SBML, where it's been, were it is going

Nicolas Le Novère, EMBL-EBI

SBML.org — The Systems Biology Markup Language

The **Systems Biology Markup Language** (**SBML**) is a computer-readable format for representing models of biological processes. It's applicable to simulations of metabolism, cell-signaling, and many other topics. SBML has been evolving since mid-2000 thanks to an international community of software developers and users. This website is the global portal for the SBML effort; here you can find information about all aspects of SBML.

For the curious

What *is* SBML? Read our **basic introduction** and then perhaps browse the **mailing lists** to get a sense for what's currently going on in the world of SBML.

For modelers

Are you looking for ready-to-run software that supports SBML? The **SBML Software Guide** lists over **175** systems today. Are you instead looking for ready-to-use models? Visit the **BioModels Database**, where you can find hundreds!

For software developers

Are you interested in developing SBML support for your software? Read our **basic introduction** and then the **SBML specifications** to understand how to use SBML. After that, you may want to look at **libSBML**, an API library supporting many programming languages.

No matter how you use SBML, we invite you to sign up for news updates either

SBML News

Review SBML on SourceForge!
(12 Nov.'09) SourceForge.net has a review system for projects. Please use it to **vote & comment** on the SBML project!

Call for SBML Editor nominations
(10 Nov.'09) The nomination phase for two new SBML Editors is **now open**.

LibSBML 4.0.0 released!
(26 Aug.'09) **LibSBML** is an API library for SBML. This release focuses on reducing opportunities for creating invalid SBML.

Older news ...

Community News

BioMet Toolbox
(29 Oct.'09) **BioMet Toolbox** is a web-based toolbox for analyzing genome-scale models.

modelMaGe v. 1.0beta
(27 Oct.'09) **modelMaGe** can generate models and fit models to data.

CycSim supports SBML
(27 Oct.'09) **CycSim** is a

What is SBML?

The Systems Biology Markup Language is a way to **exchange and reuse** (and hopefully **interface**) descriptions of quantitative models in “Systems Biology”, in fact mostly well-stirred chemical kinetics so far.

It is not a procedural language.

It is not a programming language.

It is not a format for specific software configuration files.

Tools are supposed to understand the whole of SBML but not obligatory make use of everything (will not be true for Level 3).

Development philosophy: Start small, get good support, extend.

A feature should only be included if at least two software tools can use it: It is an exchange language.

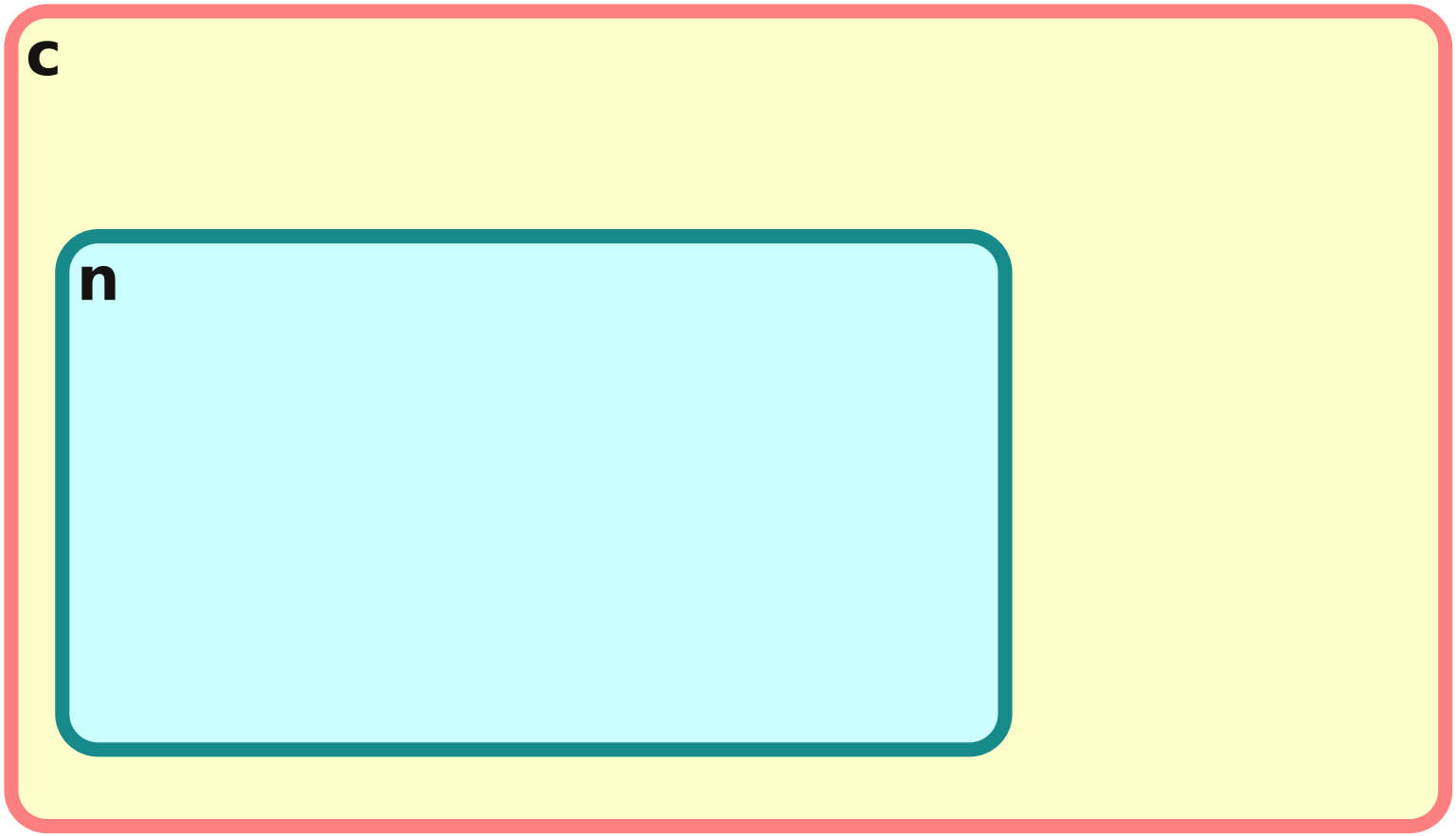
Basic tools are provided to read, validate, write and process SBML. No need to re-invent the wheel. Let's focus on science instead.

SBML itself re-uses other standards: MathML, XHTML, RDF, existing ontologies.

It is supported by a community large, diverse, active and **evolving.**

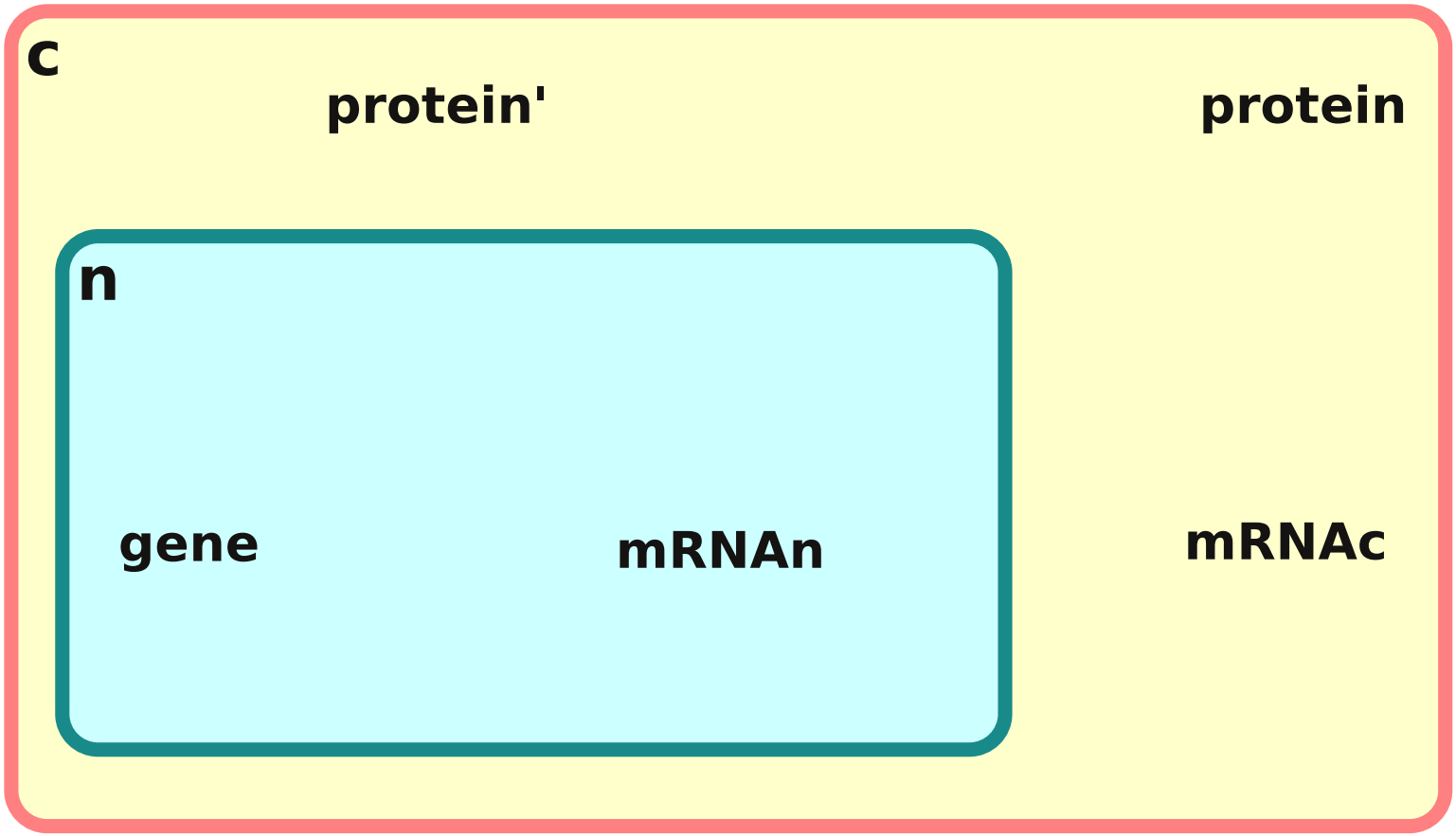
What can we encode in SBML Level 2?

containers (compartments)



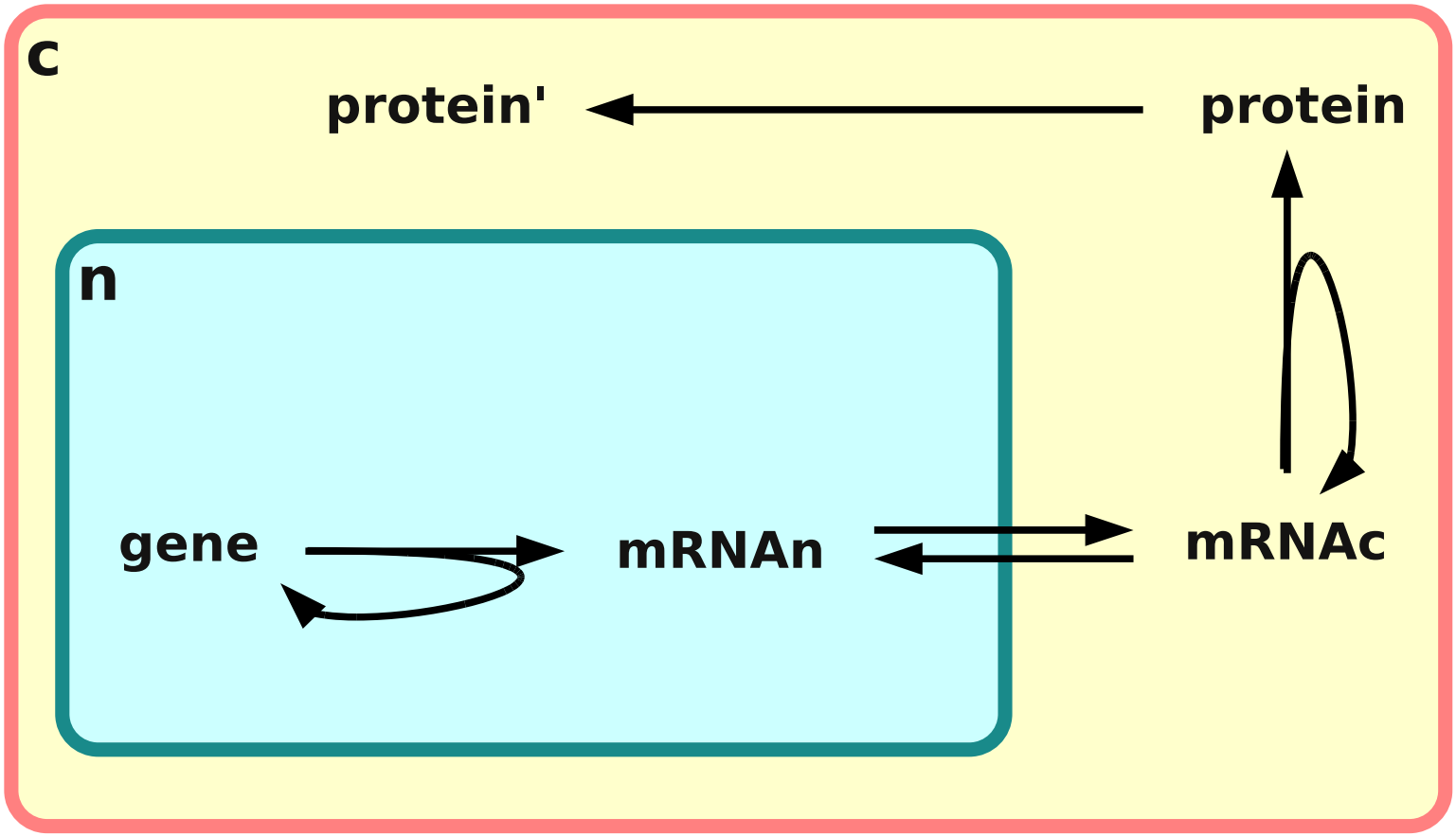
What can we encode in SBML Level 2?

species



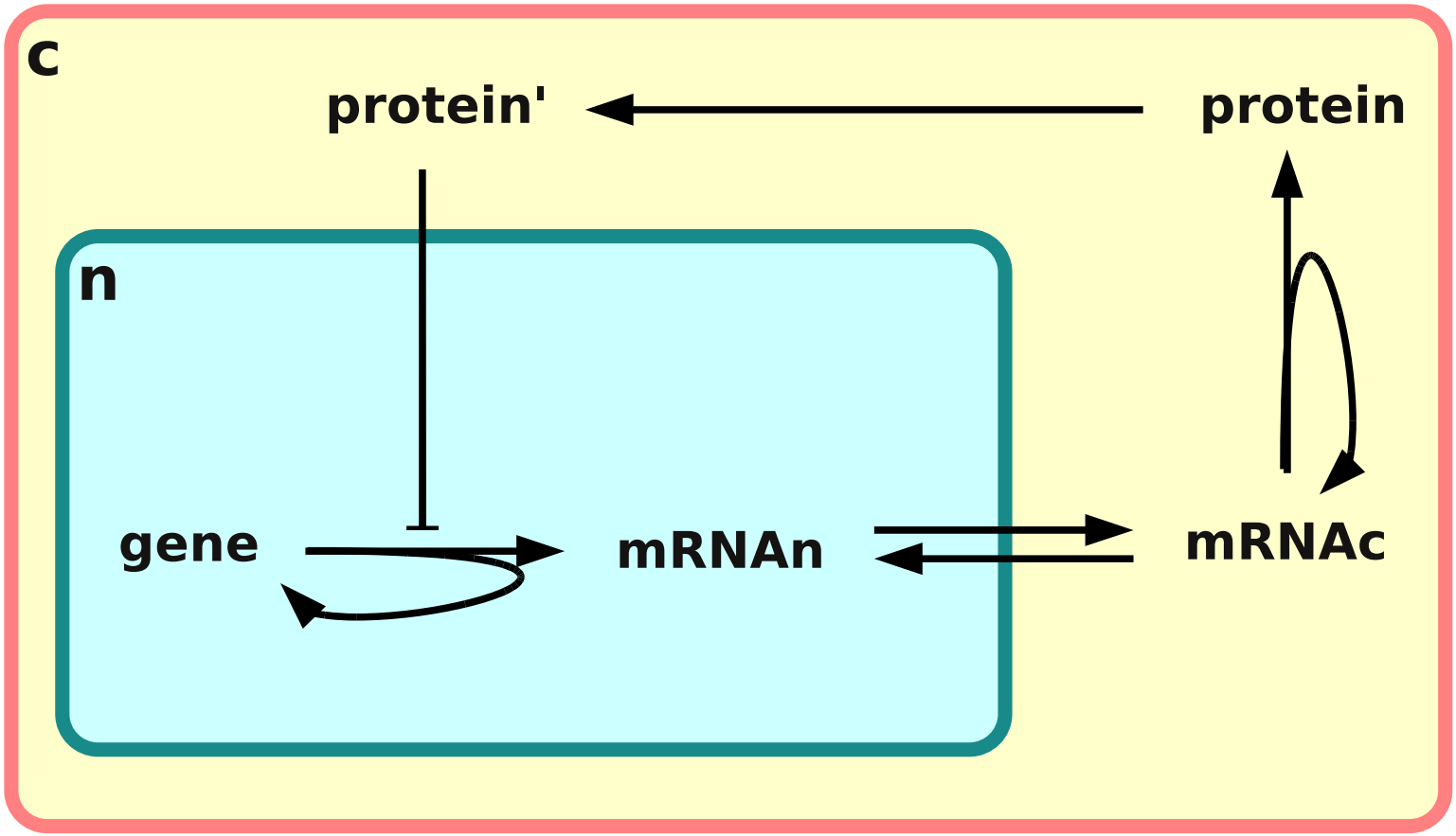
What can we encode in SBML Level 2?

reactions



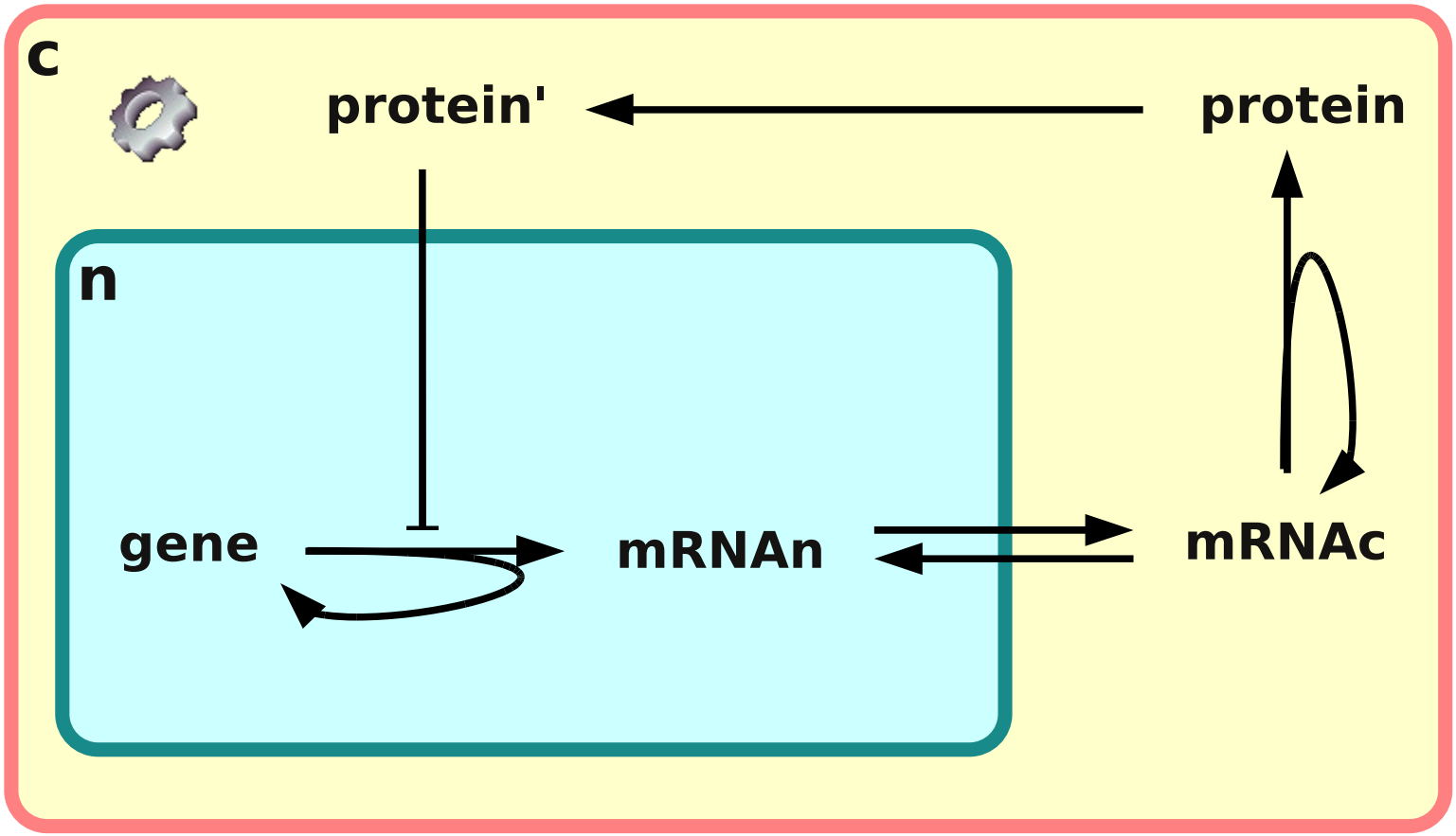
What can we encode in SBML Level 2?

modulations



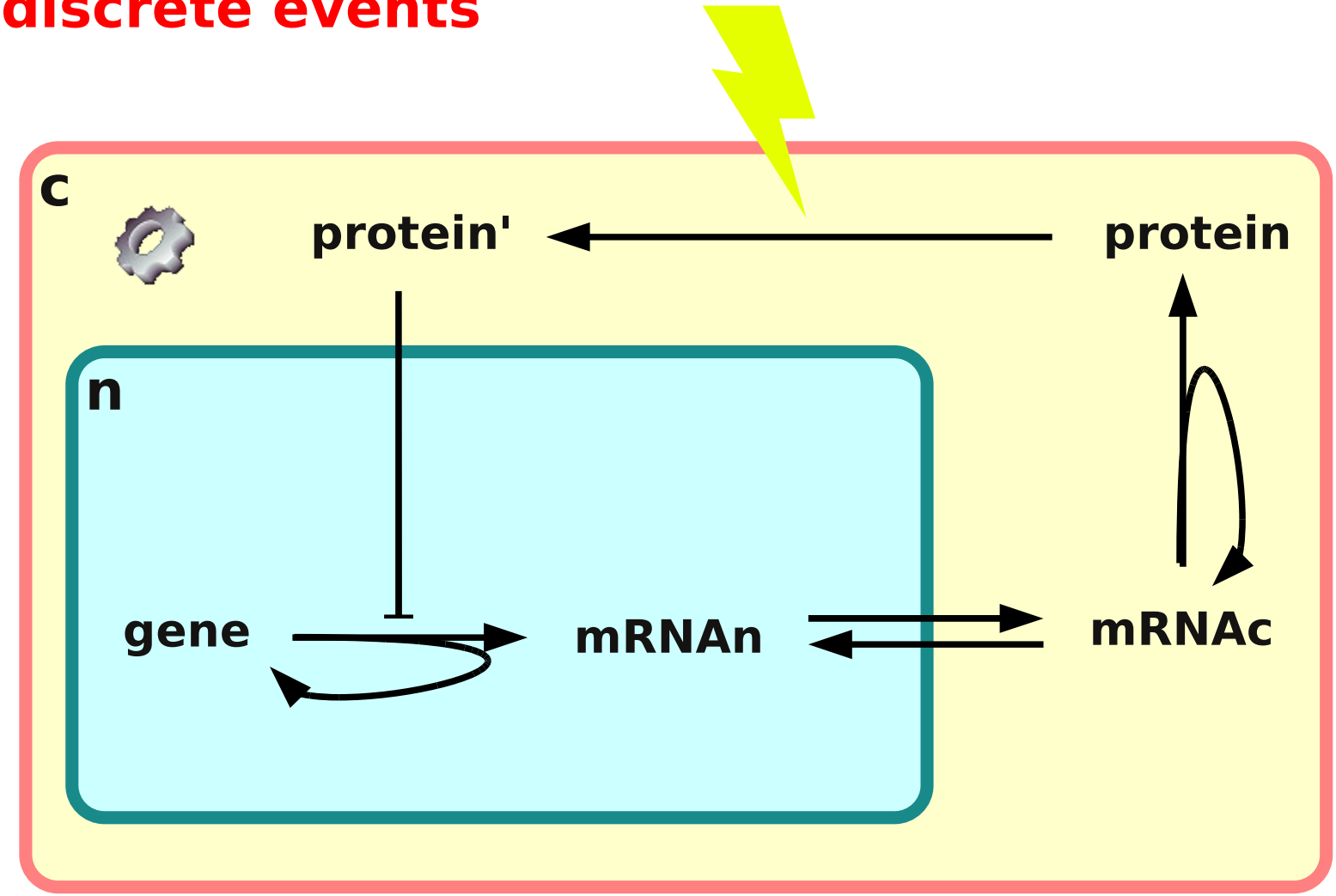
What can we encode in SBML Level 2?

arbitratry rules



What can we encode in SBML?

discrete events



SBML and XML

The Systems Biology Markup Language is defined as a set of classes represented in the Unified Modelling Language (UML)

In practise, it is used

A) as serialised in XML, using

- An XML schema 1) lists all the elements and attributes, 2) specifies the containment relationships between them, 3) precises the datatype of each
- An additional set of constraints is listed in the specification and implemented as a list of consistency checks, for instance in libSBML
- Strict system of unit consistency can be turned on

B) as an API (libSBML)

A → B

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml level="2" version="1" xmlns="http://www.sbml.org/sbml/level2">
  <model>
    <listOfCompartments>
      <compartment id="cell" />
    </listOfCompartments>
    <listOfSpecies>
      <species id="A" compartment="cell" initialConcentration="1"/>
      <species id="B" compartment="cell" initialConcentration="0"/>
    </listOfSpecies>
    <listOfParameters>
      <parameter id="kon" value="1"/>
    </listOfParameters>
    <listOfReactions>
      <reaction>
        <listOfReactants>
          <speciesReference species="A" />
        </listOfReactants>
        <listOfProducts>
          <speciesReference species="B" />
        </listOfProducts>
        <kineticLaw>
          <math xmlns="http://www.w3.org/1998/Math/MathML">
            <apply>
              <times />
              <ci>kon</ci>
              <ci>A</ci>
              <ci>cell</ci>
            </apply>
          </math>
        </kineticLaw>
      </reaction>
    </listOfReactions>
  </model>
</sbml>
```


No biological semantics in the language itself

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml level="2" version="1" xmlns="http://www.sbml.org/sbml/level2">
  <model>
    <listOfCompartments>
      <compartment id="cell" />
    </listOfCompartments>
    <listOfSpecies>
      <species id="A" compartment="cell" initialConcentration="1"/>
      <species id="B" compartment="cell" initialConcentration="0"/>
    </listOfSpecies>
    <listOfParameters>
      <parameter id="kon" value="1"/>
    </listOfParameters>
    <listOfReactions>
      <reaction>
        <listOfReactants>
          <speciesReference species="A" />
        </listOfReactants>
        <listOfProducts>
          <speciesReference species="B" />
        </listOfProducts>
        <kineticLaw>
          <math xmlns="http://www.w3.org/1998/Math/MathML">
            <apply>
              <times />
              <ci>kon</ci>
              <ci>A</ci>
              <ci>cell</ci>
            </apply>
          </math>
        </kineticLaw>
      </reaction>
    </listOfReactions>
  </model>
</sbml>
```

Elements free of biological semantics: we do not know which type of species this is

Reusing existing standards

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml level="2" version="1" xmlns="http://www.sbml.org/sbml/level2">
  <model>
    <listOfCompartments>
      <compartment id="cell" />
    </listOfCompartments>
    <listOfSpecies>
      <species id="A" compartment="cell" initialConcentration="1"/>
      <species id="B" compartment="cell" initialConcentration="0"/>
    </listOfSpecies>
    <listOfParameters>
      <parameter id="kon" value="1"/>
    </listOfParameters>
    <listOfReactions>
      <reaction>
        <listOfReactants>
          <speciesReference species="A" />
        </listOfReactants>
        <listOfProducts>
          <speciesReference species="B" />
        </listOfProducts>
        <kineticLaw>
          <math xmlns="http://www.w3.org/1998/Math/MathML">
            <apply>
              <times />
              <ci>kon</ci>
              <ci>A</ci>
              <ci>cell</ci>
            </apply>
          </math>
        </kineticLaw>
      </reaction>
    </listOfReactions>
  </model>
</sbml>
```

MathML

A more realistic example ...

```
<species
    id="A"
    name="α-tubulin"
    compartment="cell"
    initialAmount="1000"
    substanceUnits="item"
    hasOnlySubstanceUnits="true"
    boundaryCondition="true"
    constant="false"
    charge="0"
    metaid="PX"
    sboTerm="SBO:0000245" >
  <notes>
    <body xmlns="http://www.w3.org/1999/xhtml">
      <p>One of the components of a microtubule</p>
    </body>
  </notes>
  <annotation>
    <rdf:RDF
        xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
        xmlns:bqmodel="http://biomodels.net/model-qualifiers/"
        xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#">
      <rdf:Description rdf:about="#PX">
        <bqbiol:is>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P68370"/>
            <rdf:li rdf:resource="urn:miriam:obo.go:GO%3A0045298"/>
          </rdf:Bag>
        </bqbiol:is>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```

Externalisation of biological semantics

```
<species
    id="A"
    name="α-tubulin"
    compartment="cell"
    initialAmount="1000"
    substanceUnits="item"
    hasOnlySubstanceUnits="true"
    boundaryCondition="true"
    constant="false"
    charge="0"
    metaid="PX"
    sboTerm="SBO:0000245" >
  <notes>
    <body xmlns="http://www.w3.org/1999/xhtml">
      <p>One of the components of a microtubule</p>
    </body>
  </notes>
  <annotation>
    <rdf:RDF
        xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
        xmlns:bqmodel="http://biomodels.net/model-qualifiers/"
        xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#">
      <rdf:Description rdf:about="#PX">
        <bqbiol:is>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P68370"/>
            <rdf:li rdf:resource="urn:miriam:obo.go:GO%3A0045298"/>
          </rdf:Bag>
        </bqbiol:is>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```

macromolecule

Reusing existing standards again

```
<species
    id="A"
    name="α-tubulin"
    compartment="cell"
    initialAmount="1000"
    substanceUnits="item"
    hasOnlySubstanceUnits="true"
    boundaryCondition="true"
    constant="false"
    charge="0"
    metaid="PX"
    sboTerm="SBO:0000245" >
  <notes>
    <body xmlns="http://www.w3.org/1999/xhtml">
      <p>One of the components of a microtubule</p>
    </body>
  </notes>
  <annotation>
    <rdf:RDF
        xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
        xmlns:bqmodel="http://biomodels.net/model-qualifiers/"
        xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#">
      <rdf:Description rdf:about="#PX">
        <bqbiol:is>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P68370"/>
            <rdf:li rdf:resource="urn:miriam:obo.go:GO%3A0045298"/>
          </rdf:Bag>
        </bqbiol:is>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```

XHTML

RDF

SBML is not limited to biochemistry!

Rate Rules can describe the temporal evolution of any quantitative parameter, e.g. transmembrane voltage;

Events can describe any discontinuous change, e.g. neurotransmitter release or repolarisation;

A species is an entity participating to a reaction, **not always** a **chemical** entity:

- It can be a molecule
- It can be a cell
- It can be an organ
- It can be an organism

➔ Systems Biology is scale-free!

Neuron differentiation

```
<listOfCompartments>
  <compartment id="brain" />
</listOfCompartments>
<listOfSpecies>
  <species id="glia" compartment="brain" initialConcentration="1"/>
  <species id="neuroblast" compartment="brain" initialConcentration="1"/>
  <species id="neuron" compartment="brain" initialConcentration="0"/>
</listOfSpecies>
<listOfParameters>
  <parameter id="K" value="1"/>
</listOfParameters>
<listOfReactions>
  <reaction>
    <listOfReactants>
      <speciesReference species="neuroblast" />
    </listOfReactants>
    <listOfProducts>
      <speciesReference species="neuron" />
    </listOfProducts>
   <listOfModifiers>
      <modifierSpeciesReference species="glia" />
    </listOfModifiers>
    <kineticLaw>
      <math xmlns="http://www.w3.org/1998/Math/MathML">
        <apply>
          [...]
        </apply>
      </math>
    </kineticLaw>
  </reaction>
</listOfReactions>
```

Hodgkin-Huxley

```
<rateRule metaid="metaid_0000048" variable="V">
  <notes><p xmlns="http://www.w3.org/1999/xhtml">dV/dt = (I - (i_Na + i_K + i_L))/Cm</p></notes>
  <math xmlns="http://www.w3.org/1998/Math/MathML">
    <apply>
      <divide/>
      <apply>
        <minus/>
        <ci> I </ci>
        <apply>
          <plus/><ci> i_Na </ci><ci> i_K </ci><ci> i_L </ci>
        </apply>
      </apply>
      <ci> Cm </ci>
    </apply>
  </math>
</rateRule>
<assignmentRule metaid="metaid_0000042" variable="i_Na">
  <notes><p xmlns="http://www.w3.org/1999/xhtml">i_Na = g_Na * m^3.0 * h * (V - E_Na)</p></notes>
  <math xmlns="http://www.w3.org/1998/Math/MathML">
    <apply>
      <times/>
      <ci> g_Na </ci>
      <apply>
        <power/><ci> m </ci><cn> 3.0 </cn>
      </apply>
      <ci> h </ci>
      <apply>
        <minus/><ci> V </ci><ci> E_Na </ci>
      </apply>
    </apply>
  </math>
</assignmentRule>
```

rate rule:

dx/dt = f (x,y,z)

assignment rule:

x = f (y,z)

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BIOMD0000000020 - Hodgkin-Huxley1952 squid-axon

SBML L2 V1 | Other formats | Actions | Submit Model Comment/Bug

Model | Overview | Math | Physical entities | Parameters

Reference Publication

Publication ID: 12991237

J Physiol 1952 Aug;117(4):500-44.
A quantitative description of membrane current and its application to conduction and excitation in nerve.
HODGKIN AL, HUXLEY AF.
[more]

Model

Original Model: *Unspecified*

Submitter: Nicolas Le Novère

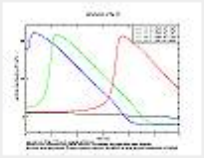
Submission Date: 2005-09-13T13:22:40+00:00

Last Modification Date: 2009-03-05T23:37:11+00:00

Creation Date: 2005-03-31T13:09:21+00:00

Creators: Maria Schilstra
Catherine Lloyd

Curation Result:

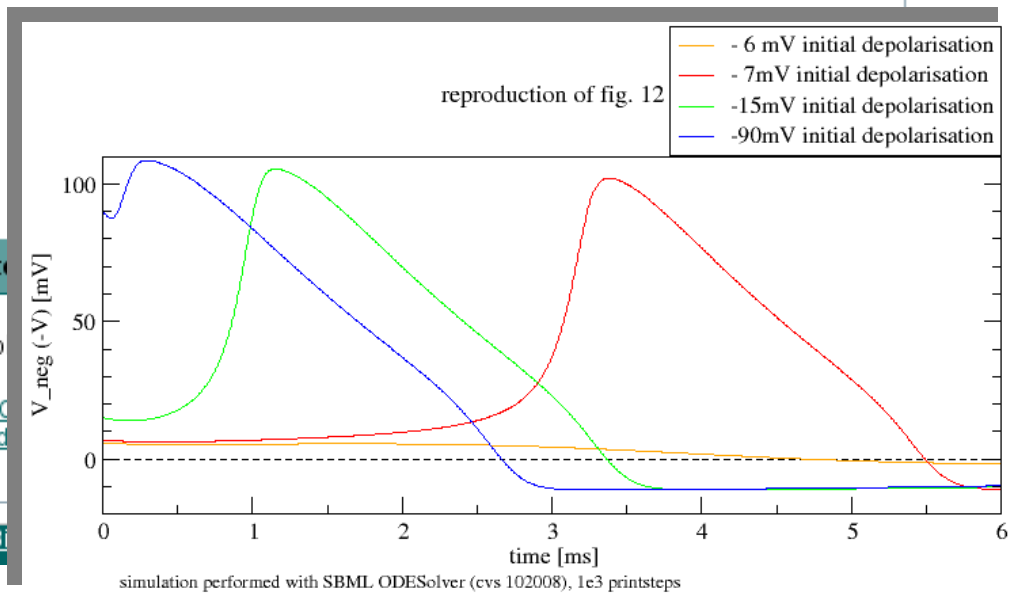


set #1	bqbiol:is	Taxonomy Loligo forbesi
set #2	bqbiol:isVersionOf	Gene Ontology voltage-gated potassium channel activity Gene Ontology voltage-gated sodium channel activity Gene Ontology action potential propagation

Not

This model originates from BioModels Database: A Database of Annotated Pub
For more information see the terms of use.
To cite BioModels Database, please use Le Novère N., Bornstein B., Broicher A., C
J.L., Hucka M. (2006) BioModels Database: A Free, Centralized Database of Curated
Nucleic Acids Res., 34: D689-D691.

Developed by BioModels Team of Computational Neurobiology Group in European Bi



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BIOMD0000000127 - Izhikevich2003_SpikingNeuron

SBML L2 V1 | Other formats | Actions | Submit Model Comment/Bug

Model | Overview | Math | Physical entities | Parameters

Publication ID: 10.1109/TNN.2003.820...

IEEE Transactions on Neural Networks. Volume 14, Issue 6, Nov. 2003 Page(s):1
Simple Model of Spiking Neurons
Eugene M. Izhikevich
[more]

Original Model: *Unspecified*

Submitter: Enuo He

Submission Date: 2007-07-27T20:22:14+00:00

Last Modification Date: 2007-09-25T10:21:27+00:00

Creation Date: 2007-07-16T09:41:14+00:00

Creators: Enuo He

Curation Result:

set #1	bqbiol:isVersionOf	Gene Ontology regulation of action potential in neuron Gene Ontology regulation of membrane potential Gene Ontology regulation of action potential
set #2	bqmodel:isDescribedBy	DOI 10.1109/TNN.2003.820440
set #3	bqbiol:is	Taxonomy Mammalia

The model is according to the paper *Simple Model of Spiking Neurons* In this paper, a simple spiking model is presented that is correspond to different values of the parameters a,b,c,d in the model. Figure2RS,IB,CH,FS,LTS have been simulated by MathSBI

RS: a=0.02, b=0.2, c=-65, d=8.

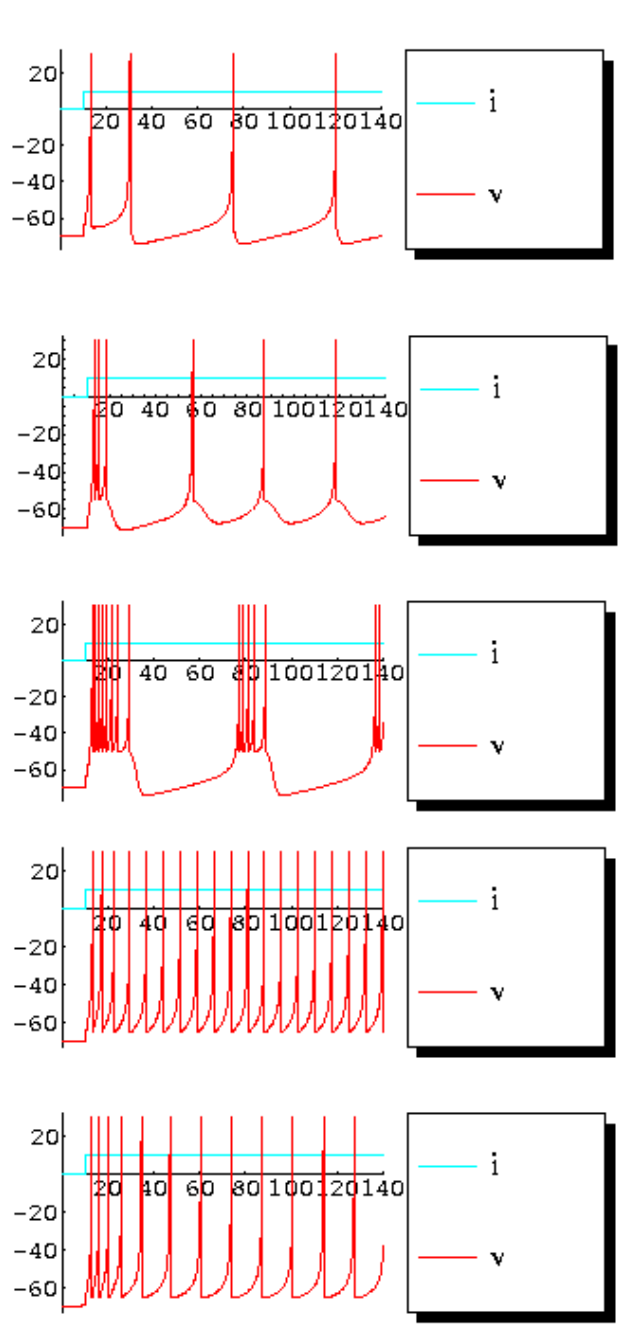
IB: a=0.02,b=0.2,c=-55,d=4

CH: a=0.02,b=0.2,c=-50,d=2

FS:a=0.1b=0.2c=-65,d=2

LTS:a=0.02,b=0.25,c=-65,d=2

This model originates from BioModels Database: A Database of Annotated Published Models. It is copyright (c) 2005-2008 The B



2007-08-10T17:20:50+00:00

Comment: Figure2 RS,IB,CH,FS,LTS have been simulated by MathSBML.

SBML roadmap

- SBML Levels are supposed to co-exist, SBML Versions override previous ones
  - Level 1 Version 1: 2 March 2001
  - **Level 1 Version 2: 28 August 2003**
  - Level 2 Version 1: 28 July 2003
  - Level 2 Version 2: 26 September 2006
  - Level 2 Version 3 release 1: 16 June 2007
  - Level 2 Version 3 release 2: 26 September 2007
  - **Level 2 Version 4: 22 December 2008**
  - **Level 3 core draft: 22 August 2009**

conversion using libSBML

- Backward compatibility within Level at the level of the XML (but not 100% at the level of semantics)
- Unambiguous and bug-free specification requires heavy work ... 166 pages, single spacing, 10pt, small margin.

Difference between L1, L2 and L3

L1	L2	L3
predefined functions	function definitions	function definitions
proprietary infix math notation	all math in MathML	all math in MathML
reserved namespaces for annotation	no reserved namespaces for annotations	no reserved namespaces for annotations
no controlled annotation	controlled RDF annotation	controlled RDF annotation
no discrete events	discrete events	discrete events
monolithic	monolithic	modular
default values	default values	no default values

Progressive simplification, generalisation and externalisation

A glimpse of SBML Level 3

Modular SBML, with core + optional packages

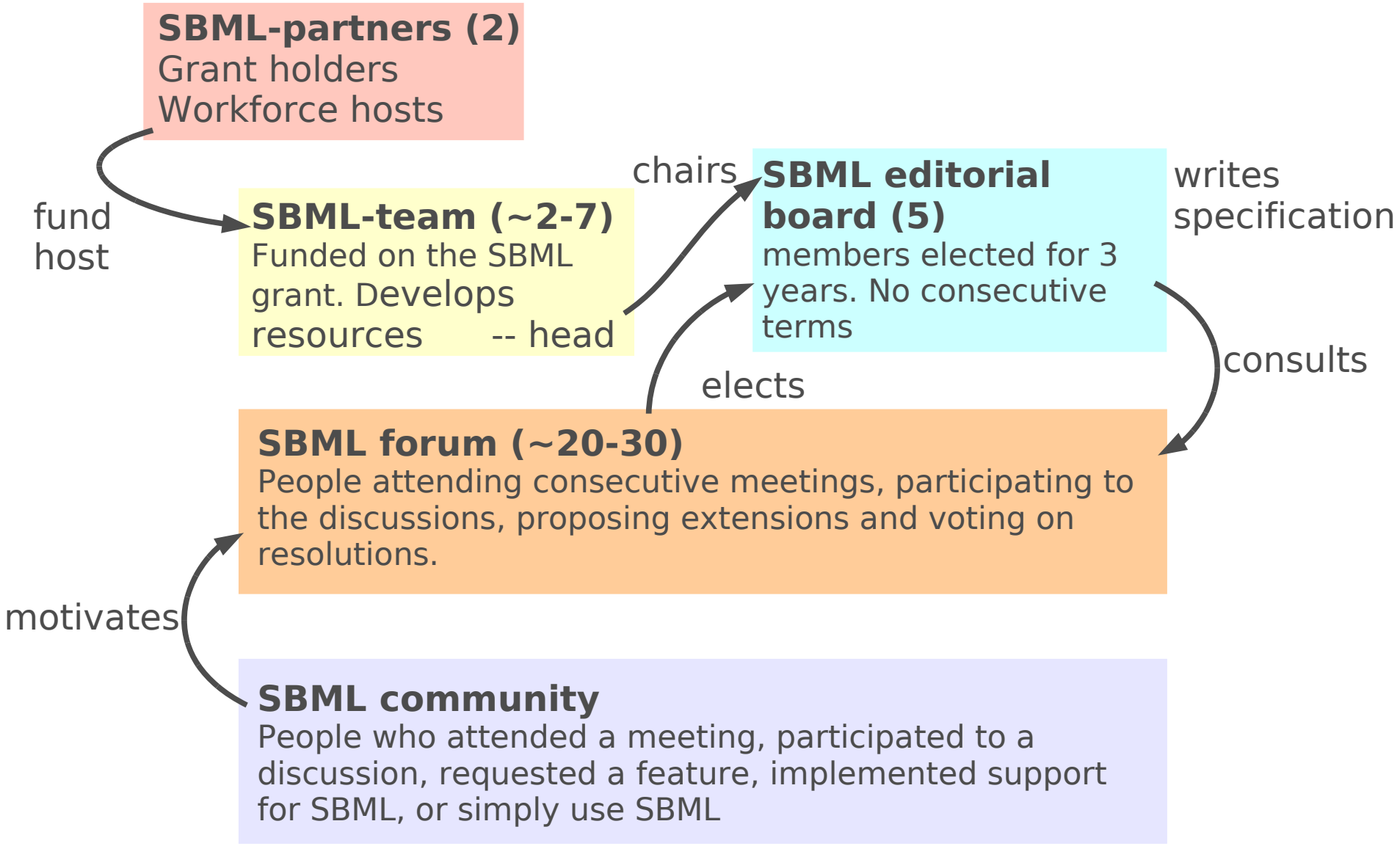
- Core package – draft specification available
- Graph Layout – specification finalised
- Complex species – specification finalised
- Groups - specification under discussion
- Model composition – specification under discussion
- Qualitative models – specification under discussion
- Graph rendering – specification proposed
- Distributions and ranges - specification proposed
- Arrays and sets – specifications proposed
- Geometry - specification proposed
- Spatial diffusion – needed
- Dynamic structures - needed

???

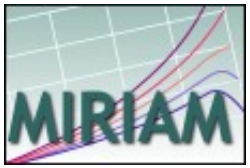
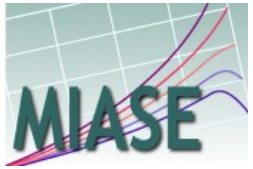
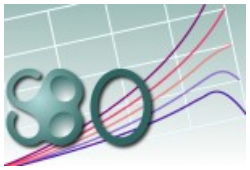
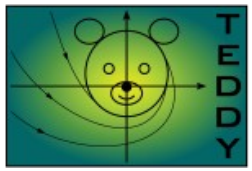
SBML development effort

- 14 community meetings, 7 technical “hackathons”, 3 focused videoconferences
- ~5500 posts on 5 mailing-lists since June 2003
- More than 170 tools claiming support
- Currently >400 models in BioModels Database
- Encoding in SBML advised in ~300 journals
- Small full-time team working on the specifications, websites, developing libraries, test suites, implementations etc.
- Uninterrupted stream of grants since 1999

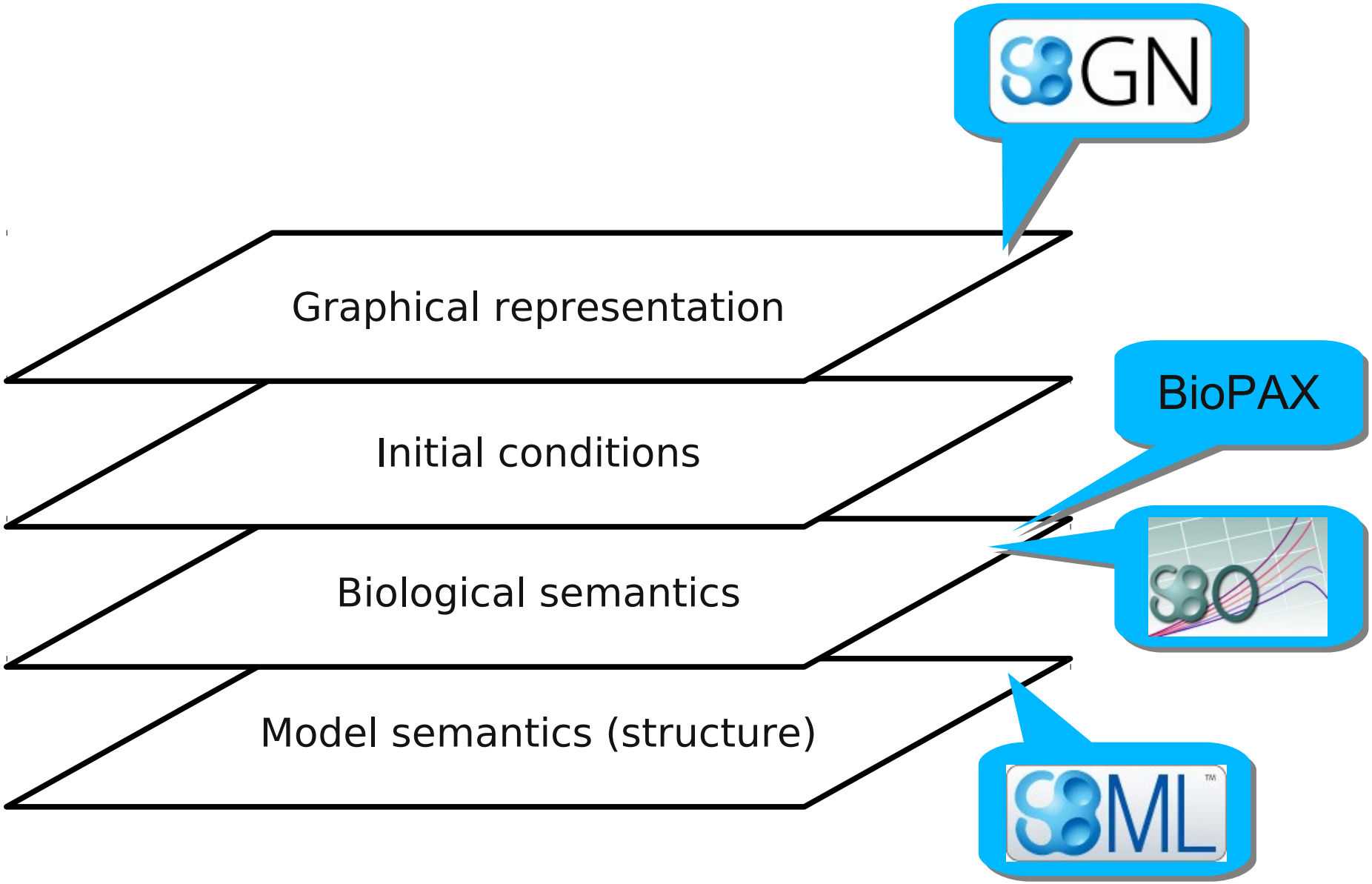
Current structure of the community



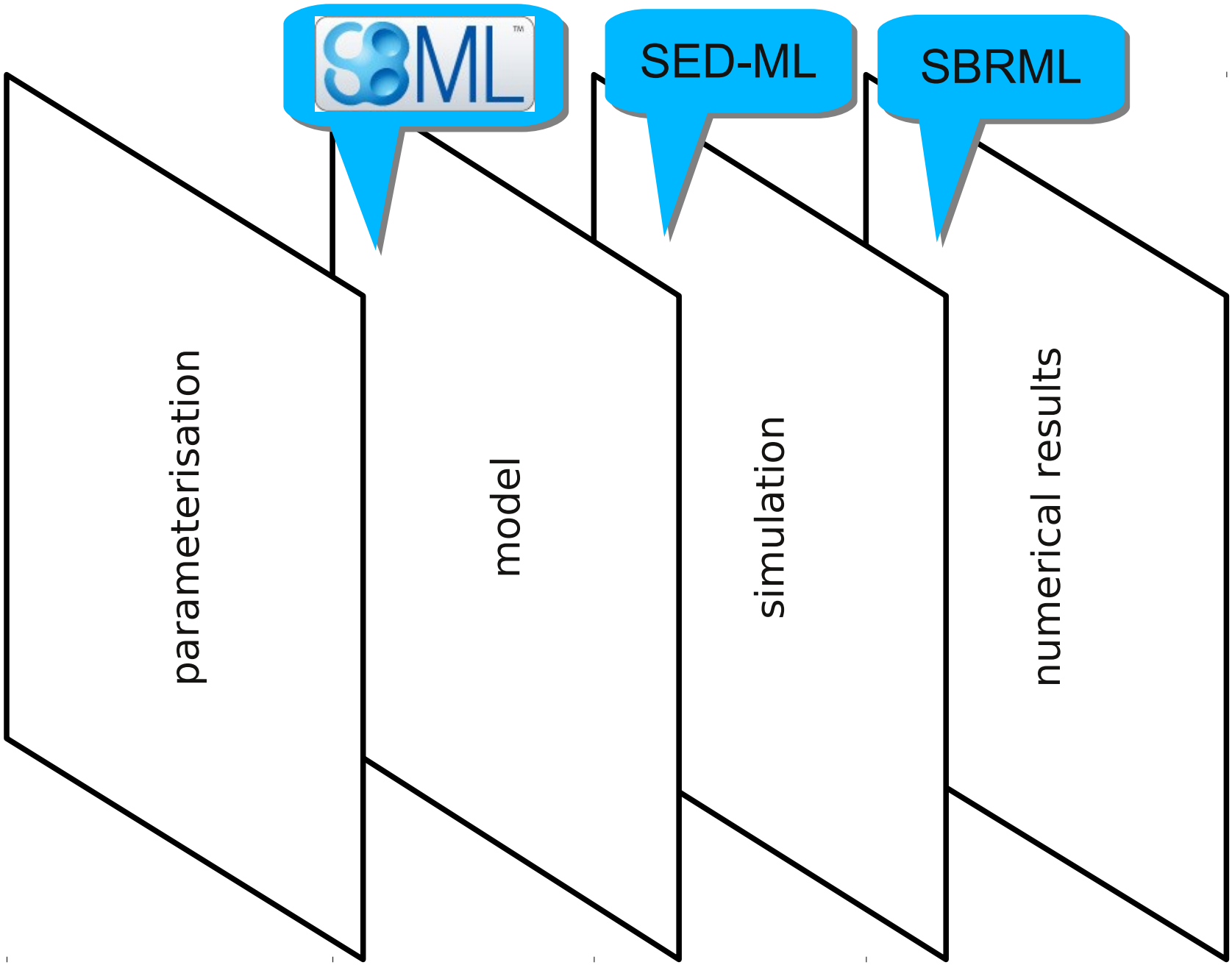
A complete mosaic of standards

	Models	Simulation	Results
Minimal requirements			
Data-models		SED-ML	SBRML
Ontologies			

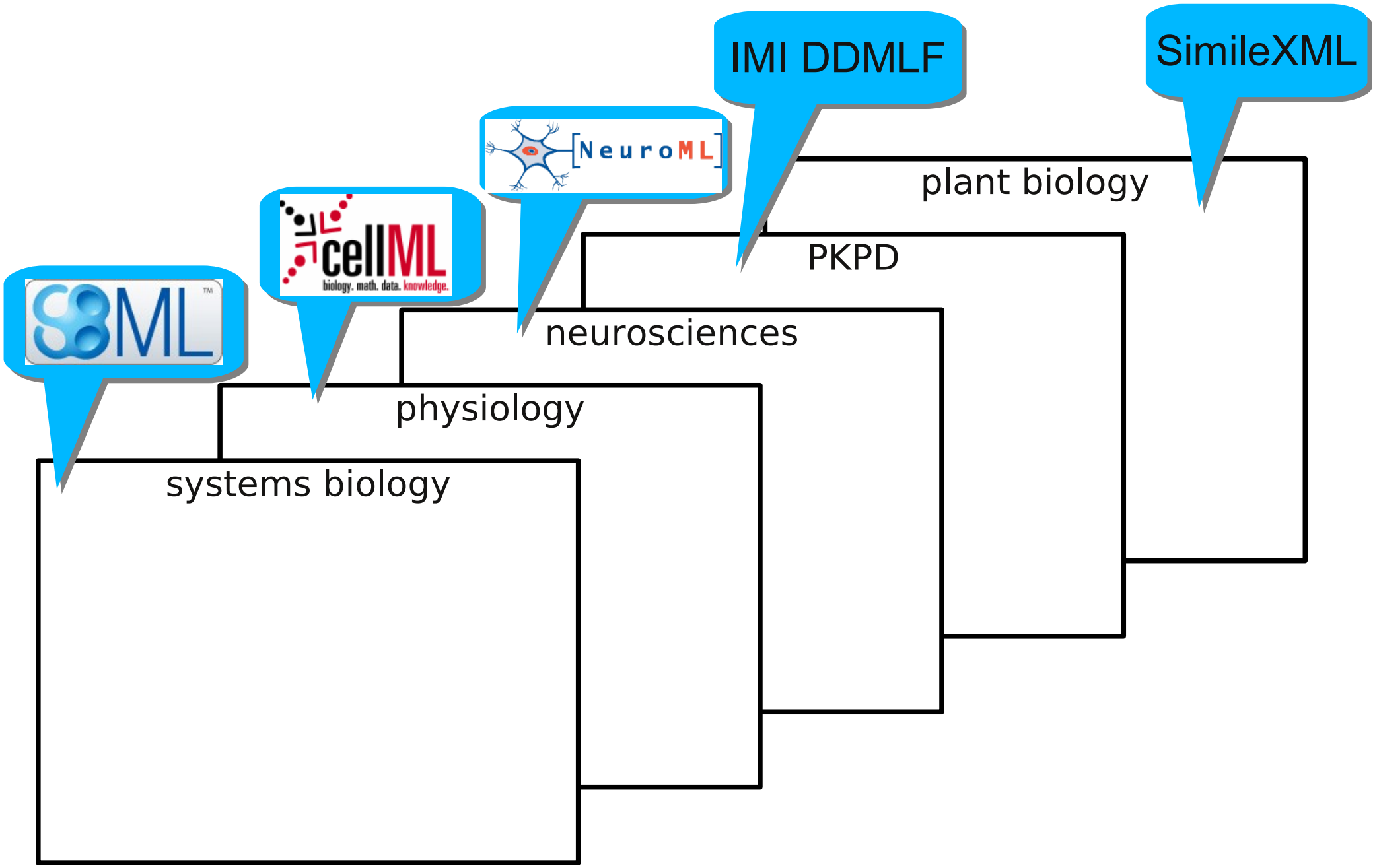
The mosaic of standards: We're going 3D



The mosaic of standards: We're going 3D



The mosaic of standards: We're going 3D

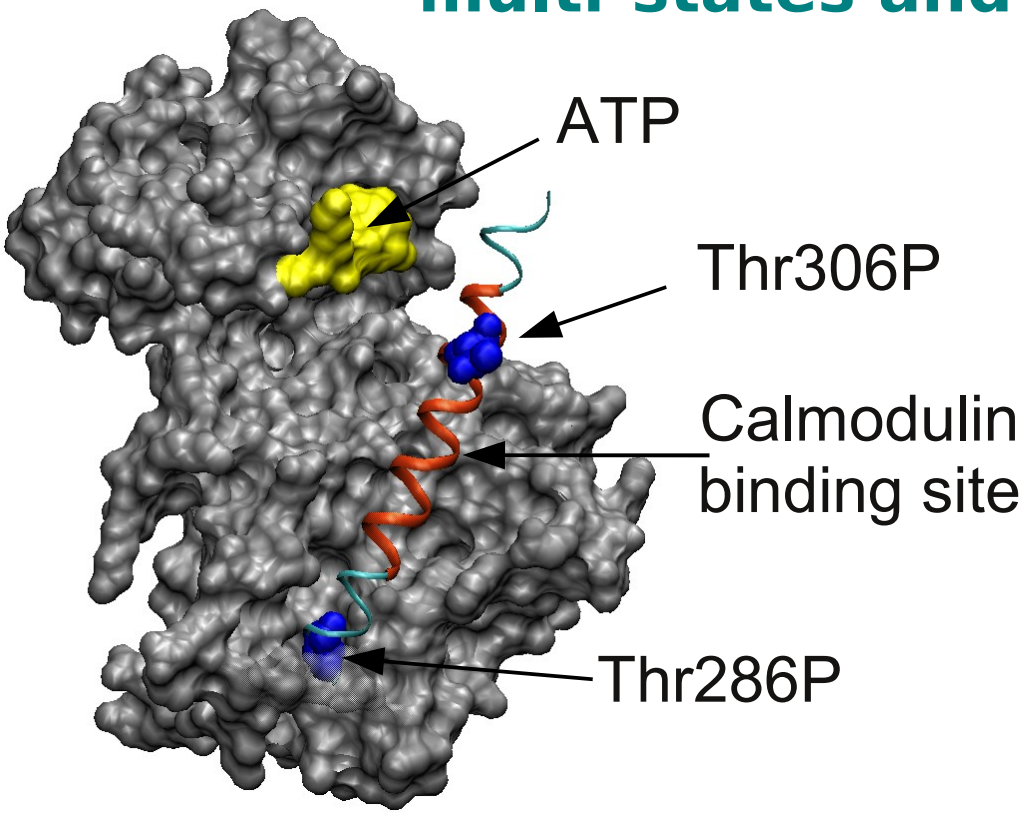


Interfacing standards in the three directions

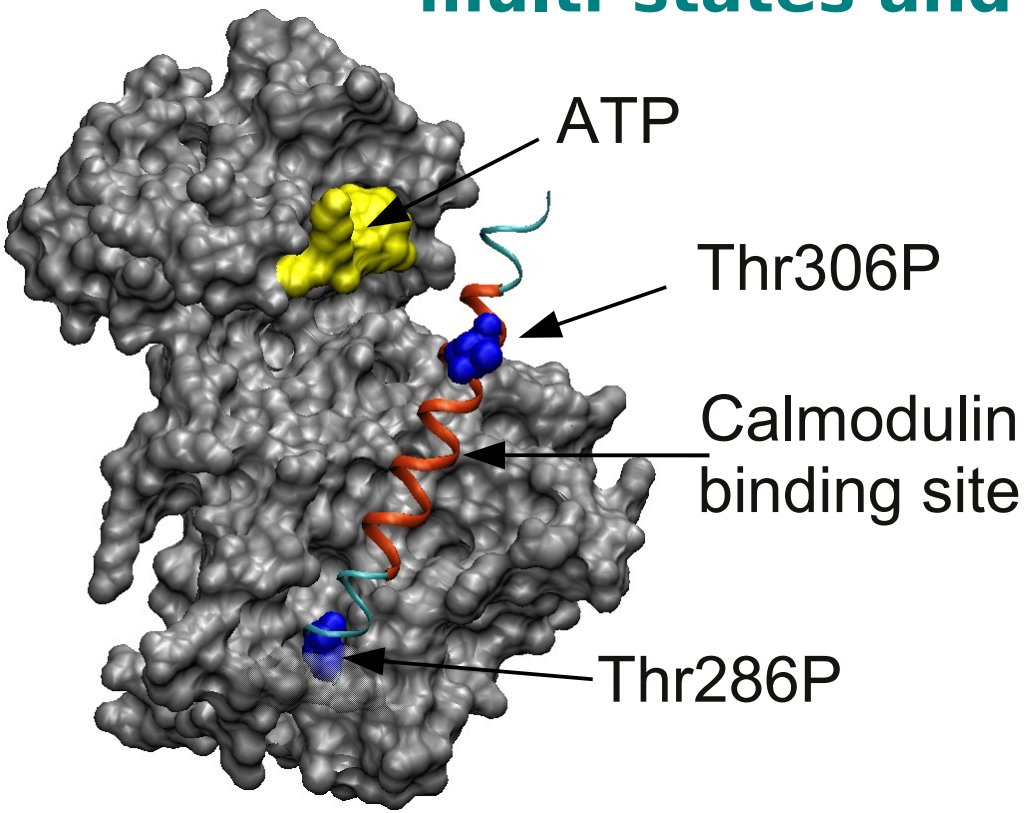
- SBML to BioPAX: interface using annotations (MIRIAM annotations and SBO terms), e.g.
  - mapping between Species and PhysicalEntity
  - mapping between Reactions and PhysicalInteraction
- Usage of SBML descriptions (or CellML or VCML) in SED-ML: Identification of variables using XPath
- Descriptions using SBML and NeuroML: Interface based on shared namespaces

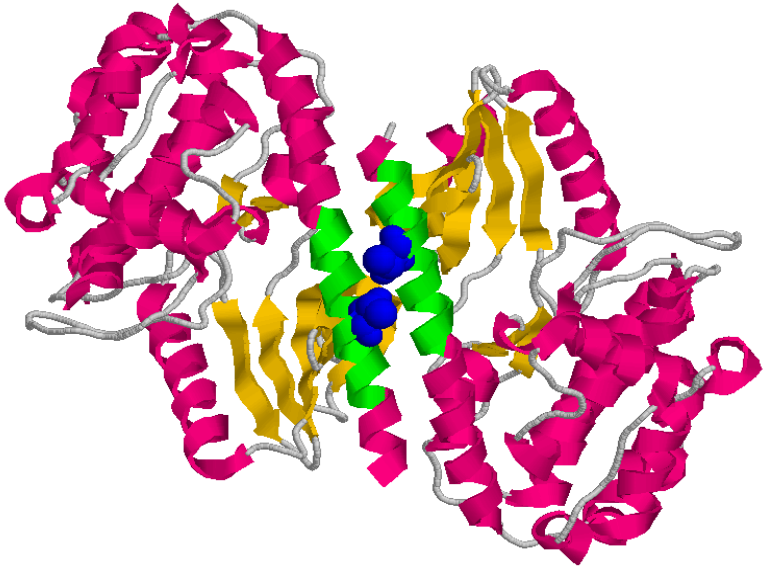
The problem of combinatorial explosion

multi-states and multicomponents complexes

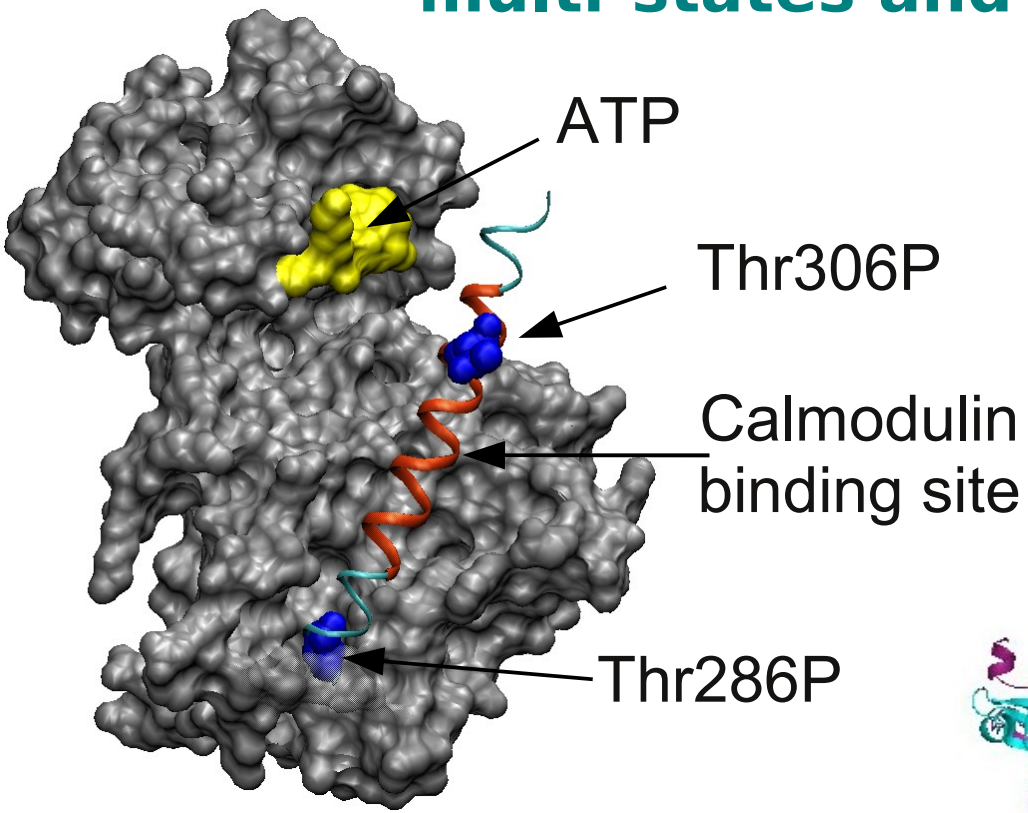


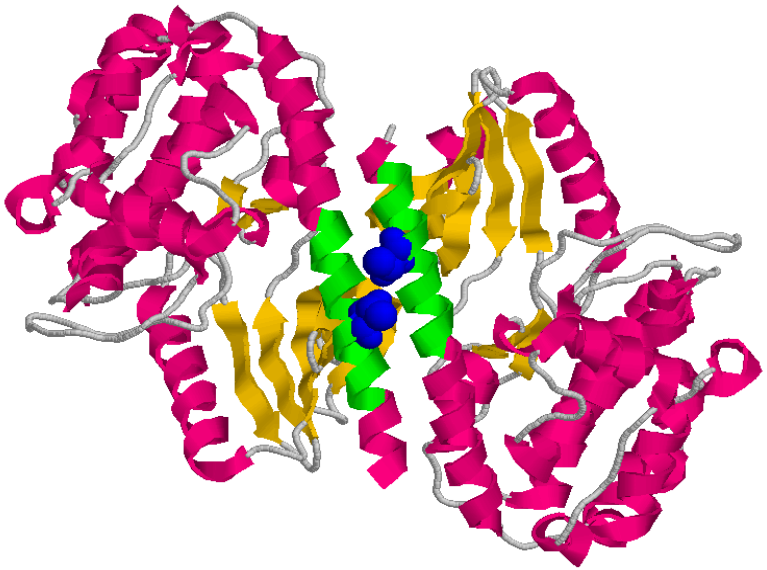
multi-states and multicomponents complexes

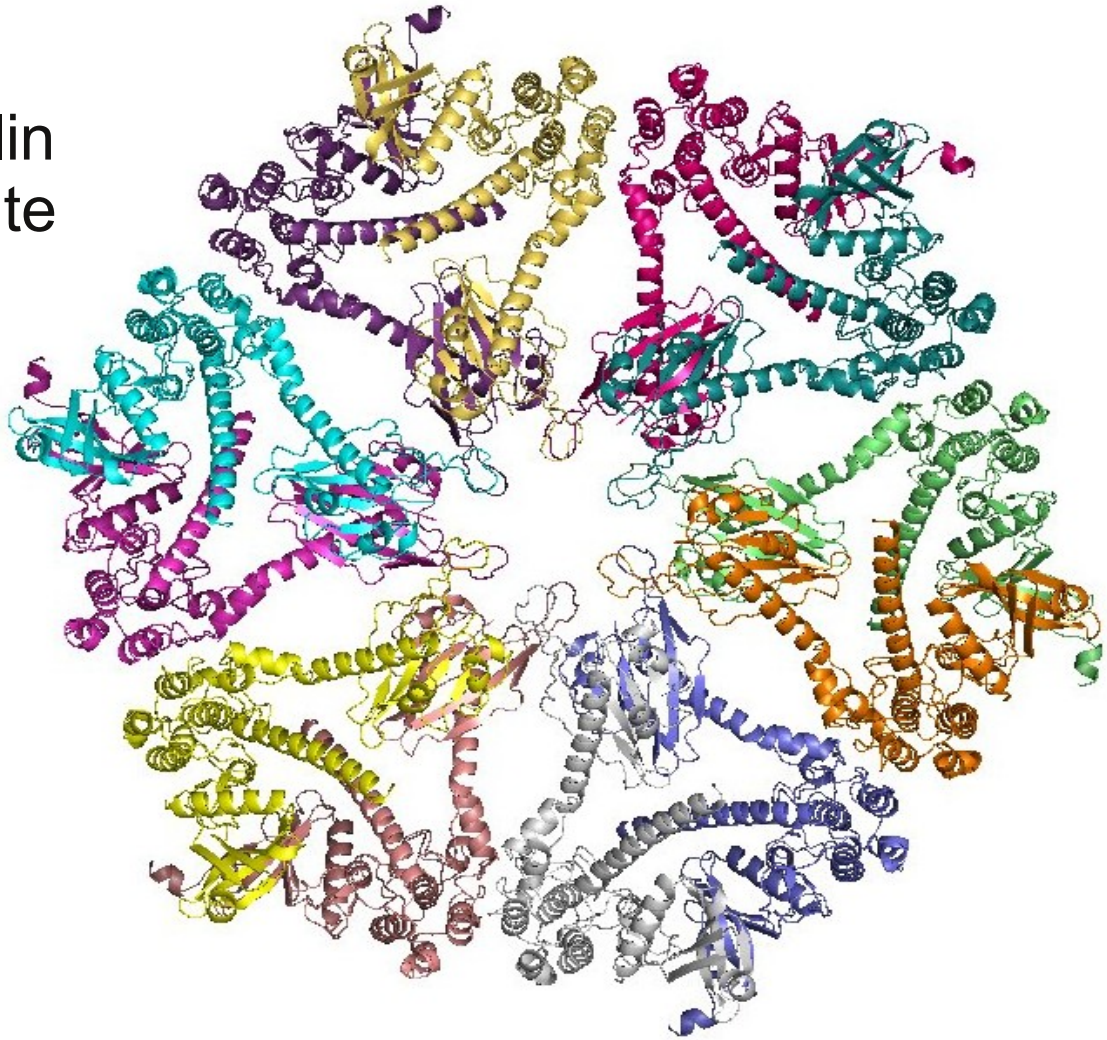




multi-states and multicomponents complexes



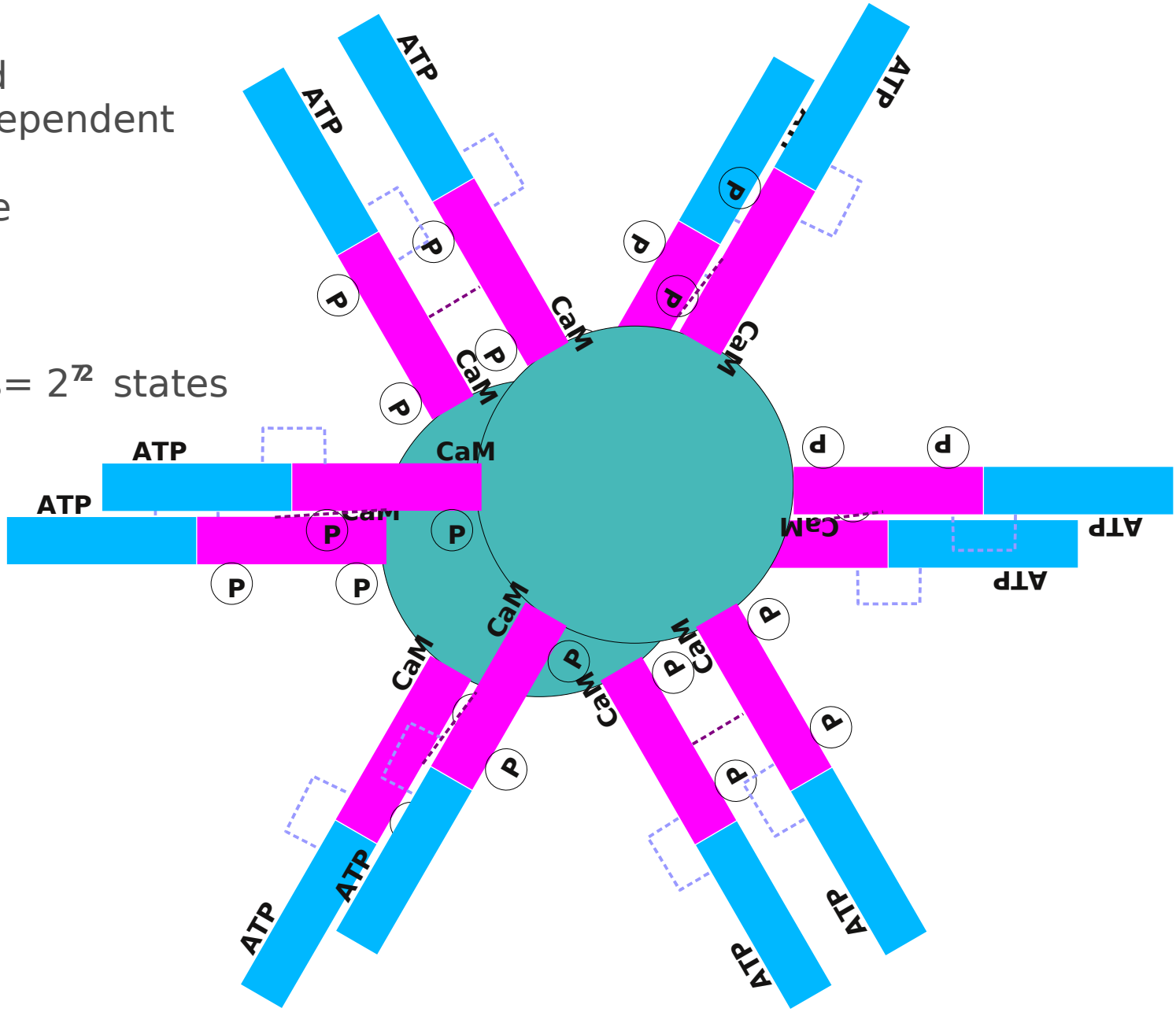




Combinatorial explosion

active/auto-inhibited
helix interaction/independent
ATP bound/ATP free
CaM bound/CaM free
T286/T286P
T306/T306P

6x12 state variables= 2^{72} states



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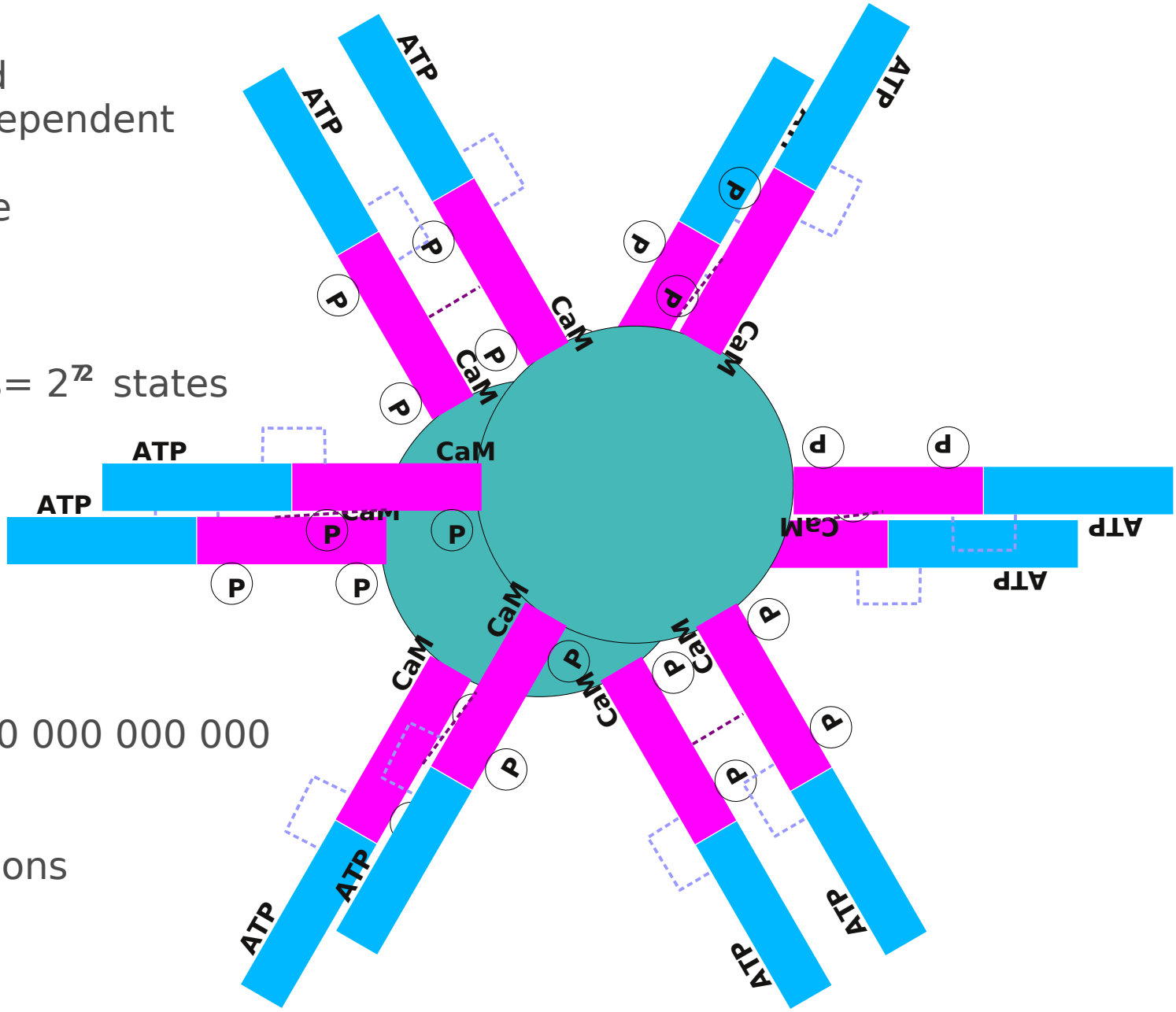
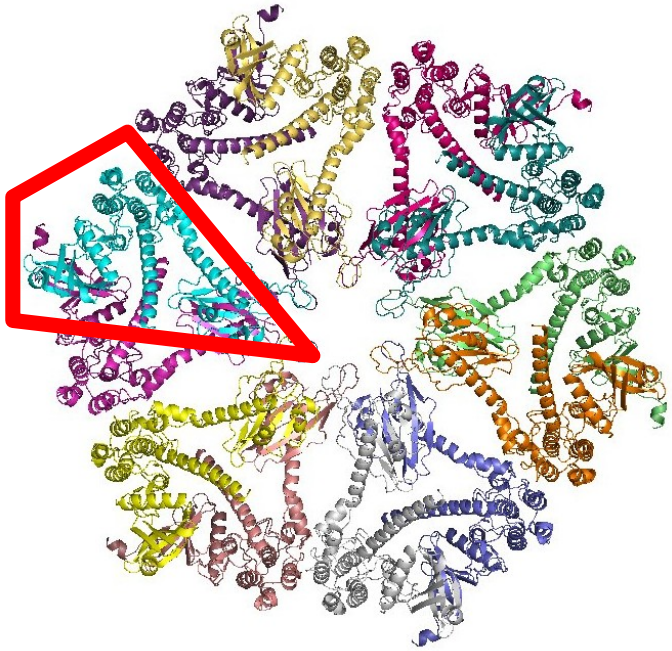
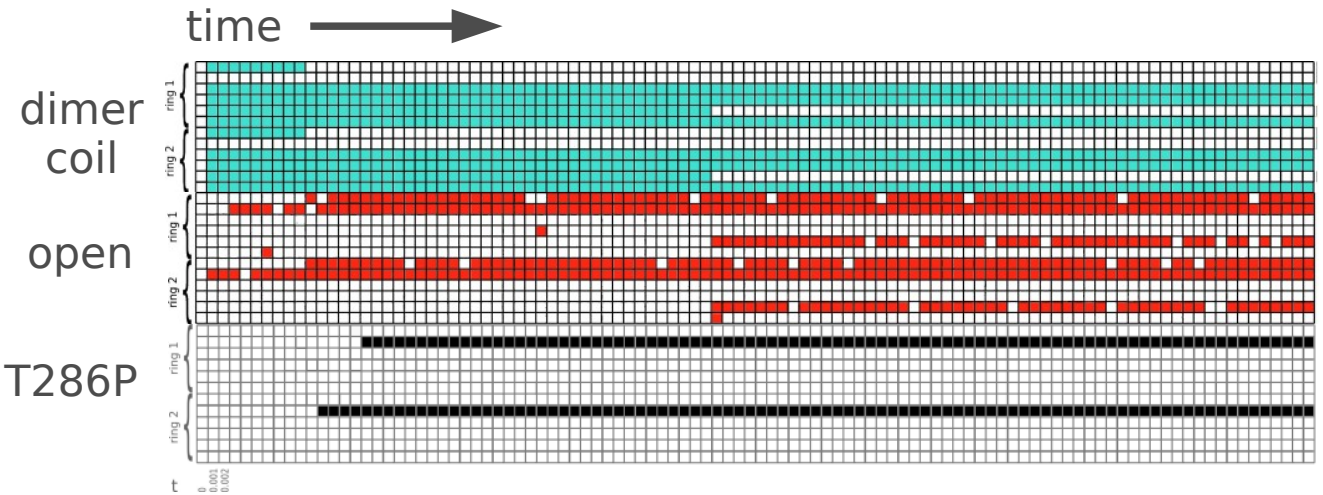


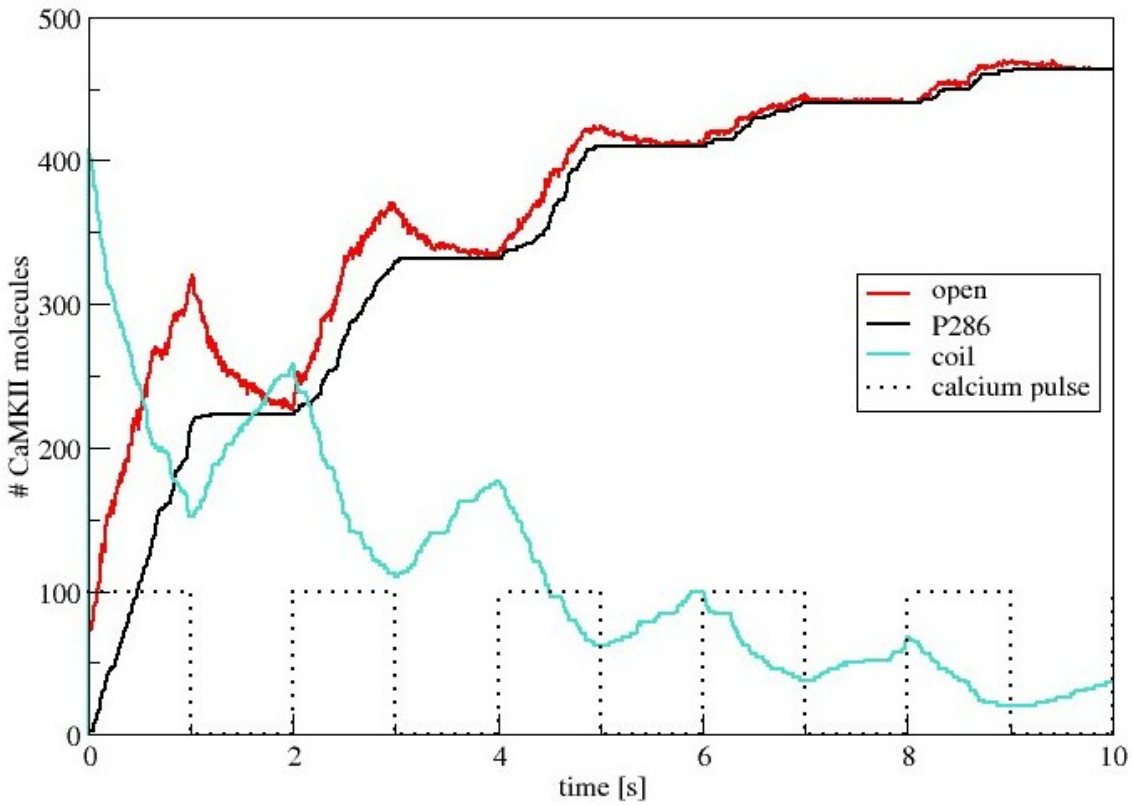
= 4 722 400 000 000 000 000 000

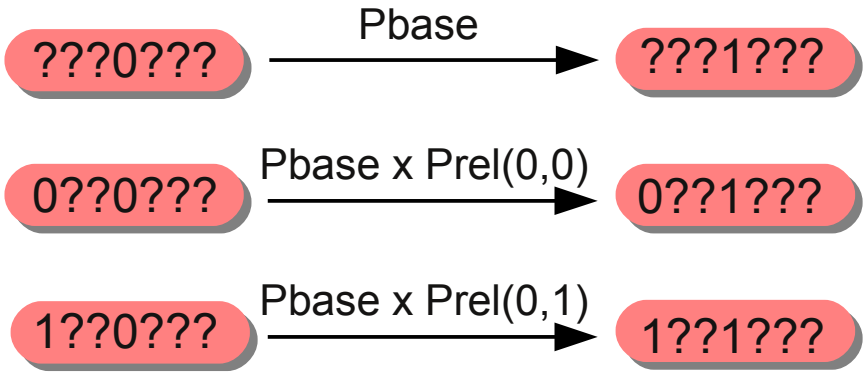
= five billions of billions

Stochastic multi-agent modeling with StochSim







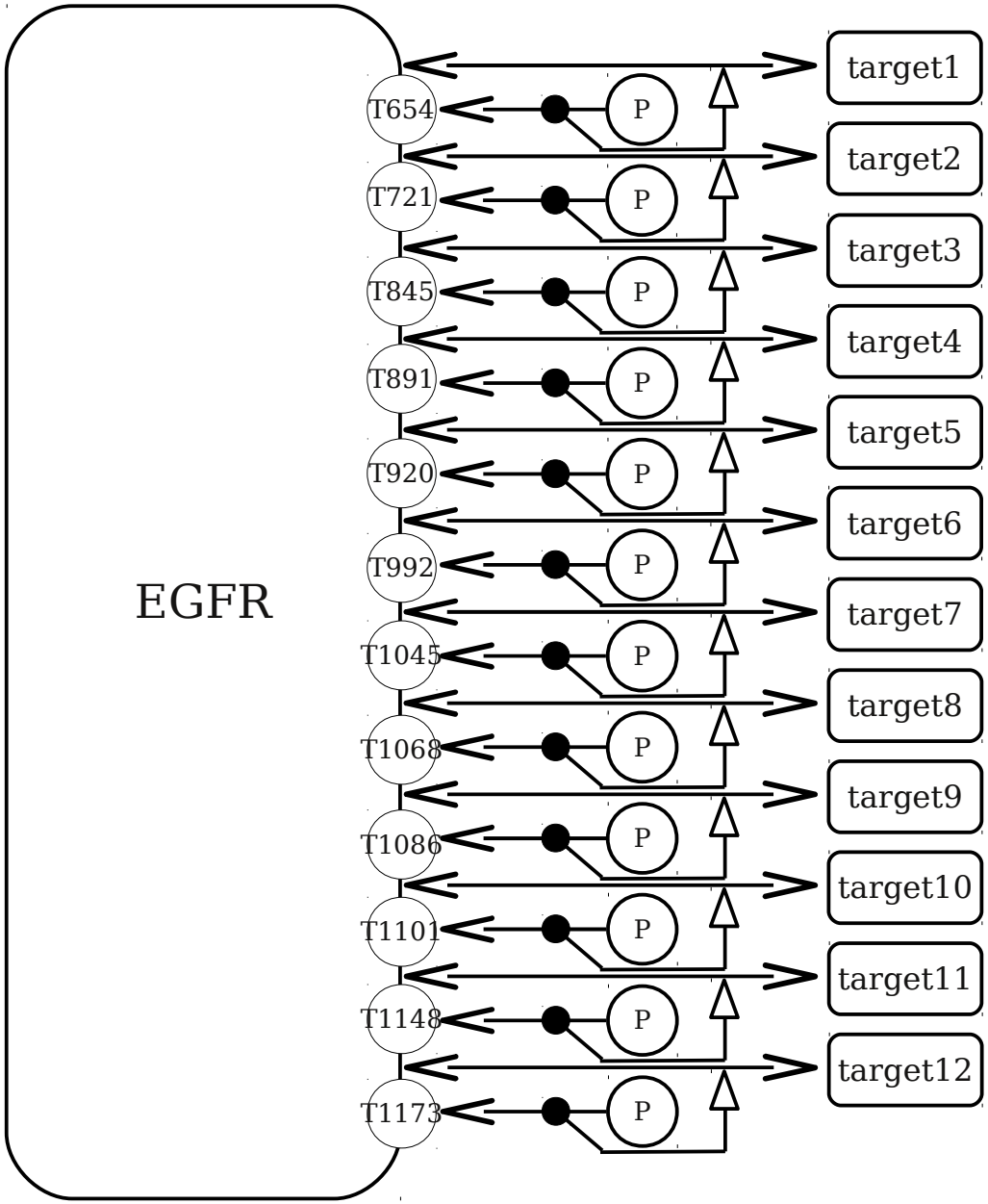


'?' Flags do not affect the reaction

only 4 species are needed instead of 128

only 2 reactions are needed instead of 64

Combinatorial explosion averted

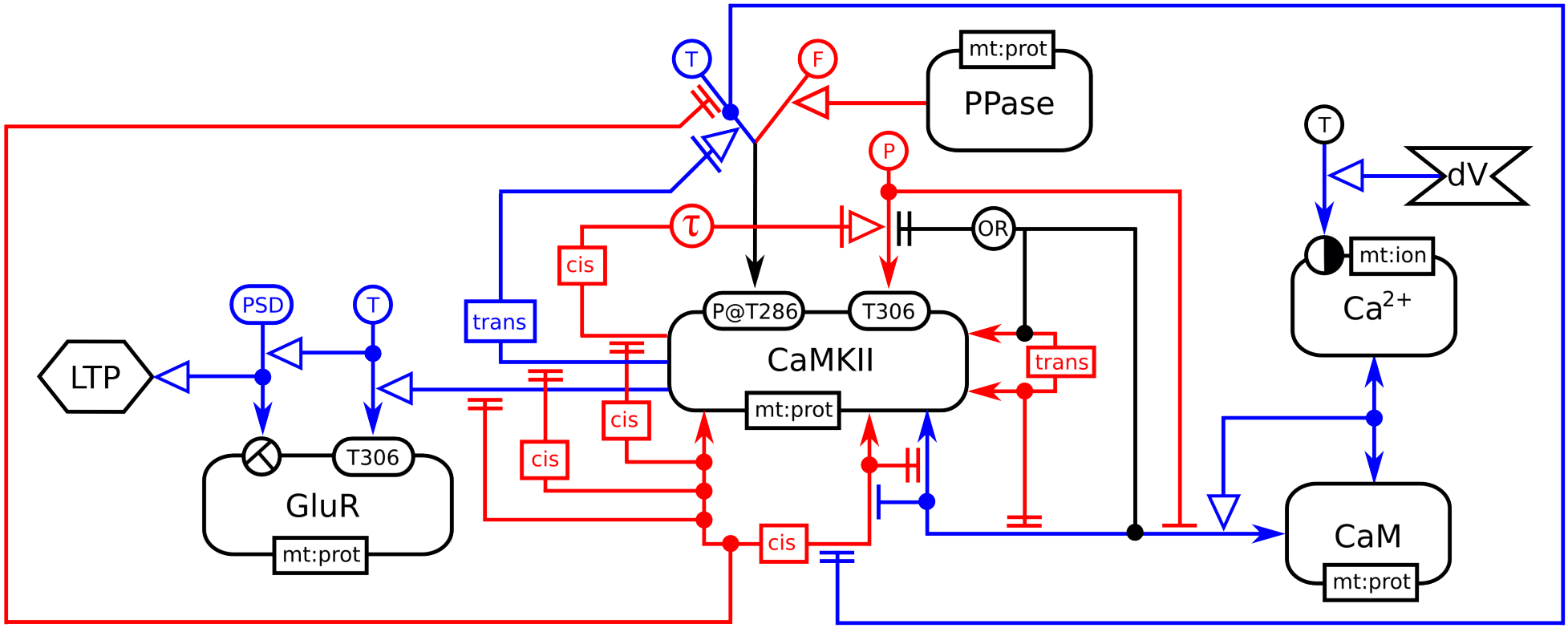


The effect of each phosphorylation is considered separately. In rule-based modeling, rules are independent

Process description:

2^{12} = 4096 states for EGFR and 4096 complexes between EGFR and targets

Calcium regulated LTP in one compact description



Rule-based modeling software

- Multi-agent systems
  - Oligo (1997, Bray, Lay)
  - Moleculizer (2005, Lok, Brent)
  - StochSim (1998, Firth, Shimizu, Emonet, Stefan, North, Le Novère, Bray)
  - Simmune (200x, Meier-Schellersheim)
  - ...
- Rule-encoding languages
  - BioNetGen (2004, Blinov, Faeder, Hlavacek, Hu)
  - kappa (2008, Danos)
  - LBS (2009, Pedersen)
  - ...

Parent pages: SBML.org / Community / Wiki / SBML Level 3 Proposals

Multistate and Multicomponent Species Proposal

Proposal title

Multistate and Multicomponent Species (abbrevation *multi*)

Proposal authors

Editors

The document summarizing the discussions and describing the proposed package is written by:

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Contents [hide]

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Proposal tracking number

The proposal for extending SBML to carry the information for multistate multi-component species relies on the extension of the following core SBML elements:

- Species
- SimpleSpeciesReference
- Reaction

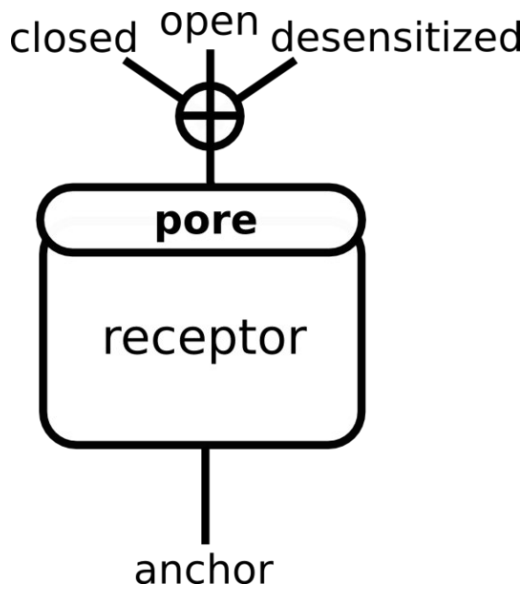
In addition, the multistate multi-component package requires the creation of new elements:

- SpeciesType
- Selector
- ReactionRule

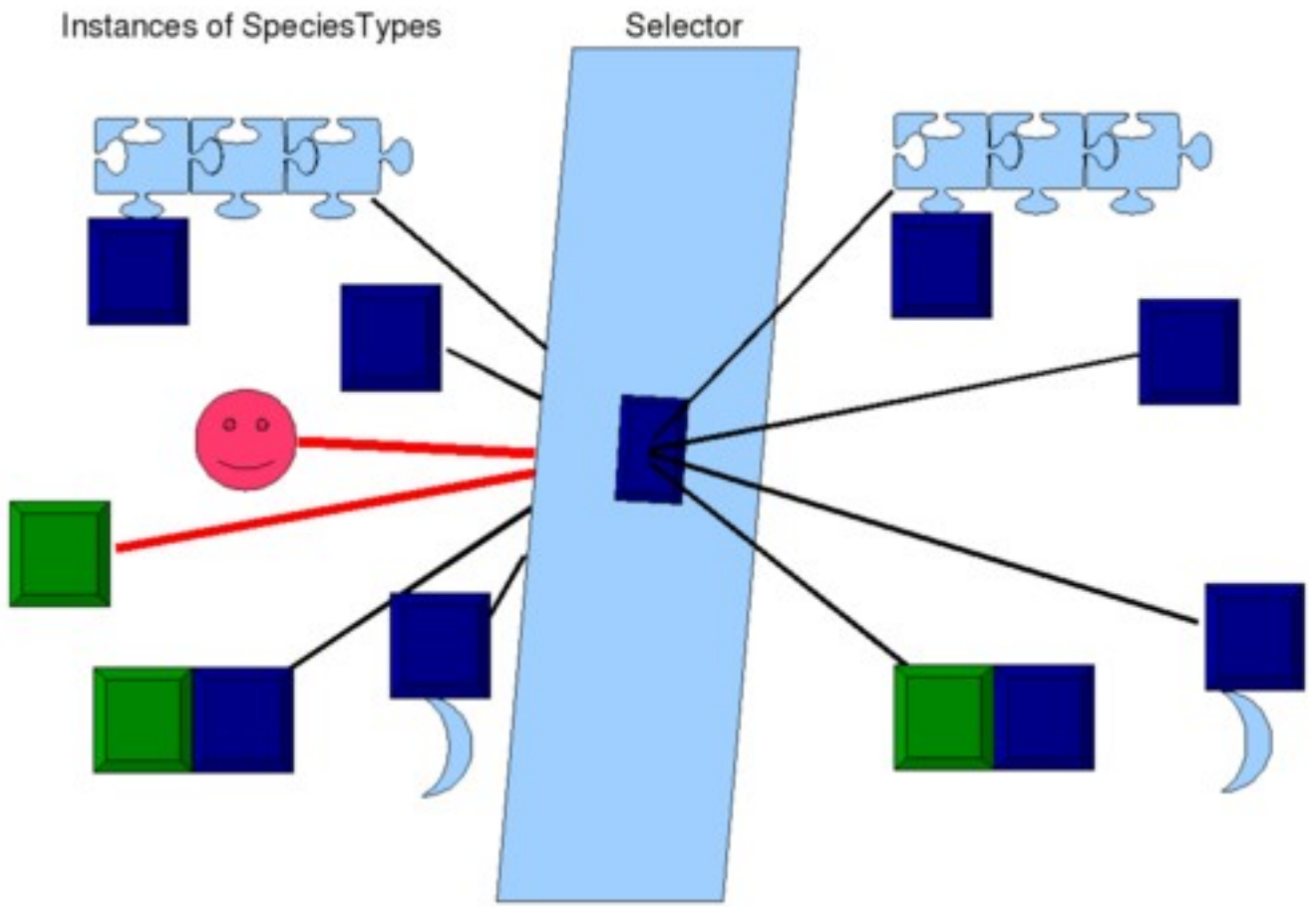
Selectors can be used in Species Rules and Reactions.

SBML multi: introduction of SpeciesType

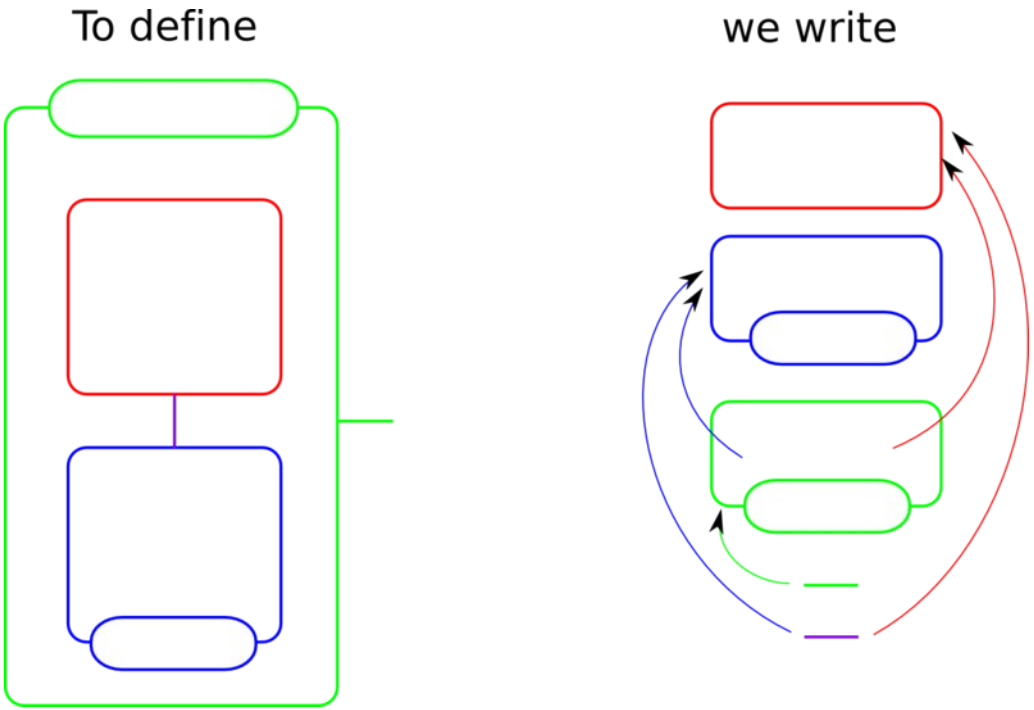
```
<speciesType xmlns="http://www.sbml.org/sbml/level3/version1/multi/version1"
             id="receptor">
  <listOfStateFeatures>
    <stateFeature id="pore">
      <listOfPossibleValues>
        <possibleValue id="open" />
        <possibleValue id="closed" />
        <possibleValue id="desensitized" />
      </listOfPossibleValues>
    </stateFeature>
  </listOfStateFeatures>
  <listOfBindingSites>
    <bindingSite id="anchor"
                 minOccur="1" maxOccur="1"/>
  <listOfBindingSites>
</speciesType>
```



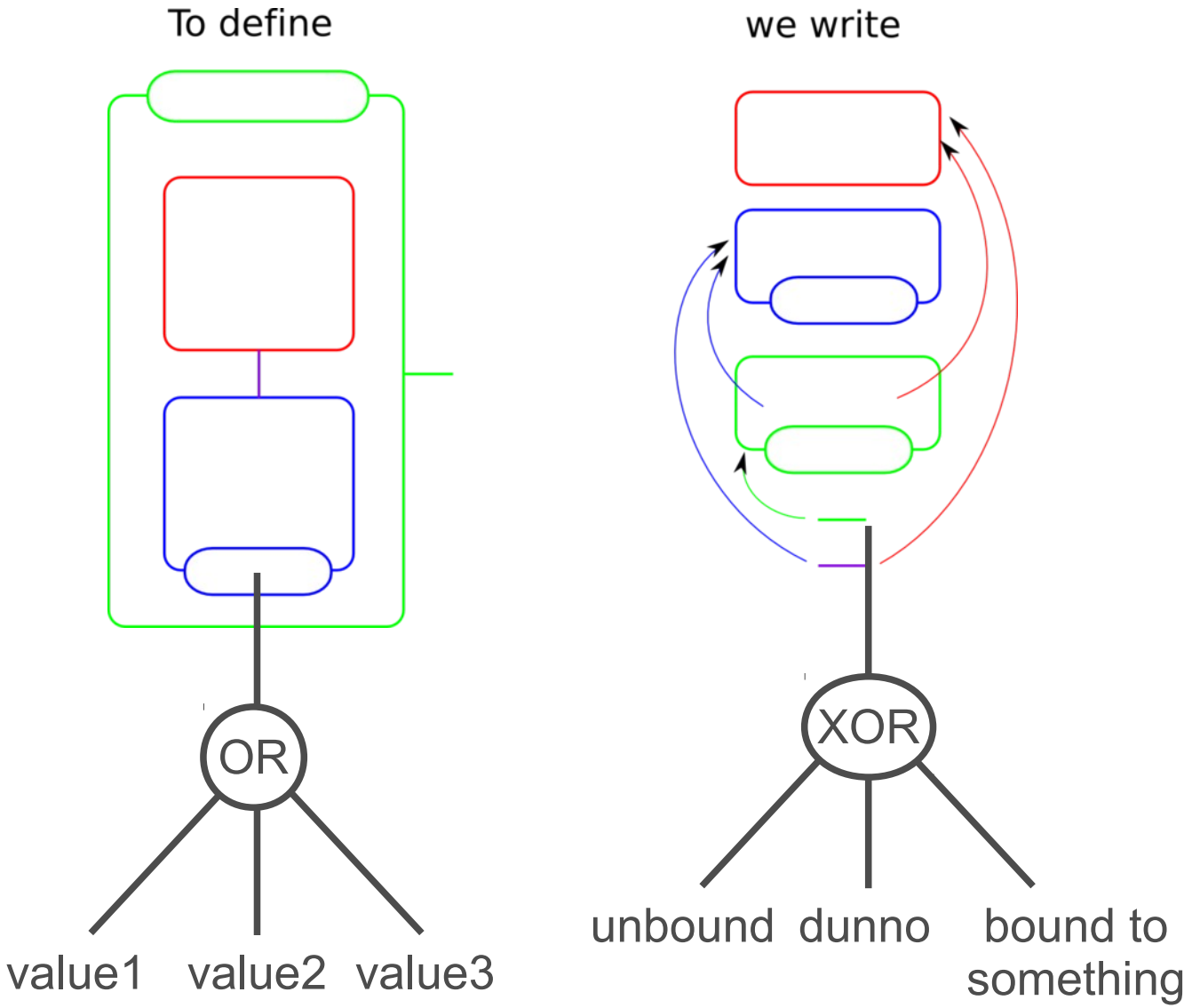
The notion of selector



How to build a selector?

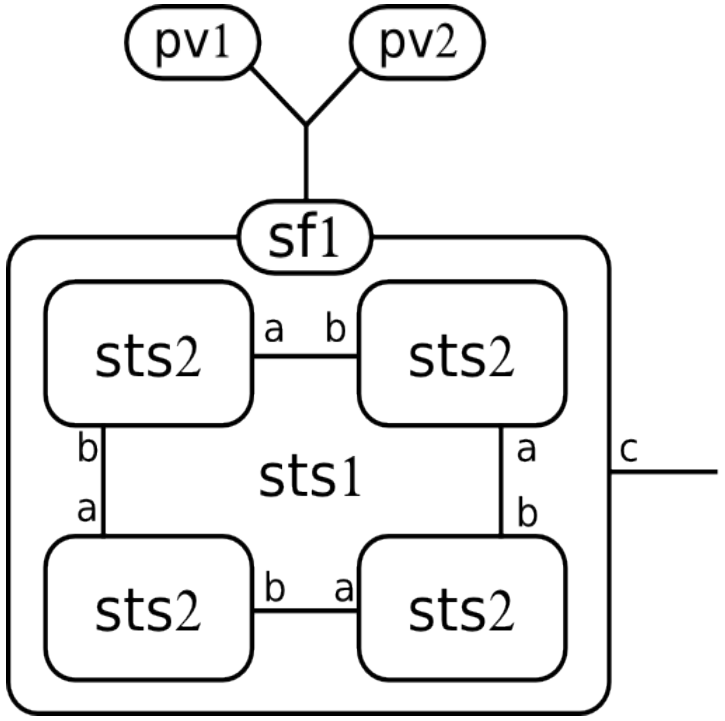


How to build a selector?



SBML multi: introduction of the selector

```
<selector xmlns="http://www.sbml.org/sbml/level3/version1/multi/version1"
          id="selector">
  <listOfSpeciesTypeStates>
    <speciesTypeState id="sts2" speciesType="st2">
    <speciesTypeState id="sts1" speciesType="st1">
      <listOfStateFeatureInstances>
        <stateFeatureInstance stateFeature="sf1">
          <listOfStateFeatureValues>
            <stateFeatureValue possibleValue="pv1" />
            <stateFeatureValue possibleValue="pv2" />
          </listOfStateFeatureValues>
        </stateFeatureInstance>
      </listOfStateFeatureInstances>
      <listOfContainedSpeciesTypes>
        <containedSpeciesType speciesTypeState="sts2"
                              minOccur="4" maxOccur="4"
                      connex="true" saturated="true" />
      </listOfContainedSpeciesTypes>
    </speciesTypeState>
  </listOfSpeciesTypeStates>
  <listOfBonds>
    <bond occurrence="required">
      <bindingSiteReference speciesTypeState="sts2" bindingSite="a" />
      <bindingSiteReference speciesTypeState="sts2" bindingSite="b" />
    </bond>
  </listOfBonds>
  <listOfUnboundBindingSites>
    <bindingSiteReference speciesTypeState="sts1" bindingSite="c" />
  </listOfUnboundBindingSites>
</selector>
```



SBML multi: extension of Species

```
<species xmlns:multi="http://www.sbml.org/sbml/level3/version1/multi/version1"
         id="sp1"
         multi:speciesType="st1"
         compartment="compartment_1"
         initialAmount="1000" >
  <multi:listOfInitialSpeciesInstances>
    <multi:initialSpeciesInstance id="initspinst1"
                                  initialProportion="0.9">
      <multi:listOfSelectorReferences>
        <multi:selectorReference  selector=”st1_sel1”
                                  negation=”false” />
        <multi:selectorReference selector=”st1_sel2”
                                 negation=”true”/>
      </multi:listOfSelectorReferences>
    </multi:initialSpeciesInstance>
  </multi:listOfInitialSpeciesInstances>
</species>
```

Need to obey BOTH selectors akin AND

Why did-I bore you stiff with all that?

- Replace SpeciesType by AnythingType ...
- Selection of dendritic branching
- Selection of firing patterns
- Selection of network structures
- Selection of EEG
- ...

Everything that be characterised by features possessing several alternative values.

Thanks in particular to

Development of the Systems Biology Markup Language

- SBML partners, past and present
- SBML editors, past and present
- Members of the SBML-team, past and present
- Members of the SBML forum, past an present
- NIH, JST, EMBL, BBSRC

(For more details, see **`http://sbml.org/About`**)

SBML Level 3 “multi” package

- Michael Blinov, James Faeder, Andrew Finney, William Hlavacek, Bin Hu, Martin Meier-Schellersheim

Anika Oellrich