EMBL-EBI

Sharing enriched computational models, a cornerstone for Integrative Biology

Nicolas Le Novère, EMBL-EBI

Computational Neurobiology

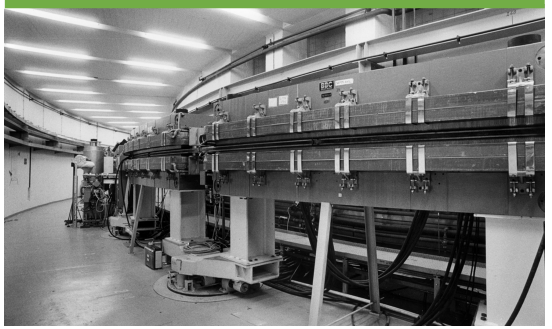
European Molecular Biology Laboratory

- EMBL is a basic research institute funded by public research monies from 20 member states and numerous external funding sources
- 1530 staffs, over 60 nationalities

Heidelberg

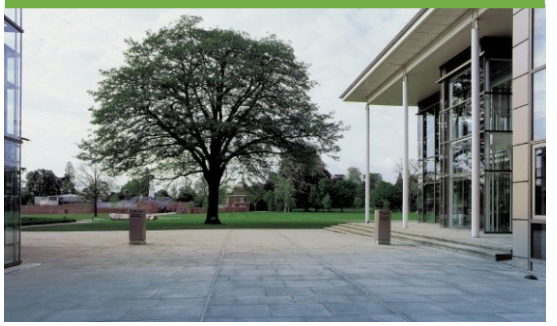
Basic research in molecular biology
Administration
EMBO

Hamburg



Structural biology

Hinxton



Bioinformatics

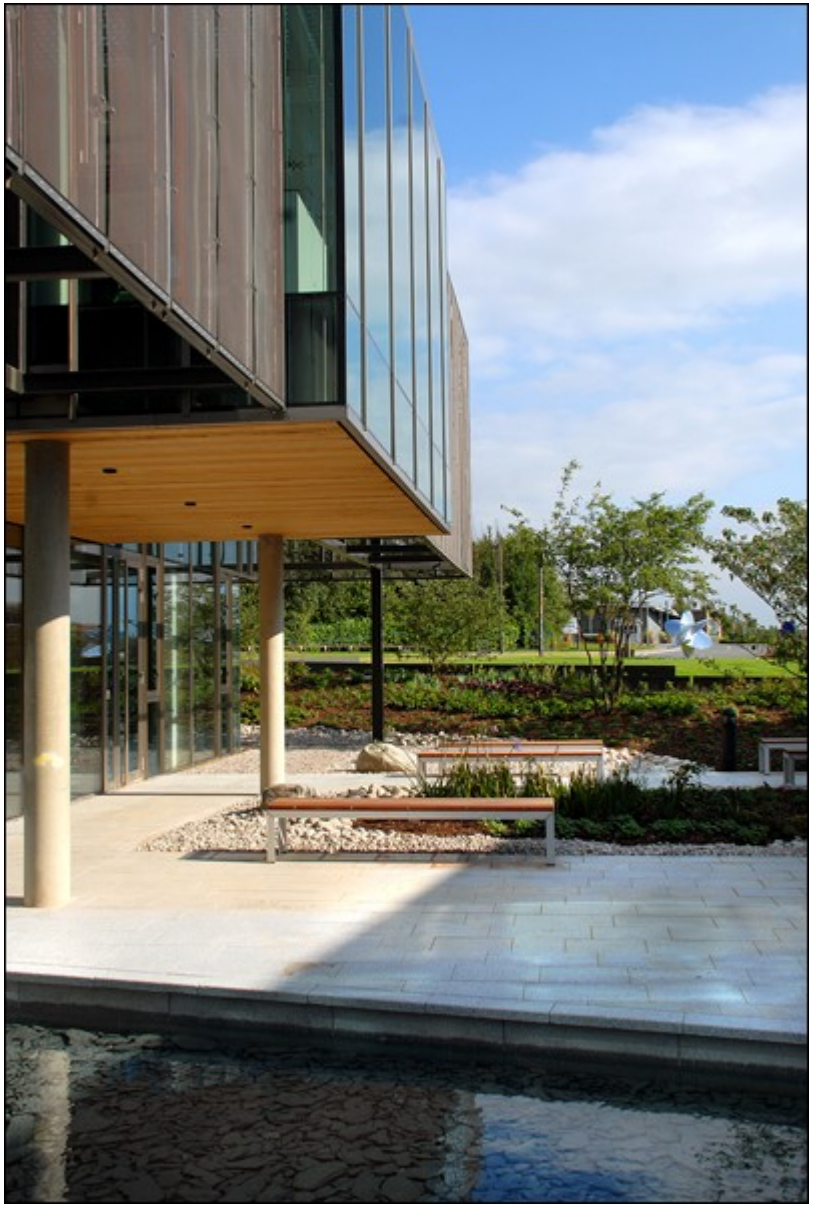
Grenoble

Structural biology

Monterotondo

Mouse biology

EMBL-European Bioinformatics Institute



Provision of services, research and training in Bioinformatics

From the molecule to the cell, and the genome to the individual

Based on the Wellcome-Trust Genome Campus near Cambridge, UK

ENA European Nucleotide Archive
Ensembl
UniProt
EMBL-EBI PDBe PROTEIN DATA BANK EUROPE
European Genome-phenome Archive
ArrayExpress
IntAct
PRIDE
BioModels
GO
ChEBI
InterPro
IntEnz
S80

What happened to biology at the end of XXth century?

Annu. Rev. Genomics Hum. Genet. 2001. 2:343–72

A New Approach to Decoding Life:
Systems Biology

Trey Ideker[1,2], Timothy Galitski[1], and Leroy Hood[1,2,3,4,5]
Institute for Systems Biology[1], Seattle, Washington 98105; Departments of

Federal Ministry
of Education
and Research

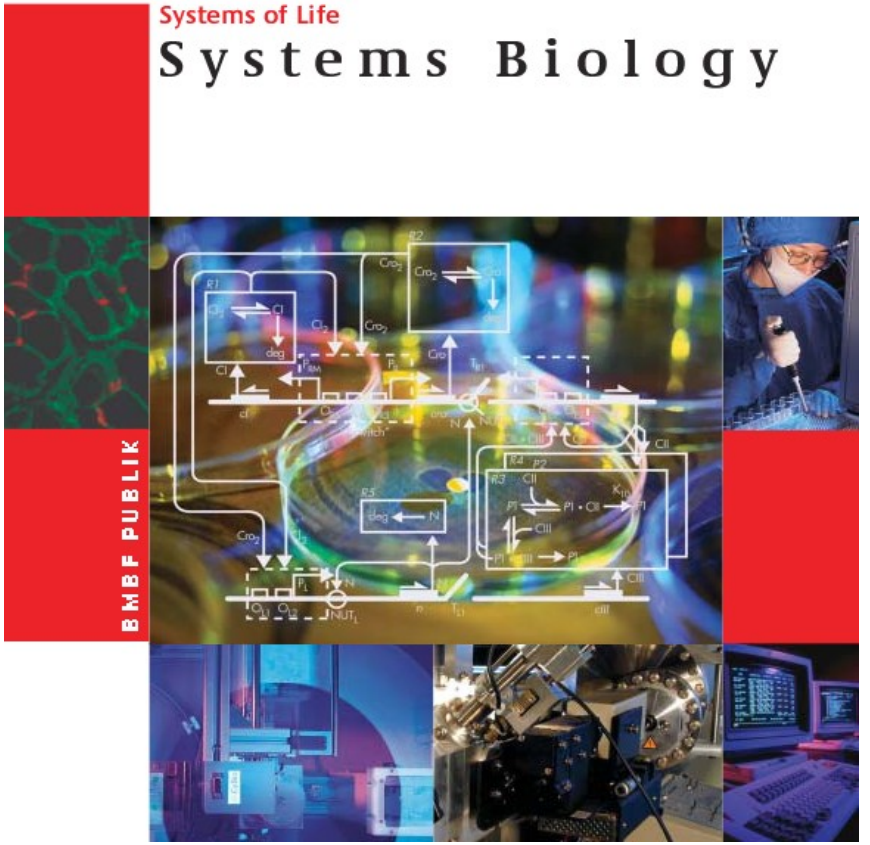
Basic science

REVIEW

Systems Biology: A Brief Overview

Hiroaki Kitano

1 MARCH 2002 VOL 295 SCIENCE www.sciencemag.org



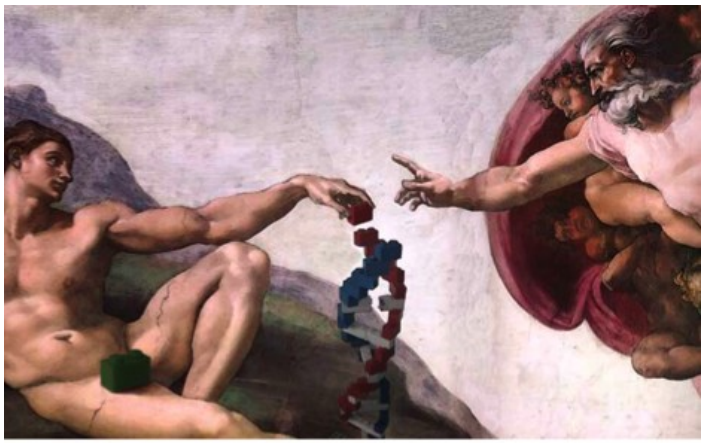
What happened to biology at the end of XXth century?

RESEARCH ARTICLE

Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome

Daniel G. Gibson,[1] John I. Glass,[1] Carole Lartigue,[1] Vladimir N. Noskov,[1] Ray-Yuan Chuang,[1] Mikkel A. Algire,[1] Gwynedd A. Benders,[2] Michael G. Montague,[1] Li Ma,[1] Monzia M. Moodie,[1] Chuck Merryman,[1] Sanjay Vashee,[1] Radha Krishnakumar,[1] Nacyra Assad-Garcia,[1] Cynthia Andrews-Pfannkoch,[1] Evgeniya A. Denisova,[1] Lei Young,[1] Zhi-Qing Qi,[1] Thomas H. Segall-Shapiro,[1] Christopher H. Calvey,[1] Prashanth P. Parmar,[1] Clyde A. Hutchison III,[2] Hamilton O. Smith,[2] J. Craig Venter[1,2]*

2 JULY 2010 VOL 329 SCIENCE www.sciencemag.org



EXTREME GENETIC ENGINEERING

An Introduction to Synthetic Biology

Induction of Pluripotent Stem Cells from Mouse Embryonic and Adult Fibroblast Cultures by Defined Factors

Cell

Kazutoshi Takahashi[1] and Shinya Yamanaka[1,2,*]
[1] Department of Stem Cell Biology, Institute for Frontier Medical Sciences, Kyoto University, Kyoto 606-8507, Japan
[2] CREST, Japan Science and Technology Agency, Kawaguchi 332-0012, Japan
*Contact: yamanaka@frontier.kyoto-u.ac.jp
DOI 10.1016/j.cell.2006.07.024 Cell *126*, 663–676, August 25, 2006 ©2006 Elsevier Inc. 663

Technology

January 2007

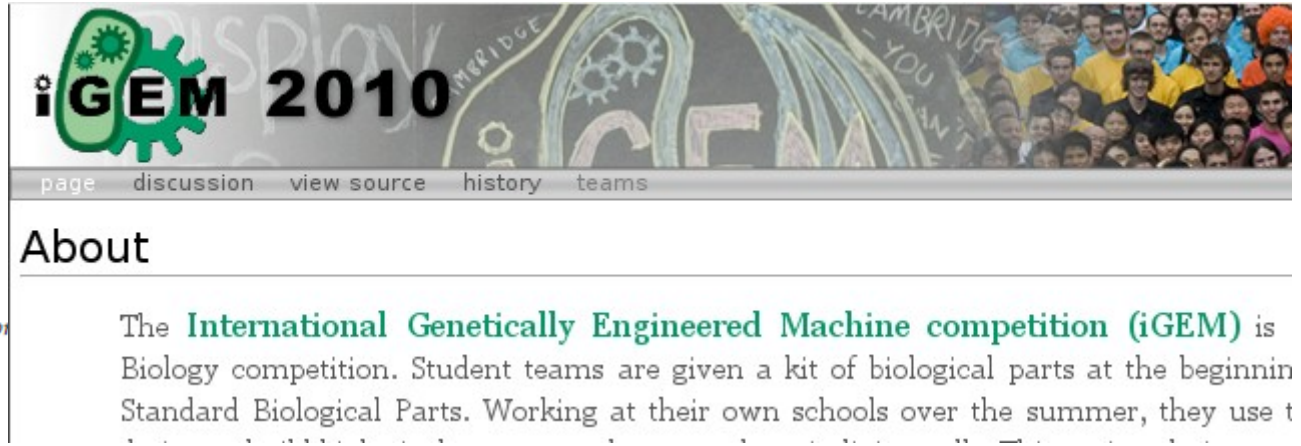
etc group

A synthetic oscillatory network of transcriptional regulators

Michael B. Elowitz & Stanislas Leibler

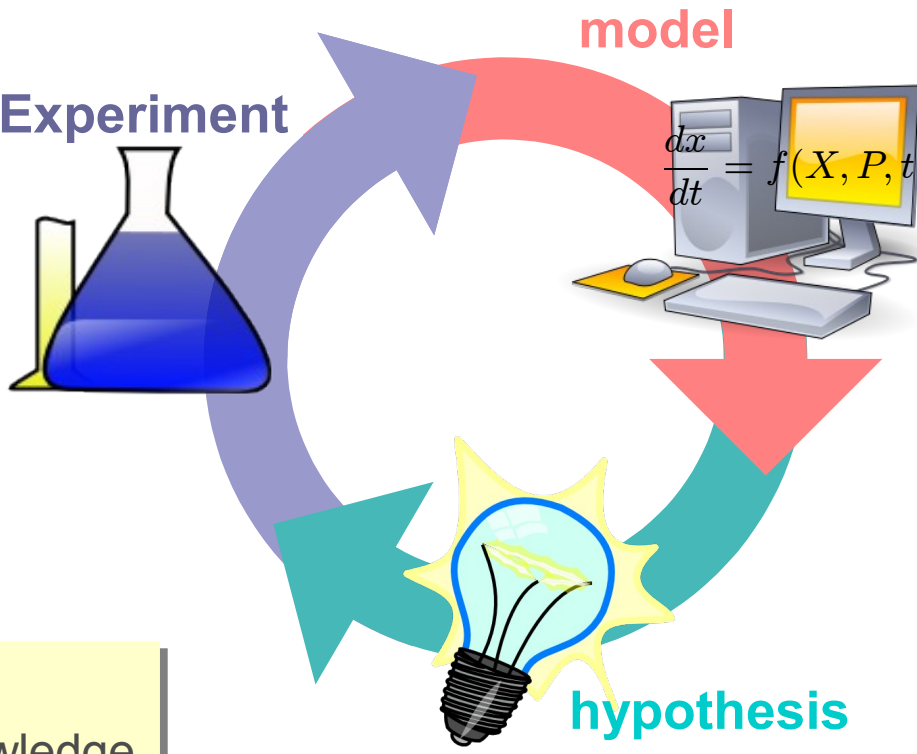
Departments of Molecular Biology and Physics, Princeton University, Princeton New Jersey 08544, USA

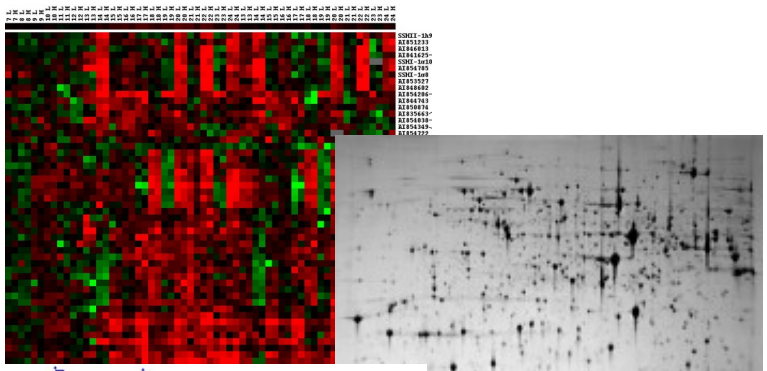
NATURE | VOL 403 | 20 JANUARY 2000 | www.nature.com

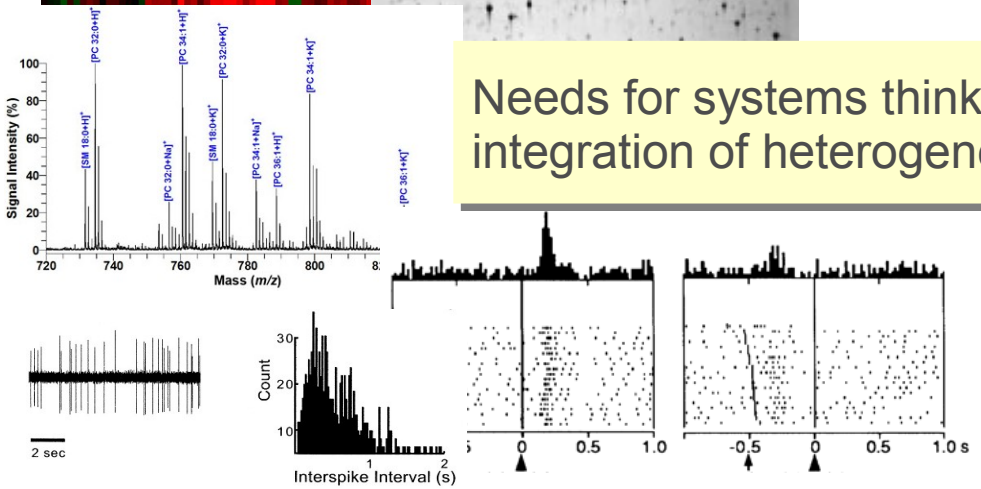


Consequences of this revolution on our activity

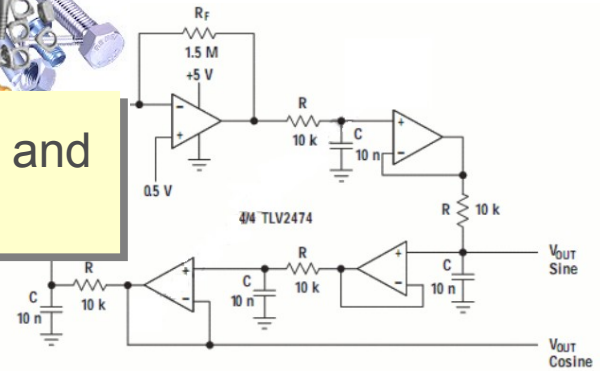
Needs for interplay between models and reality tests







Needs for systems thinking and integration of heterogeneous knowledge

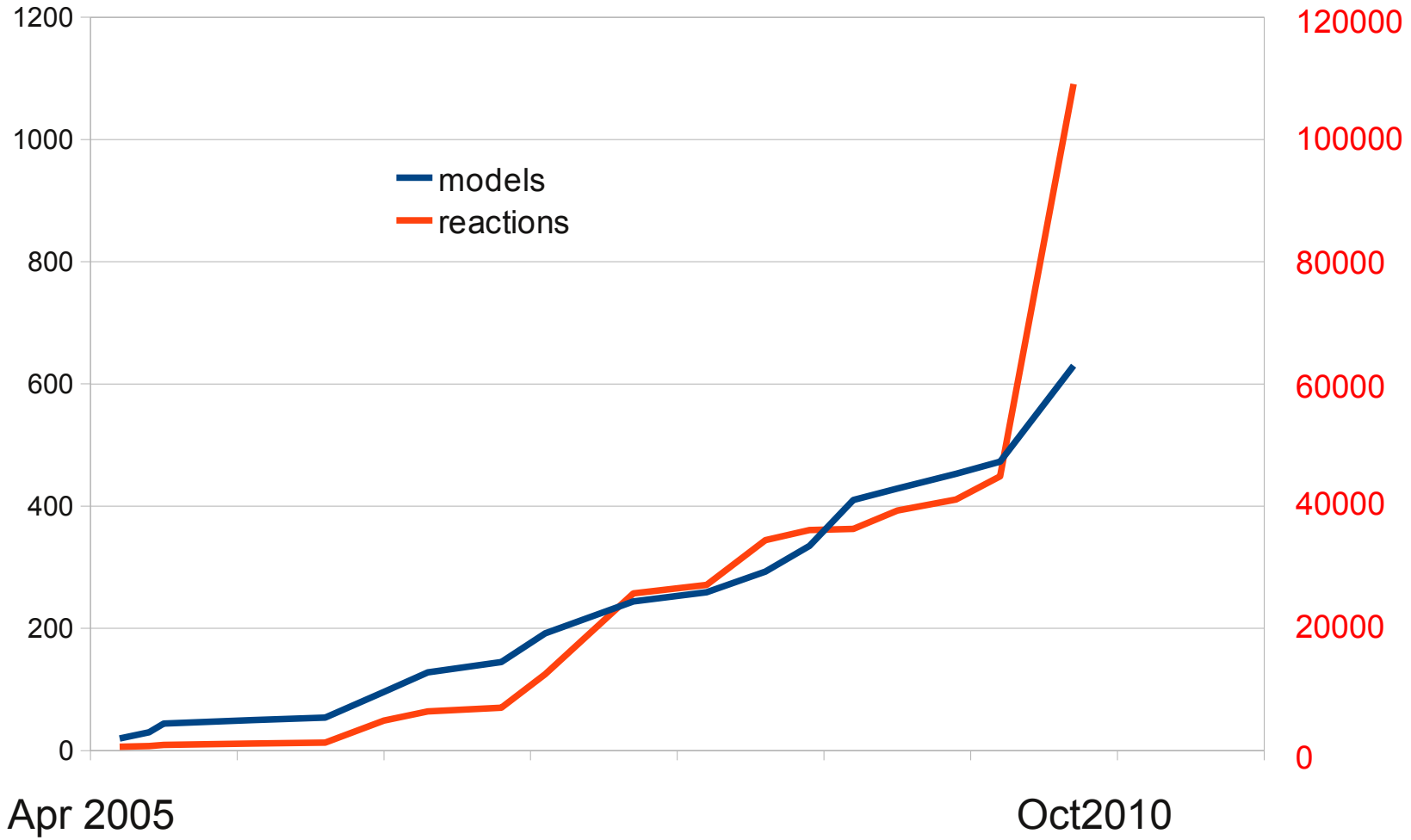


Needs for cooperation and standardisation

Computational modelling for biology and medicine left the niches and is now mainstream

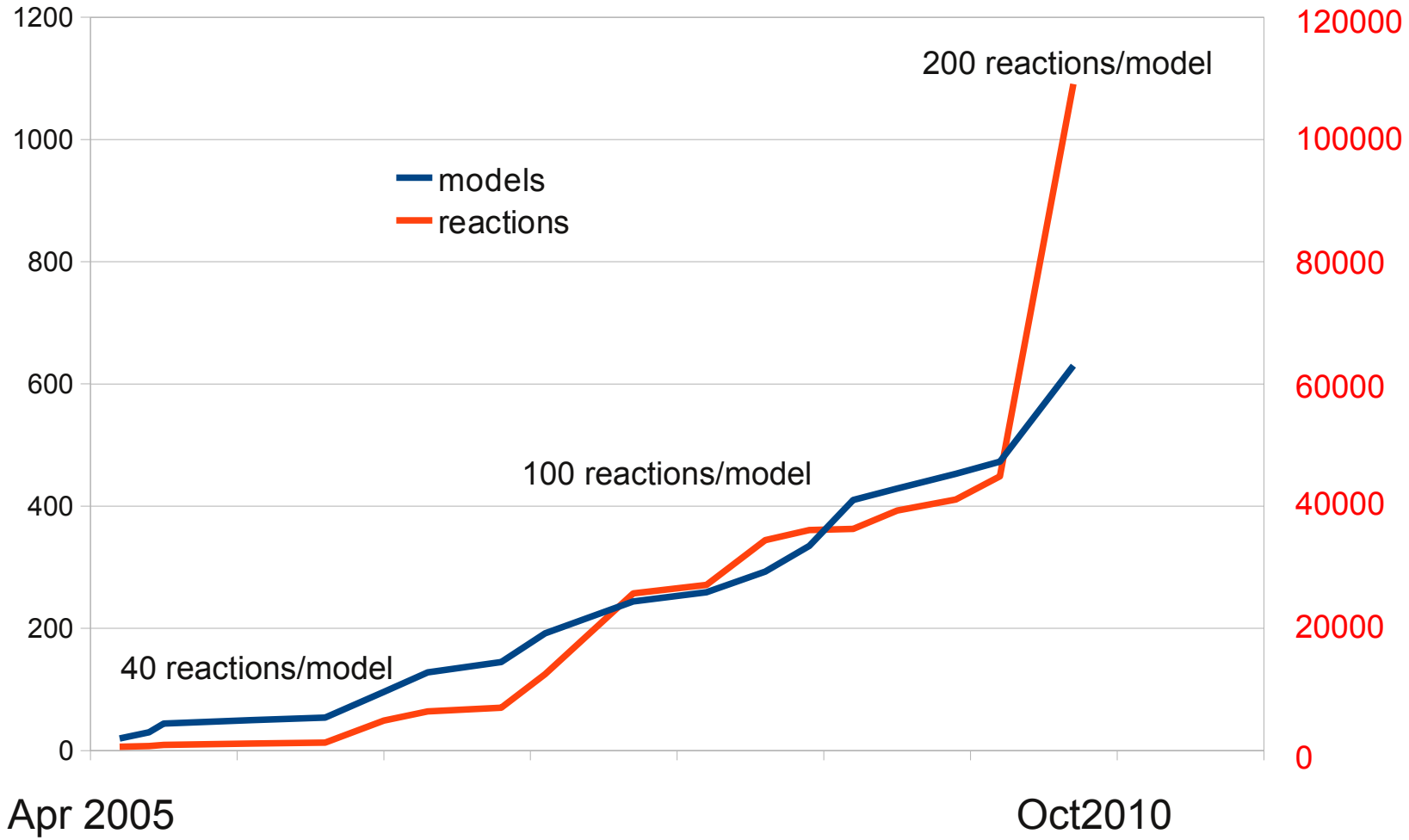
- Metabolic networks (Herrgård et al. A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. ***Nat Biotechnol*** 2008)
- Signalling pathways (Bray et al. Receptor clustering as a cellular mechanism to control sensitivity. ***Nature*** 1998; Bhalla ad Iyengar. Emergent properties of signaling pathways. ***Science*** 1998, Schoeberl et al. Computational modeling of the dynamics of the MAP kinase cascade activated by surface and internalized EGF receptors. ***Nat Biotechnol*** 2002; Nelson et al. Oscillations in NF-kB Signaling Control the Dynamics of Gene Expression. ***Science*** 2004; Ashall et al. Pulsatile Stimulation Determines Timing and Specificity of NF-kappa B-Dependent Transcription. ***Science*** 2009)
- Gene regulatory networks (McAdams and Shapiro. Circuit simulation of genetic networks. ***Science*** 1995; Yue et al. Genomic cis-regulatory logic: Experimental and computational analysis of a sea urchin gene. ***Science*** 1998; Von Dassow et al. The segment polarity network is a robust developmental module. ***Nature*** 2000)
- Pharmacokinetic/dynamic models (Labrijn et al. Therapeutic IgG4 antibodies engage in Fab-arm exchange with endogenous human IgG4 in vivo. ***Nat Biotechnol*** 2009)
- Physiological models (Noble. Modeling the heart from genes to cells to the whole organ. ***Science*** 2002; Izhikevich and Edelman. Large-scale model of mammalian thalamocortical systems. ***PNAS*** 2008)
- Infectious diseases (Perelson et al. HIV-1 dynamics in vivo: Virion clearance rate, infected cell life-span, and viral generation time. ***Science*** 1996; Neumann et al. Hepatitis C viral dynamics in vivo and the antiviral efficacy of interferon-alpha therapy. ***Science*** 1998)

Computational models on the rise



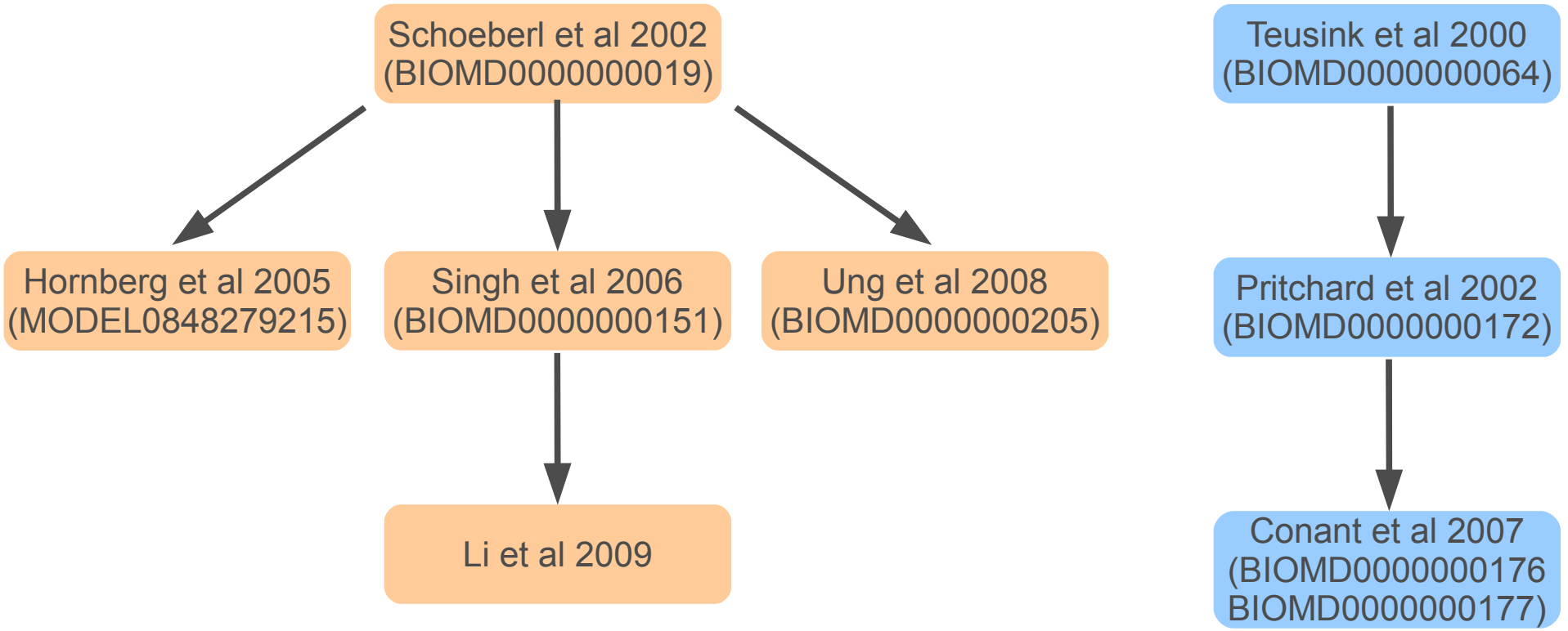
Growth of BioModels Database between its creation and release 18

Computational models on the rise



Growth of BioModels Database between its creation and release 18

Direct model re-use: EGFR signalling and glycolysis



Models at the core of integrative systems bio/physio/neuro/biology

- As any kind of output from scientific research, models must be available to the scientific community: Results based on a model that is not distributed cannot be verified and falsified. This is not valid and useful science
- Computational models must be exchanged:
  computer storable and readable
- Computational models must be related to relevant experimental datasets:
  expressive relationships and robust links
- Computational models must be amenable to many different analyses:
  standard API
- Computational models must allow modification, split, merge:
  Encoded according a suitable design

Models at the core of integrative systems bio/physio/neuro/biology

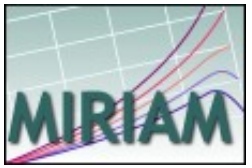
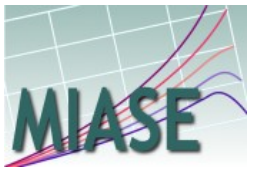
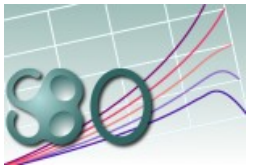
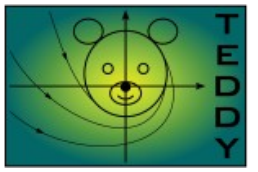
- As any kind of output from scientific research, models must be available to the scientific community: Results based on a model that is not distributed cannot be verified and falsified. This is not valid and useful science
- Computational models must be exchanged:
  computer storable and readable
- Computational models must be related to relevant experimental datasets:
  expressive relationships and robust links
- Computational models must be amenable to many different analyses:
  standard API
- Computational models must allow modification, split, merge:
  Encoded according a suitable design

➔ Standardisation is unavoidable!

A “complete” (?) mosaic of standards for Computational Systems Biology models

	Models	Simulation	Results
Minimal requirements	MIRIAM	MIASE	
Data-models	SBML, SBGN	SED ML	SBRML
Ontologies	SBO	KISAO	TEDDY

Model description

	Models	Simulation	Results
Minimal requirements			
Data-mode			SBRML
Ontologies			

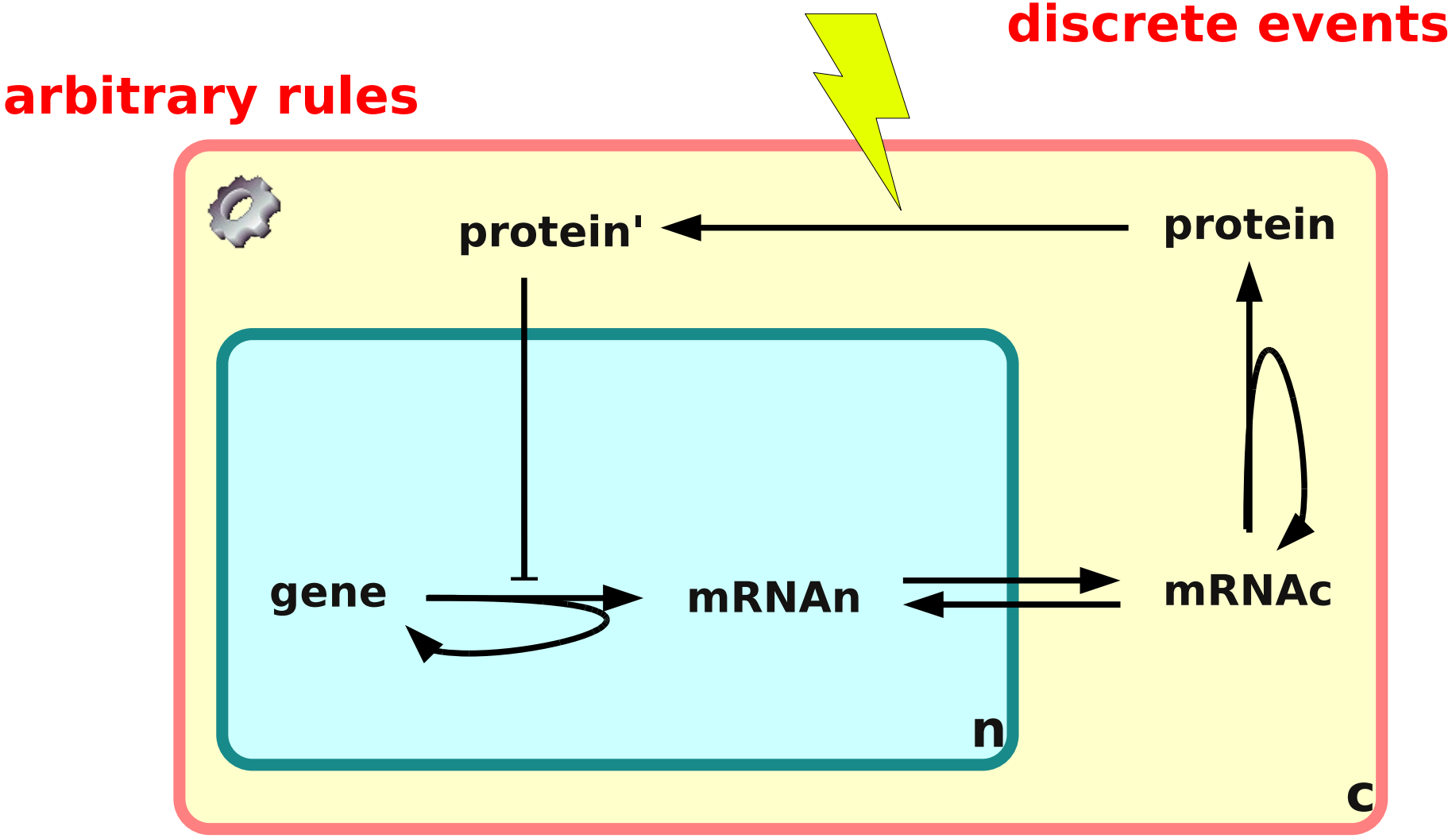
Hucka M., Bolouri H., Finney A., Sauro H.M., Doyle J.C., Kitano H.Arkin A.P., Bornstein B.J., Bray D., Cornish-Bowden A., Cuellar A.A., Dronov S., Ginkel M., Gor V., Goryanin I.I., Hedley W.J., Hodgman T.C., Hunter P.J., Juty N.S., Kasberger J.L., Kremling A., Kummer U., Le Novère N., Loew L.M., Lucio D., Mendes P., Mjolsness E.D., Nakayama Y., Nelson M.R., Nielsen P.F., Sakurada T., Schaff J.C., Shapiro B.E., Shimizu T.S., Spence H.D., Stelling J., Takahashi K., Tomita M., Wagner J., Wang J.et al (2003). The Systems Biology Markup Language (SBML): A Medium for Representation and Exchange of Biochemical Network Models. *Bioinformatics*, 19: 524-531.

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 (only 3 of the 7 SBML founding software are still maintained today

- Development philosophy: Start small, get good support, extend.
- SBML itself re-uses other standards: XML, MathML, XHTML, RDF, existing ontologies.
- It is supported by a community large, diverse, active and **evolving.**

What can we encode in SBML (core)?



Global structure of a SBML file

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml level="3" version="1"·
      xmlns="http://www.sbml.org/sbml/level3/version1/core">
  <model>
    <listOfFunctionDefinitions> <!-- --> </listOfFunctionDefinitions>
    <listOfUnitDefinitions> <!-- --> </listOfUnitDefinitions>
    <listOfCompartments> <!-- --> </listOfCompartments>
    <listOfSpecies> <!-- --> </listOfSpecies>
    <listOfParameters> <!-- --> </listOfParameters>
    <listOfInitialAssignments> <!-- --> </listOfInitialAssignments>
    <listOfRules> <!-- --> </listOfRules>
    <listOfConstraints> <!-- --> </listOfConstraints>
    <listOfReactions> <!-- --> </listOfReactions>
    <listOfEvents> <!-- --> </listOfEvents>
  </model>
</sbml>
```

Global structure of a SBML file

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml level="3" version="1"·
      xmlns="http://www.sbml.org/sbml/level3/version1/core">
  <model>
    <listOfFunctionDefinitions> <!-- --> </listOfFunctionDefinitions>
    <listOfUnitDefinitions> <!-- --> </listOfUnitDefinitions>
    <listOfCompartments> <!-- --> </listOfCompartments>
    <listOfSpecies> <!-- --> </listOfSpecies>
    <listOfParameters> <!-- --> </listOfParameters>
    <listOfInitialAssignments> <!-- --> </listOfInitialAssignments>
    <listOfRules> <!-- --> </listOfRules>
    <listOfConstraints> <!-- --> </listOfConstraints>
    <listOfReactions> <!-- --> </listOfReactions>
    <listOfEvents> <!-- --> </listOfEvents>
  </model>
</sbml>
```

variables

relationships

A very simple SBML file

```
<?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>
```

A very simple SBML file

```
<?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>
```

A very simple SBML file

```
<?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>
```

A very simple SBML file

```
<?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>
```

A very simple SBML file

```
<?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>
```

A very simple SBML file

```
<?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>
```

MathML

A more realistic example ...

```
<species·
    id="A"·
    name="a-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>
```

biological semantics

XHTML

RDF

SBML is not limited to biochemistry!

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

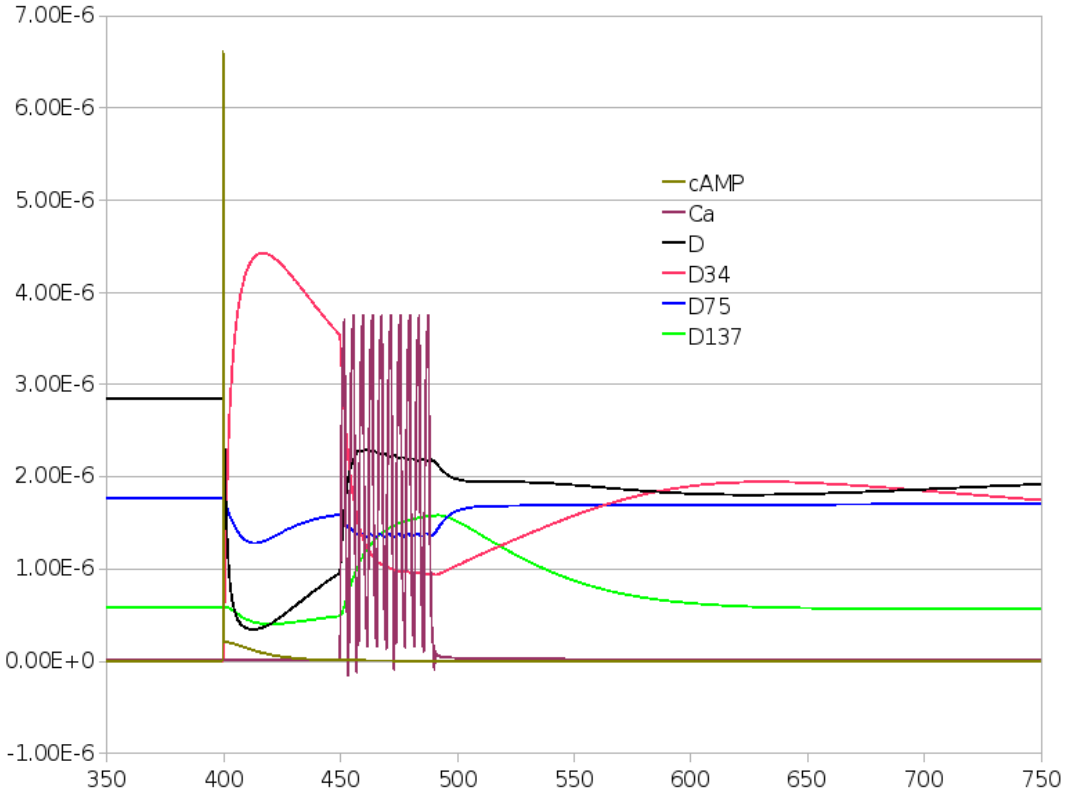
Events can describe any discontinuous change, e.g. neurotransmitter release or repolarisation;

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

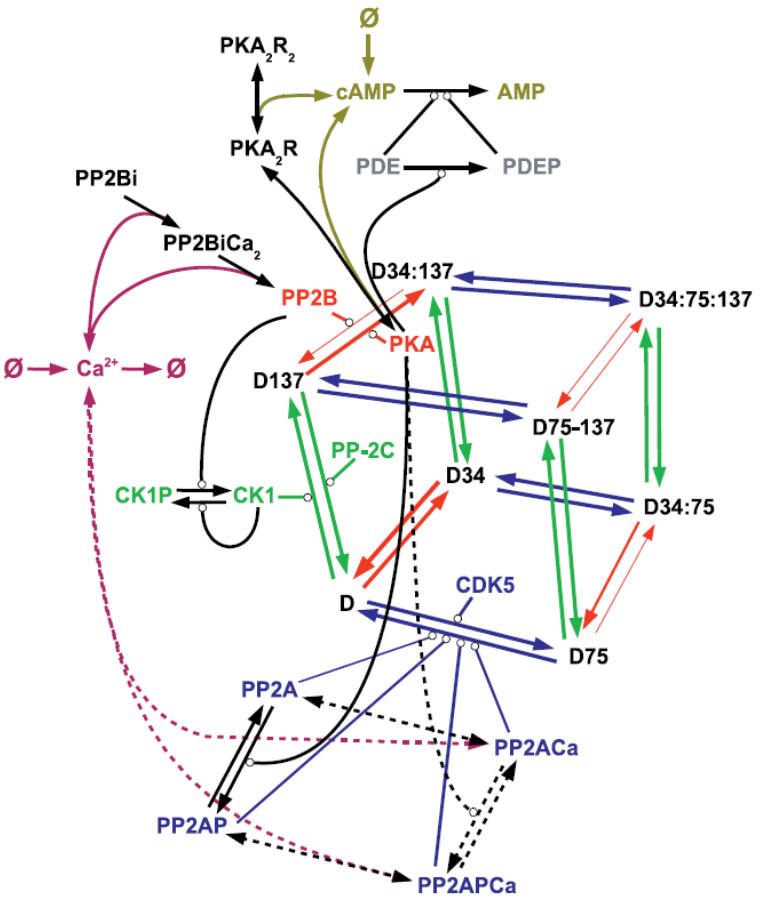
➔ SBML is about process descriptions

Model of signalling pathways



Fernandez et al. DARPP-32 is a robust integrator of dopamine and glutamate signals
PLoS Comput Biol (2006) 2: e176.

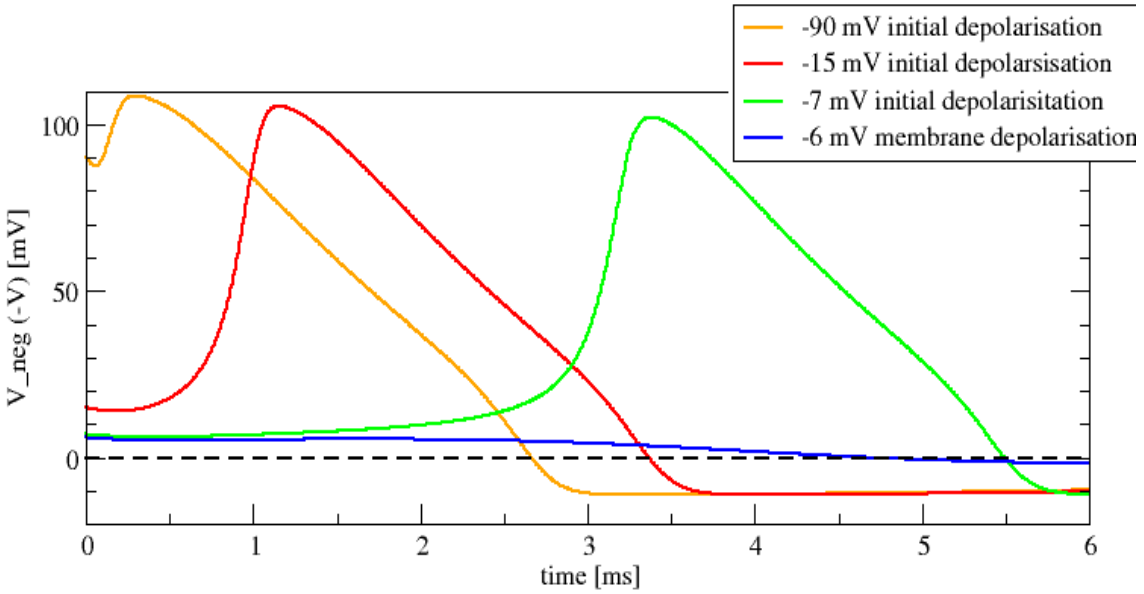
BIOMD0000000153



reaction:

$$v_{on1} = k_{on1} \times [D] \times [CDK5] \times Vol$$

Conductance-based model



Hodgkin AL, Huxley AF.
A quantitative description of membrane current and its application to conduction and excitation in nerve.
J Physiol (1952) 117:500-544.

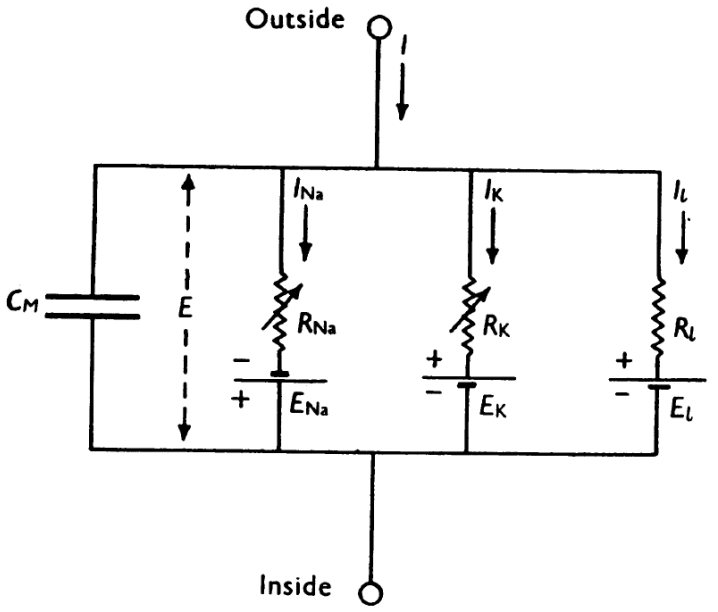
BIOMD0000000020

rate rule:

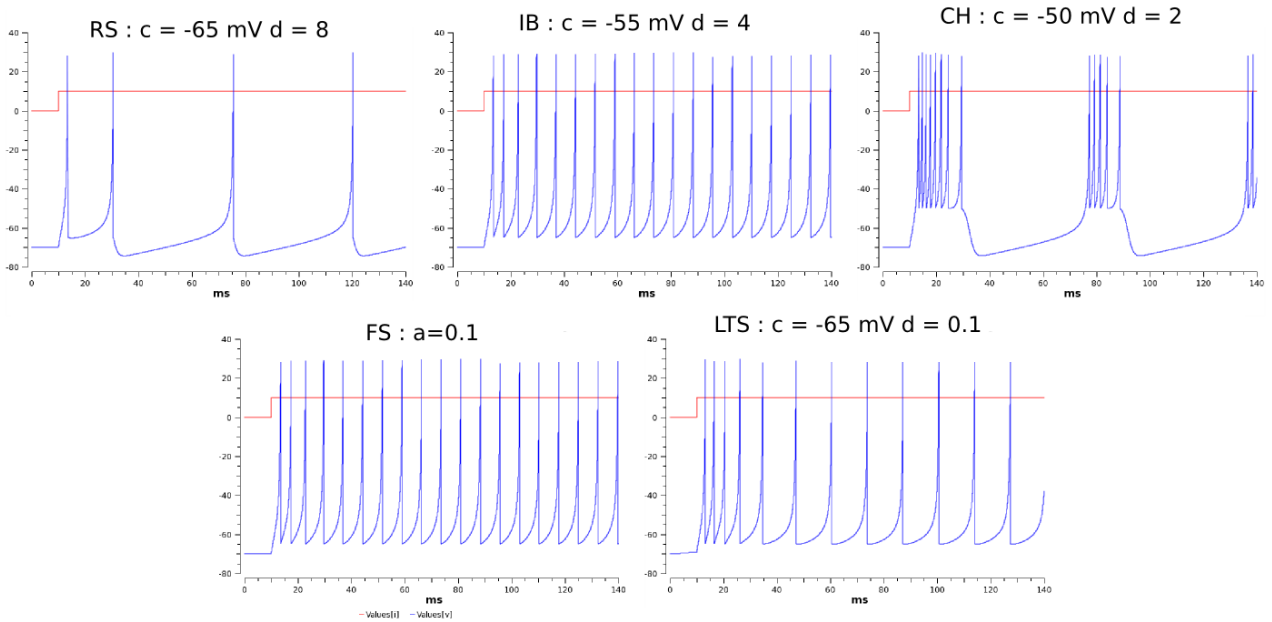
$$\frac{dv}{dt} = \frac{I - (i_{Na} + i_K + i_L)}{C_m}$$

assignment rule:

$$i_{Na} = g_{Na} \times m^3 \times h \times (V - E_{Na})$$



Single-compartment neurons



Izhikevich EM. Simple model of spiking neurons. *IEEE Trans Neural Netw* (2003) 14(6):1569-1572.

BIOMD0000000127

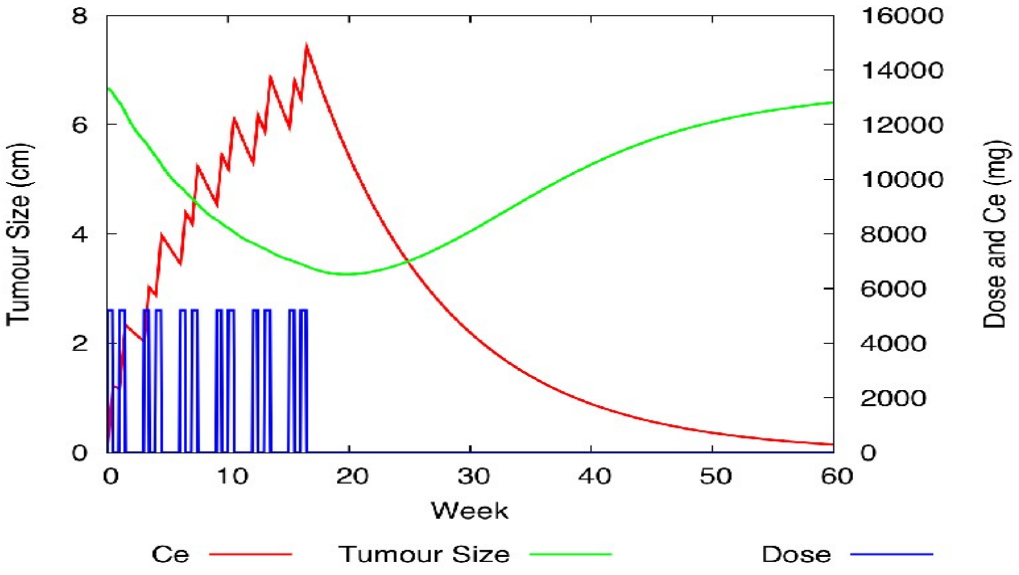
rate rule:

$$\frac{dv}{dt} = 0.04^2 + 5 \times V + 140 - U + i$$

event:

$$\text{when } v > V_{thresh} \begin{cases} v = c \\ U = U + d \end{cases}$$

Pharmacokinetic/dynamic 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.

BIOMD0000000234

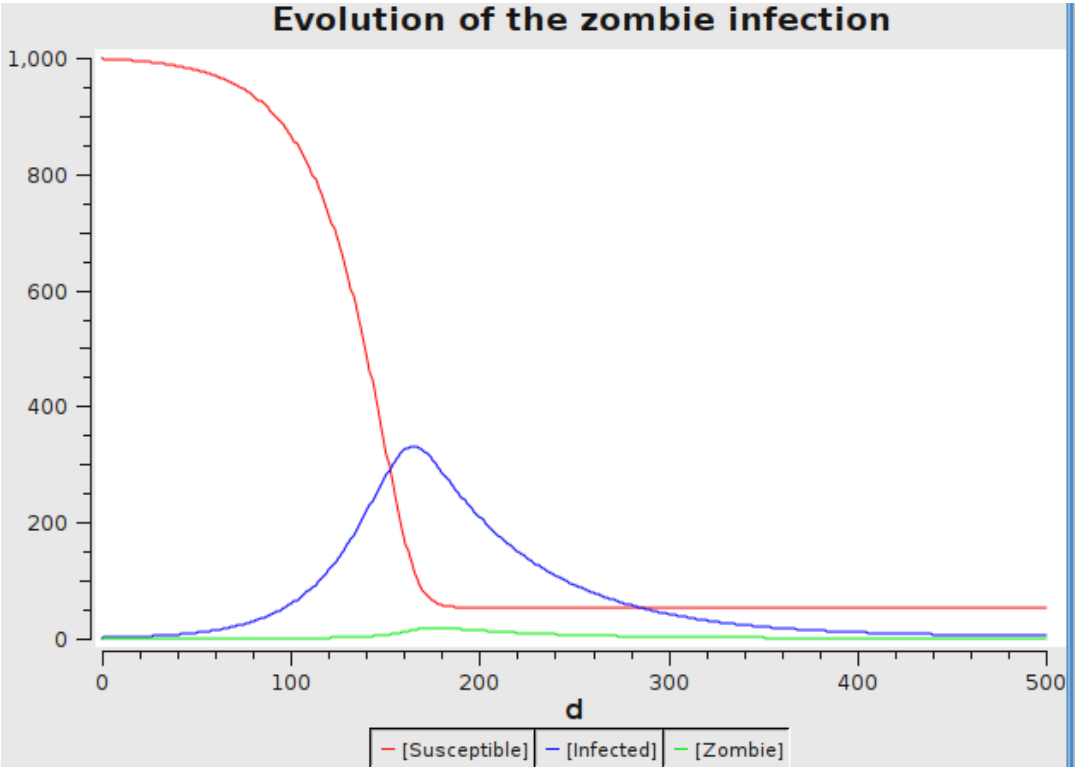
rate rule:

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

assignment rule:

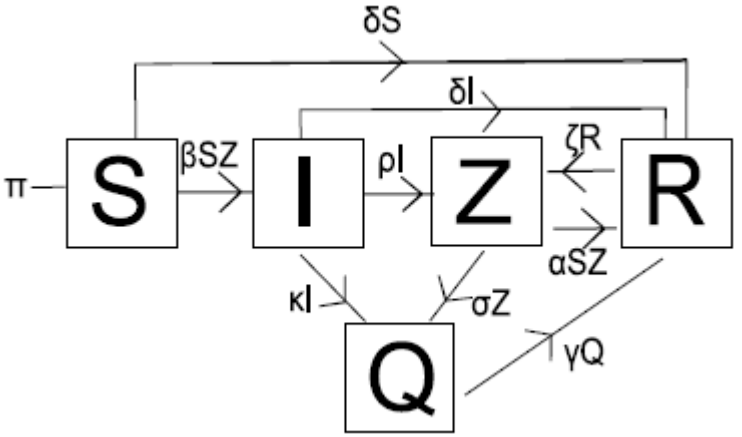
$$Effect = 1 - \frac{E_{max} - Ce}{Amt_{50} + Ce}$$

Spread of infection diseases ...



Munz P et al. When zombies attack!: Mathematical modelling of an outbreak of zombie infection. in "Infectious Disease Modelling Research Progress", (2009)133-150

MODEL1008060001



Difference between SBML 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

SBML Level 3 packages

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

???

SBML Software Guide

The following summarize all SBML-compatible systems known to us. The *matrix* provides an at-a-glance summary, whereas the *summary* provides longer descriptions of each software or project grouped by themes.

Number of software packages listed in the matrix today: **205**

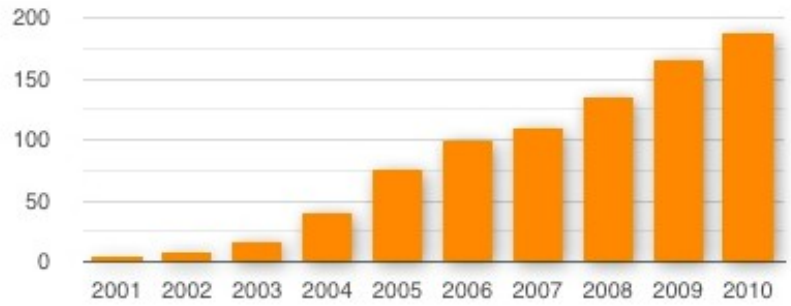
Please **use the survey form** to notify us about additions and suggestions.

Go to the SBML Software Matrix

Go to the SBML Software Summary

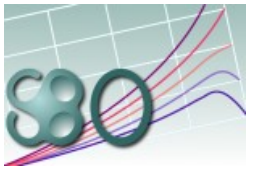
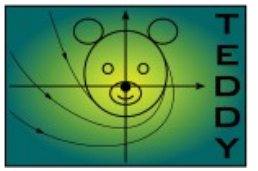
Historical trend

The following graph shows the total number of known SBML-compatible software packages each year, as counted by the SBML Team. The counts shown are for approximately the middle of each year.



(Note: the flat period in 2007 is an artifact of inadequate record keeping rather than a lull in SBML software development.)

Model semantics

	Models	Simulation	Results
Minimal requiremer			
Data-models			SBRML
Ontologies			

MIRIAM compliance (simplified)

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

Le Novère N., Finney A., Hucka M., Bhalla U., Campagne F., Collado-Vides J., Crampin E., Halstead M., Klipp E., Mendes P., Nielsen P., Sauro H., Shapiro B., Snoep J.L., Spence H.D., Wanner B.L. Minimum Information Requested In the Annotation of biochemical Models (MIRIAM). *Nature Biotechnology* (2005), 23: 1509-1515.

Why are annotations important?

Annotation of model components are essential to:

- allow efficient search strategies
- unambiguously identify model components
  - improve understanding the structure of the model
  - allow easier comparison of different models
  - ease the integration of models
- 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

Many “UniProt” accesses to EFG at the EBI:

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

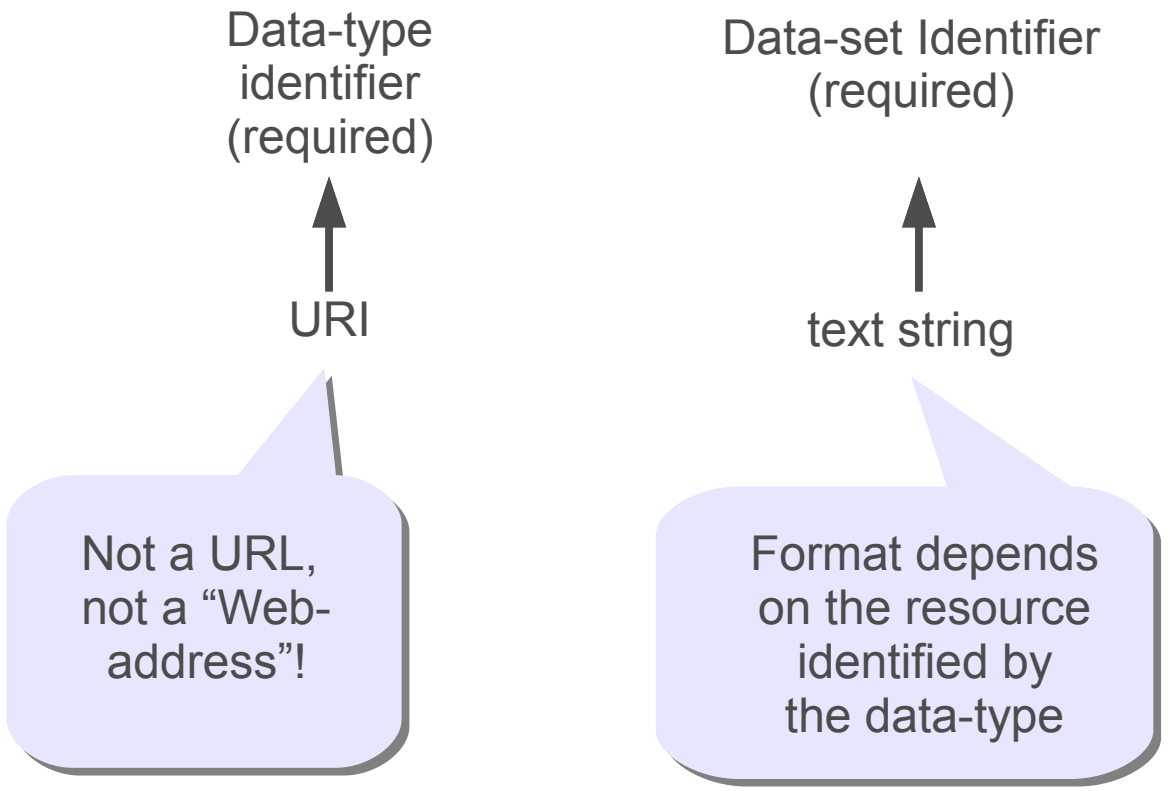
http://www.uniprot.org/uniprot/P01133?proteinId=P01133

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.

MIRIAM cross-references

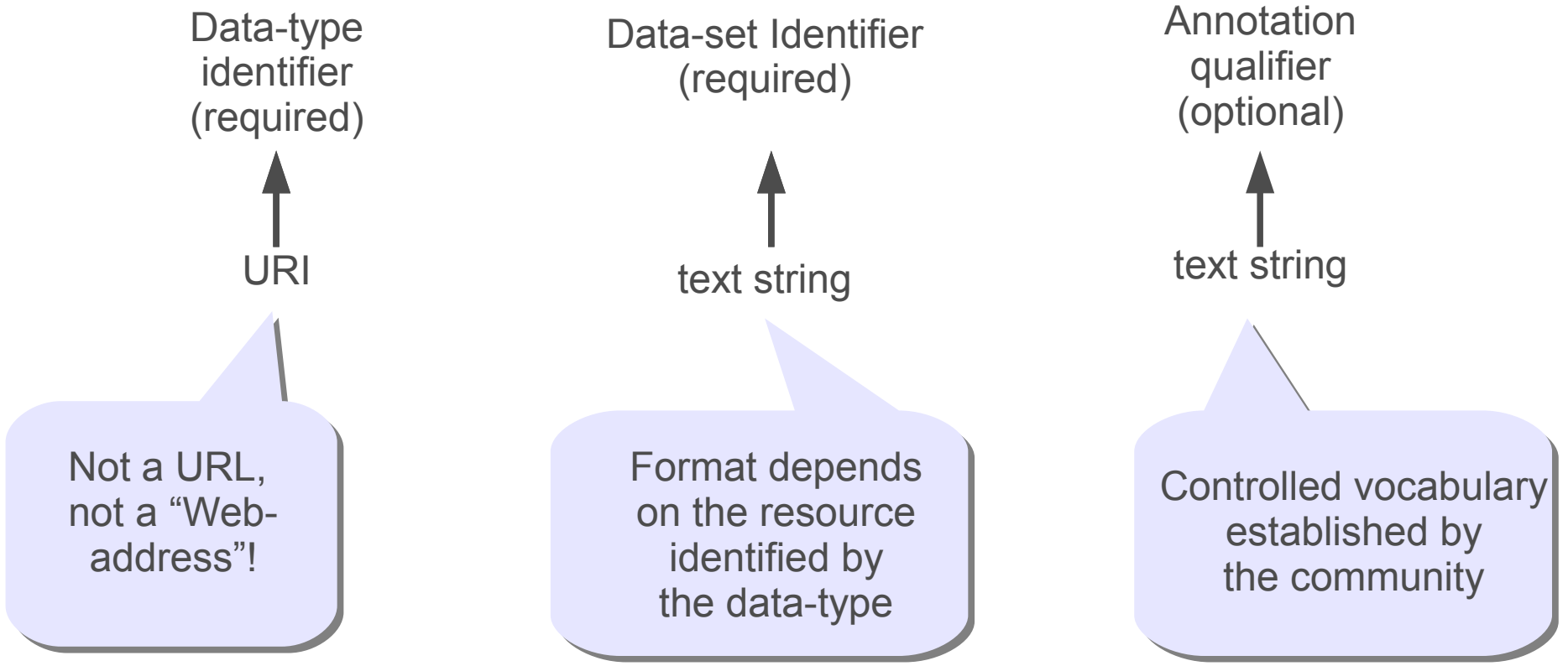


UniProt and P62158 (human calmodulin)
→ urn:miriam:uniprot:P62158

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

MIRIAM cross-references



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

- Browse
- Search
- Tags
- Query services
- Submit new
- Export
- Sign In

- Web Services
- Documents
  - MIRIAM Standard
  - FAQ
  - Documentation
  - News
  - BioModels.net Qualifiers

- MIRIAM on SourceForge

- Support
- Contact

MIRIAM Resources

MIRIAM Resources are a set of online services created to support MIRIAM Standard.

The core of *MIRIAM Resources* is a catalogue of data types (namespaces corresponding to controlled vocabularies or databases), their URIs and the corresponding physical URLs or resources. Access to this data is made available via exports (XML) and Web Services (SOAP).

Quick links

Browse

by data type name
by tags

Web Services

services available
usage of the services
online demonstration

Search

generic search

Exports

XML

Resources

MIRIAM Resources are composed of four components: a database, some Web Services, a Java library and this web application.

Database

The core of the system is a MySQL database. It allows us to store the data types (which can be controlled vocabularies or databases), their URIs and the corresponding physical URLs or resources.

Moreover,

ive model annotations, but also to generate the correct URIs based on resource name and accession numbers. You have access to the list of services available, an

Laibe C., Le Novère N. MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology. BMC Systems Biology (2007), 1: 58.

Data type: *Enzyme Nomenclature*

General | Tags | Example Usage | Web Services

General information about the data type

Name		
Identifier		MIR:00000004
Name		Enzyme Nomenclature
Synonyms		EC code
		Enzyme Classification
		EC
URIs		
MIRIAM URN		urn:miriam:ec-code
Deprecated		http://www.ec-code.org/
		urn:lsid:ec-code.org
		http://www.ebi.ac.uk/IntEnz/
Information		
Definition		The Enzyme Classification contains the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology on the nomenclature and classification of enzyme-catalysed reactions.
Identifier Pattern		^\d+\.-\.-\.-|\d+\.\d+\.-\.-|\d+\.\d+\.\d+\.-|\d+\.\d+\.\d+\.\d+$
Physical Locations		
Resource MIR:00100002	**Access URL**	http://www.genome.jp/dbget-bin/www_bget?ec:**$id** [Example: 1.1.1.1]
	Website	http://www.genome.jp/dbget-bin/www_bfind?enzyme
	Description	KEGG Ligand Database for Enzyme Nomenclature
	Institution	Kyoto University Bioinformatics Center, Japan
Resource MIR:00100003	**Access URL**	http://us.expasy.org/cgi-bin/nicezyme.pl?**$id** [Example: 1.1.1.1]
	Website	http://us.expasy.org/enzyme/
	Description	Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)
	Institution	Swiss Institute of Bioinformatics, Switzerland
Resource MIR:00100001	**Access URL**	http://www.ebi.ac.uk/intenz/query?cmd=SearchEC&ec=**$id** [Example: 1.1.1.1]
	Website	http://www.ebi.ac.uk/intenz/
	Description	IntEnZ (Integrated relational Enzyme database)
	Institution	European Bioinformatics Institute, United Kingdom
References		
URL(s)		http://www.chem.qmul.ac.uk/iubmb/enzyme/
		⊞ http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:10812475]
Miscellaneous		
Date of creation		2006-08-14 19:38:06 GMT
Date of last modification		2010-12-09 08:45:47 GMT

Go back to the list of data types

Suggest modifications to this data type

Resource: MIR:00100003

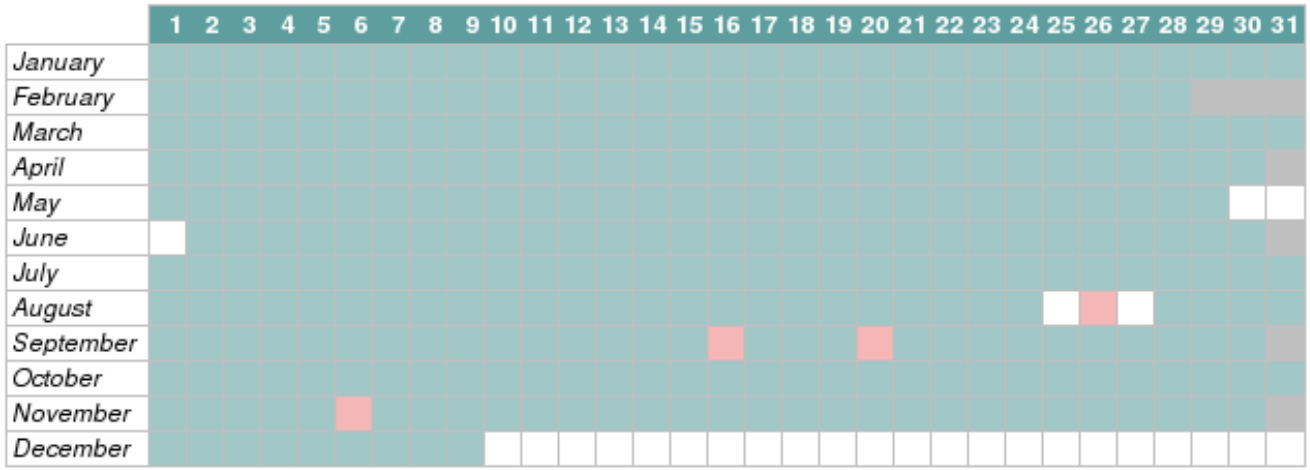
General information about the resource: ***Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)*** (associated with the data type: Enzyme Nomenclature).

Health statistics	
Last known state	up
Last check	2010-12-09 06:31:32
Uptime ratio	99% (651 checks)
Downtime ratio	0% (4 checks)
Unknown ratio	0% (0 checks)
URL used	http://us.expasy.org/cgi-bin/nicezyme.pl?1.1.1.1

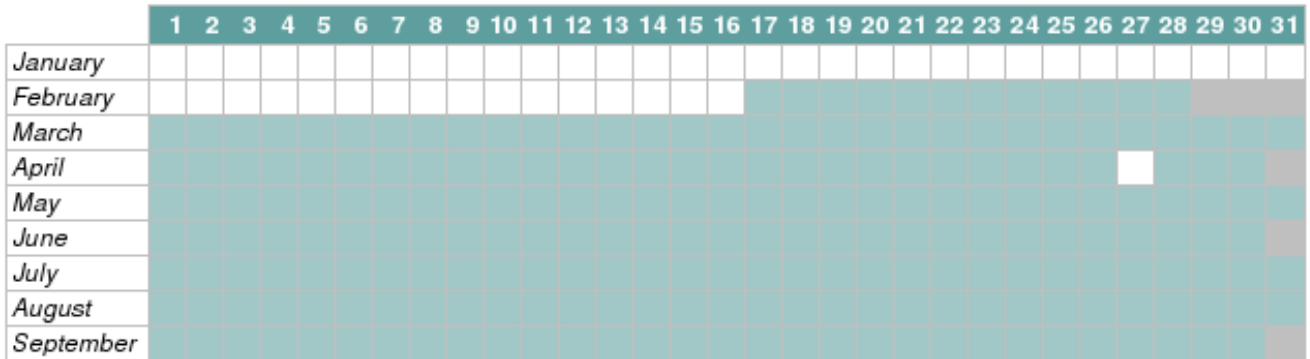
Health history

Full record of the health checks performed on this resource.

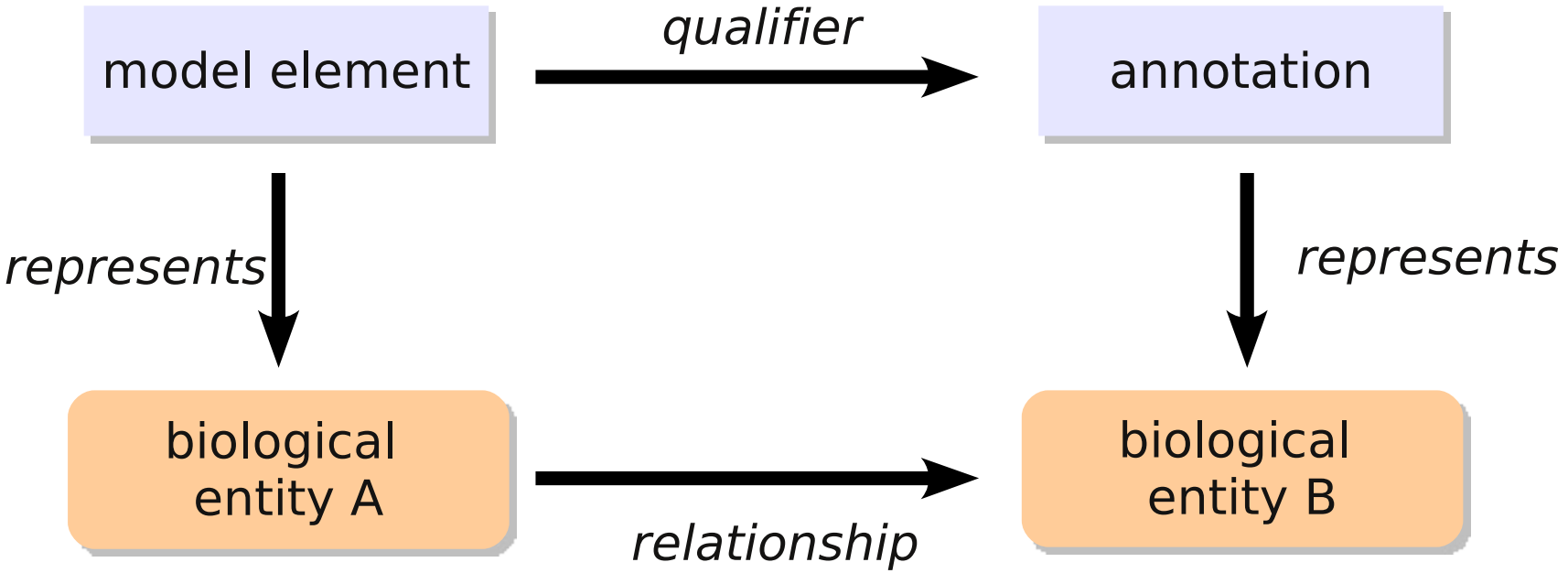
2010



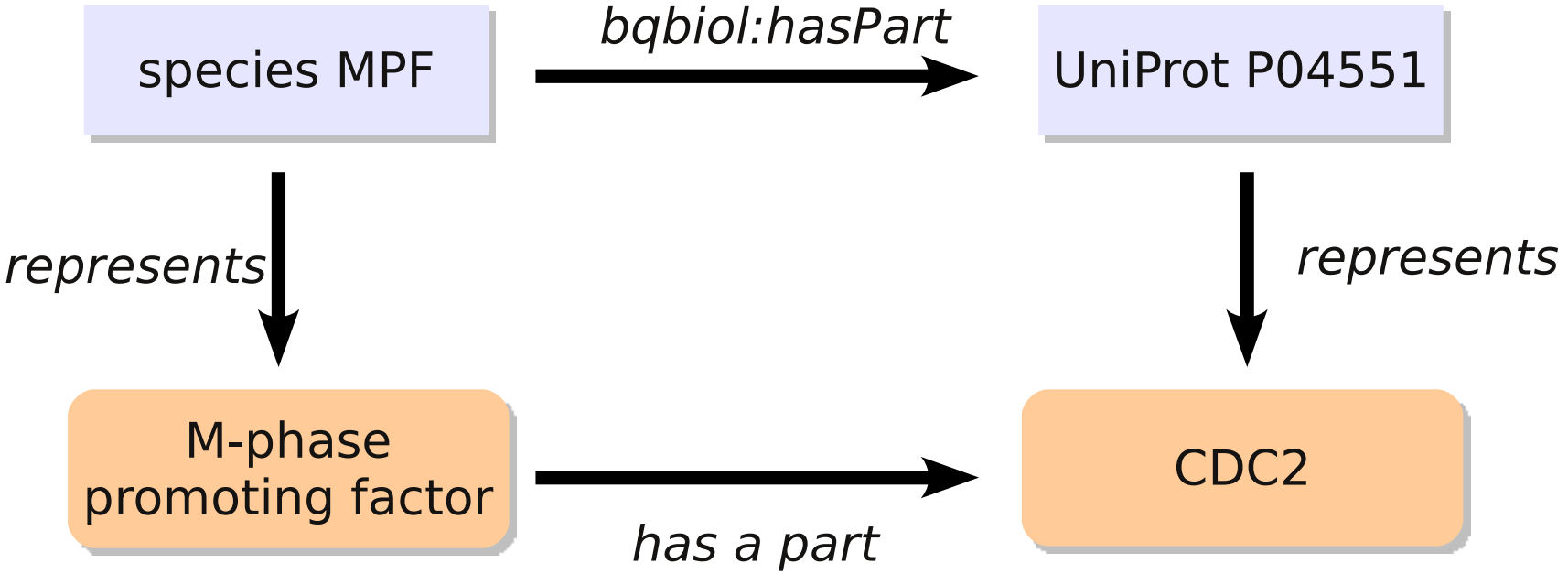
2009



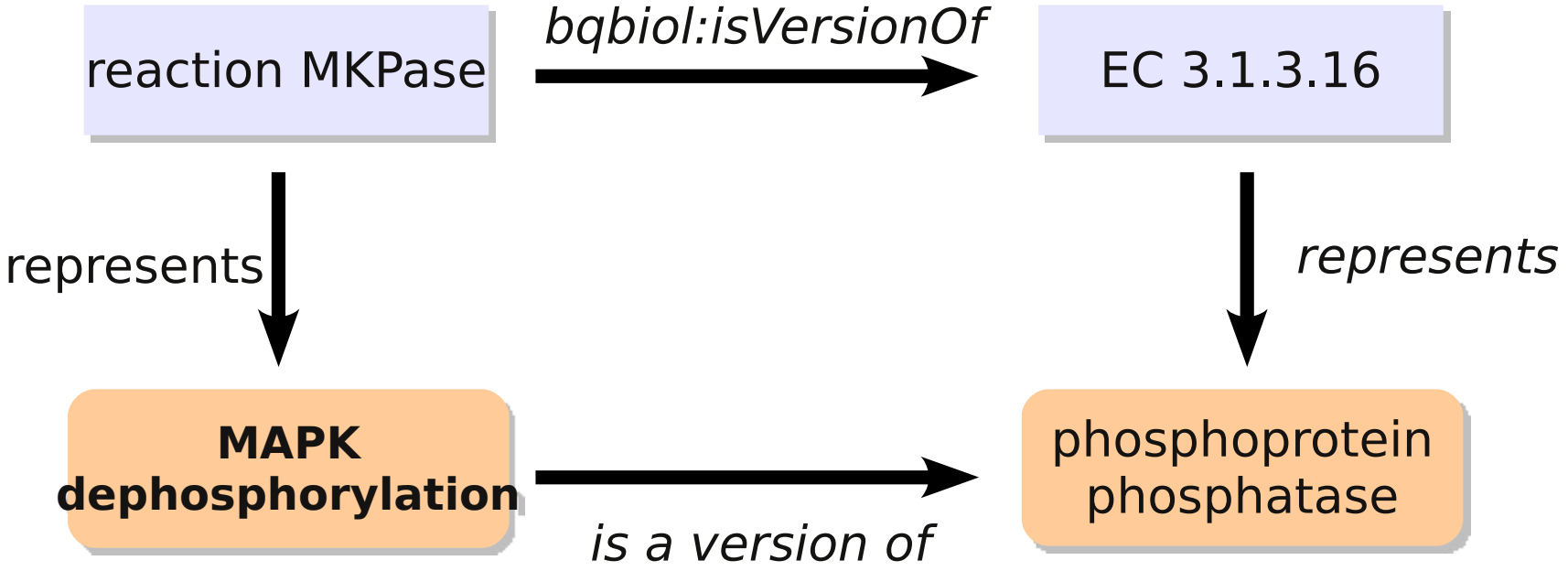
Qualification of annotation



Qualification of annotation



Qualification of annotation



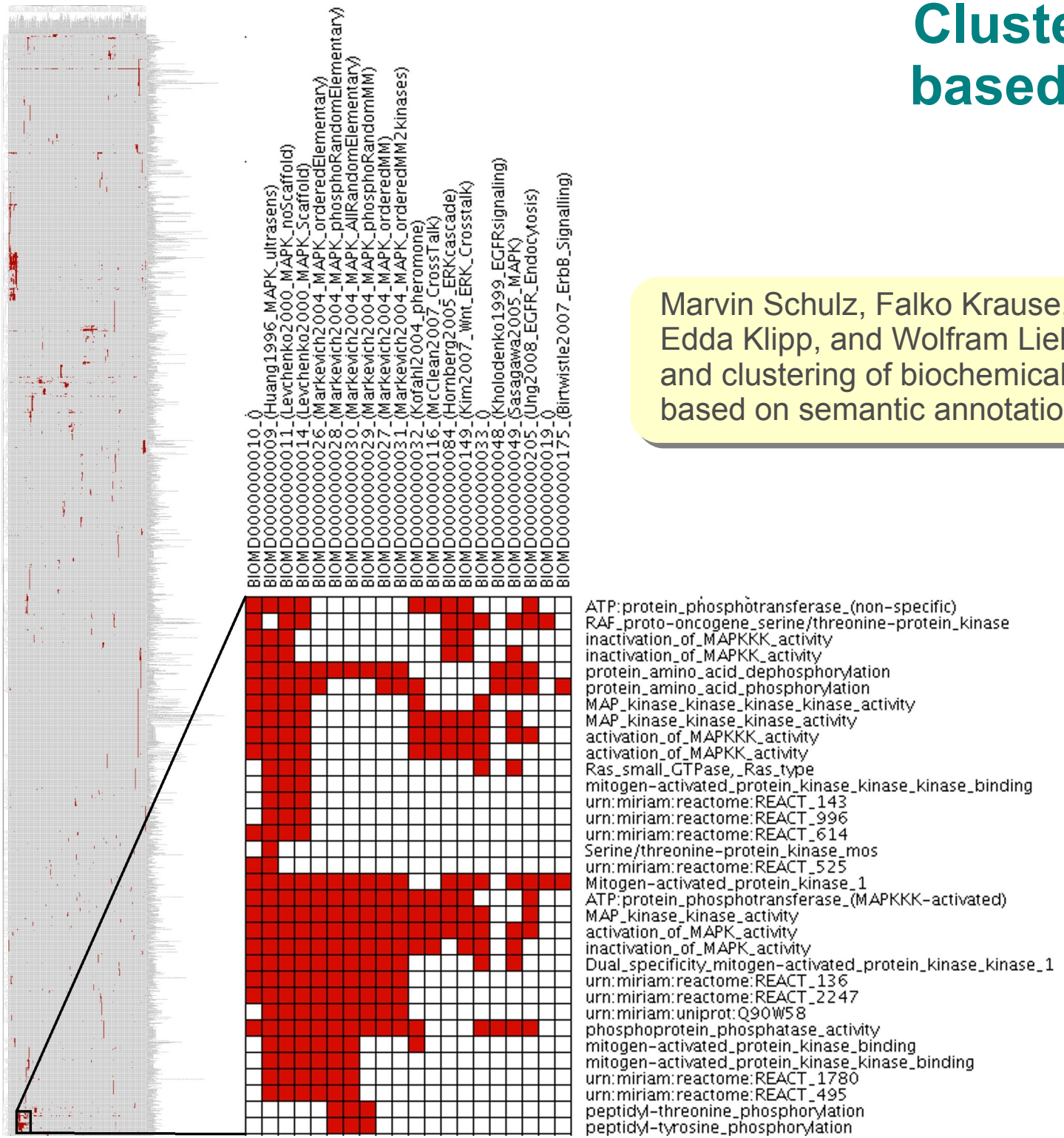
SBML and MIRIAM cross-references

```
<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)
  - Pathway commons (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)

Clustering models based on metadata



Marvin Schulz, Falko Krause, Nicolas Le Novère, Edda Klipp, and Wolfram Liebermeister: Comparison and clustering of biochemical network models based on semantic annotations. *Mol Syst Biol, in revision*

BIOMD0000000010_()
BIOMD0000000009_(Huang1996_MAPK_ultrasens)
BIOMD0000000011_(Levchenko2000_MAPK_noScaffold)
BIOMD0000000014_(Levchenko2000_MAPK_Scaffold)
BIOMD0000000026_(Markevich2004_MAPK_orderedElementary)
BIOMD0000000028_(Markevich2004_MAPK_phosphoRandomElementary)
BIOMD0000000030_(Markevich2004_MAPK_AllRandomElementary)
BIOMD0000000029_(Markevich2004_MAPK_phosphoRandomMM)
BIOMD0000000027_(Markevich2004_MAPK_orderedMM)
BIOMD0000000031_(Markevich2004_MAPK_orderedMM2kinases)
BIOMD0000000032_(Kofahl2004_pheromone)
BIOMD0000000116_(McClean2007_CrossTalk)
BIOMD0000000084_(Hornberg2005_ERKcascade)
BIOMD0000000149_(Kim2007_Wnt_ERK_Crosstalk)
BIOMD0000000033_()
BIOMD0000000048_(Kholodenko1999_EGFRsignaling)
BIOMD0000000049_(Sasagawa2005_MAPK)
BIOMD0000000205_(Ung2008_EGFR_Endocytosis)
BIOMD0000000019_()
BIOMD0000000175_(Birtwistle2007_ErbB_Signalling)
ATP:protein_phosphotransferase_(non-specific)
RAF_proto-oncogene_serine/threonine-protein_kinase
inactivation_of_MAPKKK_activity
protein_amino_acid_dephosphorylation
protein_amino_acid_phosphorylation
MAP_kinase_kinase_kinase_kinase_activity
MAP_kinase_kinase_kinase_activity
activation_of_MAPKKK_activity
Ras_small_GTPase_Ras_type
mitogen-activated_protein_kinase_kinase_kinase_binding
urn:miriam:reactome:REACT_143
urn:miriam:reactome:REACT_996
urn:miriam:reactome:REACT_614
Serine/threonine-protein_kinase_mos
urn:miriam:reactome:REACT_525
Mitogen-activated_protein_kinase_1
ATP:protein_phosphotransferase_(MAPKKK-activated)
MAP_kinase_kinase_activity
activation_of_MAPK_activity
inactivation_of_MAPK_activity
Dual_specificity_mitogen-activated_protein_kinase_kinase_1
urn:miriam:reactome:REACT_136
urn:miriam:reactome:REACT_2247
urn:miriam:uniprot:Q90W58
phosphoprotein_phosphatase_activity
mitogen-activated_protein_kinase_binding
mitogen-activated_protein_kinase_kinase_binding
urn:miriam:reactome:REACT_1780
urn:miriam:reactome:REACT_495
peptidyl-threonine_phosphorylation
peptidyl-tyrosine_phosphorylation

Ranking and retrieval

Model	BioModel	Score	p-val num
Huang1996_MAPK_ultrasens	BIOMD0000000009	1.000	< 1/1000
Levchenko2000_MAPK_noScaffold	BIOMD0000000011	0.925	< 1/1000
Levchenko2000_MAPK_Scaffold	BIOMD0000000014	0.865	< 1/1000
Kholodenko2000_MAPK_feedback	BIOMD0000000010	0.816	< 1/1000
Markevich2004_MAPK_orderedElementary	BIOMD0000000026	0.737	< 1/1000
Markevich2004_MAPK_phosphoRandomElementary	BIOMD0000000028	0.690	< 1/1000
Markevich2004_MAPK_AllRandomElementary	BIOMD0000000030	0.690	< 1/1000
Markevich2004_MAPK_orderedMM	BIOMD0000000027	0.673	< 1/1000
Markevich2004_MAPK_orderedMM2kinases	BIOMD0000000031	0.673	< 1/1000
Markevich2004_MAPK_phosphoRandomMM	BIOMD0000000029	0.617	< 1/1000
Hornberg2005_ERKcascade	BIOMD0000000084	0.468	< 1/1000
McClean2007_CrossTalk	BIOMD0000000116	0.397	< 1/1000
Kofahl2004_pheromone	BIOMD0000000032	0.348	< 1/1000
Kim2007_Wnt_ERK_Crosstalk	BIOMD0000000149	0.323	< 1/1000
Brown2004_NGF_EGF_signaling	BIOMD0000000033	0.260	< 1/1000
Goldbeter1995_CircClock	BIOMD0000000016	0.244	< 1/1000
Sasagawa2005_MAPK	BIOMD0000000049	0.240	< 1/1000
Ung2008_EGFR_Endocytosis	BIOMD0000000205	0.234	< 1/1000
Leloup1999_CircClock	BIOMD0000000021	0.229	< 1/1000
Goldbeter1991_MinMitOscil_ExplInact	BIOMD0000000004	0.222	< 1/1000
Goldbeter1991_MinMitOscil	BIOMD0000000003	0.214	< 1/1000
Leloup1998_CircClock_LD	BIOMD0000000171	0.201	< 1/1000
Tyson1991_CellCycle_6var	BIOMD0000000005	0.199	< 1/1000
Veening2008_DegU_Regulation	BIOMD0000000240	0.180	< 1/1000
Neves2008_Cell_Shape	BIOMD0000000182	0.168	4.0e-03
Fisher2006_Ca_Oscillation_dpdnt_NFAT_dynamics	BIOMD0000000122	0.164	5.0e-03
Leloup2003_CircClock_DD	BIOMD0000000073	0.163	5.0e-03

See also R. Henkel, L. Endler, A. Peters, N. Le Novère, D. Waltemath (2010) Ranked Retrieval of Computational Biology Models. *BMC Bioinformatics*, 11:423

EMBL-EBI EB-eye Search All Databases Enter

http://www.ebi.ac.uk/biomodels/

Databases | Tools | EBI Groups | Training | Ind

BioModels Home | Models | Submit | Support | About BioModels | Contact us

BioModels Database - A Database of Annotated Published Models

BioModels Database is a data resource that allows biologists to store, search and retrieve published mathematical models of biological interests. Models present in BioModels Database are annotated and linked to relevant data resources, such as publications, databases of compounds and controlled vocabularies.
BioModels Database also allows users to generate sub-models, provides access to online simulation tools and features programmatic access via Web Services.

Advanced Search

Search | Go to model

Browse models

- Curated models (269)
- Browse models using GO
- Non-curated models (361)

Simulate in JWS Online

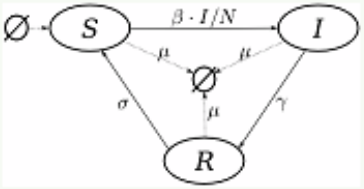
Submit a model

Links

- Main instance at EMBL-EBI, UK
- Mirror at Caltech, USA

Model of the month

November, 2010
The evolution of virulence and the occurrence of cross-immunity are of great importance for the development of pathogens and epidemics and they are rarely modelled in combination. Here is the model that explores both in one framework...
Read more...



News

17 November 2010 **New availability of the Models of the Month**
Models of the Month are now linked from BioMed Central's Systems Biology Gateway.

30 September 2010 **Eighteenth Release!**
Download All Models Under SBML Format

N. Le Novère, B. Bornstein, A. Broicher, M. Courtot, M. Donizelli, H. Dharuri, L. Li, H. Sauro, M. Schilstra, B. Shapiro, J.L. Snoep, M. Hucka. BioModels Database: A Free, Centralized Database of Curated, Published, Quantitative Kinetic Models of Biochemical and Cellular Systems. (2006) *Nucleic Acids Research*, 34: D689-D691.

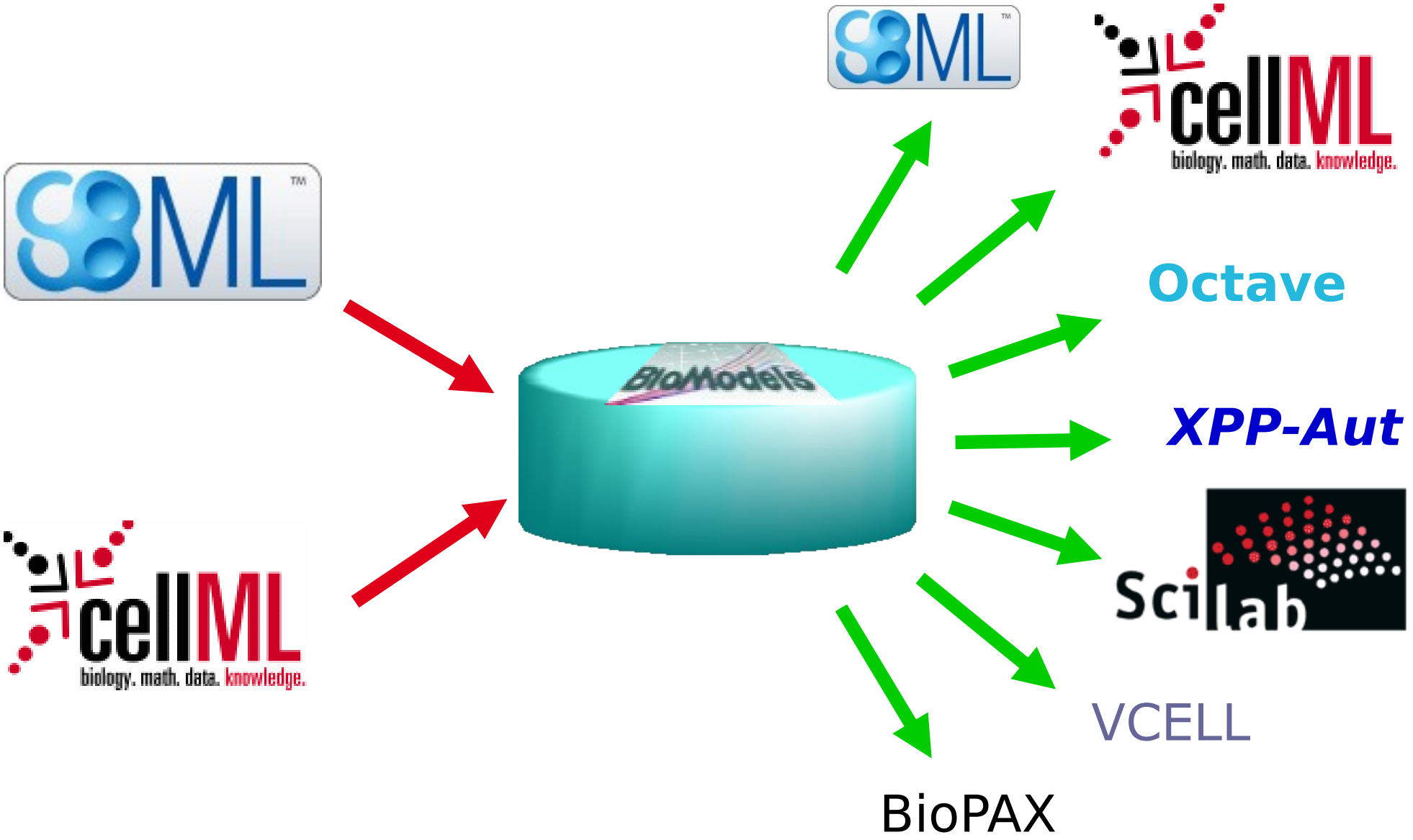
What is BioModels Database?

- Store and serve quantitative models of biomedical interest
- Only models described in the peer-reviewed scientific literature
- Models are curated: computer software check the syntax, while human curators check the semantics
- Models are simulated to ensure they provide the expected results
- Model components are annotated, to improve identification and retrieval
- Models are accepted in several formats, and served in several others

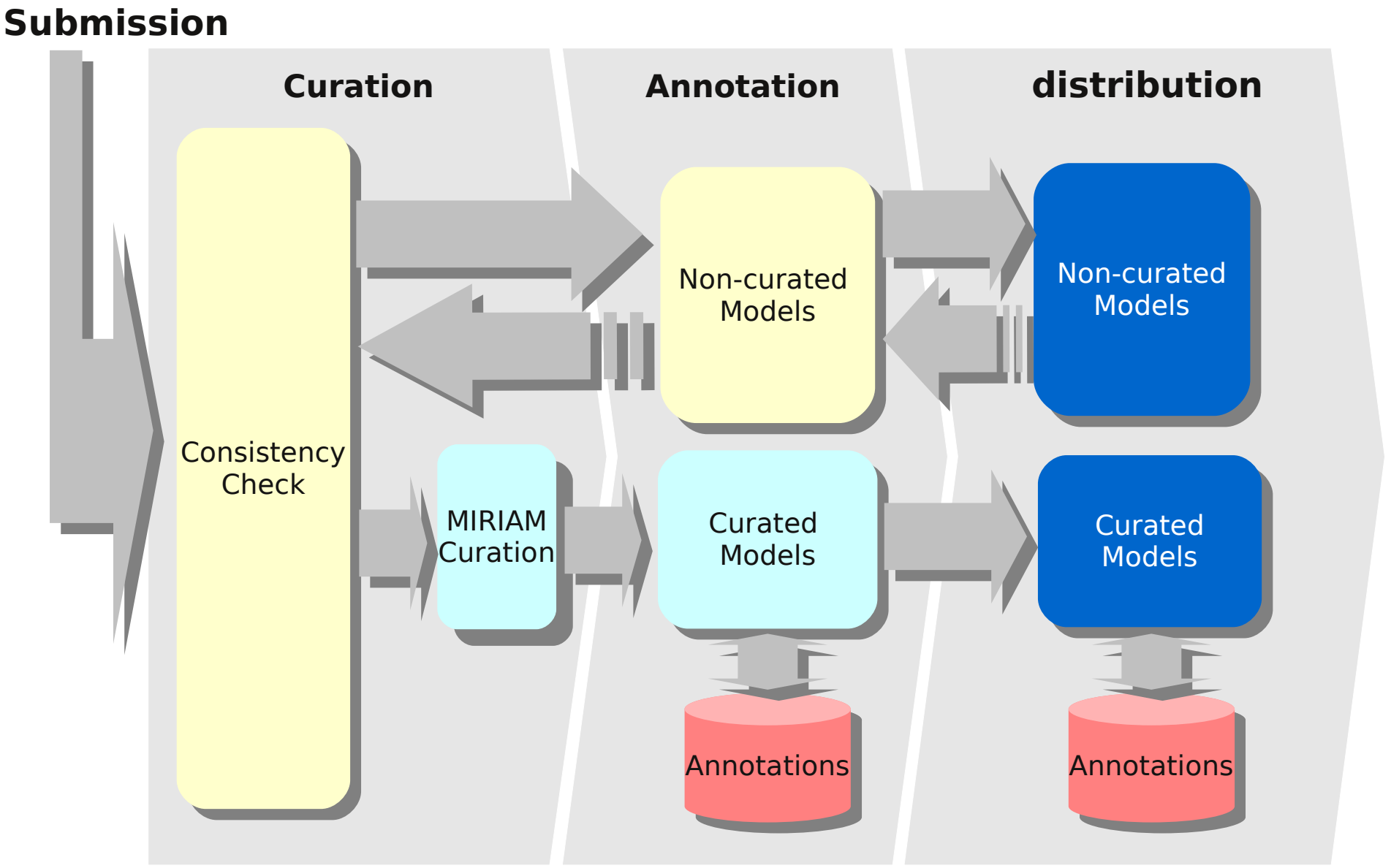
Where do models come from?

- Submitted by curators
  - imported from other repositories (DOQCS, CellML)
  - reimplemented from literature
- From authors before grant application or publication
- Over 100 scientific journals advise submission to BioModels Db:
  - Nature Molecular Systems Biology
  - Public Library of Science journals
  - BioMedCentral journals
- Various people curated models out of interest.

Input and output formats



Current production pipeline



Curated and Non-curated Models

- Curated models – Comply with the MIRIAM guidelines
- Non-Curated models – valid SBML, not curated or annotated
  - Not MIRIAM compliant:

    cannot reproduce results published in the paper.

    differ in model structure

    non-kinetic models (eg. FBA, stoichiometric maps)
  - MIRIAM compliant:

    models contain kinetics that we cannot curate at present.

    models are yet to be curated

Search - Models

You can search BioModels Database for models using one or more of the following criteria:

- *BioModels identifier* → Search BioModels Database for *exact* BioModels identifiers (for example *BIOMD0000000001* or *BIOMD0000000022*).
- *Person* → Search BioModels Database for model submitter and/or creator(s) names, or model reference publication author(s) names (for example *Nicolas Le Novère*, *Nicolas*, *Bruce Shapiro* or *Shapiro*, *Edelstein* or *Novak*).
- *SBML elements* → Search BioModels Database using the content of either "name" or "*notes*" SBML elements (for example *Edelstein* or *nicotinic*). Select the checkbox behind, if you want to find documents which matches the exact phrase; otherwise, all words will be searched as default.
- *Annotation (full text)* → Search BioModels Database for related information found in the models reference publication or third-party resources, by either publication/resource identifier or text (for example *9256450* or *cyclin* for publication, *GO:0000278* or *cell cycle* for Gene Ontology, *P04551* or *cell division* for UniProt).
- *Annotation (identifier)* → Search BioModels Database for annotations, by third-party resource identifiers (for example *IPR002394* for InterPro, *hsa04080* for KEGG Pathway, *68910* for Reactome).

A part from the *BioModels identifier*-based search, for every other criteria the search operates on a *contains the entered string basis*, case-insensitive. That is, searching *Person* for *Shapi* or *shapi* will return the same results as searching for *Shapiro* or *shapiro*. In addition, since search strings are treated as words, do not enter regular expressions.

Multiple criteria can be combined with either *and* or *or*. If *and* is selected, only those models satisfying all the criteria will be returned. If instead *or* is selected, all the models satisfying at least one of the criteria will be returned.

BioModels identifier:

Person:

SBML elements: match the **exact phrase**

Annotation (full text): UniProt

Annotation (full text): Publication — cell cycle

Annotation (full text):

Publication
ChEBI
Gene Ontology
Taxonomy
UniProt

Annotation (identifier):

Annotation (identifier): KEGG Reaction

Annotation (identifier): Enzyme Nomenclature

Compose by: and or

Search Reset

BIOMD0000000005 - Tyson1991_CellCycle_6var

Download SBML | Other formats (auto-generated) | Actions | Submit Model Comment/Bug

Model | Overview | Math | Physical entities | Parameters | Curation

Reference Publication

Publication ID: 1831270

Proc Natl Acad Sci U S A 1991 Aug;88(16):7328-32.
Modeling the cell division cycle: cdc2 and cyclin interactions.
Tyson JJ.
Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg 24061. [more]

Model

Original Model: *BIOMD0000000005.xml.origin*

Submitter: Nicolas Le Novère

Submission ID: MODEL6614644188

Submission Date: 13 Sep 2005 12:31:08 UTC

Last Modification Date: 24 May 2010 16:33:07 UTC

Creation Date: 08 Feb 2005 18:28:27 UTC

Encoders: Bruce Shapiro
Vijayalakshmi Chelliah

set #1	bqbiol:hasVersion	**Reactome** REACT_152
	bqbiol:isVersionOf	**KEGG Pathway** sce04111 **Gene Ontology** mitotic cell cycle
	bqbiol:occursIn	**Taxonomy** Fungi/Metazoa group

Notes

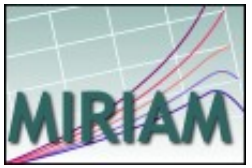
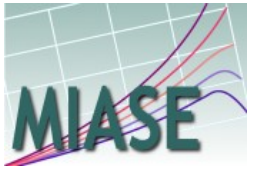
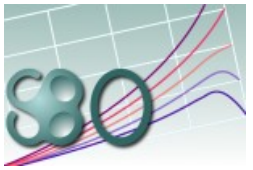
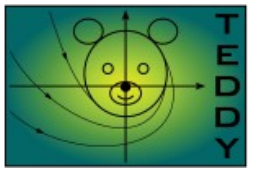
This a model from the article:
Modeling the cell division cycle: cdc2 and cyclin interactions.
Tyson JJ *Proc. Natl. Acad. Sci. U.S.A.*1991; 88(16); 7328-32 1831270,
Abstract:
The proteins cdc2 and cyclin form a heterodimer (maturation promoting factor) that controls the major events of the cell cycle. A mathematical model for the interactions of cdc2 and cyclin is constructed. Simulation and analysis of the model show that the control system can operate in three modes: as a steady state with high maturation promoting factor activity, as a spontaneous oscillator, or as an excitable switch. We associate the steady state with metaphase arrest in unfertilized eggs, the spontaneous oscillations with rapid division cycles in early embryos, and the excitable switch with growth-controlled division cycles typical of nonembryonic cells.

Future directions for BioModels Database

- Improvement of the software infrastructure
  - More portable (independent of the EBI)
  - Better authentication, logging and security
  - More flexible: groups of models, or users, more converters, views, services ...
  - Community development model
- Extension of the coverage
  - Different types of models: Neuroscience, PK/PD, physiology ...
  - Parametrisation procedures, simulation descriptions ...

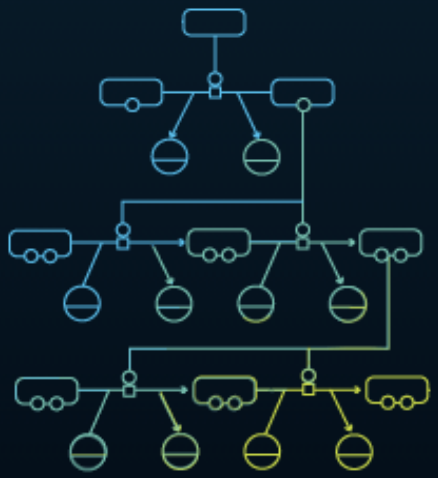
JUst a Model Management Platform

Visual representation of models

	Models	Simulation	Results
Minimal requirements			
Data-mode	 		SBRML
Ontologies			

SBGN Systems Biology Graphical Notation

Home | News | Documents | Lists | Community | Events | About | Google Site Search.



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 , software supporting SBGN, get answers to frequent questions about SBGN, access join online discussions, see current working documents 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

(23 Apr.'10) The first annual competition is opened, with categories such as Best Software, Best Map and Best Outreach.

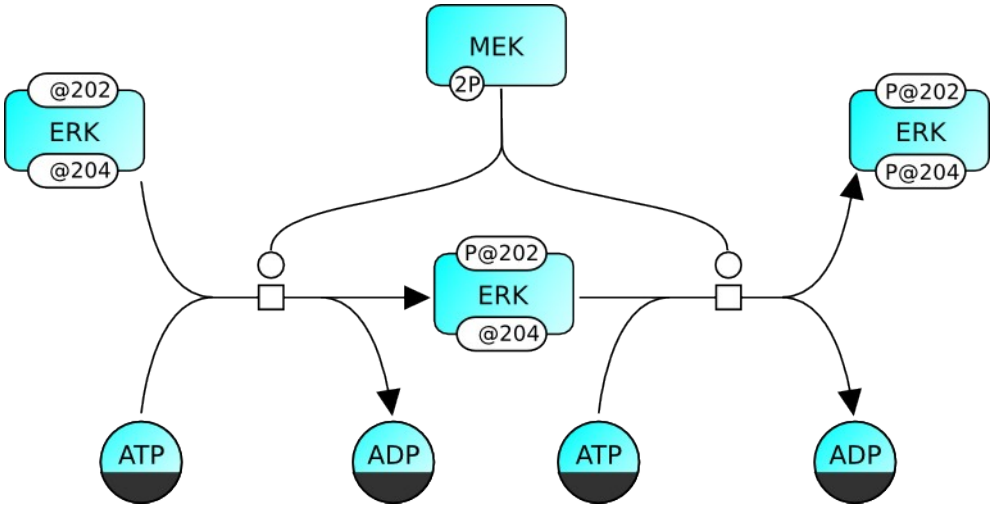
N. Le Novère *et al* (2008). *Nature Biotechnology*

What is SBGN?

- 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
- Developed over four years by a diverse community, including biologists, modellers, computer scientists etc.

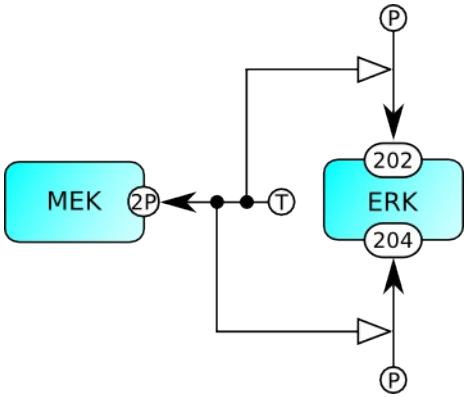
Graph trinity: three languages in one notation

Process Descriptions



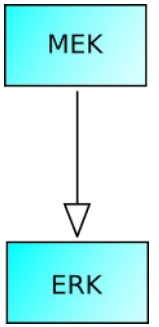
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships



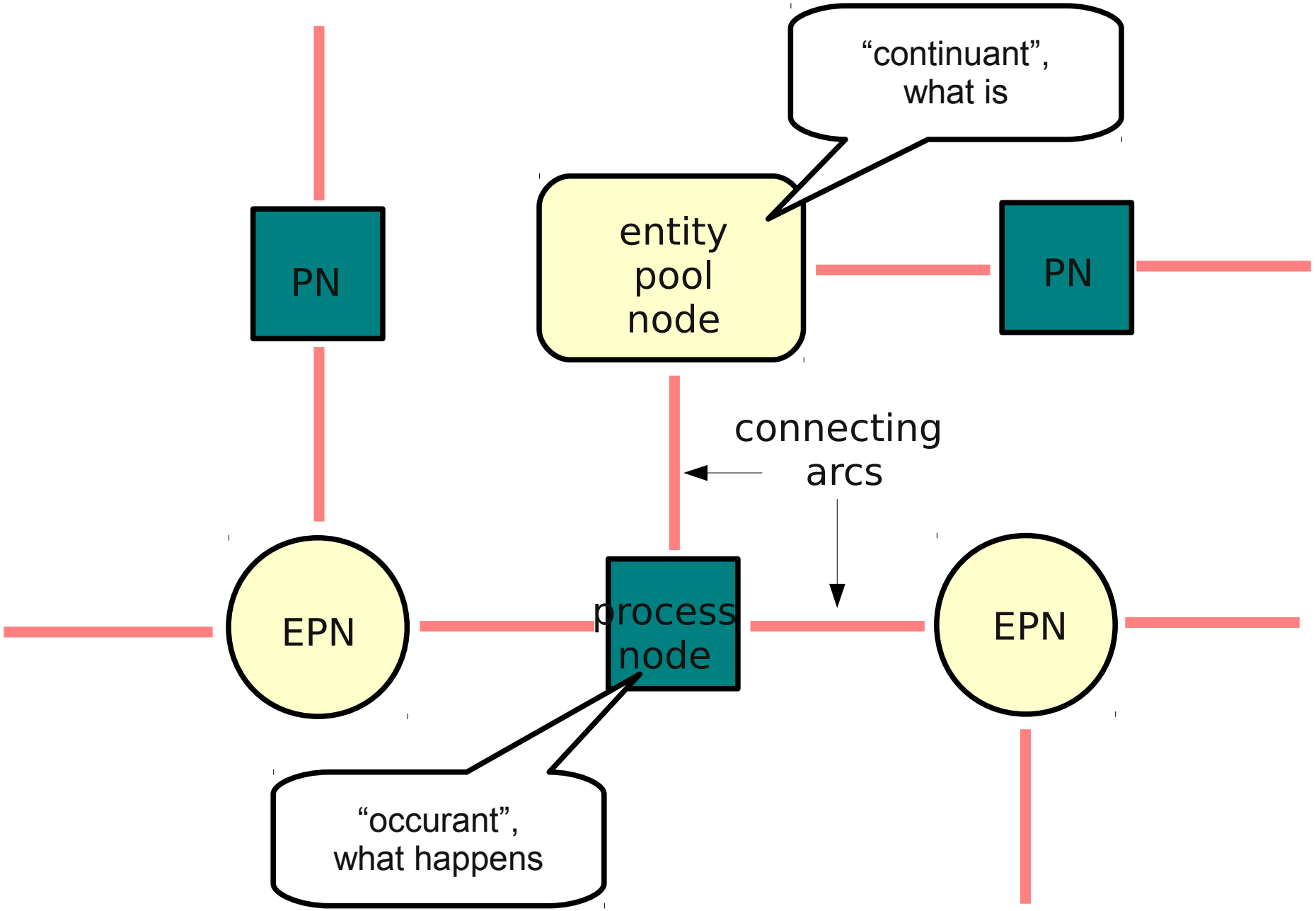
- Unambiguous
- Mechanistic
- Non-sequential
- Independence of relationships

Activity Flows

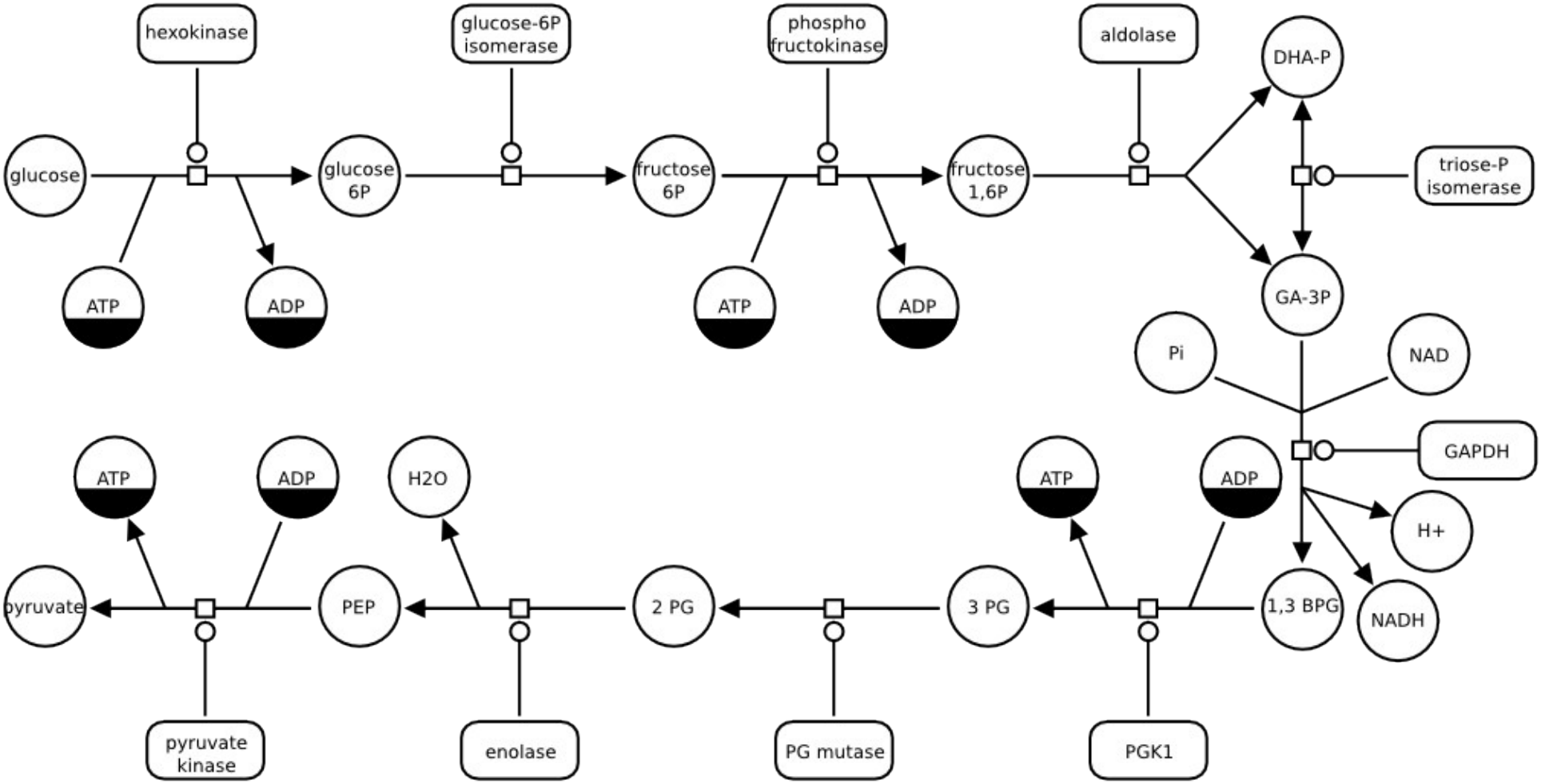


- Ambiguous
- Conceptual
- Sequential

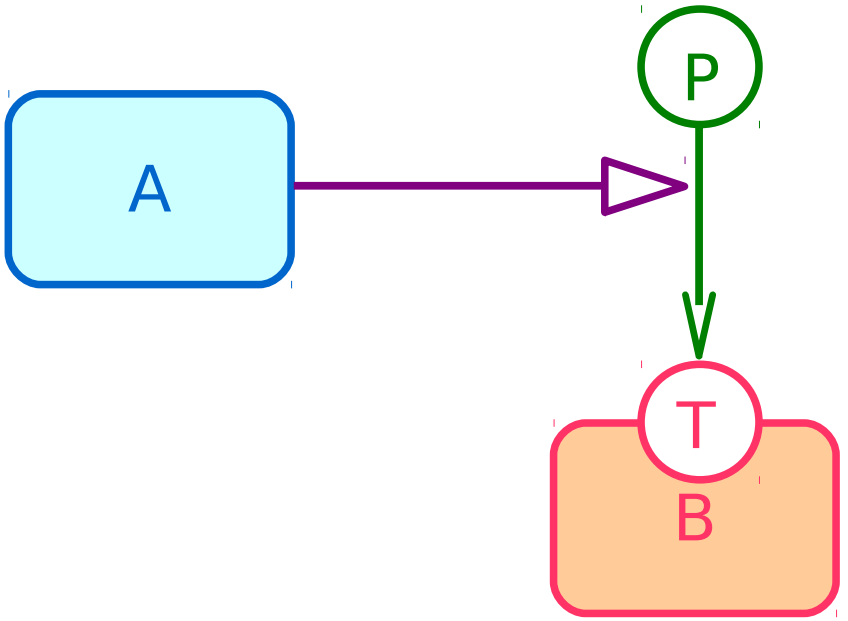
Process Descriptions are bipartite graphs



Metabolic network in Process Description Language



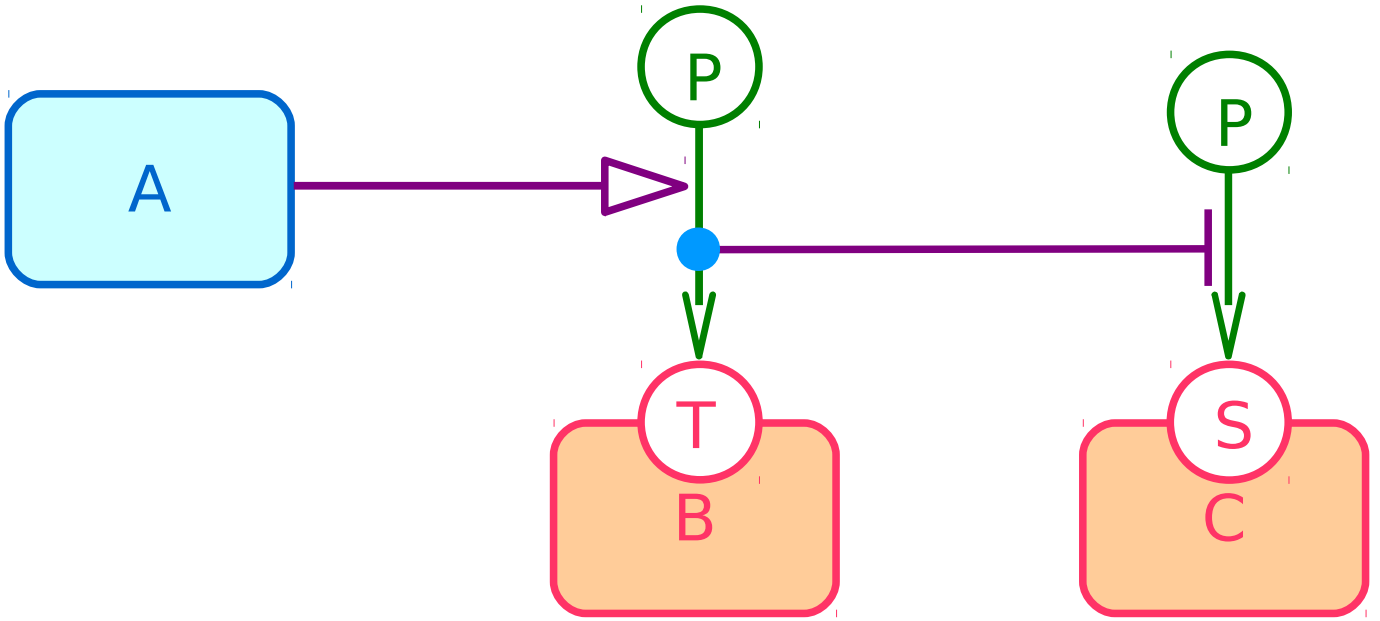
Entity Relationships can be viewed as rules



If A exists, the assignment of the value P to the state variable T of B is increased

(A stimulates the phosphorylation of B on the threonine)

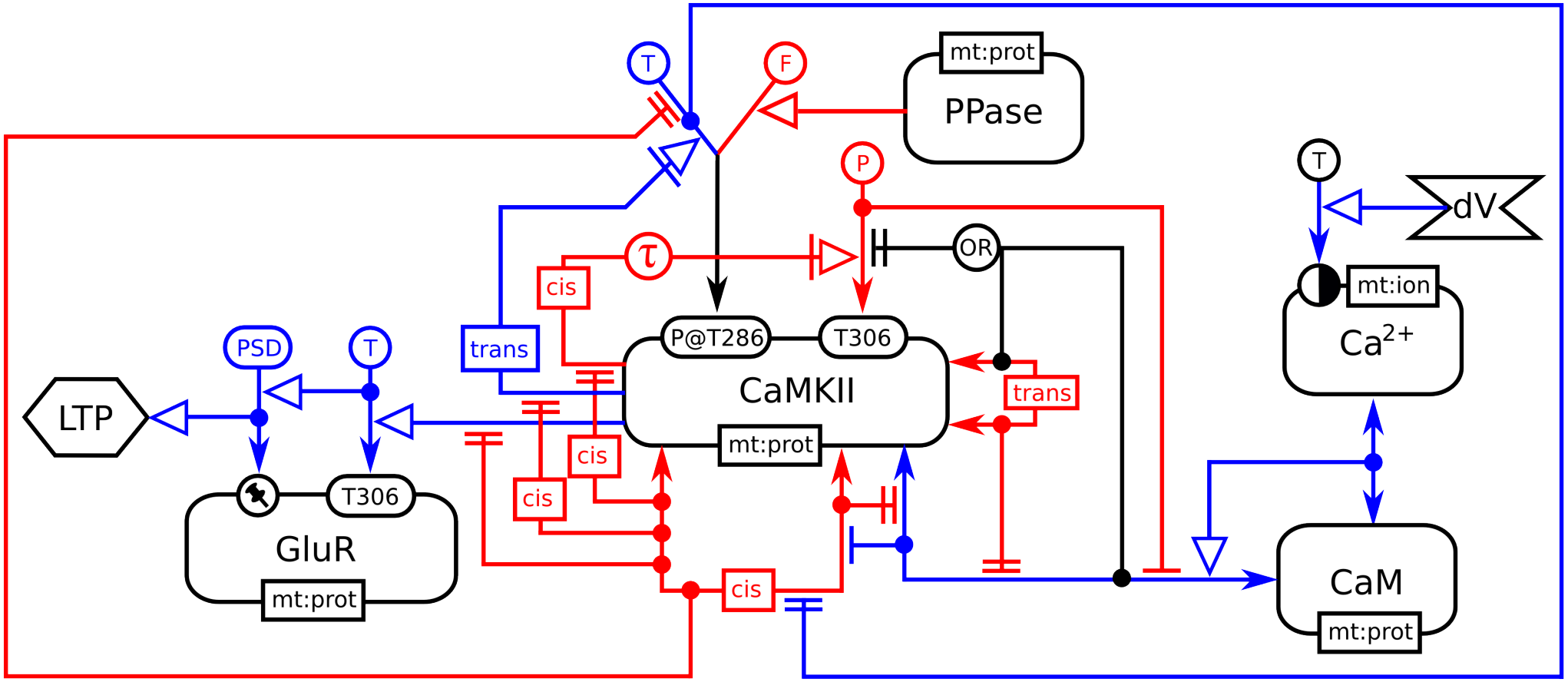
Entity Relationships can be viewed as rules



If A exists, the assignment of the value P to the state variable T of B is increased

If P is assigned to the state variable T of B, the assignment of the value P to the state variable S of B is decreased

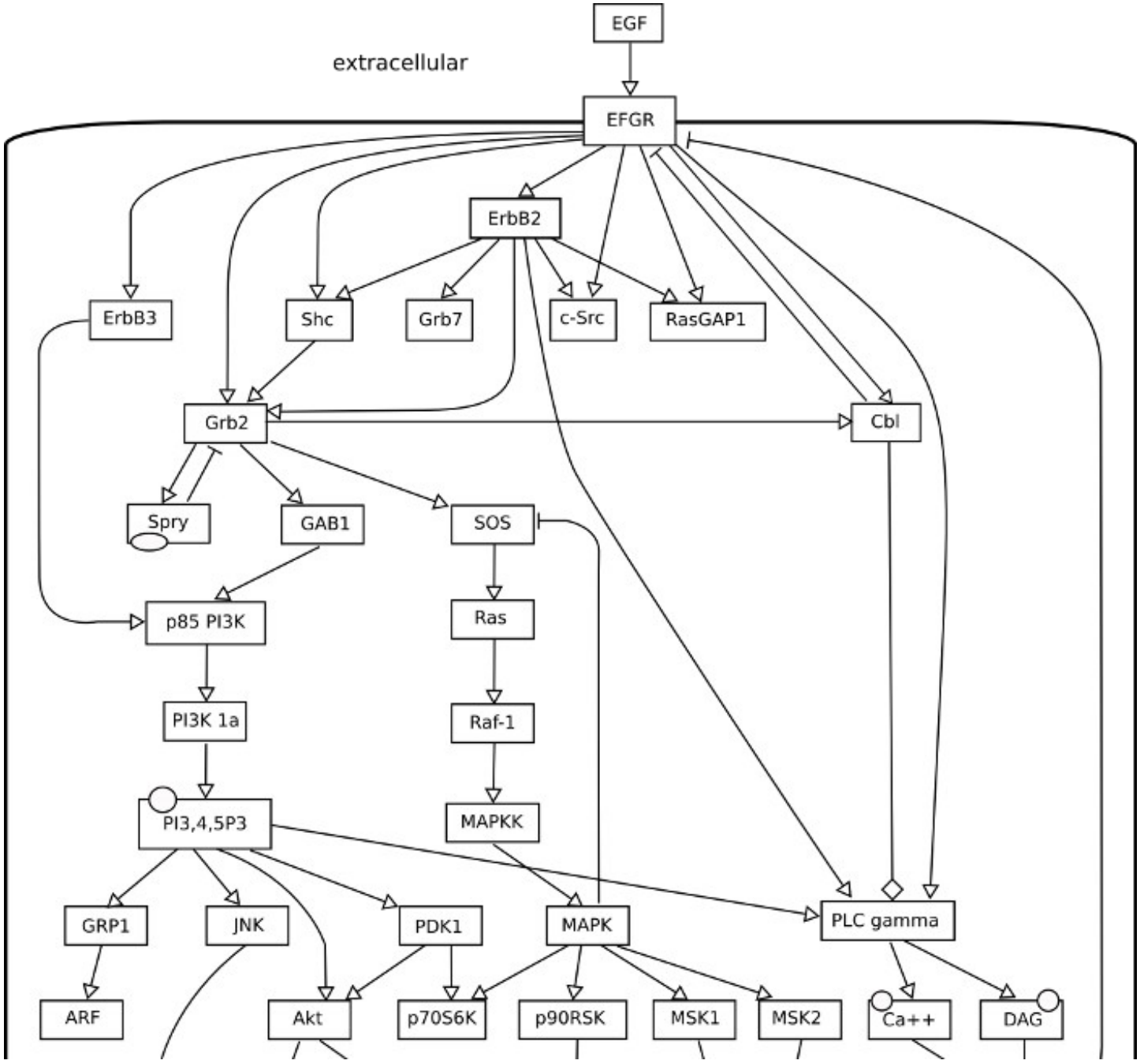
SBGN ER map of calcium-regulated synaptic plasticity

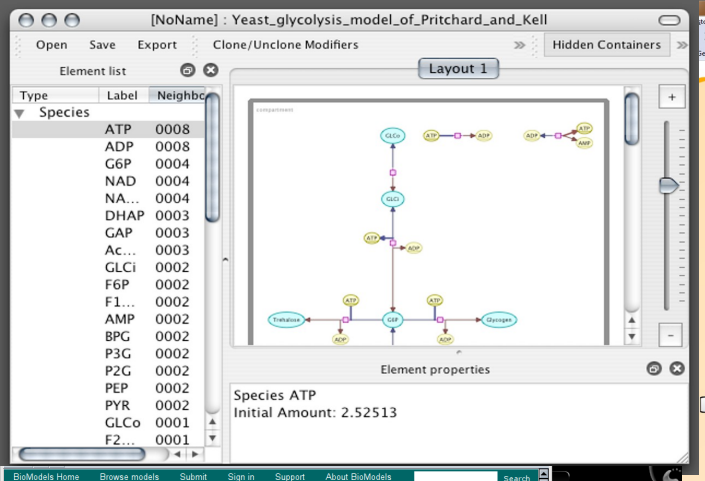


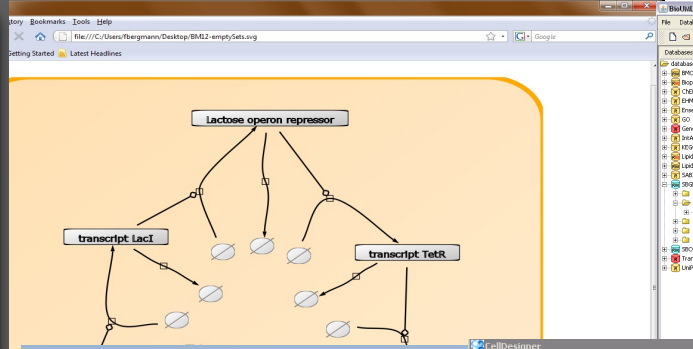
increases synaptic weight

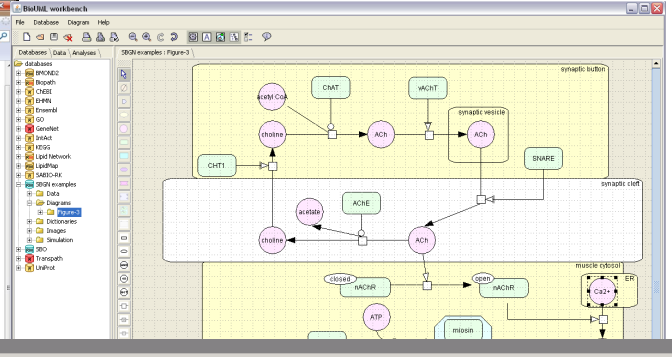
decreases synaptic weight

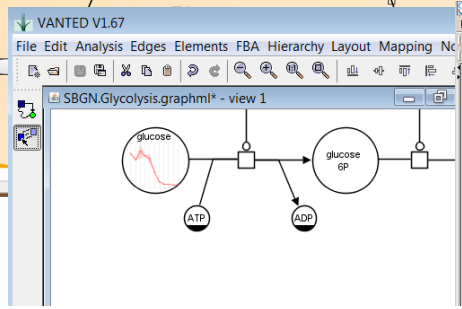
Example of Activity Flow map

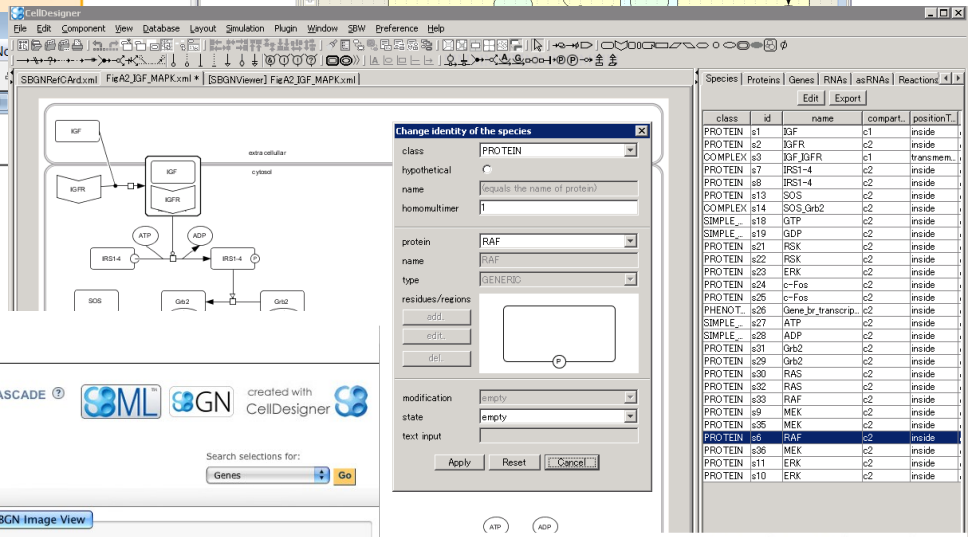


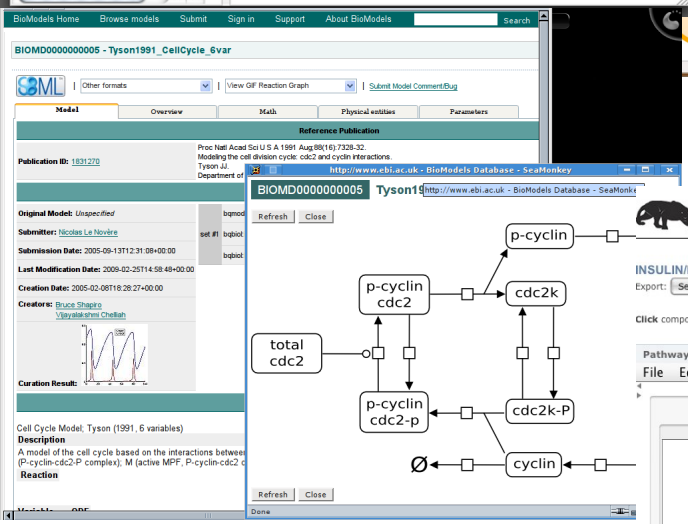

[NoName] : Yeast_glycolysis_model_of_Pritchard_and_Kell
Open
Save
Export
Clone/Unclone Modifiers
Hidden Containers
Element list
Layout 1
Type
Label
Species
ATP 0008
ADP 0008
G6P 0004
NAD 0004
DHAP 0003
GAP 0003
BPG 0002
P3G 0002
P2G 0002
PEP 0002
PYR 0002
GLCo 0001
Element properties
Species ATP
Initial Amount: 2.52513


Lactose operon repressor
transcript LacI
transcript TetR

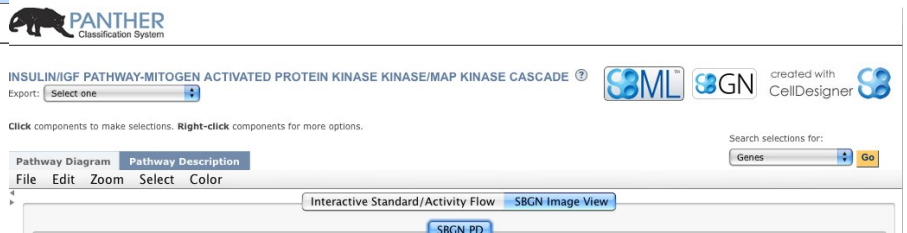

BioUML workbench
synaptic button
synaptic vesicle
synaptic cleft
muscle cytosol
ACh
choline
acetate
SNARE

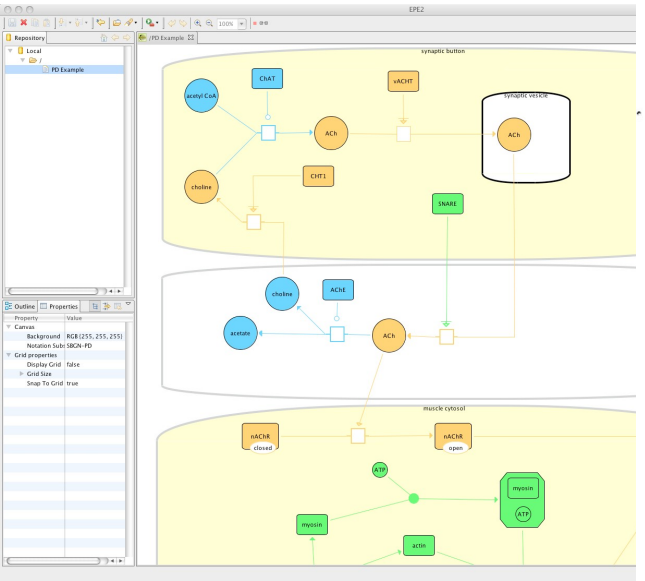

VANTED V1.67
File Edit Analysis Edges Elements FBA Hierarchy Layout Mapping
SBGN.Glycolysis.graphml* - view 1
glucose
glucose 6P
ATP
ADP

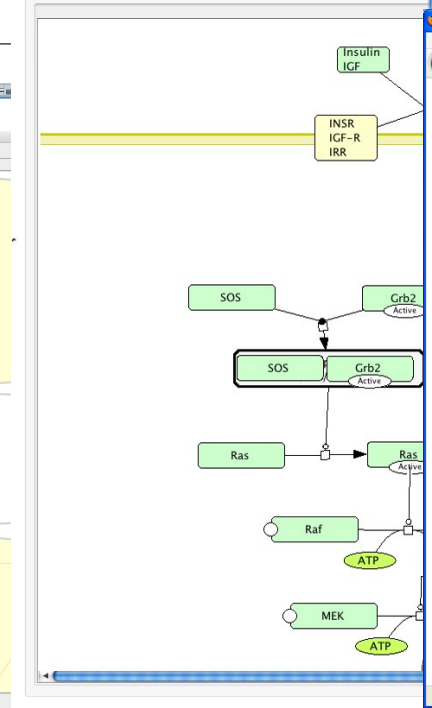

CellDesigner
Change identity of the species
class
PROTEIN
hypothetical
name
homomultimer
protein
RAF
type
residues/regions
modification
state
empty
text input
Apply
Reset
Cancel

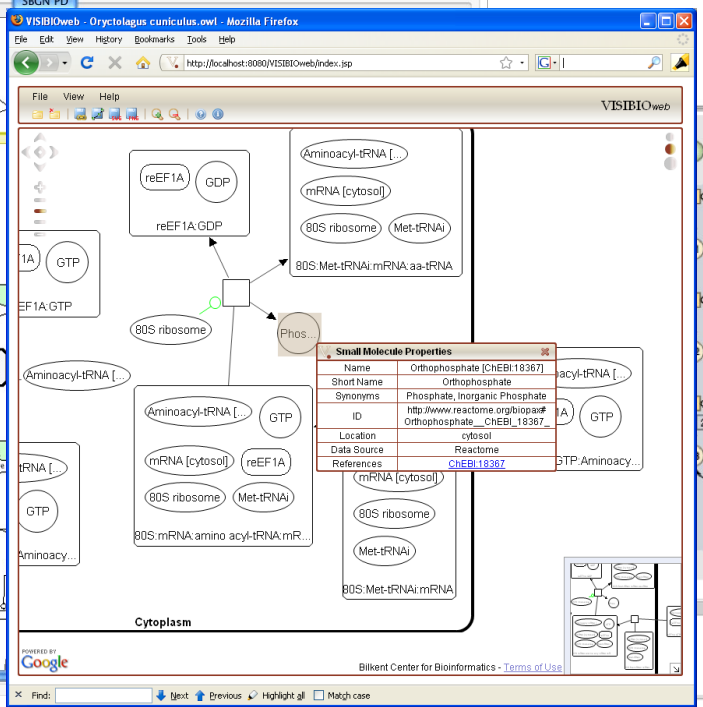

BioModels Home
Browse models
Submit
Sign in
Support
About BioModels
BIOMD0000000005 - Tyson1991_CellCycle_6var
Reference Publication
Cell Cycle Model; Tyson (1991, 6 variables)
Description
Reaction

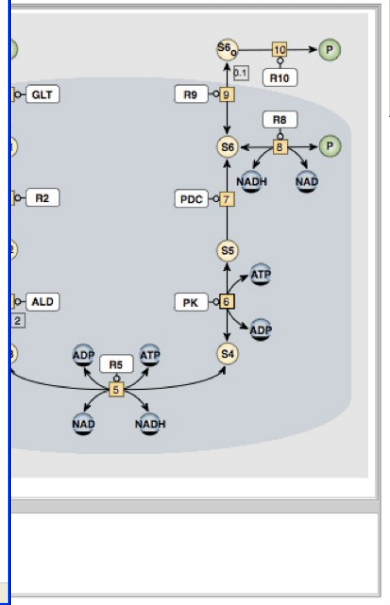
BIOMD0000000005
Refresh
Close
p-cyclin
p-cyclin cdc2
cdc2k
total cdc2
p-cyclin cdc2-p
cdc2k-P
cyclin


PANTHER
Classification System
INSULIN/IGF PATHWAY-MITOGEN ACTIVATED PROTEIN KINASE KINASE/MAP KINASE CASCADE
created with CellDesigner
Pathway Diagram
Pathway Description
File Edit Zoom Select Color
Interactive Standard/Activity Flow
SBGN Image View
SBGN PD

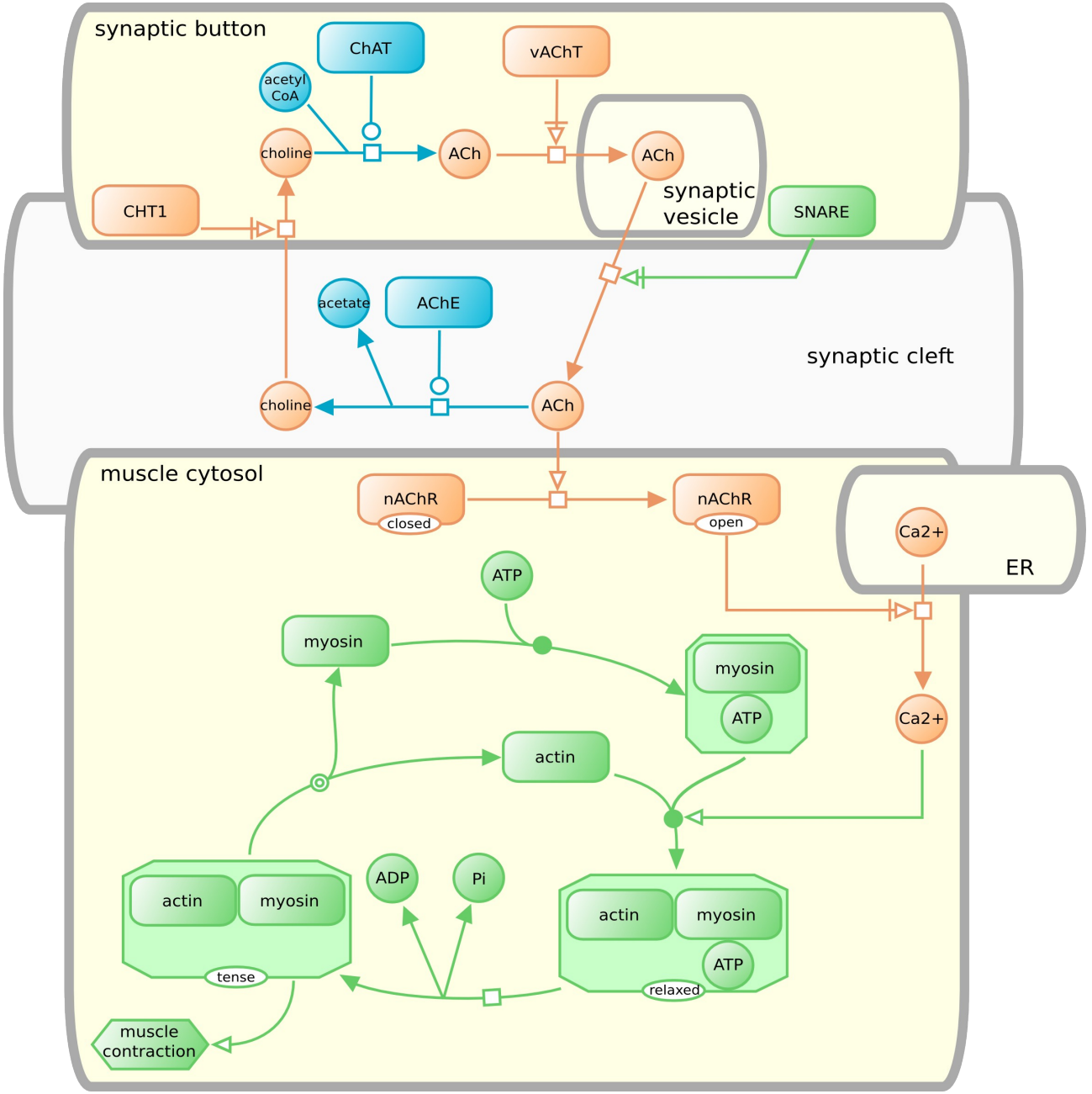

EPE2
synaptic button
synaptic vesicle
muscle cytosol
ACh
choline
acetate
SNARE


Insulin
IGF
INSR
IGF-R
IRR
SOS
Grb2
Active
Ras
Raf
ATP
MEK
ATP


VISIBIOweb - Oryctolagus cuniculus.owl - Mozilla Firefox
http://localhost:8080/VISIBIOweb/index.jsp
VISIBIOweb
reEF1A
GDP
reEF1A:GDP
Aminoacyl-tRNA [...
mRNA [cytosol]
80S ribosome
Met-tRNAi
80S:Met-tRNAi:mRNA:aa-tRNA
GTP
Small Molecule Properties
Name
Orthophosphate [ChEBI:18367]
Short Name
Orthophosphate
Synonyms
Phosphate, Inorganic Phosphate
ID
http://www.reactome.org/biopax#Orthophosphate__ChEBI_18367_
Location
cytosol
Data Source
Reactome
References
ChEBI:18367
Cytoplasm
Bilkent Center for Bioinformatics - Terms of Use


JWS Online
Search | Upload | About | Help
GLT
R9
R8
S6
NADH
NAD
R2
PDC
S5
ALD
PK
ATP
ADP
S4
R5
NAD
NADH

Linking SBGN maps to external information

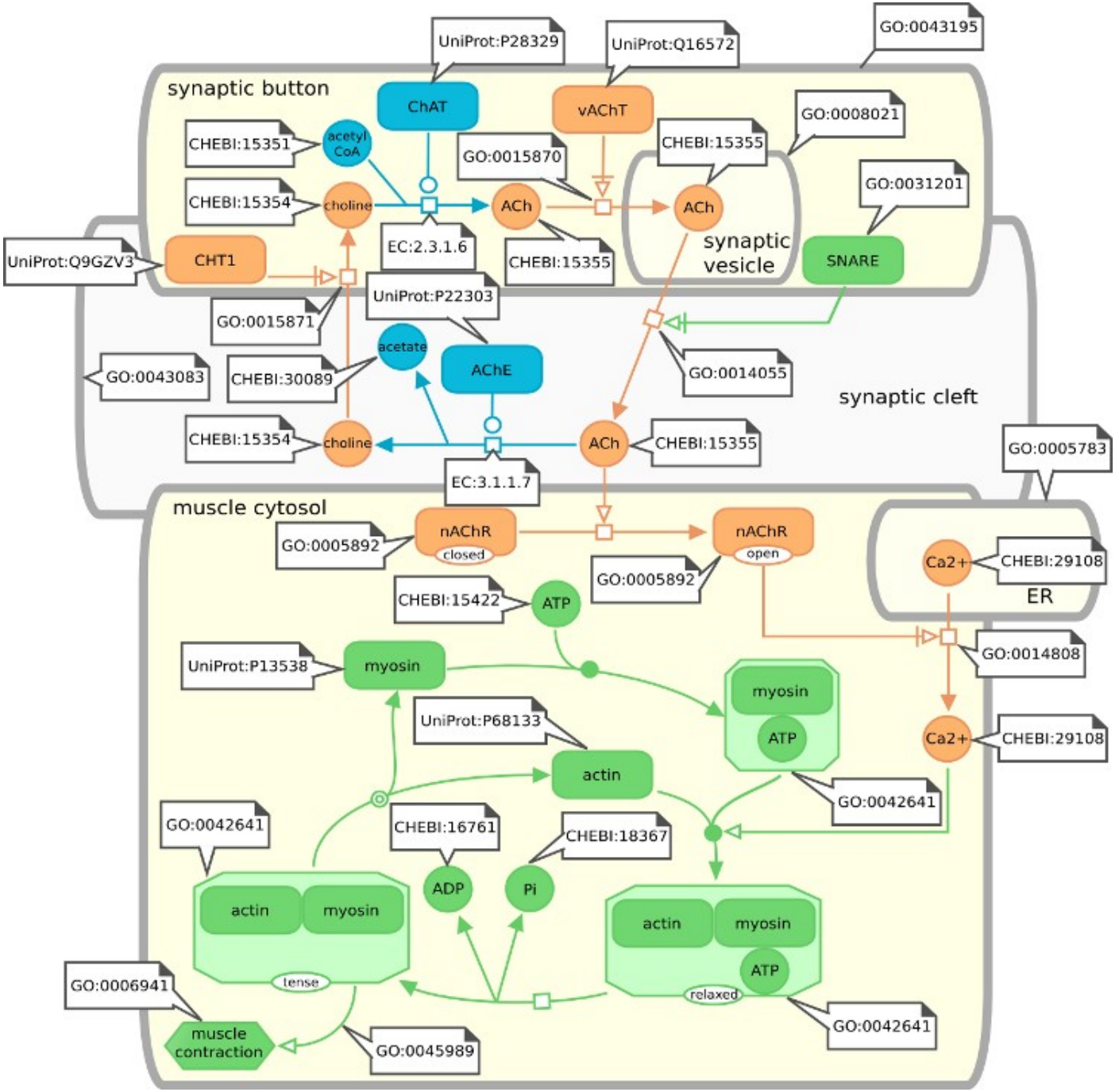


catalytic processes

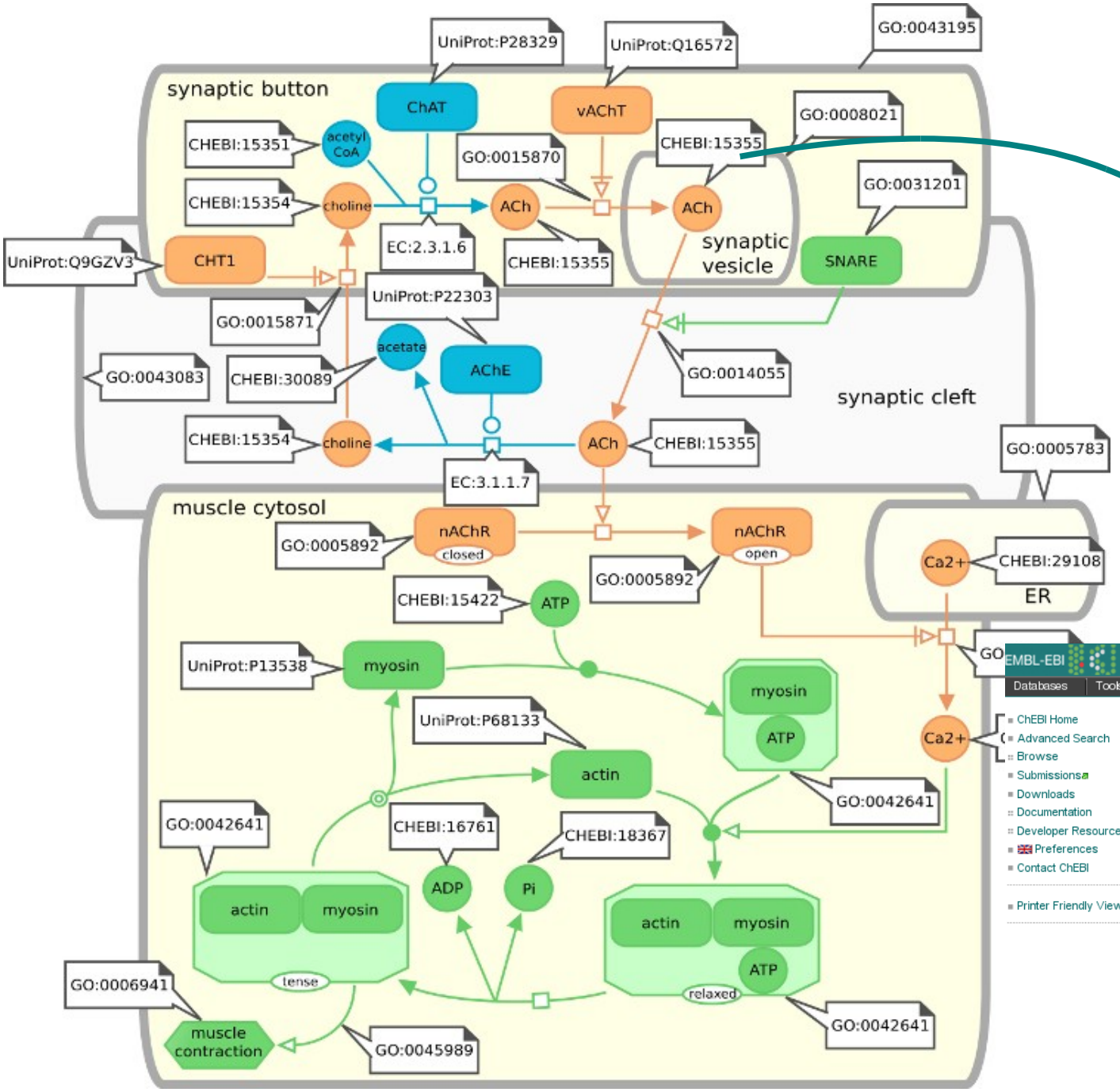
transport processes

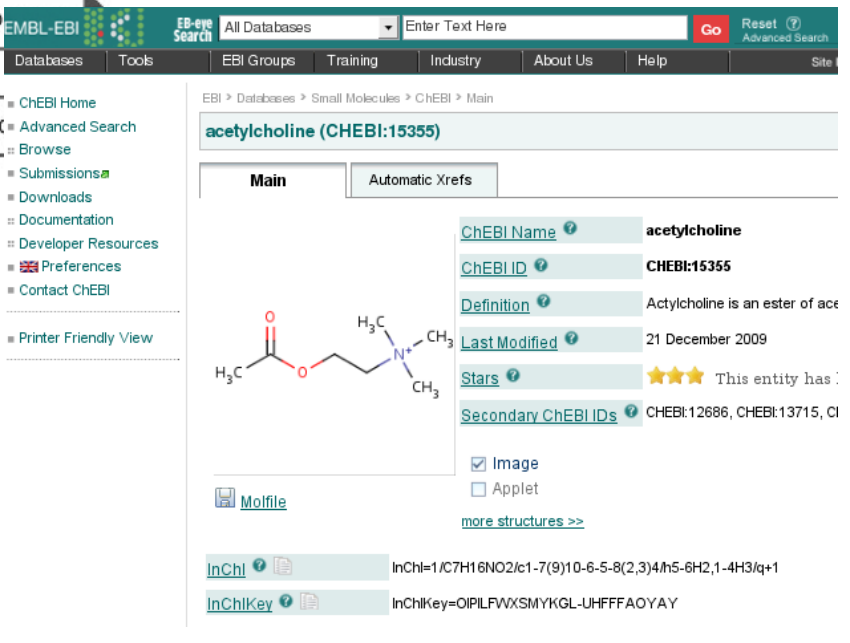
contractile proteins

Linking SBGN maps to external information



Linking SBGN maps to external information

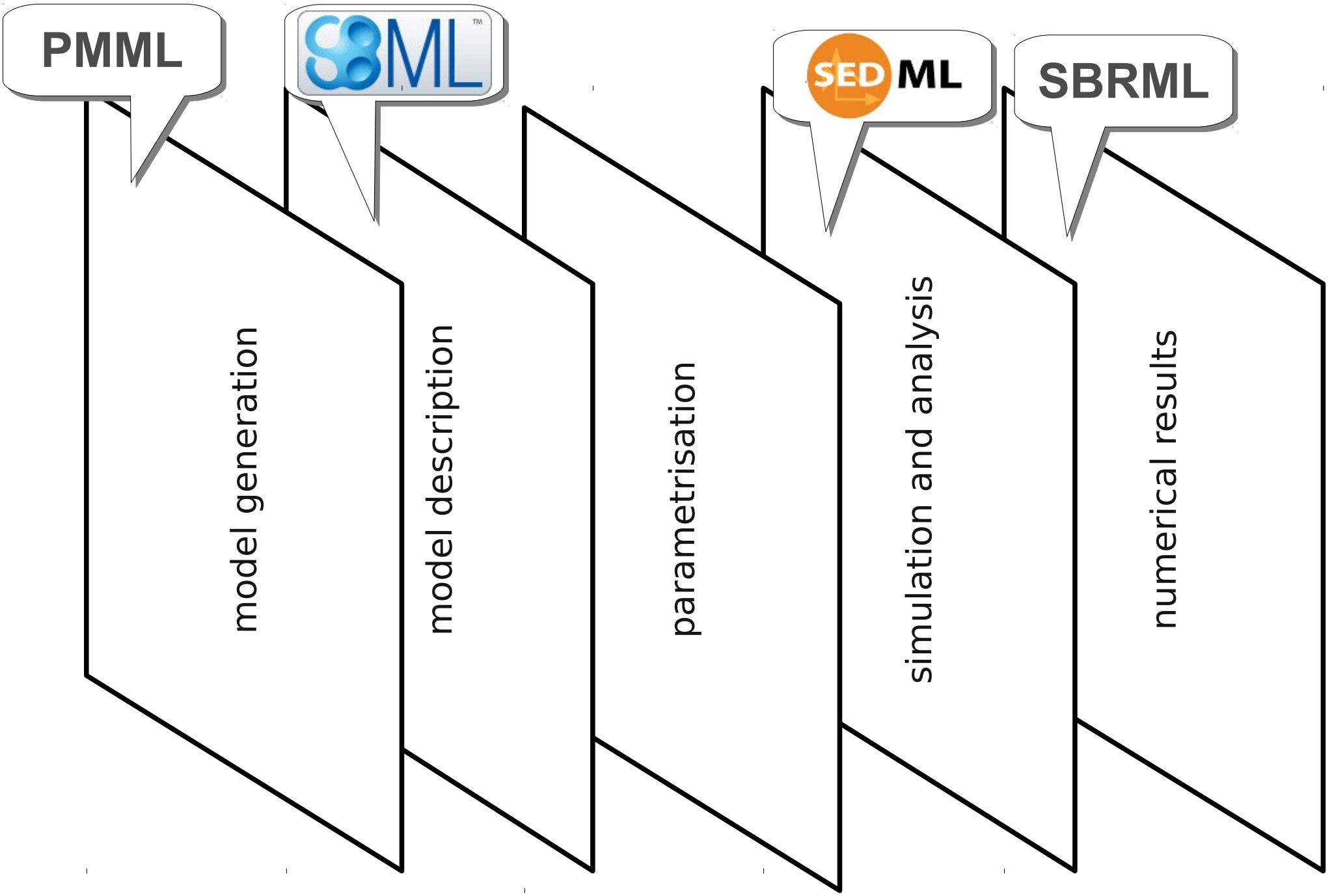




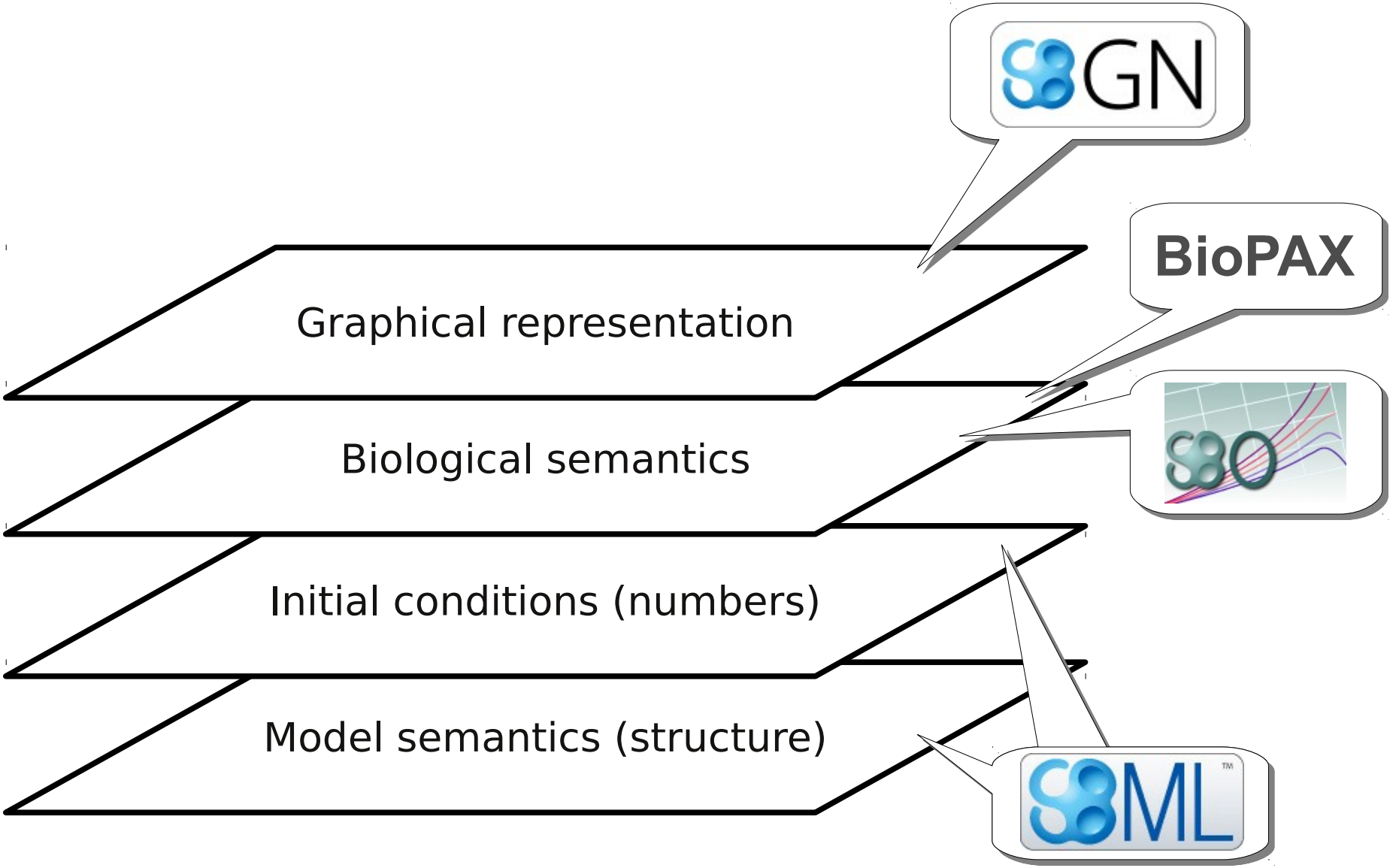
Is the mosaic of standards complete?

	Models	Simulation	Results
Minimal requirements	MIRIAM	MIASE	
Data-models	SBML, SBGN	SED ML	SBRML
Ontologies	SBO	KISAO	TEDDY

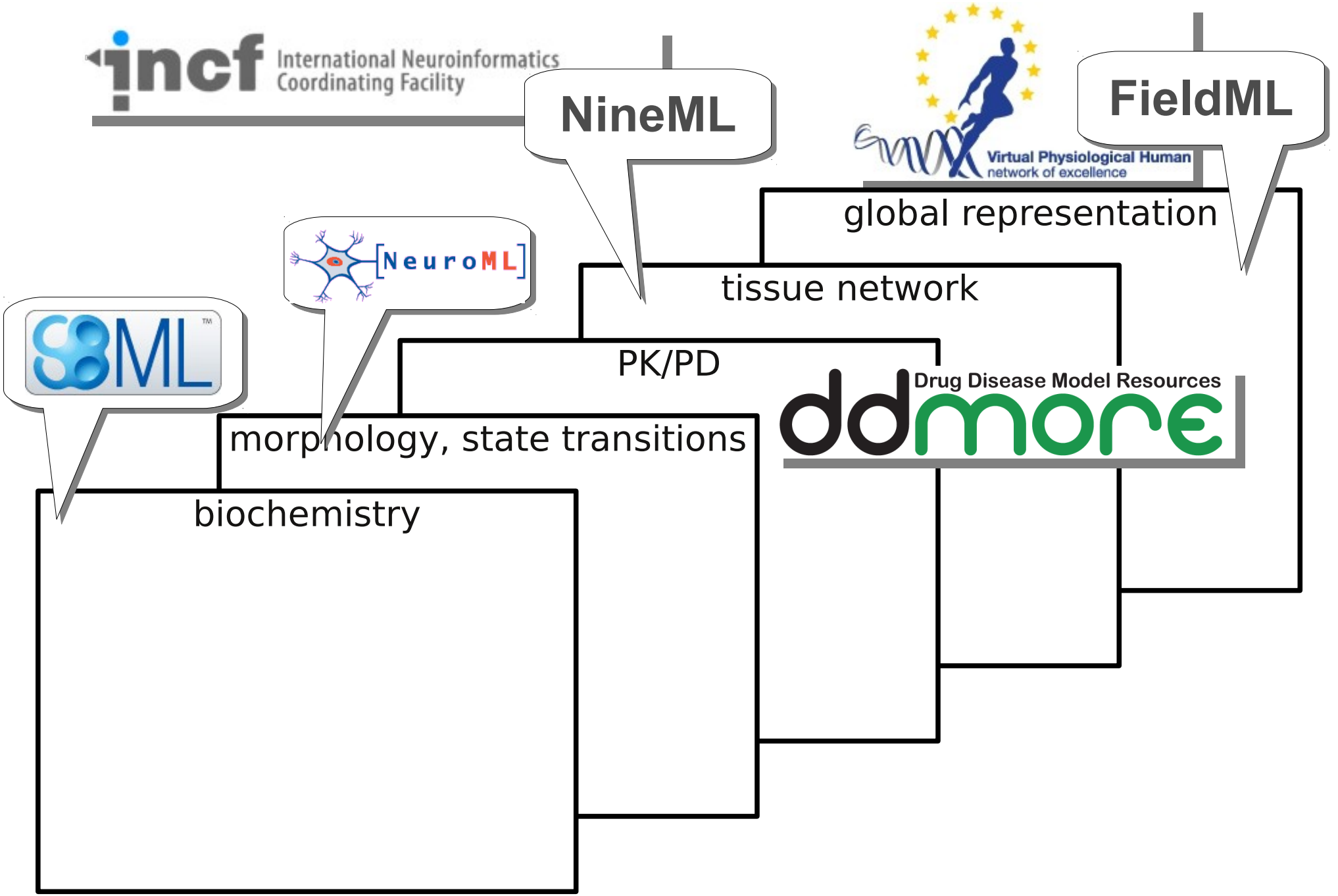
Disentangling the model life-cycle



Disentangling the level of discourse



Non-overlapping languages to cover all models



Requirements for a overarching standardisation structure

- What?
  - Set of interoperable description languages
  - Cover all aspects of modelling and simulation, all types of descriptions / views of the real
  - Role of community-maintained ontologies.
- How?
  - Independence towards Institutions, funders and individuals
  - Role of European Research Infrastructures? (ELIXIR, ISBE)
- Who?
  - Communities developing their standards: Systems Biology, Physiology (VPH), Neuroscience (INCF), Drug discovery (DDMoRe), Clinical data (CDISC) ...
  - Other players in knowledge-representation: W3C ...
  - Academic and corporate users: Modeling platforms (MatWorks ...), Pharma (Pistoia alliance) ...

Requirements for a overarching standardisation structure

- What?
  - Set of interoperable description languages
  - Cover all aspects of modelling and simulation, all types of descriptions / views of the real
  - Role of community-maintained ontologies.
- How?
  - Independence towards Institutions, funders and individuals
  - Role of European Research Infrastructures? (ELIXIR, ISBE)
- Who?
  - Communities developing their standards: Systems Biology, Physiology (VPH), Neuroscience (INCF), Drug discovery (DDMoRe), Clinical data (CDISC) ...
  - Other players in knowledge-representation: W3C ...
  - Academic and corporate users: Modeling platforms (MatWorks ...), Pharma (Pistoia alliance) ...

COmputational Modeling in Biology NEtwork (COMBINE) forthcoming: http://co.mbine.org

COMBINE 2010

- 6 to 9 October 2010, Edinburgh, before the ICSB
- 81 attendees (forecast was 50 max ...)
- 14 sessions, plus breakouts, 42 presentations, 30 posters

Physiome standards
SED-ML
SBGN languages
libSBGN and SBGN support

Encoding graph layouts
Interactions and reactions
Semantics and metadata resources
Encoding and using semantics

Format conversion
Software support
BioPAX levels
What is not covered yet

SBML Level 3
libSBML and SBML support

followed by:

SBML 10th anniversary

Acknowledgements

Visionary: **Hiroaki Kitano**

SBML editors: Frank Bergmann, *Andrew Finney, Stefan Hoops*, ***Michael Hucka***, *Nicolas Le Novère, Sarah Keating*, Sven Sahle, *Herbert Sauro*, Jim Schaff, Lucian Smith, Darren Wilkinson

MIRIAM: Nick Juty, Camille Laibe

SBGN editors: Emek Demir, *Michael Hucka*, Nicolas Le Novère, Huaiyu Mi, Stuart Moodie, Falk Schreiber, *Anatoly Sorokin*

BioModels Database: Vijilashkimi Chelliah, Marco Donizelli, Harish Dharuri, Arnaud Henry, Michael Hucka, Lukas Endler, Enuo He, Camille Laibe, Nicolas Le Novère, Chen Li, Lu Li, Melanie I Stefan, Nicolas Rodriguez, Jacky L Snoep

The whole community of Computational Systems Biology

The EBI group Computational Systems Neurobiology