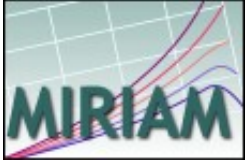
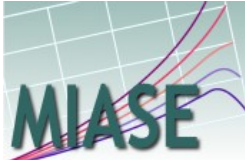
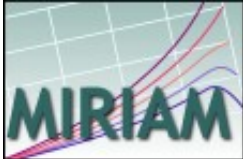
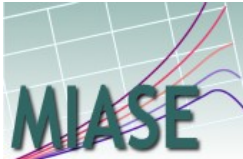
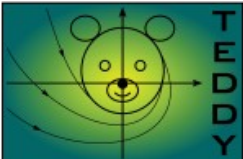


Toward a consistent set of interoperable
standards to represent models and simulations.

Nicolas Le Novère, EMBL-EBI

A “complete” (?) mosaic of standards

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

	Models	Simulation	Results
Minimal requirements			
Data-model	 	ED-ML	SBRML
Ontologies			



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 **180** 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 through our [RSS feed](#), our [Twitter feed](#), or one of the [mailing lists](#), and get involved with community efforts to help keep improving SBML. You can also call attention to your project's support of SBML by displaying the [SBML logo](#).

SBML would not have been possible without support from [multiple agencies and organizations](#), as well as intellectual contributions from many motivated individuals, including the [major contributors](#) who are shaping SBML Level 3.

SBML News

SBML-BioModels.net Hackathon

(25 Jan.'10) The next Hackathon will be held **May 1-4 in Seattle**. Please [let us know](#) if you're coming.



LibSBML 4.0.1 released!

(21 Jan.'10) This release of the libSBML version 4.x series fixes many reported small bugs in 4.0.0.



LibSBML 5 preview!

(18 Jan.'10) A preview version of libSBML version 5, with a plug-in architecture for Level 3 packages, is **now available**.



[Older news ...](#)

Community News

BioModels release 16

(26 Jan.'09) The latest release of the [BioModels Database](#) features over 450 total models.



Cain 1.2 released!

(1 Jan.'09) [Cain](#) is a stochastic simulator with highly efficient implementations of many methods.



BioUML Web Edition

(30 Nov.'09) BioUML, the Java-based modeling platform, now has a [web edition](#).



[Older news ...](#)

- 14 Nov 1996 - First XML working draft
- 11 Feb 1998 - XML as W3C recommendation
- The origins of CellML
 - 1998 - Start of the development of CellML by dept of Engineering Science at the University of Auckland and Physiome Sciences Inc.
 - Late 1998 - Watten Headley and David Nickerson suggest to use XML
 - 11 Aug 2001 - CellML 1.0 is released
- The origins of SBML
 - 1998 - Launch of ERATO Kitano, to produce a platform for modeling
 - April 1999 - Start of an effort to develop a biochemical format
 - 9 Sep 1999 - Herbert Sauro announces the Portable Metabolic Binary Standard
 - 18 Sep 1999 - Igor Goryanin suggests to use XML
 - 10 May 2000 - XML standard for cellular models (MML). ERATO
 - 8 Aug 2000 - Hucka, Finney, Sauro and Bolouri. An XML-based Model Description Language for Systems Biology Simulations. ERATO Kitano Systems Biology Project (first tracable version of a draft specification for the language called SBML)
 - 2 Mar 2001 - SBML Level 1 Version 1

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**.

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml level="2" version="4" xmlns="http://www.sbml.org/sbml/level2/version4">
  <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="4" xmlns="http://www.sbml.org/sbml/level2/version4">
  <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


```
<?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

```
<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>
```

```

<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" >
</species>

```

macromolecule

```

<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>

```

```
<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" >
```

XHTML

```
<notes>
  <body xmlns="http://www.w3.org/1999/xhtml">
    <p>One of the components of a microtubule</p>
  </body>
</notes>
```

RDF

```
<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>
```



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!

```

<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:

$$x = f(y,z)$$

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.

[\[more\]](#)

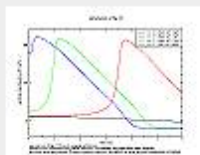
Model

Original Model: *Unspecified*set #1 bqbiol:is [Taxonomy Loligo forbesi](#)Submitter: [Nicolas Le Novère](#)
 set #2 bqbiol:isVersionOf [Gene Ontology voltage-gated potassium channel activity](#)
[Gene Ontology voltage-gated sodium channel activity](#)
[Gene Ontology action potential propagation](#)

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

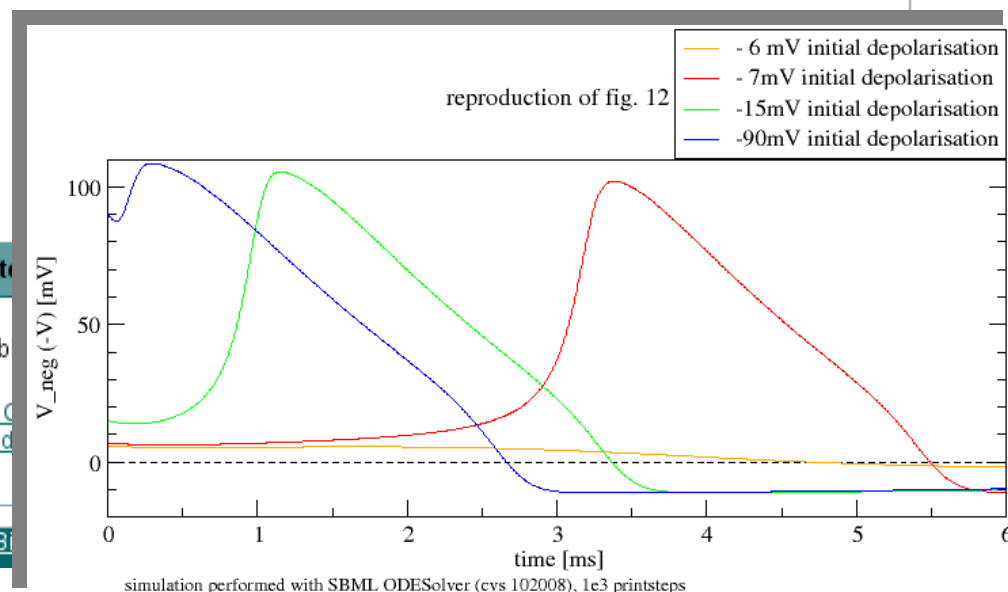
 Creators: [Maria Schilstra](#)
[Catherine Lloyd](#)


Curation Result:

Note

This model originates from BioModels Database: A Database of Annotated Publications. For more information see the [terms of use](#).

To cite BioModels Database, please use [Le Novère N., Bornstein B., Broicher A., Coudane J.L., Hucka M. \(2006\) BioModels Database: A Free, Centralized Database of Curated Models. Nucleic Acids Res., 34: D689-D691.](#)

Developed by BioModels Team of [Computational Neurobiology Group](#) in European Bioinformatics Institute

An example of pharmacodynamic model

Tham et al (2008) A pharmacodynamic model for the time course of tumor shrinkage by gemcitabine + carboplatin in non-small cell lung cancer patients. Clin Cancer Res. 2008 14(13): 4213-8.

```
<rateRule metaid="metaid_0000031" variable="Size">
  <math xmlns="http://www.w3.org/1998/Math/MathML">
    <apply>
      <times/>
      <apply>
        <minus/>
        <apply>
          <times/><ci> RateIn </ci><ci> Effect </ci>
        </apply>
        <apply>
          <times/><ci> Kover </ci><ci> Size </ci>
        </apply>
      </apply>
      <ci> Size </ci>
    </apply>
  </math>
</rateRule>
```

$$\frac{Size}{dt} = (Rate_{in} \times Effect - K_{over} \times Size) \times Size$$

```
<assignmentRule metaid="metaid_0000027" variable="Effect">
  <math xmlns="http://www.w3.org/1998/Math/MathML">
    <apply>
      <minus/>
      <cn> 1 </cn>
      <apply>
        <divide/>
        <ci> Ce </ci>
        <apply>
          <plus/><ci> AE50 </ci><ci> Ce </ci>
        </apply>
      </apply>
    </math>
</assignmentRule>
```

$$Effect = 1 - \frac{E_{max} - Ce}{Amt_{50} + Ce}$$

BIOMD0000000234 - Tham2008_PDmode_TumourShrinkage



[SBML formats](#)
[Other formats](#)
[Actions](#)
[Curation Comment](#)

[Model](#)
[Overview](#)
[Math](#)
[Physical entities](#)
[Parameters](#)
[Curation](#)

Reference Publication

Publication ID: [18594002](#)

Clin Cancer Res 2008 Jul;14(13):4213-8.

A pharmacodynamic model for the time course of tumor shrinkage by gemcitabine + carboplatin in non-small cell lung cancer patients.

Tham LS, Wang L, Soo RA, Lee SC, Lee HS, Yong WP, Goh BC, Holford NH.

Department of Hematology-Oncology, National University Hospital, Singapore. Tham_lai_san@lilly.com [\[more\]](#)

Model

Original Model: [BIOMD0000000234.xml.origin](#)

Submitter: [Nick Holford](#)

Submission ID: MODEL0911120001

Submission Date: 2009-11-16T19:41:59+00:00

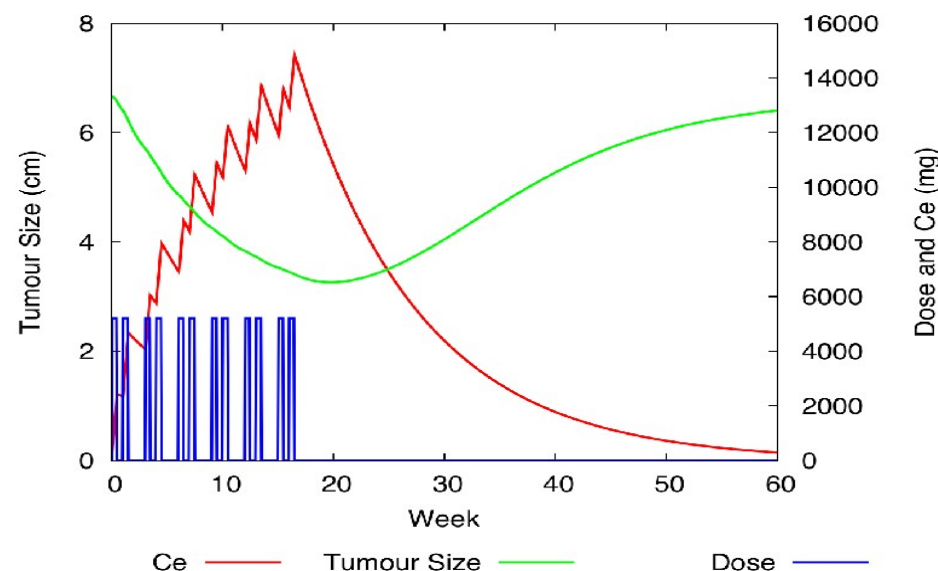
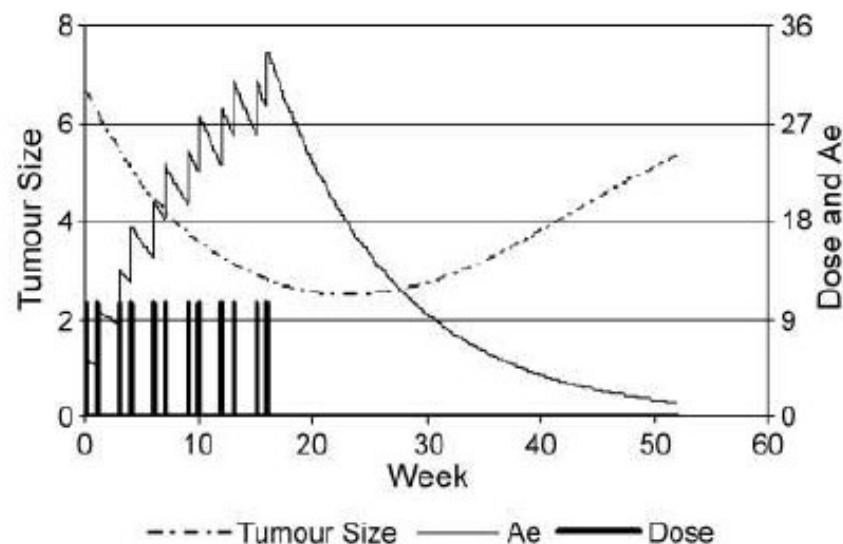
Last Modification Date: 2009-11-23T13:24:05+00:00

set #1 bqbiol:occursIn [Taxonomy](#) [Homo sapiens](#)

set #2 bqbiol:isVersionOf [ICD C34](#)
[OMIM 211980](#)

original article

reproduction with SBMLodeSolver



predicting tumor shrinkage in primary lung cancer lesions. Gemcitabine dose-based models did marginally better than treatment-based models that ignored doses of drug administered to patients. Modeling tumor shrinkage in primary lesions can be used to quantify individual sensitivity and response to antitumor effects of anticancer

- 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: 31 December 2009**
- Backward compatibility within Level at the level of the XML (but not 100% at the level of semantics)

**conversion
using libSBML**



L1

- predefined functions
- proprietary infix math notation
- reserved namespaces for annotation
- no controlled annotation
- no discrete events
- monolithic
- default values

L2

- function definitions
- all math in MathML
- no reserved namespaces for annotations
- controlled RDF annotation
- discrete events
- monolithic
- default values

L3

- function definitions
- all math in MathML
- no reserved namespaces for annotations
- controlled RDF annotation
- discrete events
- modular
- no default values

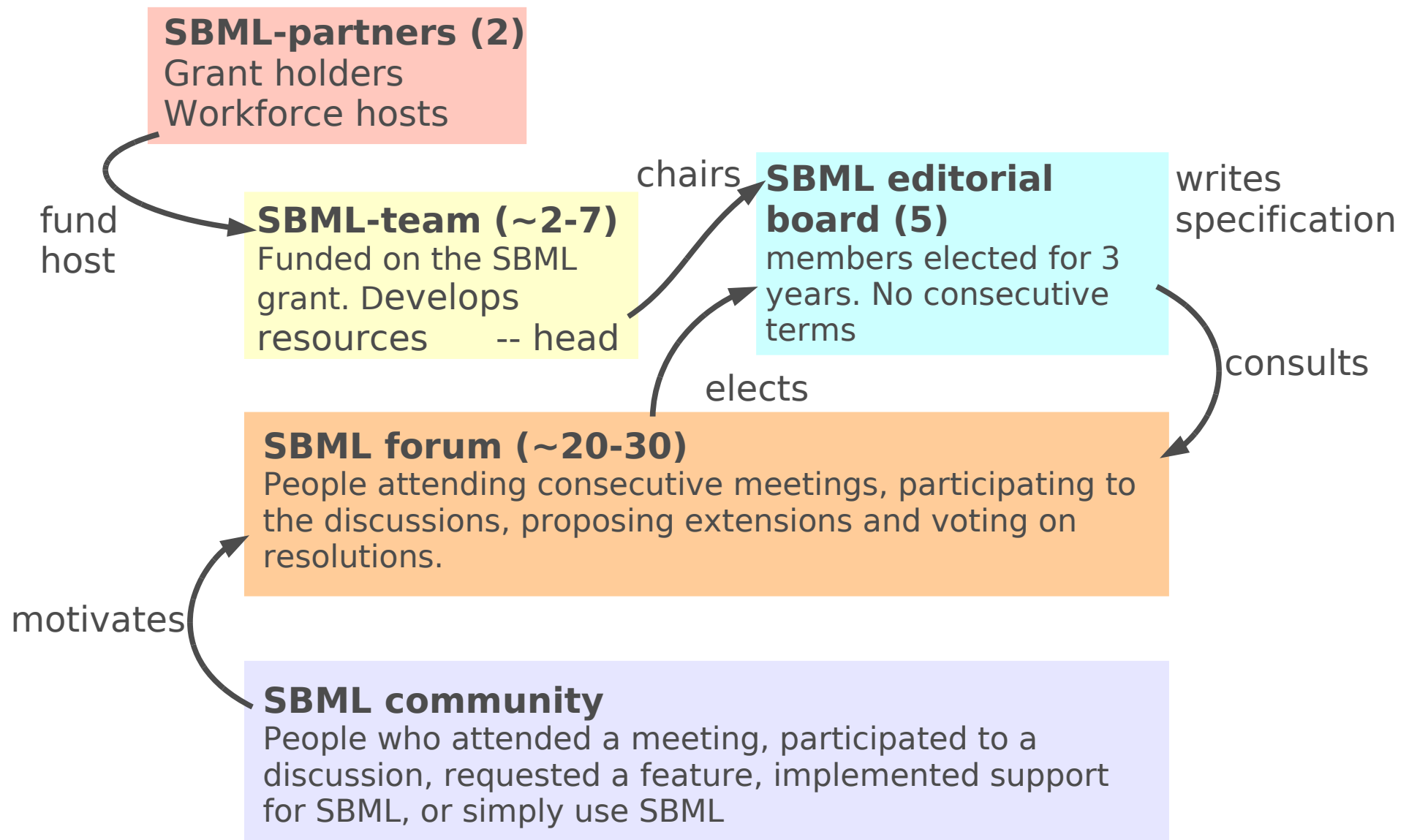
Progressive simplification, generalisation and externalisation

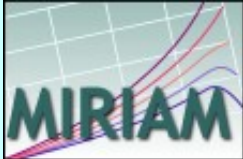
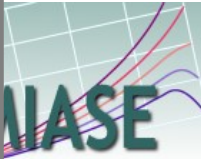
Modular SBML, with core + optional packages

- Core package – Release candidate
- 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

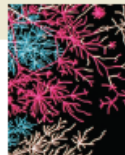
???

Current structure of the community



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

- Reporting guidelines for curation of quantitative models
 - Specifically about encoding & annotation
 - Limited for the moment to models that can be numerically evaluated
- Not specific to SBML; applicable to any structured model format



computational
BIOLOGY

PERSPECTIVE

Minimum information requested in the annotation of biochemical models (MIRIAM)

Nicolas Le Novère^{1,15}, Andrew Finney^{2,15}, Michael Hucka³, Upinder S Bhalla⁴, Fabien Campagne⁵, Julio Collado-Vides⁶, Edmund J Crampin⁷, Matt Halstead⁷, Edda Klipp⁸, Pedro Mendes⁹, Poul Nielsen⁷, Herbert Sauro¹⁰, Bruce Shapiro¹¹, Jacky L Snoep¹², Hugh D Spence¹³ & Barry L Wanner¹⁴

Most of the published quantitative models in biology are lost for the community because they are either not made available or they are insufficiently characterized to allow them to be reused. The lack of a standard description format, lack of stringent reviewing and authors' carelessness are the main causes for incomplete model descriptions. With today's increased interest in detailed biochemical models, it is necessary to define a minimum quality standard for the encoding of those models. We propose a set of rules for curating quantitative models of biological systems. These rules define procedures for encoding and annotating models represented in machine-readable form. We believe their application will enable users to (i) have confidence that curated models are an accurate reflection of their associated reference descriptions, (ii) search collections of curated models with precision, (iii) quickly identify the biological phenomena that a given curated model or model constituent represents and (iv) facilitate model reuse and composition into large subcellular models.

During the genomic era we have witnessed a vast increase in availability of large amounts of quantitative data. This is motivating a shift in the focus of molecular and cellular research from qualitative descriptions of biochemical interactions towards the quantification of such interactions and their dynamics. One of the tenets of systems biology is the use of quantitative models (see Box 1 for definitions) as a mechanism for capturing precise hypotheses and making predictions^{1,2}. Many specialized models exist that attempt to explain aspects of the cellular machinery. However, as has happened with other types of biological information, such as sequences, macromolecular structures or

Box 1 Glossary

Some terms are used in a very specific way throughout the article. We provide here a precise definition of each one.

Quantitative biochemical model. A formal model of a biological system, based on the mathematical description of its molecular and cellular components, and the interactions between those components.

Encoded model. A mathematical model written in a formal machine-readable language, such that it can be systematically parsed and employed by simulation and analysis software without further human translation.

MIRIAM-compliant model. A model that passes all the tests and fulfils all the conditions listed in MIRIAM.

Reference description. A unique document that describes, or references the description of the model, the structure of the model, the numerical values necessary to instantiate a simulation from the model, or to perform a mathematical analysis of the model, and the results one expects from such a simulation or analysis.

Curation process. The process by which the compliance of an encoded model with MIRIAM is achieved and/or verified. The curation process may encompass some or all of the following tasks: encoding of the model, verification of the reference correspondence and annotation of the model.

Reference correspondence. The fact that the structure of a model and the results of a simulation or an analysis match the information present in the reference description.

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1509

Models must :

- be encoded in a public machine-readable format
- be clearly linked to a single reference description
- reflect the structure of the biological processes described in the reference paper (list of reactions etc.)
- be instantiable in a simulation (possess initial conditions etc.)
- be able to reproduce the results given in the reference paper
- contain creator's contact details
- annotation to unambiguously identify each model constituent

Why are annotations important?

Annotation of model components are essential to:

- unambiguously identify model components
 - improve understanding the structure of the model
 - allow easier comparison of different models
 - ease the integration of models
- allow efficient search strategies
- add a semantic layer to the model
 - improve understanding of the biology behind the model
 - allow conversion and reuse of the model
 - ease the integration of model and biological knowledge

Why annotations should not be raw text

- EMBL bank version 45 (04-DEC-1995):
/db_xref="PID:g984120"
- EMBL bank version 47 (07-JUN-1996):
/db_xref="PID:g984120"
/db_xref="SWISS-PROT:P49581"
- EMBL bank version 60 (03-SEP-1999):
/db_xref="SWISS-PROT:P49581"
/protein_id="CAA58766.1"
- EMBL bank version 73 (30-NOV-2002):
/db_xref="SWISS-PROT:P49581"
/protein_id="CAA58766.1"
/db_xref="GOA:P49581"
- EMBL bank version 79 (08-JUN-2004):
/db_xref="UniProt/Swiss-Prot:P49581"
/protein_id="CAA58766.1"
/db_xref="GOA:P49581"
- EMBL bank version 84 (12-SEP-2005):
/db_xref="UniProtKB/Swiss-Prot:P49581"
/protein_id="CAA58766.1"
/db_xref="GOA:P49581"

Why annotations should not be uncontrolled XML

Extracted from a BioPAX version of "Signaling by EGFR":

```
<bp:unificationXref rdf:ID="UniProt_P01133">  
  <bp:DB rdf:datatype="http://www.w3.org/2001/XMLSchema#string">UniProt</bp:DB>  
  <bp:ID rdf:datatype="http://www.w3.org/2001/XMLSchema#string">P01133</bp:ID>  
</bp:unificationXref>
```

What is "UniProt"?

- CGD is the official acronym for:
 - Candida Genome Database
 - Cattle Genome Database
 - Comparative Genomics Database
 - Chronic Granulomatous Disease

Why annotations should not be uncontrolled URLs

[http://srs6.ebi.ac.uk/srs6bin/cgi-bin/wgetz?\[swissprot-AccNumber:P01133\]+-e](http://srs6.ebi.ac.uk/srs6bin/cgi-bin/wgetz?[swissprot-AccNumber:P01133]+-e)

<http://www.ebi.uniprot.org/uniprot-srv/uniProtView.do?proteinId=P01133>

<http://www.ebi.uniprot.org/entry/P01133>

<http://www.uniprot.org/uniprot/P01133?proteinId=P01133>

<http://www.uniprot.org/uniprot/P01133>

Characteristics of a useful identifier

- **Unique**
an identifier must never be assigned to two different objects;
- **Perennial**
the identifier is constant and its lifetime is permanent;
- **Standards compliant**
must conform on existing standards, such as URI;
- **Resolvable**
identifiers must be able to be transformed into locations of online resources storing the object or information about the object;
- **Free of use**
everybody should be able to use and create identifiers, freely and at no cost.

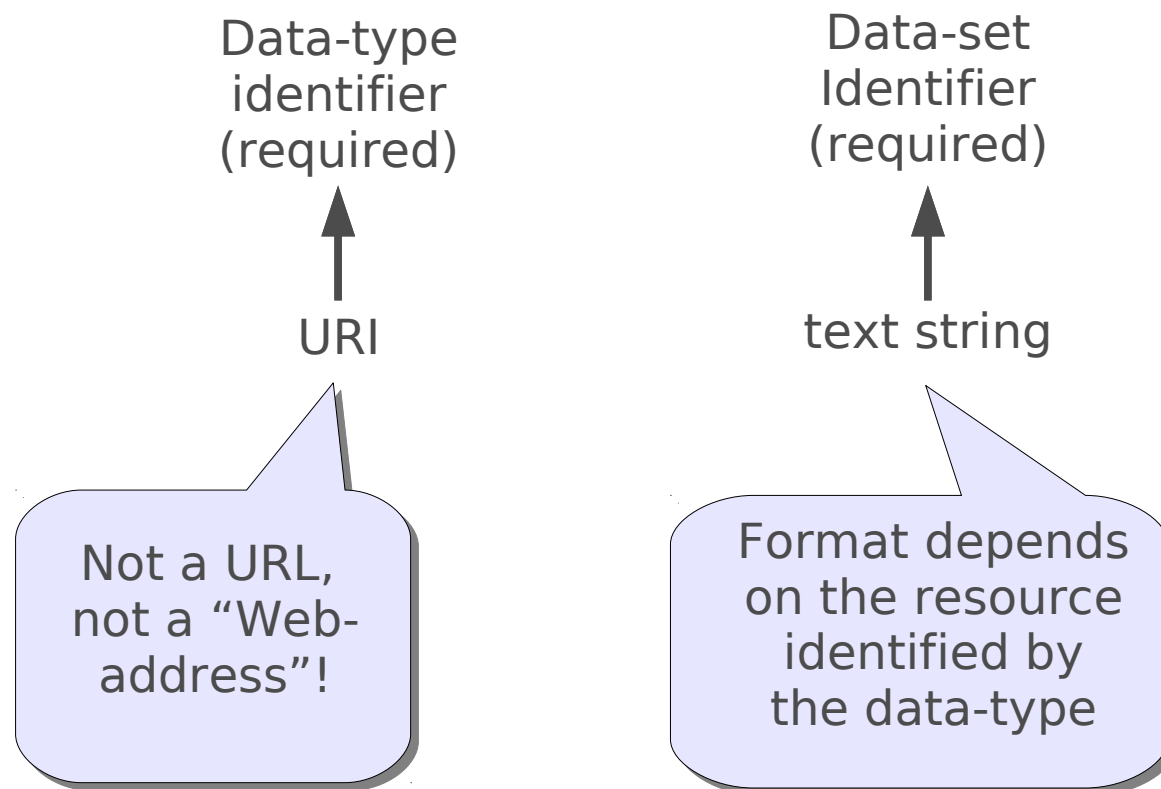
Data-type
identifier
(required)

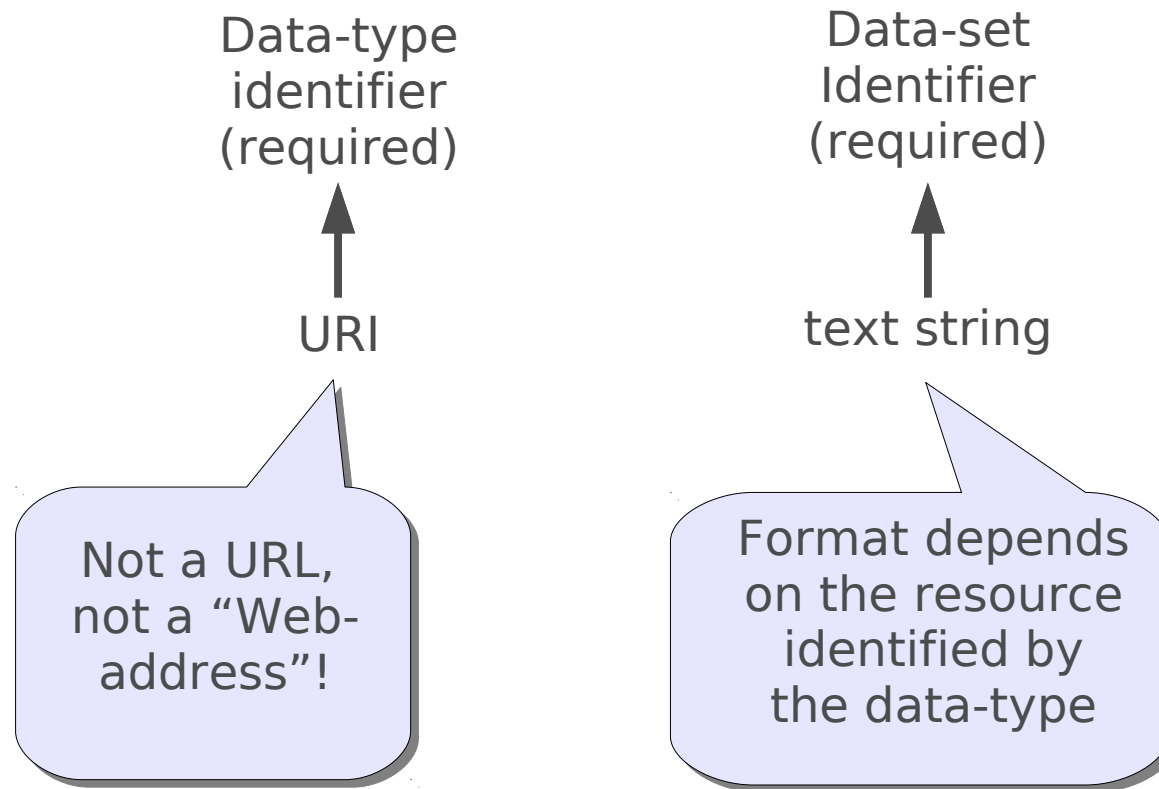


URI

Corresponds to a namespace

Not a URL,
not a “Web-
address”!





UniProt and P62158 (human calmodulin)

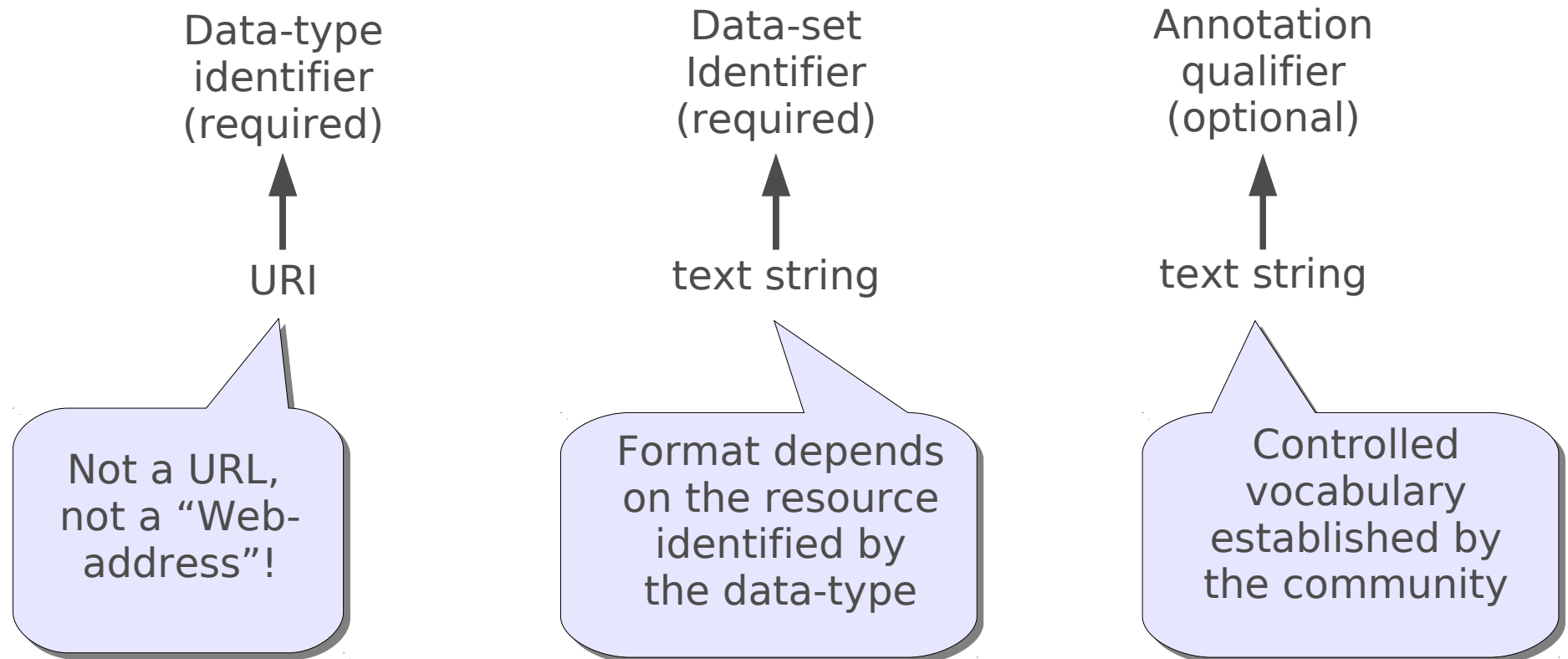
urn:miriam:uniprot:P62158

EC code and 1.1.1.1 (alcohol dehydrogenase)

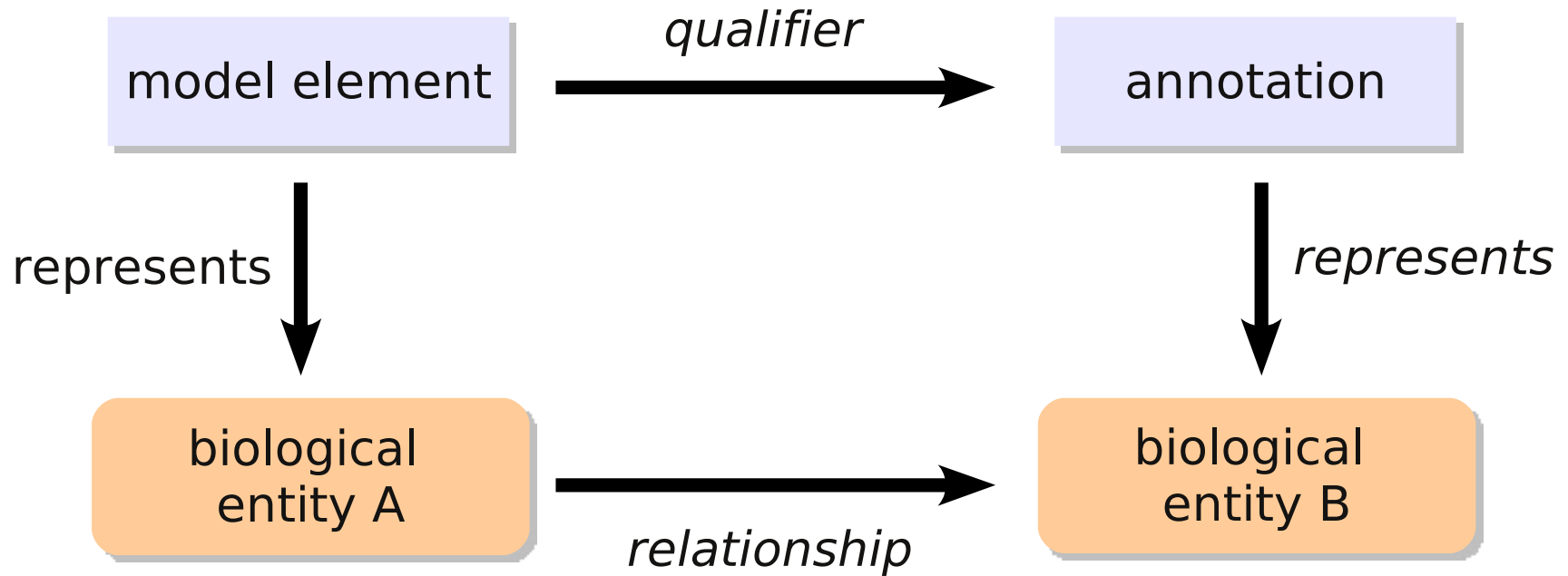
urn:miriam:ec-code:1.1.1.1

Gene Ontology and GO:0000186 (activation of MAPKK activity)

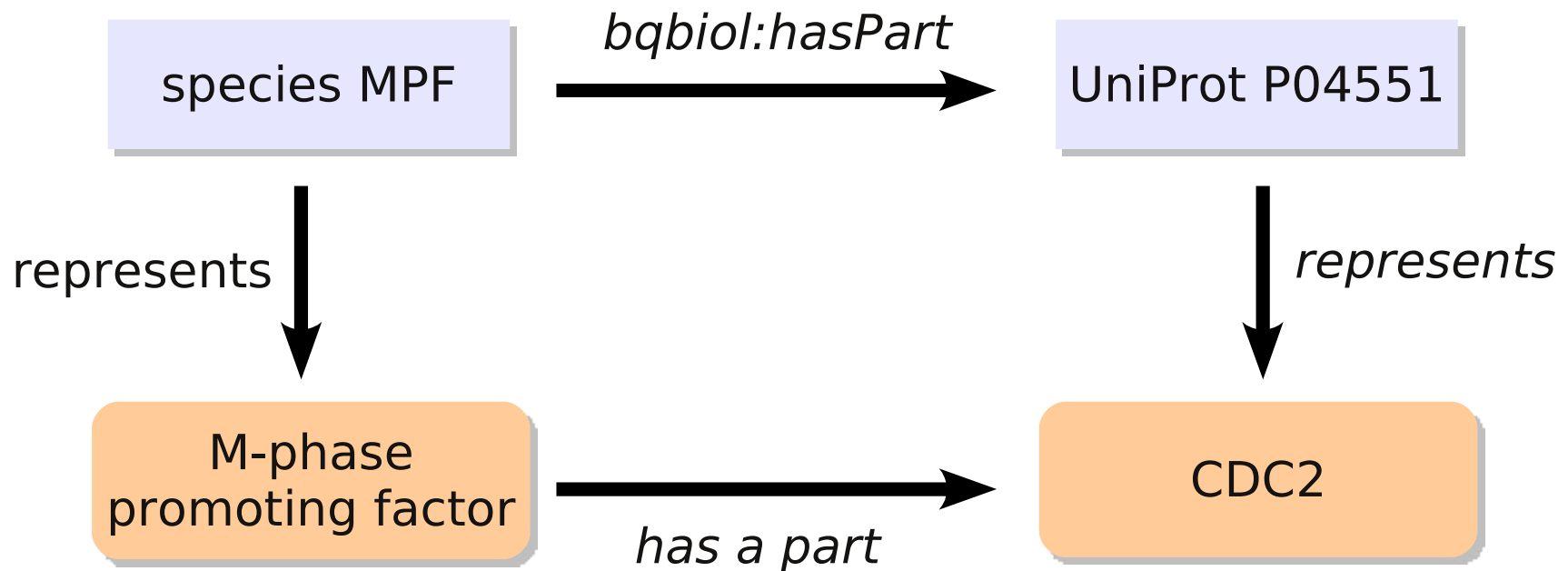
urn:miriam:obo.go:GO%3A0000186



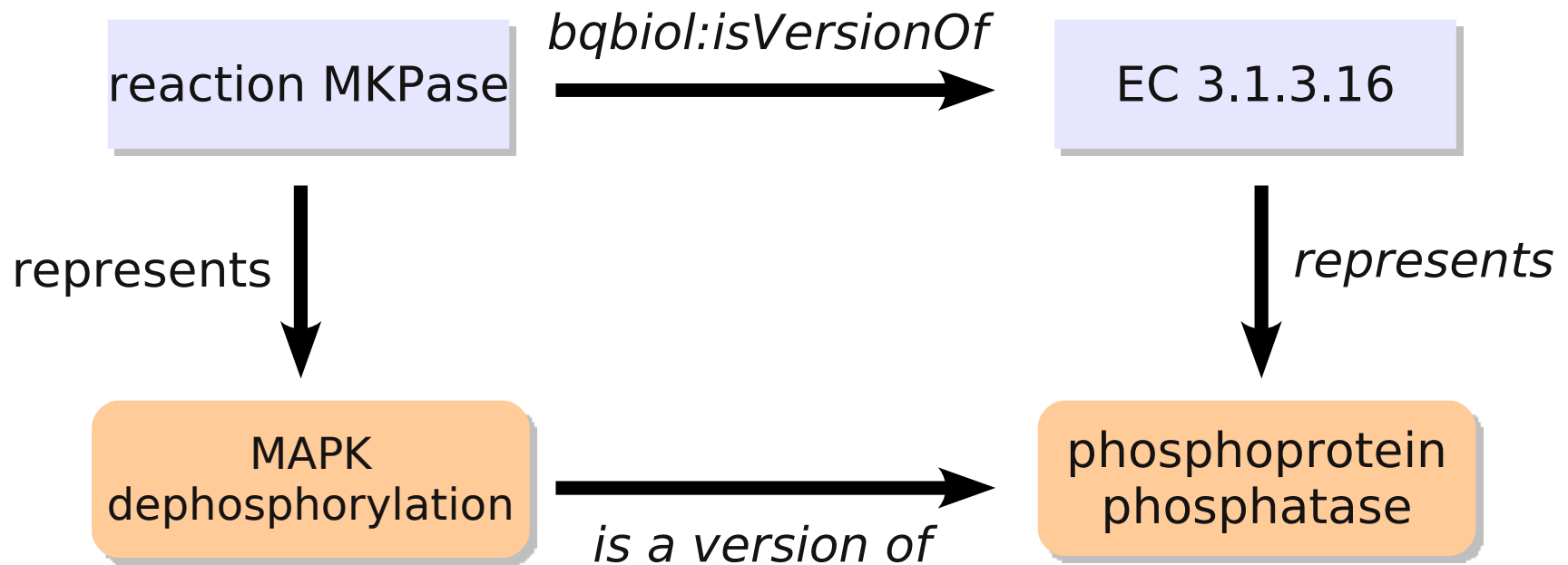
Qualification of annotation



Qualification of annotation



Qualification of annotation



Current BioModels.net Qualifiers

- **bqmodel:is** The modelling object represented by the model component is the subject of the referenced resource.
- **bqmodel:isDescribedBy** The modelling object represented by the component of the encoded model is described by the referenced resource.
- **bqbiol:is** The biological entity represented by the model component is the subject of the referenced resource.
- **bqbiol:hasPart** The biological entity represented by the model component includes the subject of the referenced resource, either physically or logically.
- **bqbiol:isPartOf** The biological entity represented by the model component is a physical or logical part of the subject of the referenced resource
- **bqbiol:isVersionOf** The biological entity represented by the model component is a version or an instance of the subject of the referenced resource.
- **bqbiol:hasVersion** The subject of the referenced resource is a version or an instance of the biological entity represented by the model component.
- **bqbiol:isHomologTo** The biological entity represented by the model component is homolog, to the subject of the referenced resource, i.e. they share a common ancestor.
- **bqbiol:isDescribedBy** The biological entity represented by the model component is described by the referenced resource.

- **bqbiol:encodes** The biological entity represented by the model component encodes, directly or by transitivity the subject of the referenced resource.
- **bqbiol:isEncodedBy** The biological entity represented by the model component is encoded, directly, or by transitivity, by the subject of the referenced resource.
- **bqbiol:occursIn** The biological entity represented by the model component takes place in the subject of the referenced resource.

PROPOSED

- **bqbiol:isPropertyOf** The biological entity represented by the model component is a property of the subject of the referenced resource.
- **bqbiol:hasProperty** The subject of the referenced resource is a property of the biological entity represented by the model component .

```
<species id="Ca_calmodulin" metaid="cacam">
  <annotation>
    <rdf:RDF
      xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
      xmlns:bqbiol="http://biomodels.net/biology-qualifiers/">
      <rdf:Description rdf:about="#cacam">
        <bqbiol:hasPart>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P62158"/>
            <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A29108"/>
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```


Tools developing support for MIRIAM identifiers

- Data resources
 - BioModels Database (kinetic models)
 - PSI consortium (protein interactions)
 - Reactome (pathways)
 - SABIO-RK (reaction kinetics)
 - Yeast consensus model database
 - Human consensus model database
 - E-MeP (structural genomics)
- MIRIAM Resources statistics
 - ~5000 web page requests per month
 - ~550000 web service requests per month
- Application software
 - ARCADIA (graph editor)
 - BIOUML (modeling and simulation)
 - COPASI (Simulation)
 - libAnnotationSBML
 - libSBML
 - SAINT (semantic annotation)
 - SBML2BioPAX
 - SBML2LaTeX
 - SBMLeditor (model editor)
 - SemanticSBML (annotation and merging)
 - Snazer (Network analysis, Simulations)
 - Systems Biology Workbench (model design and simulation)
 - The Virtual Cell (Simulation)

Tools using MIRIAM identifiers

- Data resources
 - BioModels Database (kinetic models)
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 - BIOUML (modeling and simulation)
 - COPASI (Simulation)
 - libAnnotationSBML
 - libSBML
 - SAINT (semantic SBML merging) 
 - SBML2BioPAX
 - SBML2LaTeX
 - SBMLEditor (n  merging) ations)
 - SemanticSBM
 - Snazer (Network)
 - Systems Biology (model design and simulation)
 - The Virtual Cell (Simulation)

Application: whole-cell metabolic models

- Yeast Metabolic Model

Herrgård M.J., Swainston N., Dobson P., Dunn W.B., Arga K.V., Arvas M., Blüthgen N., Borger S., Costenoble R, Heinemann M., Hucka M., Le Novère N., Li P., Liebermeister W., Mo M.L., Oliveira A.P., Petranovic D., Pettifer S., Simeonidis E., Smallbone K., Spasic I., Weichart D., Brent R., Broomhead D.S., Westerhoff H.V., Kirdar B., Penttilä M., Klipp E., Palsson B.Ø., Sauer U., Oliver S.G., Mendes P., Nielsen J., Kell D.B. (2008) A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnology*, 26: 1155-1160.

2152 species, 1857 reactions, 4861 MIRIAM annotations

- Human Metabolic Model

4889 species, 8866 reactions, **66968** MIRIAM annotations

0
KEGG_Reaction:R01429
042 Nielsen1998_Glycolysis

015 Curto1998_purineMetabol
070 Holzhutter2004_Erythrocyte_Metabolism
051 Chassagnole2002_Carbon_Metabolism
088 Maeda2006_MyosinPhosphorylation
071 Bakker2001_Glycolysis
064 Teusink2000_Glycolysis
063 Galazzo1990_pathway_kinetics
061 Hynne2001_Glycolysis
042 Nielsen1998_Glycolysis
013 Poolman2004_CalvinCycle
018 Morrison1989_FolateCycle
017
056 Chen2004_CellCycle
106 Yang2007_ArachidonicAcid
049 Sasagawa2005_MAPK

Krause F, Liebermeister W (2009)
A simple clustering of the BioModels
database using semanticSBML.
***Nature Precedings*, doi:10.1038/npre.2009.3444.1**



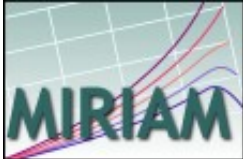
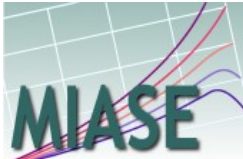
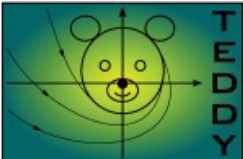
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</listOfCompartments>
<listOfSpecies>
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  <species id="B"/>
  <species id="C"/>
</listOfSpecies>
<listOfReactions>
  <reaction>
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      <speciesReference species="A"/>
    </listOfReactants>
    <listOfProducts>
      <speciesReference species="B"/>
    </listOfProducts>
    <listOfModifiers>
      <speciesReference species="C"/>
    </listOfModifiers>
    <kineticLaw>
      <math></math>
      <listOfParameters>
        <parameter id="U"/>
        <parameter id="V"/>
      </listOfParameters>
    </kineticLaw>
  </reaction>
</listOfReactions>
```

What are those?

("who" has been answered
by MIRIAM annotations)

Do those affect/are
affected by the reaction?

How should-I
understand this?

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

Systems Biology Ontology vocabularies

- Entities, that is existing objects, whether functional or material, such as “**macromolecule**”, or “**channel**”.
- Roles of reaction participants, including terms like “**substrate**”, “**catalyst**” etc.
- Parameter used in quantitative models. This vocabulary includes terms like “**Michaelis constant**”, “**forward unimolecular rate constant**” etc. A term may contain a precise mathematical expression stored as a MathML lambda function. The variables refer to other parameters.
- Mathematical expressions. Examples of terms are “**mass action kinetics**”, “**Henri-Michaelis-Menten equation**” etc. A term may contain a precise mathematical expression stored as a MathML lambda function. The variables refer to the other vocabularies.
- Modelling framework to precise how to interpret the rate-law. E.g. “**continuous modelling**”, “**discrete modelling**” etc.
- Event type, such as “**catalysis**” or “**addition of a chemical group**”.

Le Novère N., Courtot M., Laibe C. Adding semantics in kinetics models of biochemical pathways. *Proc 2nd Intl Symp Experimental Standard Conditions of Enzyme Characterizations* (2007), 137-153. Available at <http://www.beilstein-institut.de/index.php?id=196>

EBI > SBO > Browsing

Systems Biology Ontology

SBO:0000000 - sbo term

- SBO:0000236 - entity
- SBO:0000231 - interaction
- SBO:0000064 - mathematical expression
 - SBO:0000355 - conservation law
 - SBO:0000001 - rate law
 - SBO:0000268 - enzymatic rate law
 - SBO:0000150 - enzymatic rate law for irreversible reaction
 - SBO:0000151 - enzymatic rate law for irreversible reaction with no allosteric modulation
 - SBO:0000152 - enzymatic rate law for irreversible reaction with allosteric modulation
 - SBO:0000028 - enzymatic rate law for irreversible reaction with allosteric modulation and inhibition
 - SBO:0000031 - Briggs-Haldane rate law
 - SBO:0000029 - Henri-Michaelis-Menten rate law
 - SBO:0000199 - normalised enzyme rate law
 - SBO:0000030 - Van Slyke-Cullen rate law
 - SBO:0000269 - enzymatic rate law for unireactant enzymes
 - SBO:0000192 - Hill-type rate law, generalised form
 - SBO:0000012 - mass action rate law
 - SBO:0000391 - steady state expression
 - SBO:0000004 - modelling framework
 - SBO:0000003 - participant role
 - SBO:0000002 - quantitative parameter

Legend

I "is a" relationship

http://www.ebi.ac.uk - Systems Biology Ontology - SeaMonkey

SBO:0000031

Name
Briggs-Haldane rate law

Definition
Rate-law presented in "G.E. Briggs and J.B.S. Haldane (1925) A note on the kinetics of enzyme action, Biochem. J., 19: 338-339". It is a general rate equation that does not require the restriction of equilibrium of Henri-Michaelis-Menten or irreversible reactions of Van Slyke, but instead make the hypothesis that the complex enzyme-substrate is in quasi-steady-state. Although of the same form than the Henri-Michaelis-Menten equation, it is semantically different since Km now represents a pseudo-equilibrium constant, and is equal to the ratio between the rate of consumption of the complex (sum of dissociation of substrate and generation of product) and the association rate of the enzyme and the substrate.

MathML

```
<math xmlns="http://www.w3.org/1998/Math/MathML">
  <semantics definitionURL="http://biomodels.net/SBO/#SBO:0000062">
    <lambda>
      <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000025">kcat</ci></bvar>
      <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000014">Et</ci></bvar>
      <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000015">S</ci></bvar>
      <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000371">Km</ci></bvar>
      <apply>
        <divide/>
        <apply>
          <times/>
          <ci>kcat</ci>
          <ci>Et</ci>
          <ci>S</ci>
        </apply>
        <plus/>
        <ci>Km</ci>
      </apply>
    </lambda>
  </semantics>
</math>
```

Rendered equation

$$\lambda(kcat, Et, S, Km) = \frac{kcat \times Et \times S}{Km + S}$$

Miscellaneous

Date of creation:
23 February 2006, 14:00

Date of last modification:
25 November 2008, 16:27

Parent(s)
SBO:0000028 enzymatic rate law for irreversible non-modulated non-interacting unireactant enzymes (is a)

Children
This term has no child.

History [\[+\]](#)

Done


```
<listOfCompartments>
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  <species id="C" sboTerm="SBO:0000014" />
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    </kineticLaw>
  </reaction>
</listOfReactions>
```

```

<listOfCompartments>
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</listOfCompartments>
<listOfSpecies>
  <species id="A" sboTerm="SBO:0000247">
  <species id="B" sboTerm="SBO:0000247">
  <species id="C" sboTerm="SBO:0000014">
</listOfSpecies>
<listOfReactions>
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        <parameter id="U" sboTerm="SBO:0000008"/>
        <parameter id="V" sboTerm="SBO:0000025"/>
      </listOfParameters>
    </kineticLaw>
  </reaction>
</listOfReactions>

```

functional compartment

simple chemical

simple chemical

enzyme

catalysis

substrate

product

catalyst

Briggs-Haldane equation

K_m

k_{cat}

Conversion between modeling frameworks

```
<listOfCompartments>
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</listOfCompartments>
<listOfSpecies>
  <species id="A" sboTerm="SBO:0000247" />
  <species id="B" sboTerm="SBO:0000247" /
  <species id="C" sboTerm="SBO:0000014" />
</listOfSpecies>
<listOfReactions>
  <reaction sboTerm="SBO:0000172">
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    </listOfReactants>
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      <speciesReference species="B" sboTerm="SBO:0000011"/>
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    </listOfModifiers>
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        <parameter id="U" sboTerm="SBO:0000008"/>
        <parameter id="V" sboTerm="SBO:0000025"/>
      </listOfParameters>
    </kineticLaw>
  </reaction>
</listOfReactions>
```

discrete simulator

$$v1 = \frac{(k_{-1} + V)}{U} \cdot [A] \cdot [C]$$

$$v2 = k_{-1} \cdot [D]$$

$$v3 = V \cdot [D]$$

continuous simulator

$$v = \frac{C \cdot V \cdot [A]}{(U + [A])}$$



to BioPAX conversion using SBO

```
<listOfCompartments>
  <compartment id="C" sboTerm="SBO:0000289">
</listOfCompartments>
<listOfSpecies>
  <species id="A" sboTerm="SBO:0000247">
  <species id="B" sboTerm="SBO:0000247">
  <species id="C" sboTerm="SBO:0000014">
</listOfSpecies>
<listOfReactions>
  <reaction sboTerm="SBO:0000172">
    <listOfReactants>
      <speciesReference species="A" sboTerm="SBO:0000015"/>
    </listOfReactants>
    <listOfProducts>
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        <parameter id="U" sboTerm="SBO:0000008"/>
        <parameter id="V" sboTerm="SBO:0000025"/>
      </listOfParameters>
    </kineticLaw>
  </reaction>
</listOfReactions>
```

GO annotation

Small molecule

Small molecule

Protein

catalysis

physicalEntityParticipant

physicalEntityParticipant

physicalEntityParticipant

<http://www.biopax.org/>

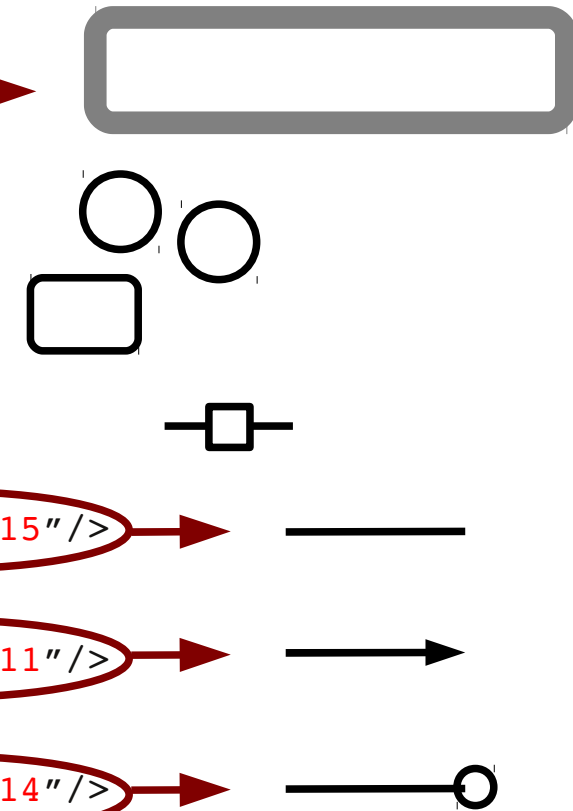


to



conversion using SBO

```
<listOfCompartments>
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</listOfCompartments>
<listOfSpecies>
  <species id="A" sboTerm="SBO:0000247">
  <species id="B" sboTerm="SBO:0000247">
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    </kineticLaw>
  </reaction>
</listOfReactions>
```

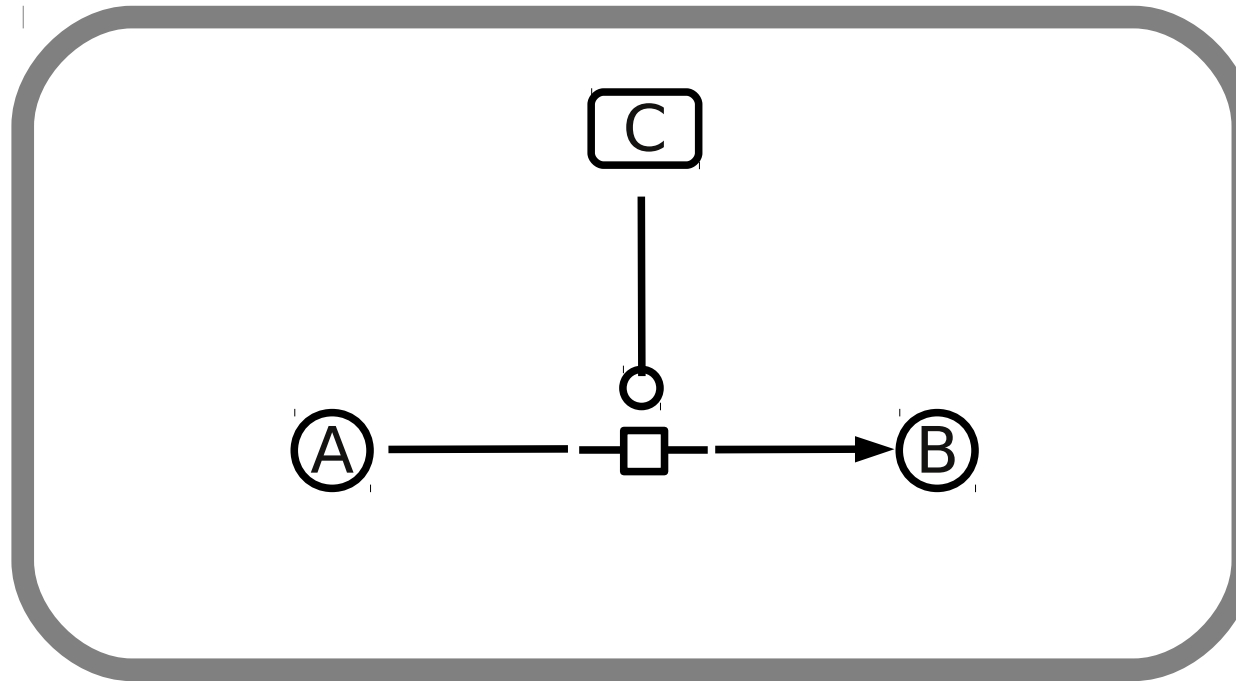


<http://www.sbgn.org/>

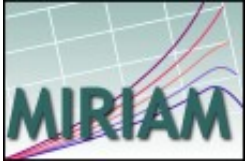
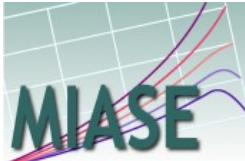
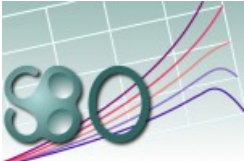


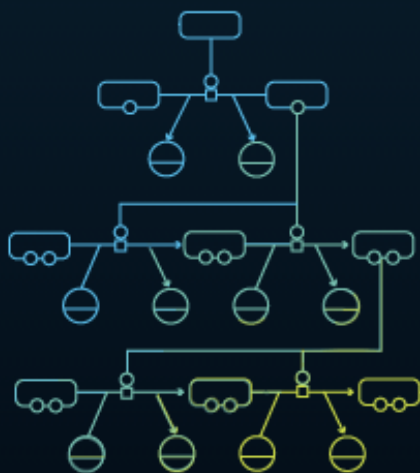
to SBGN

conversion using SBO



Model representation

	Models	Simulation	Results
Minimal requirements			
Data-model	 	ED-ML	SBRML
Ontologies			



A Visual Notation for Network Diagrams in Biology

SBGN.org is the global portal for documentation, news, and other information about the Systems Biology Graphical Notation (SBGN) project, an effort to standardize the graphical notation used in maps of biochemical and cellular processes studied in systems biology.

Standardizing the visual representation is crucial for more efficient and accurate transmission of biological knowledge between different communities in research, education, publishing, and more. When biologists are as familiar with the notation as electronics engineers are familiar with the notation of circuit schematics, they can save the time and effort required to familiarize themselves with different notations, and instead spend more time thinking about the biology being depicted.

SBGN is made up of [[three orthogonal languages](#)], representing different visions of biological systems. Each language defines a comprehensive set of symbols with precise semantics, together with detailed syntactic rules how maps are to be interpreted.

On this site, you can browse some [example maps](#) to get a feeling for SBGN, read the SBGN [specification documents](#), join [online discussions](#), see current working documents and software support in the [SBGN wiki](#), and much more.

SBGN is the work of many people. It would not have been possible without the generous [support of multiple organizations](#) over the years, for which we are very thankful.

To quote SBGN as a whole, please use:

Le Novère N, Hucka M, Mi H, Moodie S, Schreiber F, Sorokin A, Demir E, Wegner K, Aladjem MI, Wimalaratne SM, Bergman FT, Gauges R, Ghazal P, Kawaji H, Li L, Matsuoka Y, Villéger A, Boyd SE, Calzone L, Courtot M, Dogrusoz U, Freeman TC, Funahashi A, Ghosh S, Jouraku A, Kim S, Kolpakov F, Luna A, Sahle S, Schmidt E, Watterson S, Wu G, Goryanin I, Kell DB, Sander C, Sauro H, Snoep JL, Kohn K, Kitano H. The Systems Biology Graphical Notation. [Nat Biotechnol. 2009 27\(8\):735-41.](#)

SBGN News

(02 Sep. '09) The first specifications for [SBGN Entity Relationships](#) and [SBGN Activity Flows](#) are out.

- An unambiguous way of graphically describing and interpreting biochemical and cellular events
- Limited amount of symbols
Re-use existing symbols
 - 👉 Smooth learning curve
- Can represent logical or mechanistic models, biochemical pathways, at different levels of granularity
- Detailed technical specification, precise data-models and growing software support
- Initiated by Hiroaki Kitano. Developed over four years by a diverse community

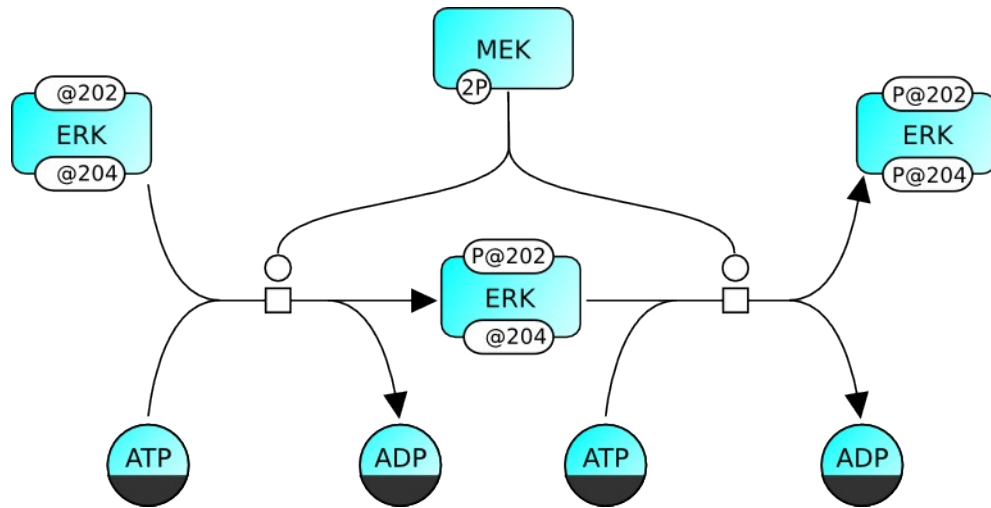
The Systems Biology Graphical Notation

Nicolas Le Novère¹, Michael Hucka², Huaiyu Mi³, Stuart Moodie⁴, Falk Schreiber^{5,6}, Anatoly Sorokin⁷, Emek Demir⁸, Katja Wegner⁹, Mirit I Aladjem¹⁰, Sarala M Wimalaratne¹¹, Frank T Bergman¹², Ralph Gauges¹³, Peter Ghazal^{4,14}, Hideya Kawaji¹⁵, Lu Li¹, Yukiko Matsuoka¹⁶, Alice Villéger^{17,18}, Sarah E Boyd¹⁹, Laurence Calzone²⁰, Melanie Courtot²¹, Ugur Dogrusoz²², Tom C Freeman^{14,23}, Akira Funahashi²⁴, Samik Ghosh¹⁶, Akiya Jouraku²⁴, Sohyoung Kim¹⁰, Fedor Kolpakov^{25,26}, Augustin Luna¹⁰, Sven Sahle¹³, Esther Schmidt¹, Steven Watterson^{4,22}, Guanming Wu²⁷, Igor Goryanin⁴, Douglas B Kell^{18,28}, Chris Sander⁸, Herbert Sauro¹², Jacky L Snoep²⁹, Kurt Kohn¹⁰ & Hiroaki Kitano^{16,30,31}

¹EMBL European Bioinformatics Institute, Hinxton, UK. ²Engineering and Applied Science, California Institute of Technology, Pasadena, California, USA. ³SRI International, Menlo Park, California, USA. ⁴Centre for Systems Biology at Edinburgh, University of Edinburgh, Edinburgh, UK. ⁵Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany. ⁶Institute of Computer Science, University of Halle, Halle, Germany. ⁷School of Informatics, University of Edinburgh, Edinburgh, UK. ⁸Memorial Sloan Kettering Cancer Center - Computational Biology Center, New York, NY, USA. ⁹Science and Technology Research Institute, University of Hertfordshire, Hatfield, UK. ¹⁰National Cancer Institute, Bethesda, Maryland, USA. ¹¹Auckland Bioengineering Institute, University of Auckland, Auckland, New Zealand. ¹²Department of Bioengineering, University of Washington, Seattle, Washington, USA. ¹³BIOQUANT, University of Heidelberg, Heidelberg, Germany. ¹⁴Division of Pathway Medicine, University of Edinburgh Medical School, Edinburgh, UK. ¹⁵Riken OMICS Science Center, Yokohama City, Kanagawa, Japan. ¹⁶The Systems Biology Institute, Tokyo, Japan. ¹⁷School of Computer Science, University of Manchester, Manchester, UK. ¹⁸Manchester Interdisciplinary Biocentre, Manchester, UK. ¹⁹Clayton School of Information Technology, Faculty of Information Technology, Monash University, Melbourne, Victoria, Australia. ²⁰U900 INSERM, Paris Mines Tech, Institut Curie, Paris, France. ²¹Terry Fox Laboratory, British Columbia Cancer Research Center, Vancouver, British Columbia, Canada. ²²Bilkent Center for Bioinformatics, Bilkent University, Ankara, Turkey. ²³The Roslin Institute, University of Edinburgh, Midlothian, UK. ²⁴Department of Biosciences and Informatics, Keio University, Hiyoshi, Kouhoku-ku, Yokohama, Japan. ²⁵Institute of Systems Biology, Novosibirsk, Russia. ²⁶Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia. ²⁷Ontario Institute for Cancer Research, Toronto, Ontario, Canada. ²⁸School of Chemistry, University of Manchester, Manchester, UK. ²⁹Department of Biochemistry, Stellenbosch University, Matieland, South Africa. ³⁰Sony Computer Science Laboratories, Tokyo, Japan. ³¹Okinawa Institute of Science and Technology, Okinawa, Japan. Correspondence should be addressed to N.L.N. (lenov@ebi.ac.uk).

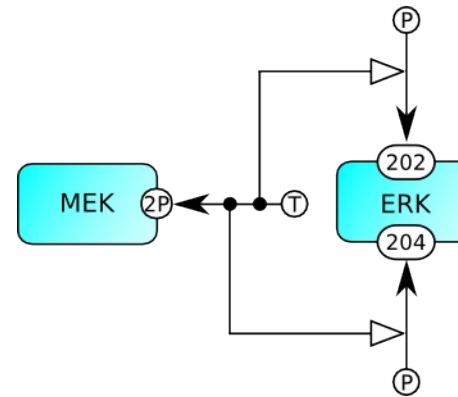
39 authors, 31 affiliations

Process Descriptions



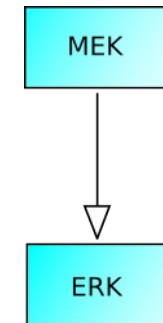
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships



- Unambiguous
- Mechanistic
- Non-sequential
- Independence of relationships

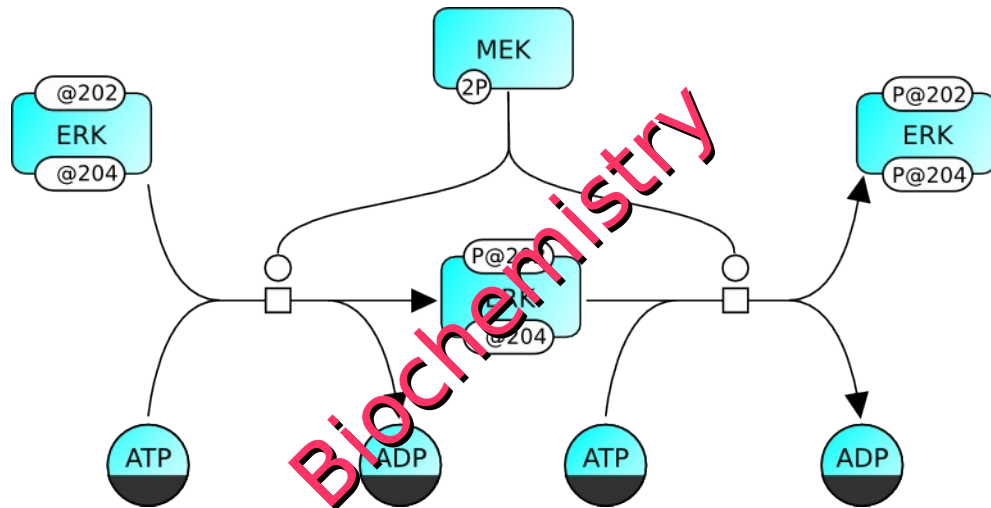
Activity Flows



- Ambiguous
- Conceptual
- Sequential

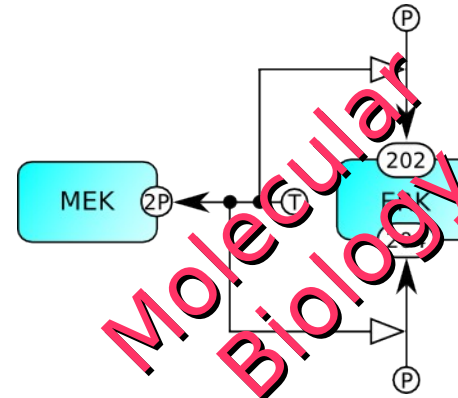
Graph trinity: three languages in one notation

Process Descriptions



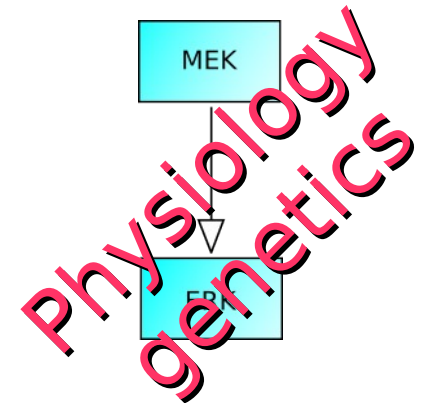
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships



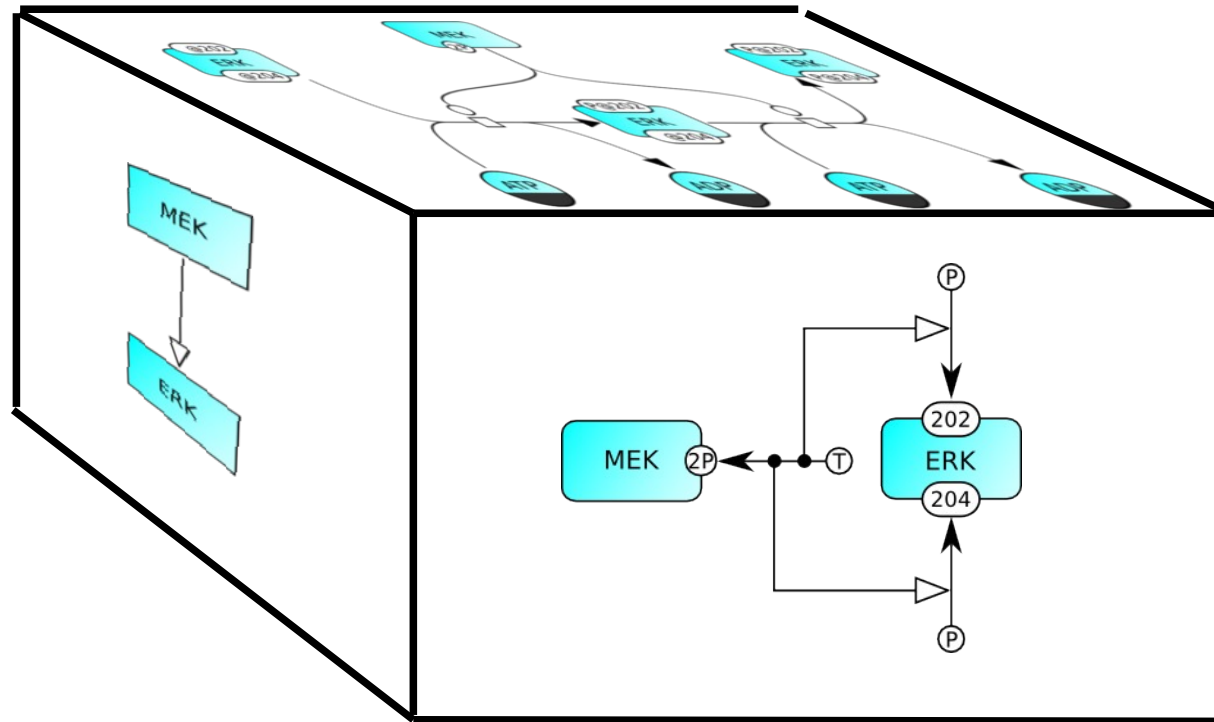
- Unambiguous
- Mechanistic
- Non-sequential
- Independence of relationships

Activity Flows

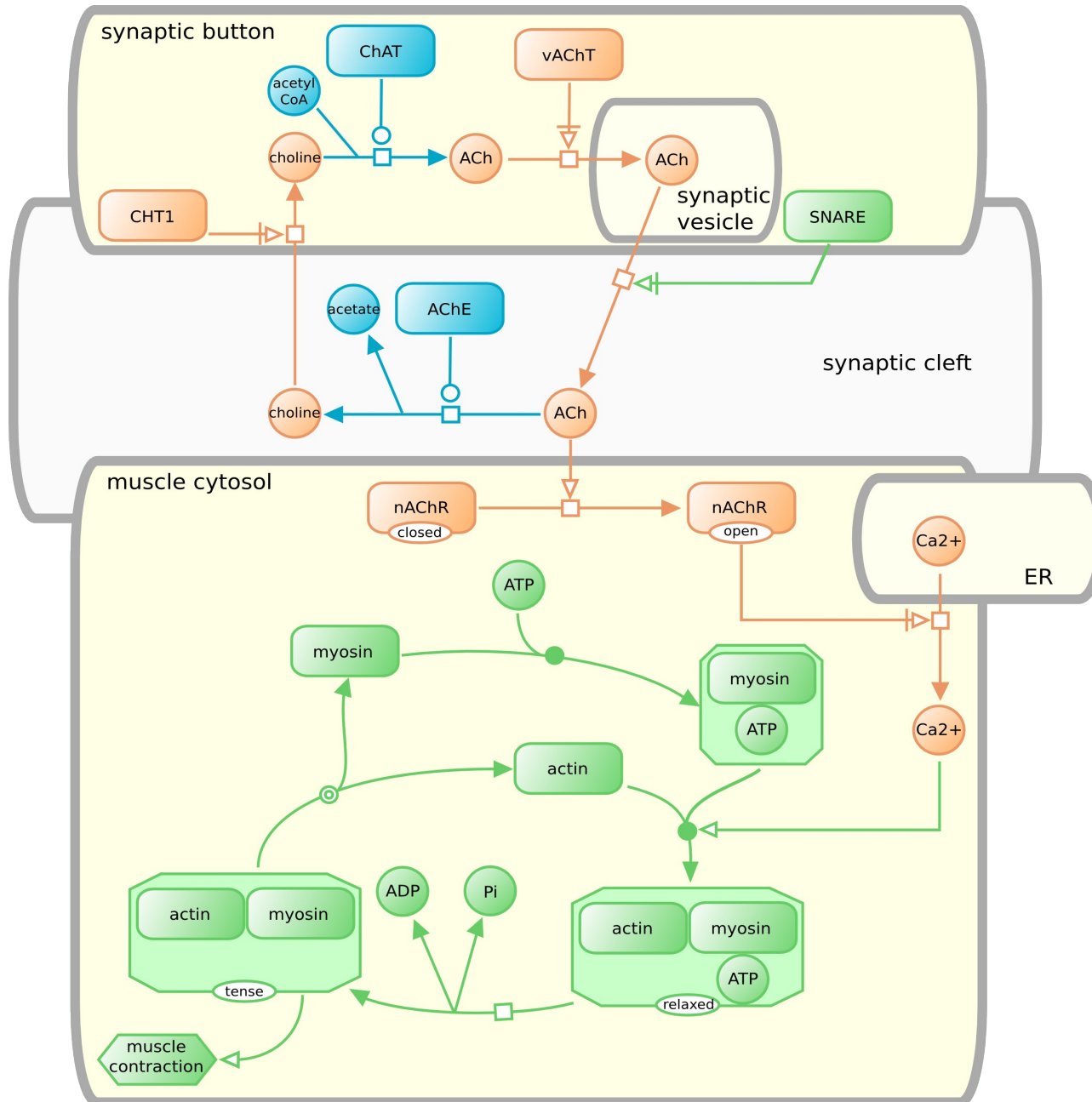


- Ambiguous
- Conceptual
- Sequential

Three orthogonal projections of biology



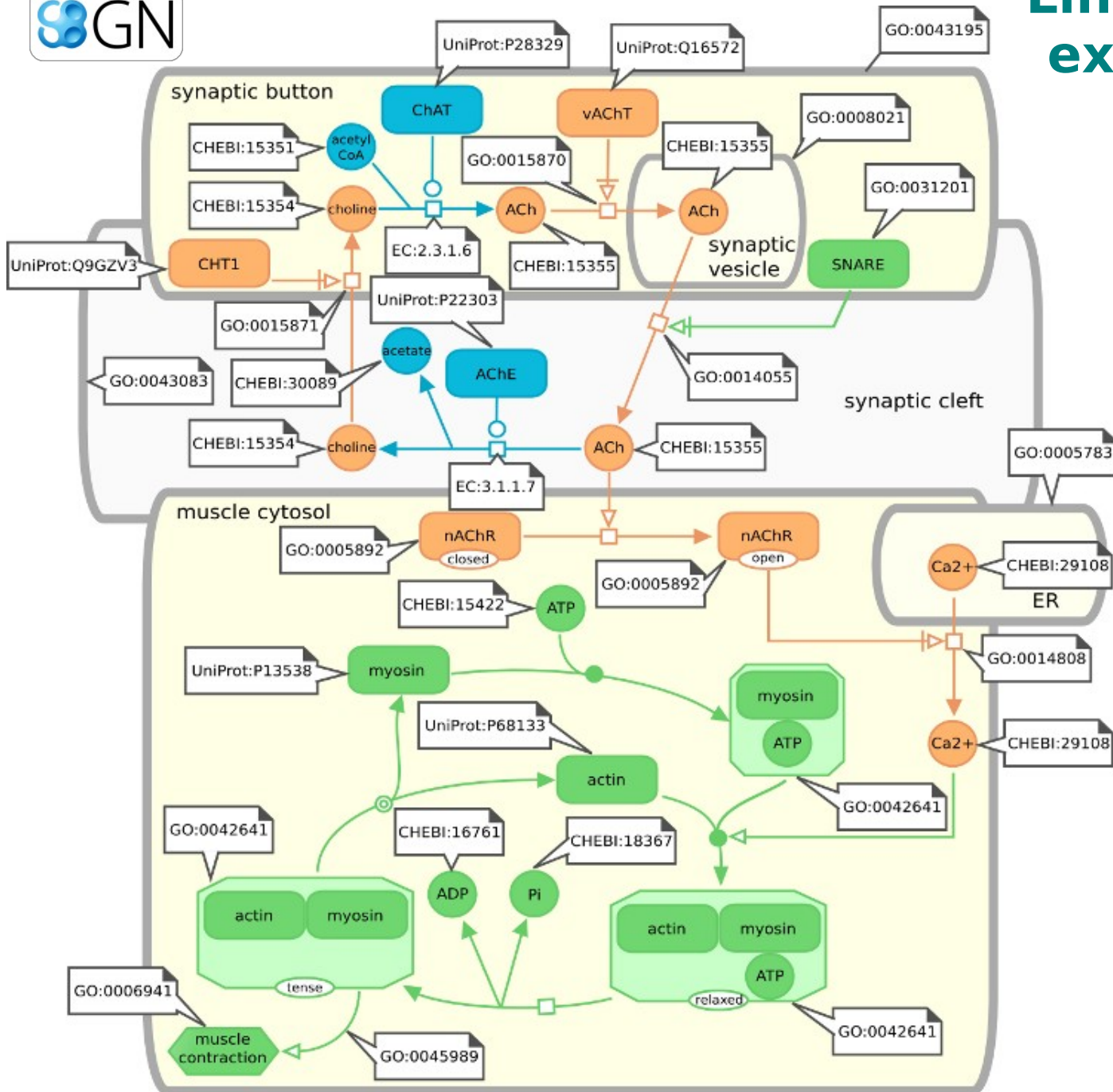
multi-cellular processes in Process Description language

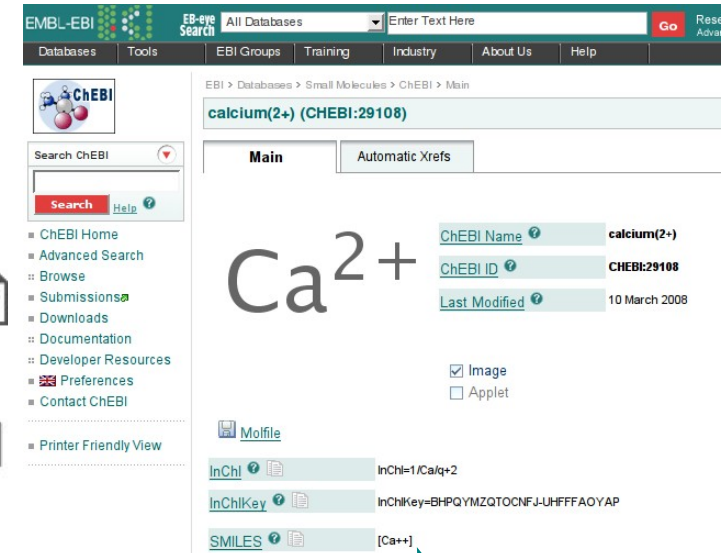


catalytic processes

transport processes

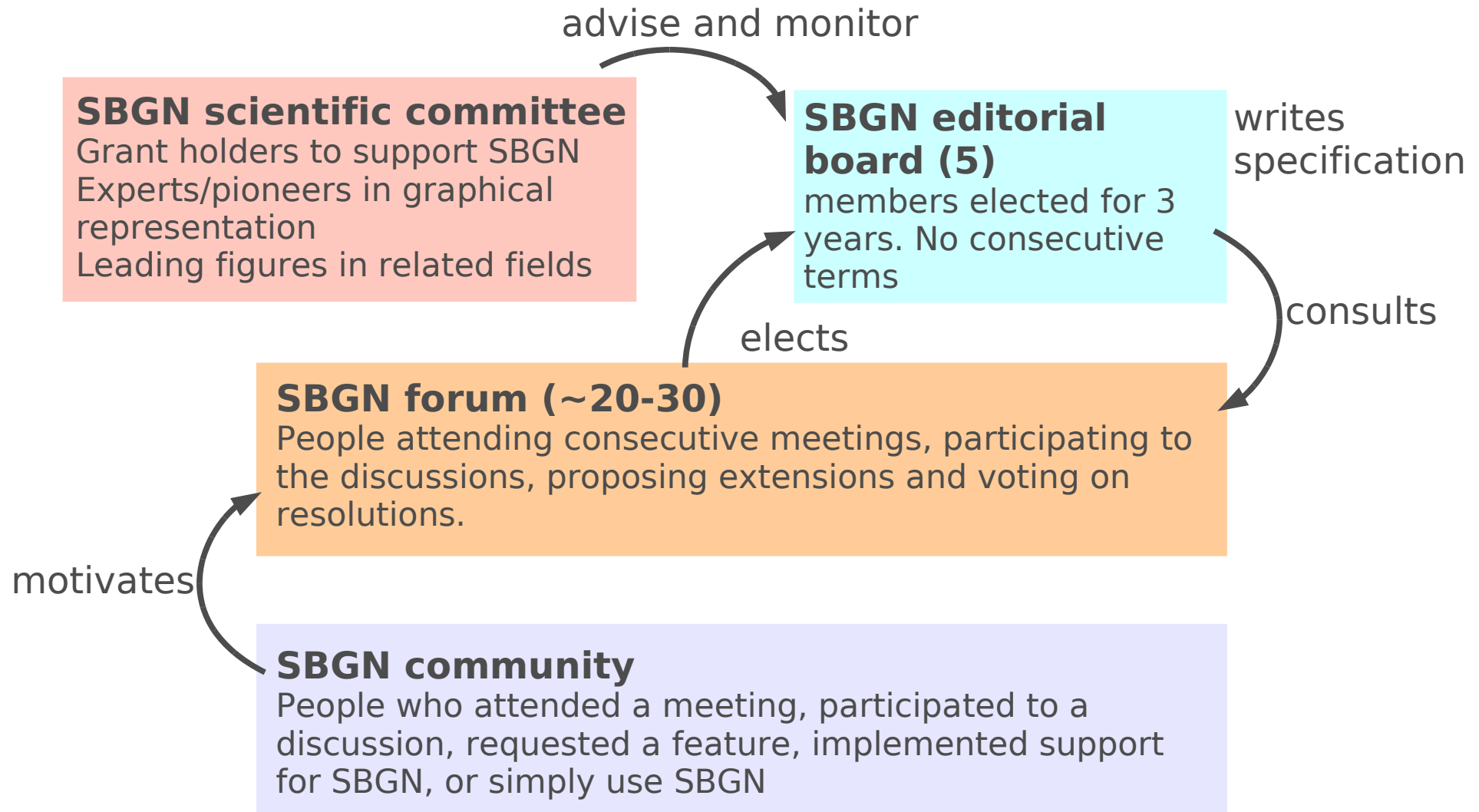
contractile proteins



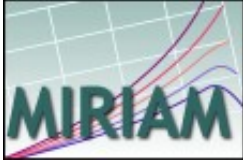
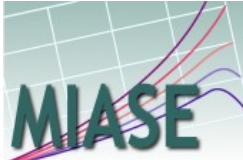


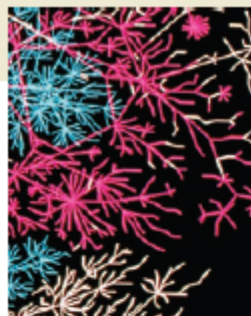
- SBGN Process Descriptions
 - Level 1 Version 1.0 released on August 23rd 2008
 - Level 1 Version 1.1 released on September 1st 2009
 - Level 1 Version 2 under discussion
- SBGN Entity Relationships
 - Level 1 Version 1.0 released on September 1st 2009
- SBGN Activity Flows
 - Level 1 Version 1.0 released on September 1st 2009

Current structure of the SBGN community



Simulation description

	Models	Simulation	Results
Minimal requirements			
Data-models	  		
Ontologies			

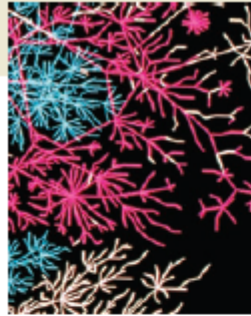


Minimum information requested in the annotation of biochemical models (MIRIAM)

Nicolas Le Novère^{1,15}, Andrew Finney^{2,15}, Michael Hucka³, Upinder S Bhalla⁴, Fabien Campagne⁵, Julio Collado-Vides⁶, Edmund J Crampin⁷, Matt Halstead⁷, Edda Klipp⁸, Pedro Mendes⁹, Poul Nielsen⁷, Herbert Sauro¹⁰, Bruce Shapiro¹¹, Jacky L Snoep¹², Hugh D Spence¹³ & Barry L Wanner¹⁴

Most of the published quantitative models in biology are lost for the community because they are either not made available or they are insufficiently characterized to allow them to be reused. The lack of a standard description format, lack of stringent reviewing and authors' carelessness are the main causes for incomplete model descriptions. With today's increased interest in detailed biochemical models, it is necessary to define a minimum quality standard for the encoding of those models. We propose a set of rules for curating quantitative models of biological systems. These rules define procedures for encoding and annotating models represented in machine-readable form. We believe their

During the genomic era we have witnessed a vast increase in availability of large amounts of quantitative data. This is motivating a shift in the focus of molecular and cellular research from qualitative descriptions of biochemical interactions towards the quantification of such interactions and their dynamics. One of the tenets of systems biology is the use of quantitative models (see Box 1 for definitions) as a mechanism for capturing precise hypotheses and making predictions^{1,2}. Many specialized models exist that attempt to explain aspects of the cellular machinery. However, as has happened with other types of biological information, such as sequences, macromolecular structures or



Minimum biochem

Nicolas Le Novère
Julio Collado-Vides
Herbert Sauro^{10,11}

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6. The model, when instantiated within a suitable simulation environment, must be able to reproduce all relevant results given in the reference description that can readily be simulated. Not only does the simulation have to provide results qualitatively similar to the reference description, such as oscillation, bistability, chaos, but the quantitative values of variables, and their relationships (e.g., the shape of the phase portrait) must be reproduced within some epsilon, the difference being attributable to the algorithms used to run the simulation, and the

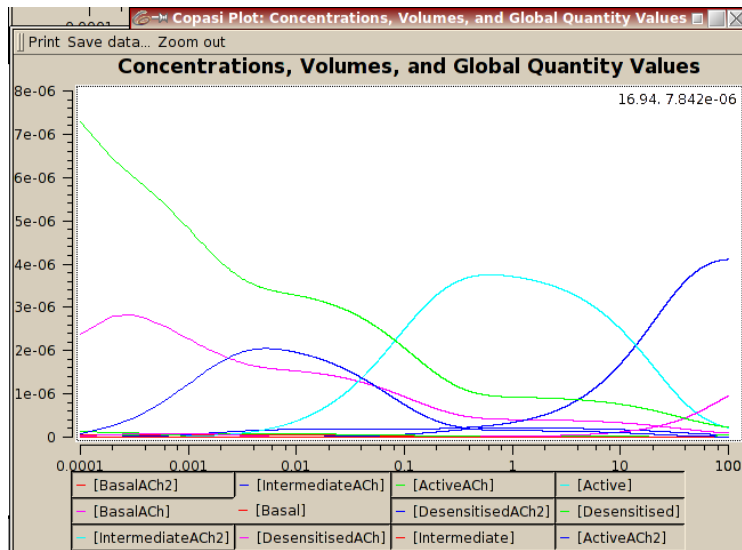
tion of

en⁷,

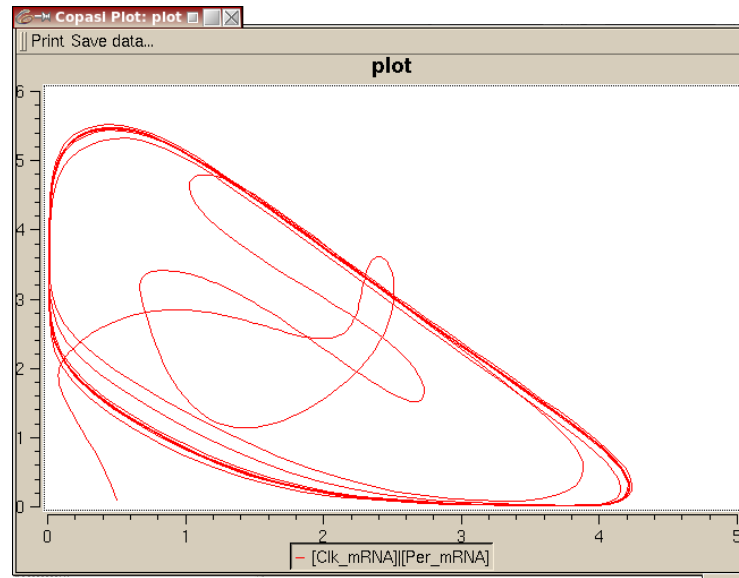
During the genome era, the massive increase in availability of large amounts of quantitative data. This is motivating a shift in the focus of molecular and cellular research from qualitative descriptions of biochemical interactions towards the quantification of such interactions and their dynamics. One of the tenets of systems biology is the use of quantitative models (see Box 1 for definitions) as a mechanism for capturing precise hypotheses and making predictions^{1,2}. Many specialized models exist that attempt to explain aspects of the cellular machinery. However, as has happened with other types of biological information, such as sequences, macromolecular structures or

Reproduction of published simulation results

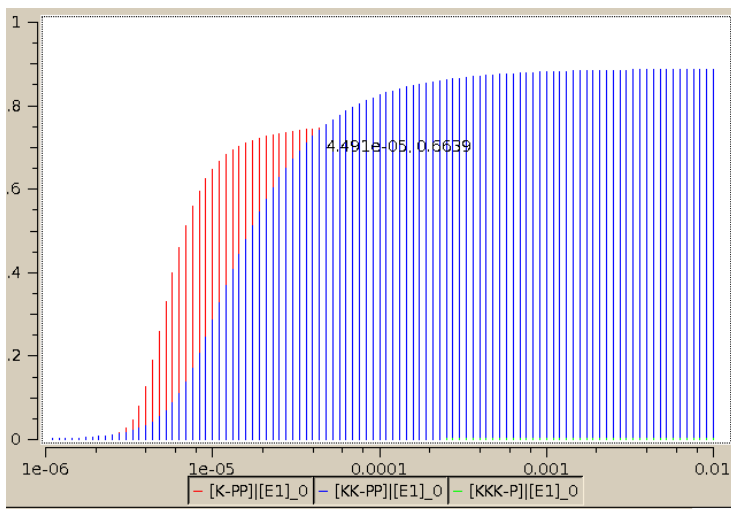
Edelstein et al 1996 (BIOMD0000000002)



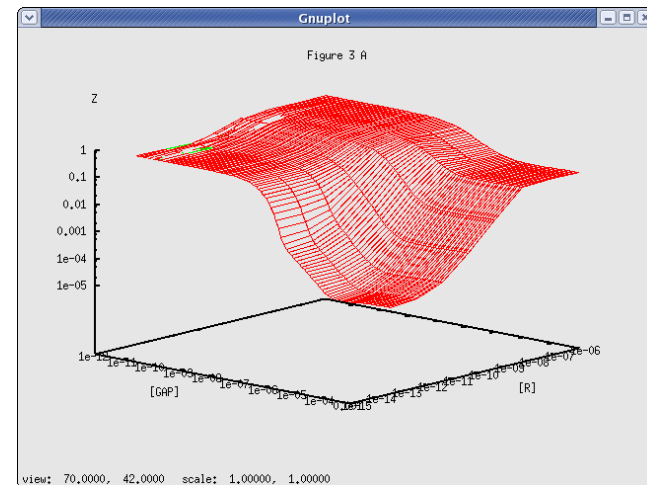
Ueda, Hagiwara, Kitano 2001 (BIOMD0000000022)



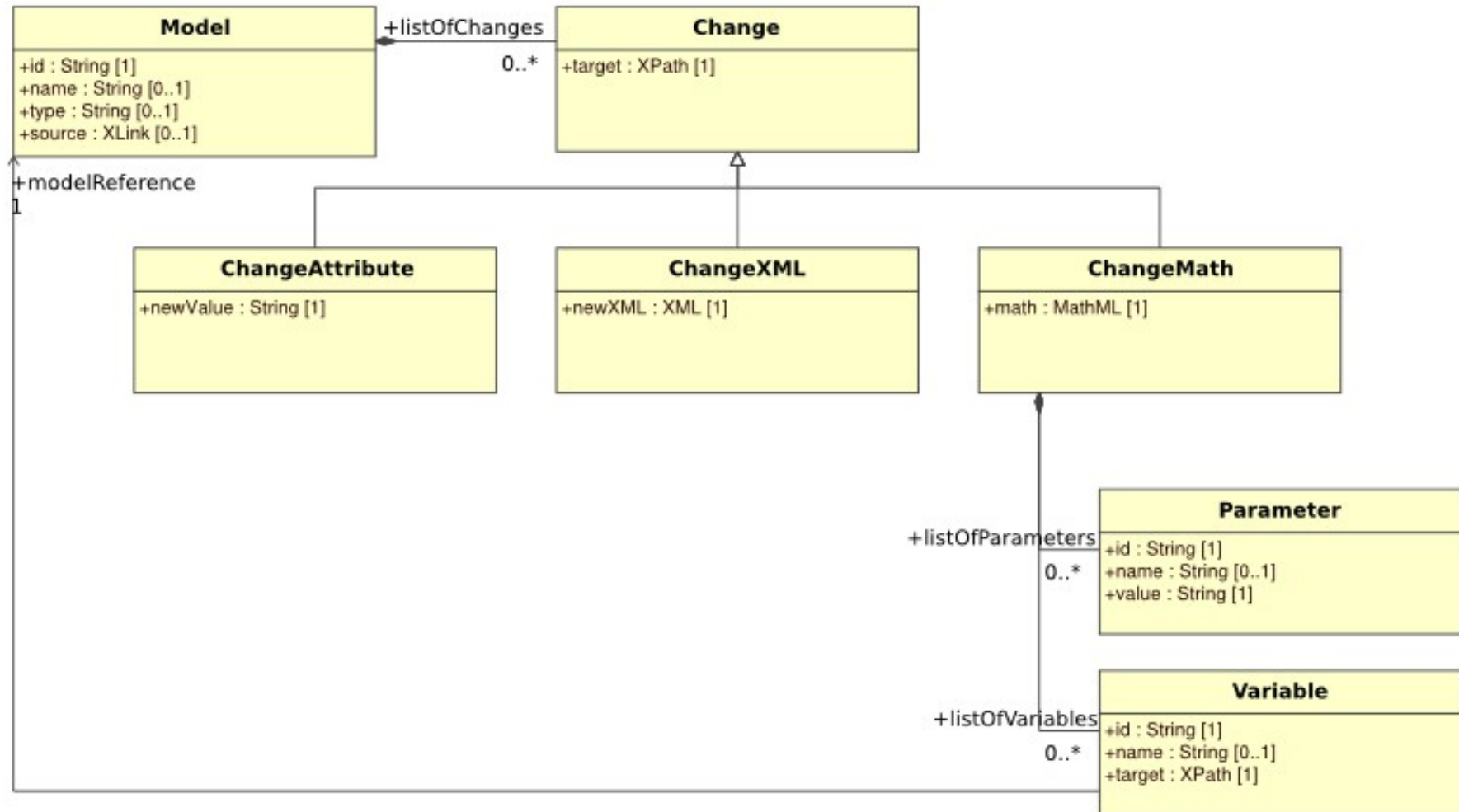
Huang & Ferrell (BIOMD0000000009)



Bornheimer et al 2004 (BIOMD0000000086)



Description of models




```
<?xml version="1.0" encoding="utf-8"?>
<sedML version="1.0" xmlns="http://www.miase.org/">
  <notes>Changing a system from oscillation to chaos</notes>
  <listOfModels>
    <model id="model1"
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    </model>
  </listOfModels>
```


Description of models

```
<?xml version="1.0" encoding="utf-8"?>
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  </listOfModels>
```

Any model description
in XML such as SBML, CellML
VCML etc.

```
<?xml version="1.0" encoding="utf-8"?>
<sedML version="1.0" xmlns="http://www.miase.org/">
  <notes>Changing a system from oscillation to chaos</notes>
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    </model>
  </listOfModels>
```

Description of models

MIRIAM Resources

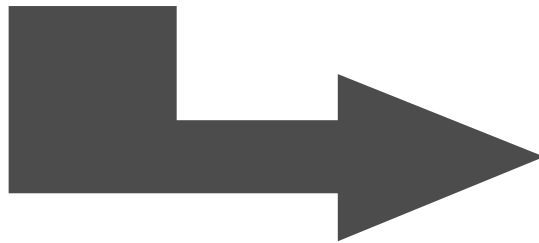
Data type: *BioModels Database*

General Tags Annotation

General information about the data type

Name		
Identifier	MIR:00000007	
Name	BioModels Database	
Synonyms	BioModels	
URIs		
Official URN	urn:miriam:biomodels.db	
Deprecated	http://www.ebi.ac.uk/biomodels/	
Information		
Definition	BioModels Database is a data resource that allows biologists to models of biological interests.	
Identifier Pattern	^(BIOMD MODEL)d{10}\$	
Physical Locations		
Resource #1	Data Entry	http://www.ebi.ac.uk/biomodels-main/\$id [Example: BIOMD0000000001]
	Data Resource	http://www.ebi.ac.uk/biomodels/
	Information	BioModels, a Database of Annotated Published Models
	Institution	European Bioinformatics Institute, United Kingdom
Resource #2	Data Entry	http://biomodels.caltech.edu/\$id [Example: BIOMD00000000048]
	Data Resource	http://biomodels.caltech.edu/
	Information	Mirror of BioModels Database
	Institution	California Institute of Technology, USA
Documentation		
URL(s)	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?view+MedlineFull+	
Miscellaneous		
Date of creation	2006-08-14 19:38:06 GMT	
Date of last modification	2009-06-05 17:43:08 GMT	

[Go back to the list of data types](#)



BioModels Home Browse Models Submit Sign In Support About

BIOMD0000000021 - Leloup1999_CircClock

SBML L2 V1 | Other formats | Actions | [Submit Model](#) [Comment/Bug](#)

Overview

Model

Math

Physical entities

Parameters

Reference Publication

Publication ID: [10366496](#)

J Theor Biol 1999 Jun;198(3):445-59.
Chaos and birhythmicity in a model for circadian oscillations of the PER and TIM proteins in drosophila.
Leloup JC, Goldbeter A.
Unite de Chronobiologie Theorique, Faculte des Sciences, Universite Libre de Bruxelles, Campus
B-1050 Brussels, Belgium. [\[more\]](#)

Model

Original Model: *Unspecified*

set #1 bqbiol:is [Taxonomy Drosophila melanogaster](#)
[KEGG Pathway dne04710](#)

Submitter: [Nicolas Le Novère](#)

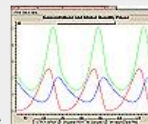
set #2 bqbiol:isVersionOf [Gene Ontology circadian rhythm](#)

Submission Date: 2005-09-13T13:24:15+00:00

Last Modification Date: 2007-09-25T09:32:00+00:00

Creation Date: 2005-06-29T10:27:52+00:00

Creators: [Nicolas Le Novère](#)
[Bruce Shapiro](#)

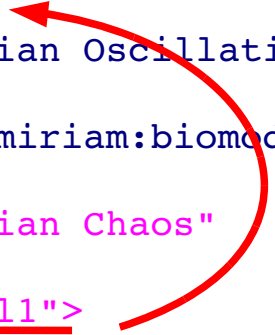


Curation Result:

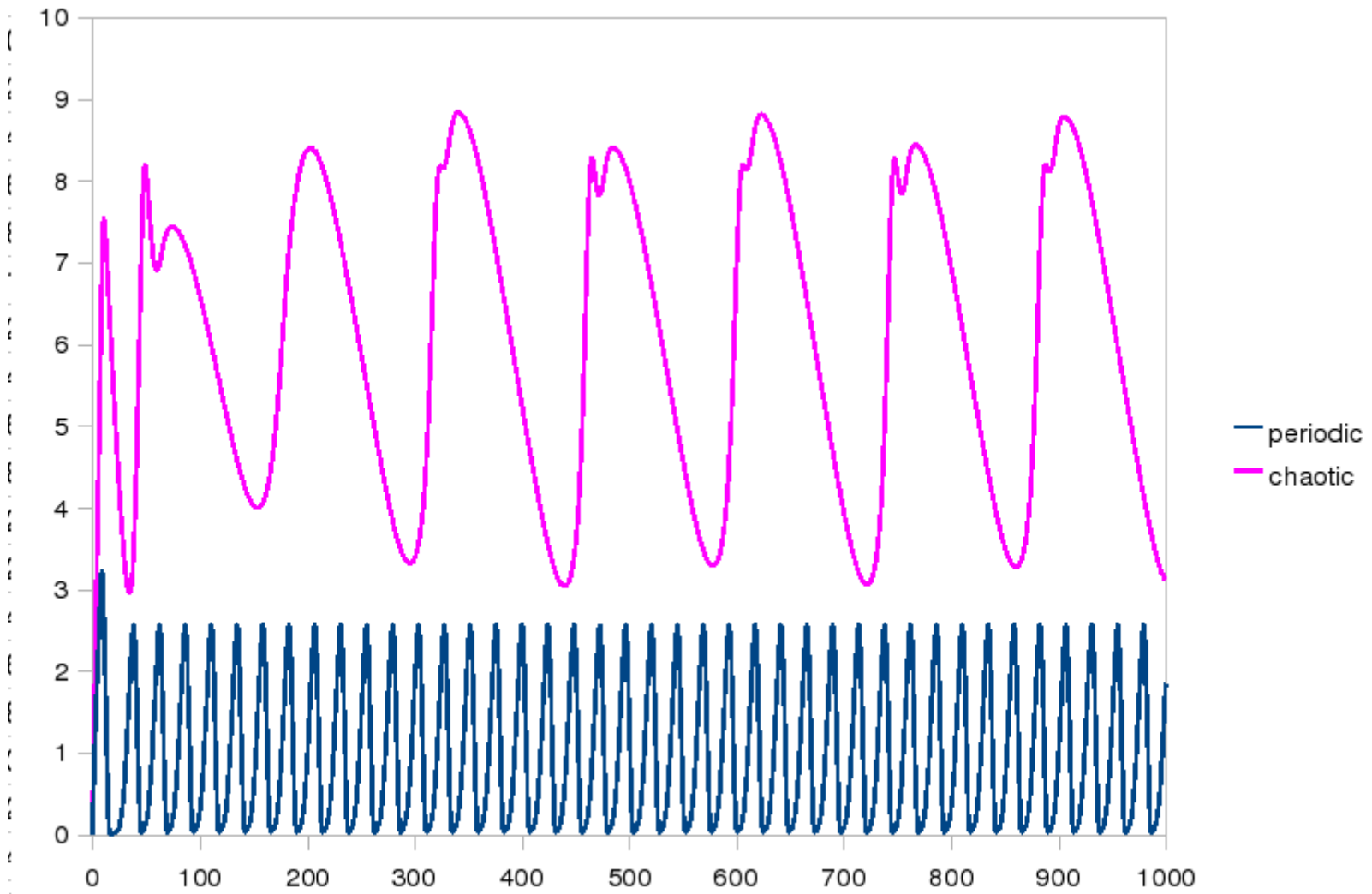
Notes

[Terms of Use](#) | [EBI Funding](#) | [Contact EBI](#) | © European Bioinformatics Institute 2006-2008. EBI is an Outstation of the [European Molecular Biology Laboratory](#).

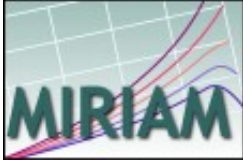
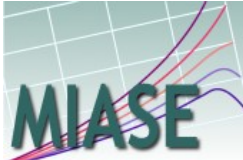
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          "/sbml/model/listOfParameters/parameter[@id='V_mT']/@value" newValue="0.28">
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      </listOfChanges>
    </model>
  </listOfModels>
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<?xml version="1.0" encoding="utf-8"?>
<sedML version="1.0" xmlns="http://www.miase.org/">
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    </model>
  </listOfModels>
```



Is the mosaic of standards really complete?

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

Disentangling the model life-cycle

PMML



SED-ML

SBRML

model generation

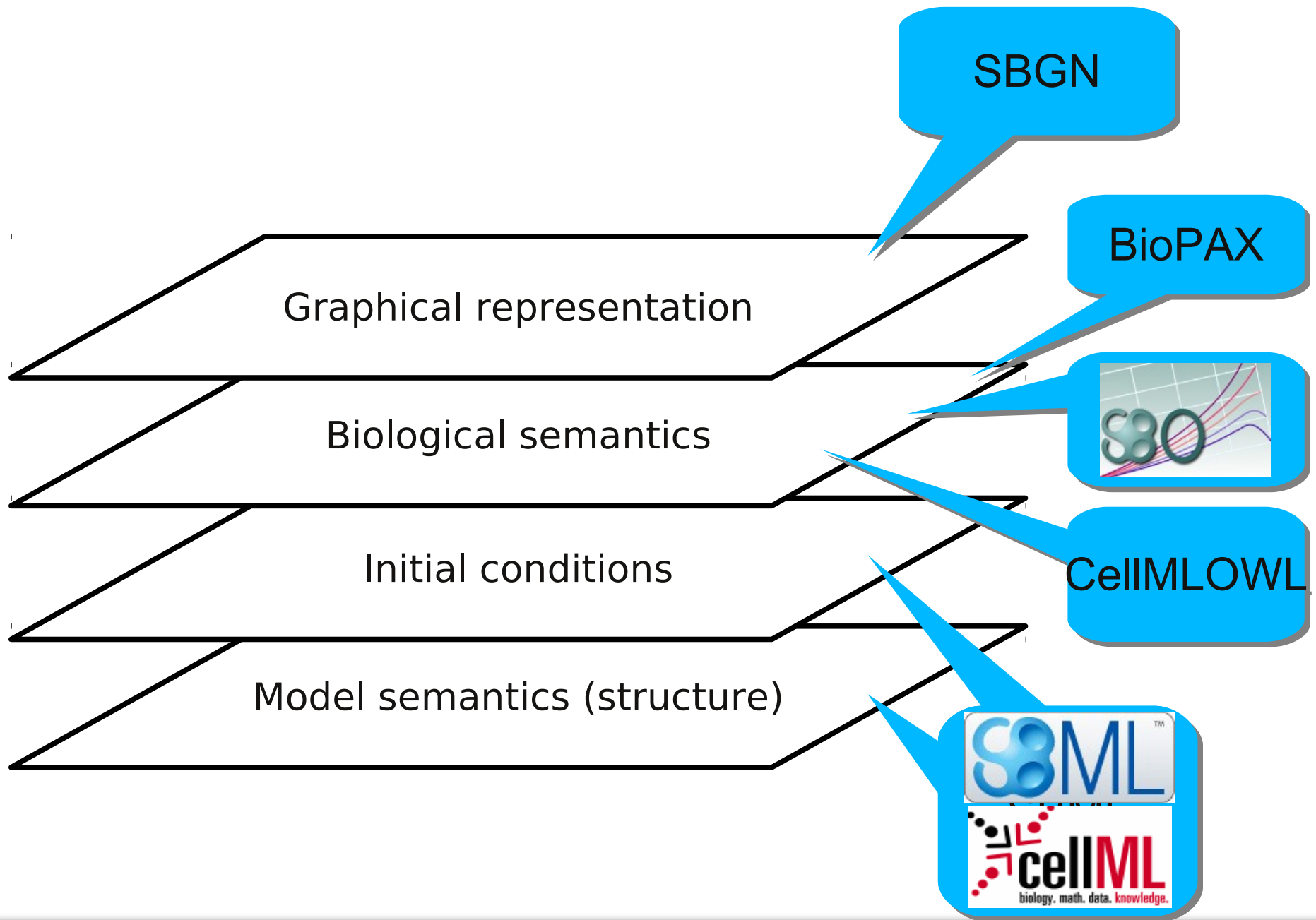
model description

parameterisation

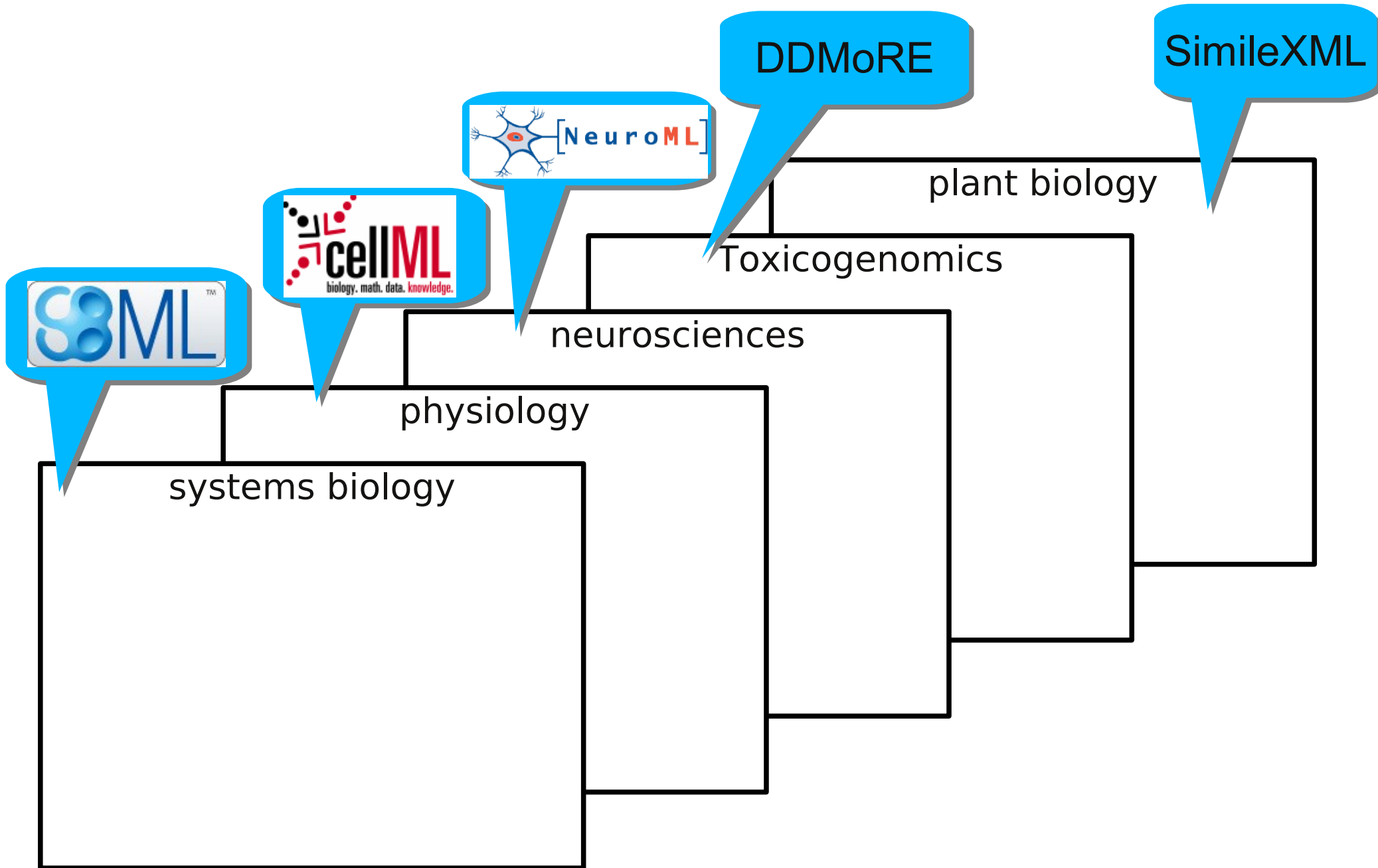
simulation and analysis

numerical results

Disentangling the level of discourse



Covering the whole life-science



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

Separating scales and representations

example of neurosciences

- Brain function is a multi-scale process
 - Molecular: Opening of ion channels
 - Subcellular: Signalling pathways
 - Cellular: Propagation of the action potentials
 - Multi-cellular: Computation by micro-circuits
 - Tissular: Consciousness and depolarization waves
- Modelling neuronal processes requires many approaches
 - Modelling biochemistry
 - Modelling electrical activity
 - Modelling mechanics
- Role of the International Neuroinformatics Coordinating Facility

Existing standardisation efforts

- ChannelML: state-based representation of molecule behaviour (part of NeuroML)
- SynapseML: (part of NeuroML)
- MorphML: cable representation of neurons (part of NeuroML)
- SBML: description of biochemical processes (interoperate with NeuroML)
- NeuML (temporary name): Effort started by the INCF to describe networks of single-compartment neurons
- Missing: Representation of mechanical processes
- Missing: Description of mean-field measurements

Existing standardisation efforts

electrical behaviours

- ChannelML: state-based representation of molecule behaviour (part of NeuroML)
- SynapseML: (part of NeuroML)
- MorphML: cable representation of neurons (part of NeuroML)
- SBML: description of biochemical processes (interoperate with NeuroML)
- Missing: Representation of mechanical processes
- NeuML (temporary name): Effort started by the INCf to describe networks of single-compartment neurons
- Missing: Representation of tissues
- Missing: Description of mean-field measurements

biochemical processes

- ChannelML: state-based representation of molecule behaviour (part of NeuroML)
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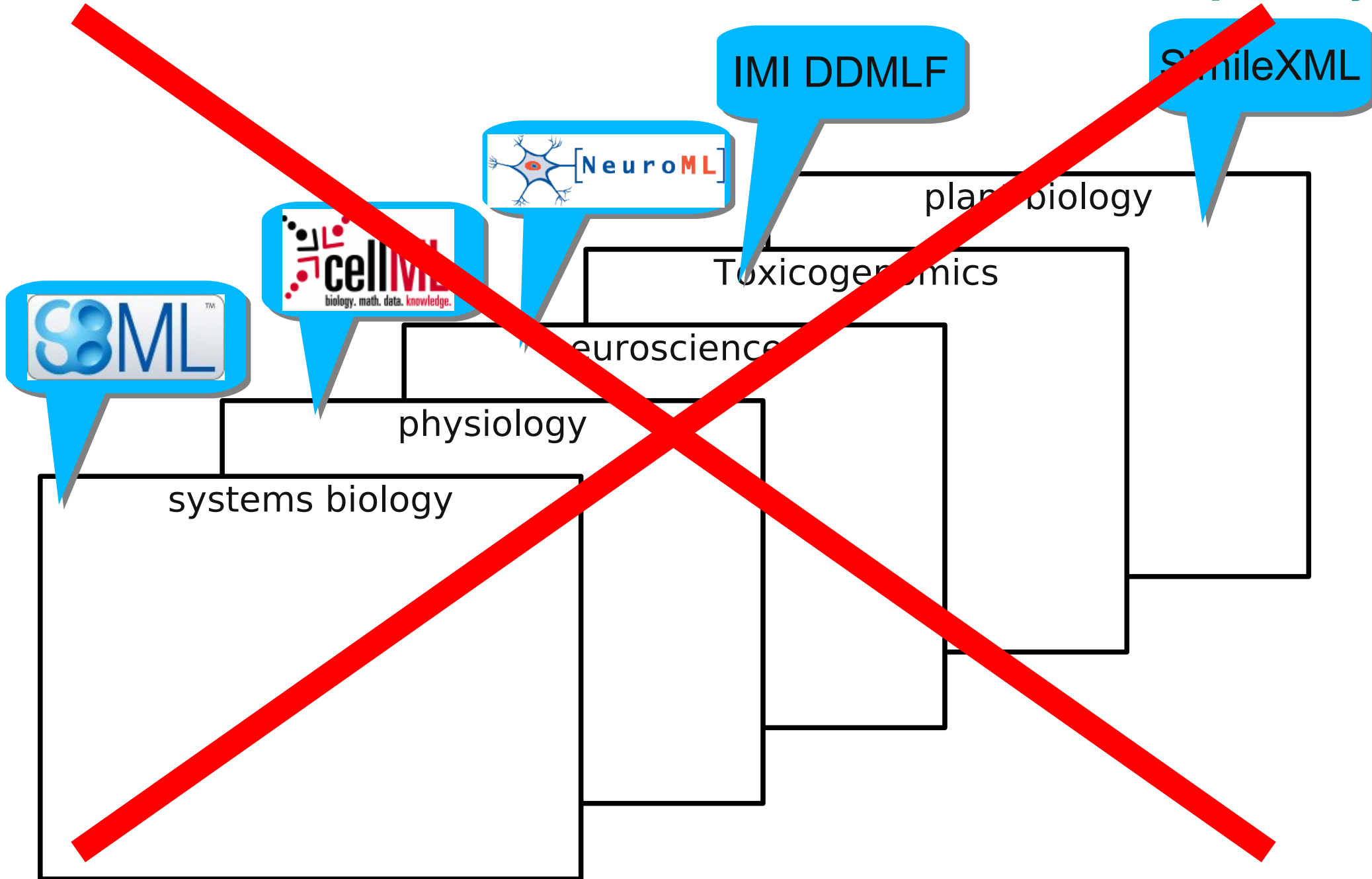
mechanical processes

- ChannelML: state-based representation of molecule behaviour (part of NeuroML)
- SynapseML: (part of NeuroML)
- MorphML: cable representation of neurons (part of NeuroML)
- SBML: description of biochemical processes (interoperate with NeuroML)
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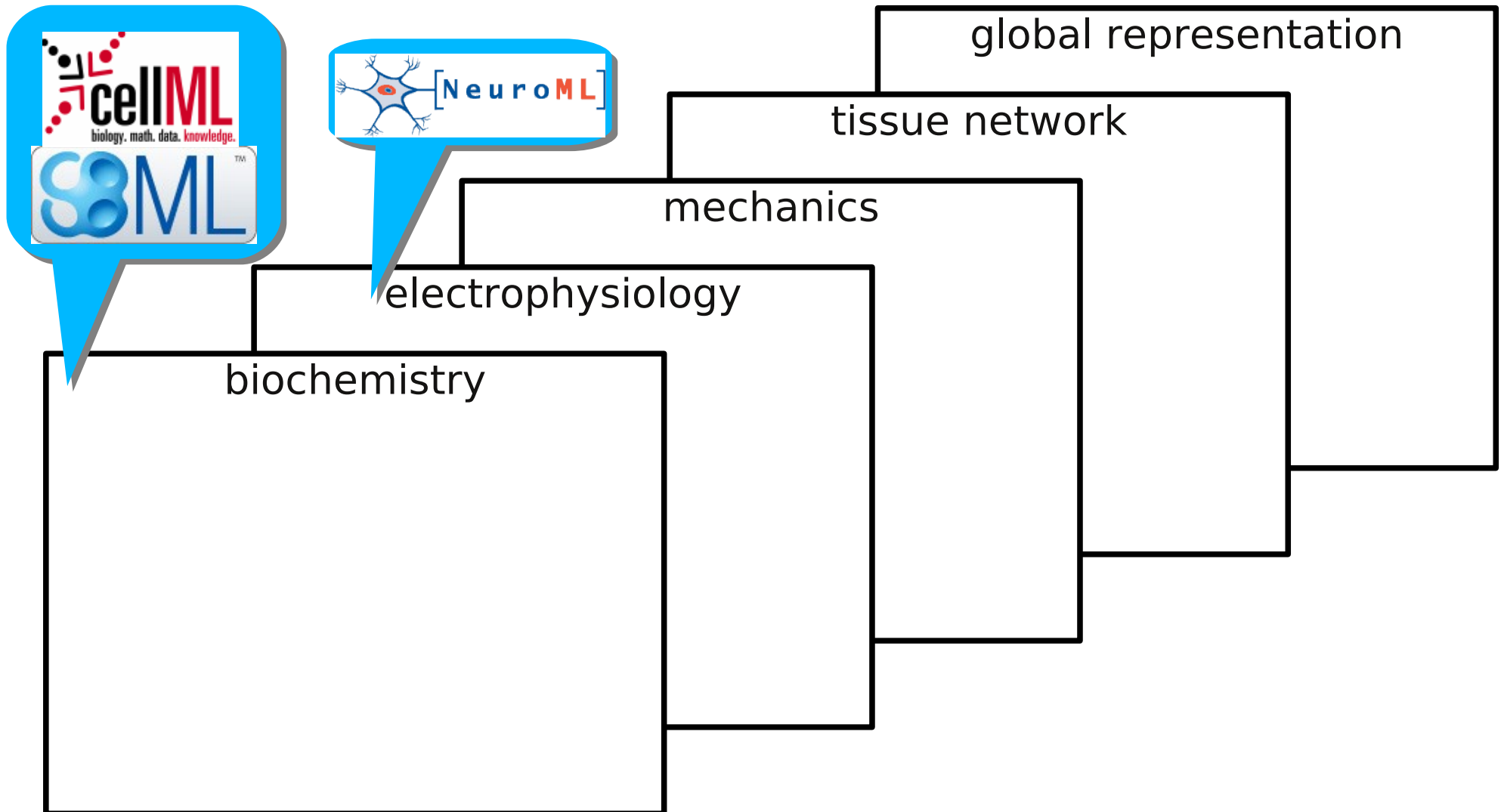
Networks of coupled cells

- ChannelML: state-based representation of molecule behaviour (part of NeuroML)
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- SBML: description of biochemical processes (interoperate with NeuroML)
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The issues to tackle are trans-disciplinary

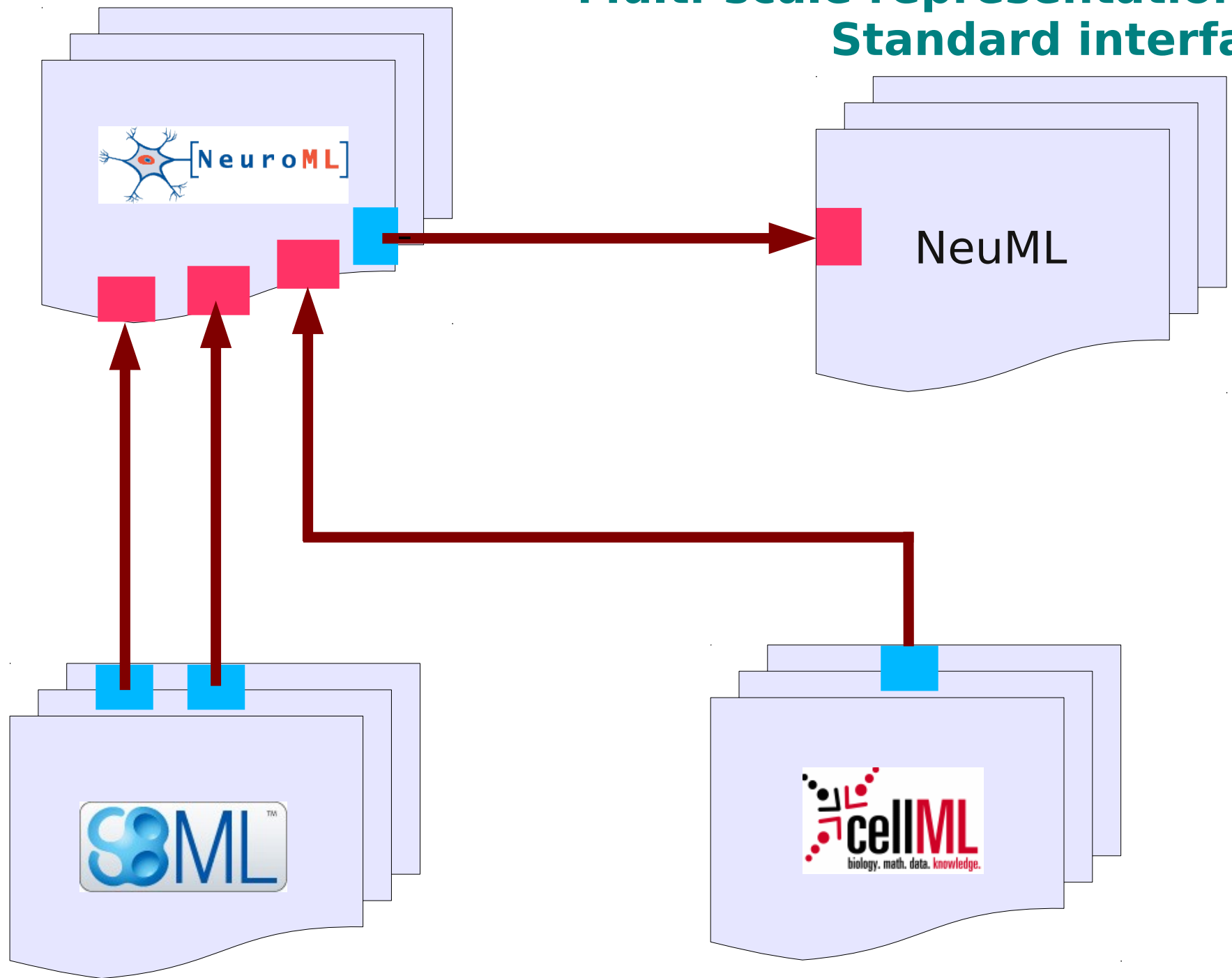


The issues to tackle are trans-disciplinary



Multi-scale representation (1)

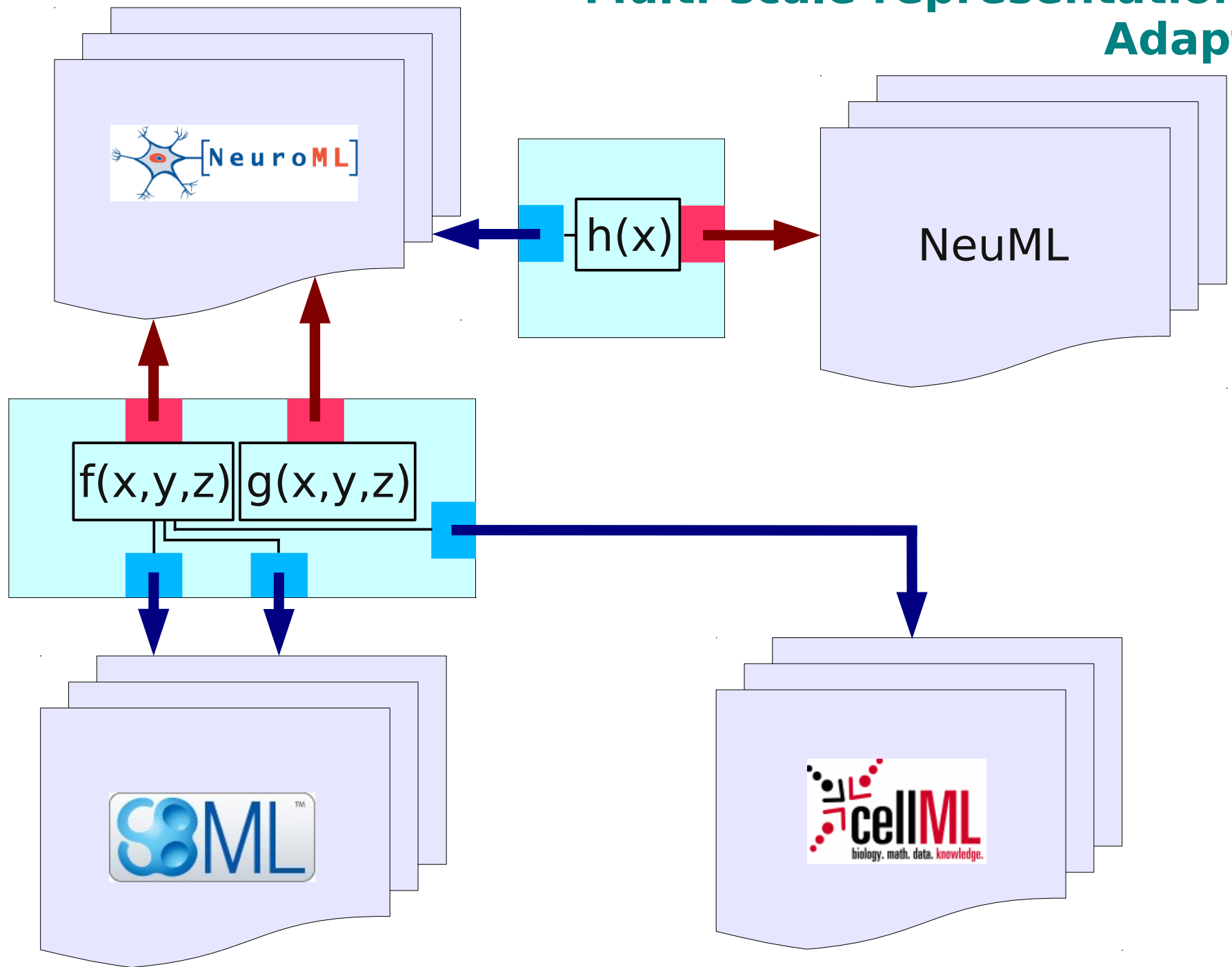
Standard interfaces



Requirement for multi-scale representation (1)

- Agreement on data-types and units
- The components contain the addressing
- The components with input terminals cannot be readily reused

Multi-scale representation (2) Adapters



Requirement for multi-scale representation (2)

- Able to connect any format as input and any format as output, as far as it is XML.
- Contains all the information necessary for building the model. The components do not know about it.
- The bridges cannot be reused. They are specific of a given set of components (because of the pointers).
- The components can be reused.

Threats to the whole enterprise

- Current efforts are entirely dependent on key people (SBML: Mike Hucka, CellML: Peter Hunter/Poul Nielsen, NeuroML: Padraig Gleeson, SBGN: NLN). Their disengagement means disaggregation.
- Current funding structure is fragile. Many different grants, sometimes only supporting meetings (SBGN), none of them infrastructure rolling funding, often tied to individuals.
- Current efforts are not immune against intellectual property claims that would destroy the community (e.g. Caltech and SBML)
- Existing standards are developed with very different approaches, quality checks, and are based on completely different assumptions (e.g. NeuroML assumes implicit knowledge)
- APIs needs industry-grade support, incompatible with standard academic usages and possibilities



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W3C By Region

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STANDARDS

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STANDARDS



Web Design and Applications



Web Architecture



Semantic Web



XML Technology



Web of Services



Web of Devices



Browsers and Authoring Tools

... or view all

WEB FOR ALL

W3C A to Z

Accessibility

Internationalization

Mobile Web

eGovernment

Developing Economies

▼ Interested in Next Steps for RDF? Come to the W3C Workshop!

20 January 2010 | [Archive](#)

W3C is organizing a [Workshop on the Next Steps for RDF](#) around June 2010; we will announce the exact dates and location as soon as possible. Since its publication in 2004, the [Resource Description Framework \(RDF\)](#) has become the core architectural block of the [Semantic Web](#). The standard is now widely deployed in terms of tools and applications. Due to this wide deployment, additional R&D activities, and the publication of newer standards (e.g., [SPARQL](#), [OWL](#), [POWDER](#), and [SKOS](#)), a number of issues regarding RDF have come to the fore. Workshop participants will discuss these issues and help determine whether it is time for a new version of RDF. W3C Membership is not required to participate in the Workshop, but each participant must be associated with an accepted position paper. The deadline for position papers is 29 March 2010; see the [Call for Participation](#) for more information. Updates (including the exact date and location of the Workshop) will be added to the Call for Participation and will be announced on the [Semantic Web Activity News Blog](#).

► W3C Seeks Feedback on Early Draft of SPARQL 1.1 Property Paths; Six SPARQL Drafts Updated

27 January 2010 | [Archive](#)

▼ UK Government Launches Open Data Site

25 January 2010 | [Archive](#)

The UK Government has unveiled its open data website, [data.gov.uk](#), developed with the help of Tim Berners-Lee (W3C Director) and John Sheridan (Linked Data Lead for data.gov.uk and co-Chair of the [W3C eGovernment Interest Group](#)). Like [data.gov](#) in the United States, the UK site reflects a growing awareness inside and outside of government that standards-based open data is a key enabler of government services and a building block for new information services across government and industry. Additionally, this new site showcases [Semantic Web](#) and [Linked Data](#) technologies. Learn more about [Publishing Open Government Data](#) and [eGovernment at W3C](#).

► Uniform Messaging Policy, Level One Draft Published

25 January 2010 | [Archive](#)

The World Wide Web Consortium (W3C) is an international community that develops [standards](#) to ensure the long-term growth of the Web. Join [groups](#), and participate in [W3C blogs](#) and other [discussion](#). We welcome your help to fulfill the [W3C mission](#): to lead the Web to its full potential.

JOBS

W3C is seeking a [Chief Executive Officer](#); learn more about [job opportunities](#).

W3C BLOG

SWSWiki

18 January 2010 by [Ivan Herman](#)

Take a few minutes to encourage web accessibility. You can make a difference.

6 January 2010 by [Shawn Henry](#)

Share Resources Supporting the Web Accessibility Business Case

14 December 2009 by [Shawn Henry](#)

VALIDATORS AND OTHER SOFTWARE

The W3C Community has created useful [Open Source Software](#). The most popular is the [W3C validator](#), which can help you with [HTML](#), [CSS](#), [mobileOK](#) content, and

STANDARDS

W3C develops technical specifications and guidelines through a process designed to maximize consensus about the content of a technical report, to ensure high technical and editorial quality, and to earn endorsement by W3C and the broader community.

W3C provides a number of **views** of its specifications, including:

- by [technology topic](#) (such as "all the HTML-related specifications")
- by [status](#) (this is an approximation of the "classic" TR view, with recent publications at the top and then all specifications grouped by status, from Recommendations to drafts)
- by [date](#) (most recent at the top)
- by [group](#) (who is working on the specification)

If you are learning about Web technology, you may wish to start with the introduction below, and follow links for more and more detail.



Web Design and Applications

Web Design and Applications involve the standards for building and Rendering Web pages, including HTML, CSS, SVG, Ajax, and other technologies for Web Applications ("WebApps"). This section also includes information on how make pages accessible to people with disabilities (WCAG), internationalized, and work on mobile devices.



Web Architecture

Web Architecture focuses on the foundation technologies and principles which sustain the Web, including URIs and HTTP.



Semantic Web

In addition to the classic "Web of documents" W3C is helping to build a technology stack to support a "Web of data", the sort of data you find in databases. The ultimate goal of the Web of data is to enable computers to do more useful work and to develop systems that can support trusted interactions over the network. The term "Semantic Web" refers to W3C's vision of the Web of linked data. Semantic Web technologies enable people to create data stores on the Web, build

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STANDARDS

Web Design and Applications

Web Architecture

Semantic Web

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Web of Services

Web of Devices

Browsers and Authoring Tools

All Standards and Drafts

About W3C Standards

WEB DESIGN AND APPLICATIONS

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Web Design and Applications involve the standards for building and Rendering Web pages, including HTML, CSS, SVG, Ajax, and other technologies for Web Applications ("WebApps"). This section also includes information on how make pages accessible to people with disabilities (WCAG), internationalized, and work on mobile devices.

HTML & CSS

HTML and CSS are the fundamental technologies for building Web pages: HTML (html and xhtml) for structure, CSS for style and layout. Find resources for good Web page design as well as helpful tools.

Scripting and Ajax

Standard APIs for client-side Web Application development include those for Geolocation, XMLHttpRequest (Ajax), and mobile widgets. W3C standards for document models (the "DOM") and technologies such as XBL allow content providers to create interactive documents through scripting.

Graphics

W3C is the home of the widely deployed PNG raster format, SVG vector format, and the Canvas API. WebCGM is a more specialized format used, for example, in the fields of automotive engineering, aeronautics.

Audio and Video

Some of the W3C formats that enable authoring audio and video presentations include HTML, SVG, and SMIL (for synchronization). W3C is also working on a timed text format for captioning and other applications.

Accessibility

W3C's Web Accessibility Initiative (WAI) has published Web Content Accessibility Guidelines (WCAG) to help authors create content that is accessible to people with disabilities. WAI-ARIA gives authors more tools to create accessible Web Applications by providing additional semantics about widgets and behaviors.

Internationalization

W3C has a mission to design technology that works across cultures and languages. W3C standards such as HTML and XML are built on Unicode, for instance. In addition, W3C has published guidance for authors related to language tags bi-directional (bidi) text, and more.

Mobile Web

W3C promotes "One Web" that is available on any device. W3C's Mobile Web Best Practices help authors understand how to

Privacy

The Web is a powerful tool for communications and transactions of all sorts. It is important to consider privacy and security

Math on the Web

Mathematics and formula are used on the Web for business reports, education materials and scientific research. W3C's

Poster presented
by Mike Hucka
at the 6th ICSB
Boston 2005

BioModels.net

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For computational modeling to become more widely used in biology, researchers must be able to exchange and share their results. The development and broad acceptance of common representation formats such as SBML is a crucial step in that direction, allowing researchers to exchange and build upon each other's work with greater ease and accuracy.

BioModels.net is another step: an international effort to

- 1) define agreed-upon standards for model curation
- 2) define agreed-upon vocabularies for annotating models, and
- 3) provide a free, centralized, publicly-accessible database of annotated models in SBML and other structured formats.

SBO

The **Systems Biology Ontologies (SBO)** are a set of interlinked controlled vocabularies tailored to the needs of the systems biology modeling community. The aim is to capture consensus definitions of commonly-used concepts and their relationships. Using SBO terms as a basis for annotating models and performing database searches (e.g., in BioModels Database) can lead to a greater degree of consistency, quality and interoperability.

BioModels Database

BioModels Database is a free, public repository of published quantitative models of biochemical and cellular systems. The models are curated to verify that they correspond to the reference publication and give the proper numerical results. Curators annotate the components of the models with terms from controlled vocabularies and links to external relevant data resources, allowing users to search accurately for the models they need and precisely identify their components.

BioModels.net

References

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Le Novère N, Finney A, Hucka M, Bhalla U, Campagne F, Collado-Vides J, Crampin EJ, Halstead M, Klipp E, Mendes P, Nielsen P, Sauro H, Shapiro B, Snoep JL, Spence HD, Wanner BL. Minimal Information Requested in the Annotation of biochemical Models (MIRIAM). (2005) *Nature Biotechnology*, in press.

MIRIAM

The **Minimum Information Requested in the Annotation of Models (MIRIAM)** is a proposed set of rules for curating quantitative models of biological systems. The rules define procedures for encoding and annotating models represented in machine-readable form. Their application will enable users to (a) have confidence that curated models are an accurate reflection of their associated reference description; (b) search collections of curated models with precision; (c) quickly identify the biological phenomena that a given curated model or model constituent represents; and (d) facilitate model reuse and composition into large subcellular models.

Acknowledgments

Funding for different aspects of the BioModels.net effort currently comes from the following organizations: the National Institute of General Medical Sciences (USA, grant GM070923-02S1), the International Joint Research Program of NEDO (Japan), DARPA BioComp Bio-SPICE (USA), the European Molecular Biology Laboratory (EU), the California Institute of Technology (USA), the Systems Biology Institute (Japan), and the University of Hertfordshire (UK).



[Home](#) [Database](#) [MIRIAM](#) [SBO](#) [MIASE](#) [SED-ML](#) [Qualifiers](#) [Events](#) [Contact](#)

BioModels.net

The Next Step After Standard Formats

For computational modeling to become more widely used in biological research, researchers must be able to exchange and share their results. The development and broad acceptance of common model representation formats such as [SBML](#) is a crucial step in that direction, allowing researchers to exchange and build upon each other's work with greater ease and accuracy.

The BioModels.net project is another step: an international effort to:

1. define agreed-upon standards for model curation
2. define agreed-upon vocabularies for annotating models with connections to biological data resources
3. provide a free, centralized, publicly-accessible database of annotated, computational models in SBML and other structured formats

Helping to Define Community Standards

To facilitate assembling useful collections of quantitative models of biological phenomena, it is crucial to establish standards for the vocabularies used in model annotations as well as criteria for minimum quality levels of those models. The BioModels.net project aims to bring together a community of interested researchers to address these issues. We are working towards defining these standards through white papers and process definitions. All of the products of our efforts are open and freely available through this site.

Standards and Processes Developed Hand-in-Hand with a New Database

The database component of BioModels.net is especially designed for working with *annotated* computational models: each model is carefully reviewed and augmented by human annotators on the BioModels.net team to add metadata linking the model elements to other biological databases and resources. The [BioModels Database](#) at the [EBI](#) system goes far beyond other collections of models by being a *true* database, featuring browsing, cross-referencing, searching, and facilities for visualization, exporting models in different formats, and remote API access.

Projects

The projects we are currently coordinating are:

- [BioModels Database](#)
- [MIRIAM](#) and the associated [set of qualifiers](#) and [MIRIAM Resources](#)
- [SBO](#)

A first step: common meetings

- January 2008: SBGN hackathon; BioModels DB; MIRIAM; SBO
- March 2009: SBML hackathon; BioModels DB; MIRIAM; SBO
- April 2009: CellML; SED-ML; SBGN hackathon
- May 2010: SBML hackathon; BioModels DB; MIRIAM; SBO; SED-ML
- October 2010: 1st **COMBINE** MEETING with SBML; SBGN; ??
- From now on, two grouped annual meetings
 - **COMBINE** forum: presentation of support, discussion about future developments and collaboration etc.
 - **HARMONY** hackathon: developing support, writing specifications, tinkering with interoperability etc.

Requirements for a global coordination structure

- What?
 - Set of interoperable description languages
 - Cover all aspects of modelling and simulation
 - Cover all type of descriptions / views of the real
 - Role of community-maintained ontologies.
- How?
 - Independance towards Institution, funders and individuals
 - ?
- Who?
 - Community developing their standards: Systems Biology, Physiology, Neuroscience (INCF), Drug discovery
 - Other players in knowledge-representation (W3C, ...)
 - Academic and corporate users: Modeling platforms (Matworks ...), Pharma (Pistoia alliance) ...

THE END

THE ~~X~~ END

THE BEGINNING