml">
            <p>the molecule under state Y</p>
          </body>
        </notes>
      </species>
    </listOfSpecies>
    <listOfCompartments>
      <compartment volume="1e-021" name="compl" />
    </listOfCompartments>
  </model>
</sbml>
```



A real situation: Stochastic simulation of a nicotinic EPSP

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

