EMBL-EBI

Sharing enriched computational models, a cornerstone for Integrative Biology

(Desperate attempt to justify my existence)

Computational Neurobiology

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

REVIEW

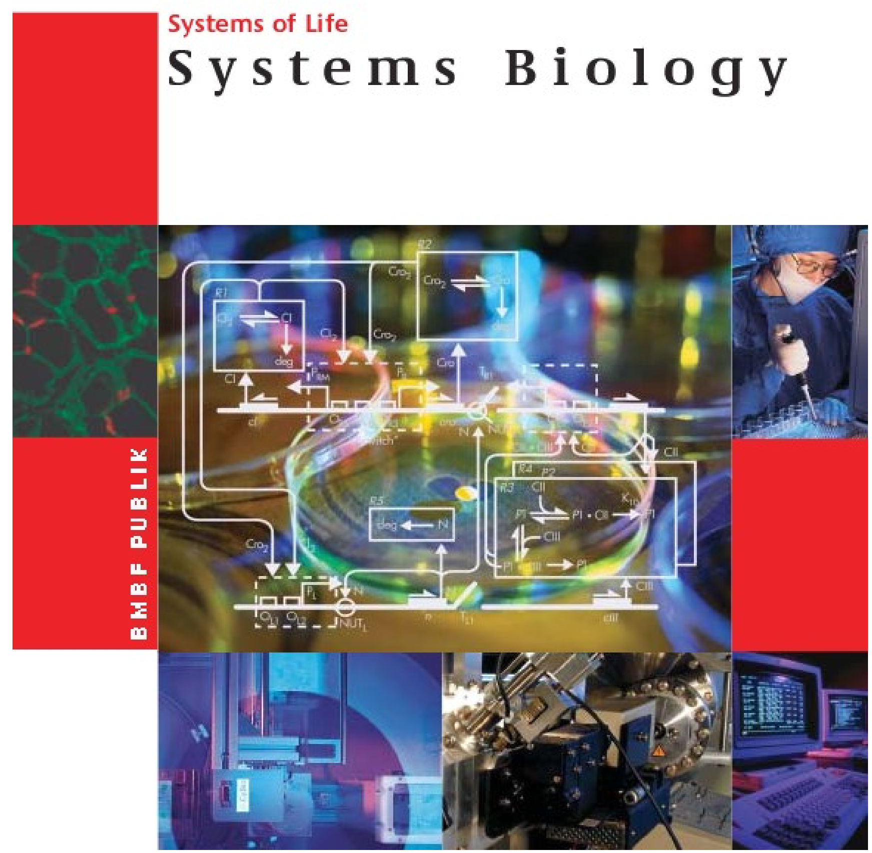
Systems Biology: A Brief Overview

Hiroaki Kitano

1 MARCH 2002 VOL 295 SCIENCE www.sciencemag.org

Federal Ministry of Education and Research

Basic science



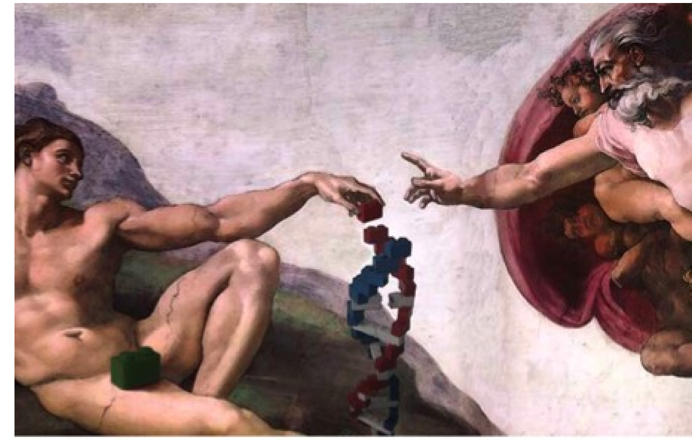
What happened to biology at the end of XXth century?

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

January 2007

etc group

Technology

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

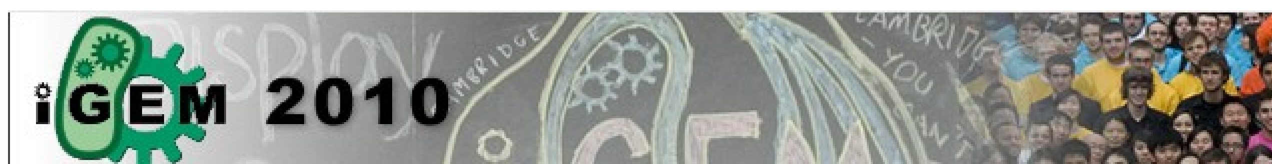
Cell

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

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

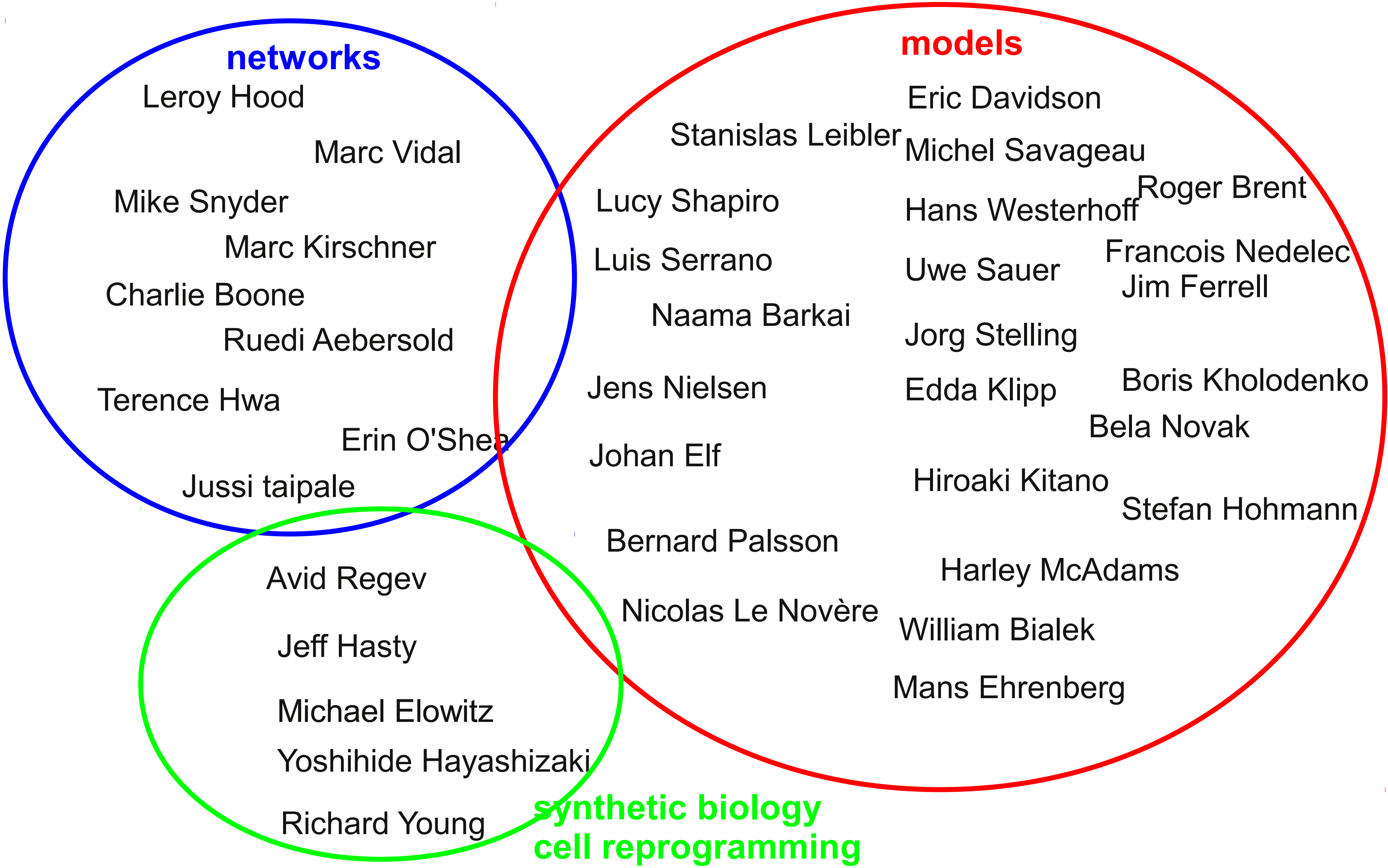


page discussion view source history teams

About

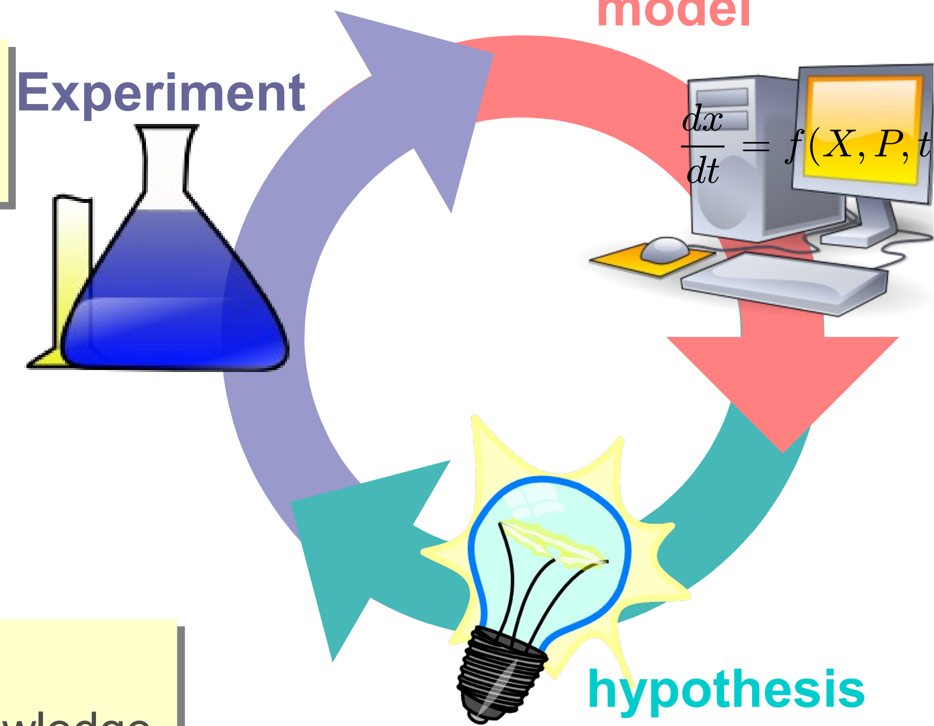
The International Genetically Engineered Machine competition (iGEM) is
Biology competition. Student teams are given a kit of biological parts at the beginnin
Standard Biological Parts. Working at their own schools over the summer, they use t

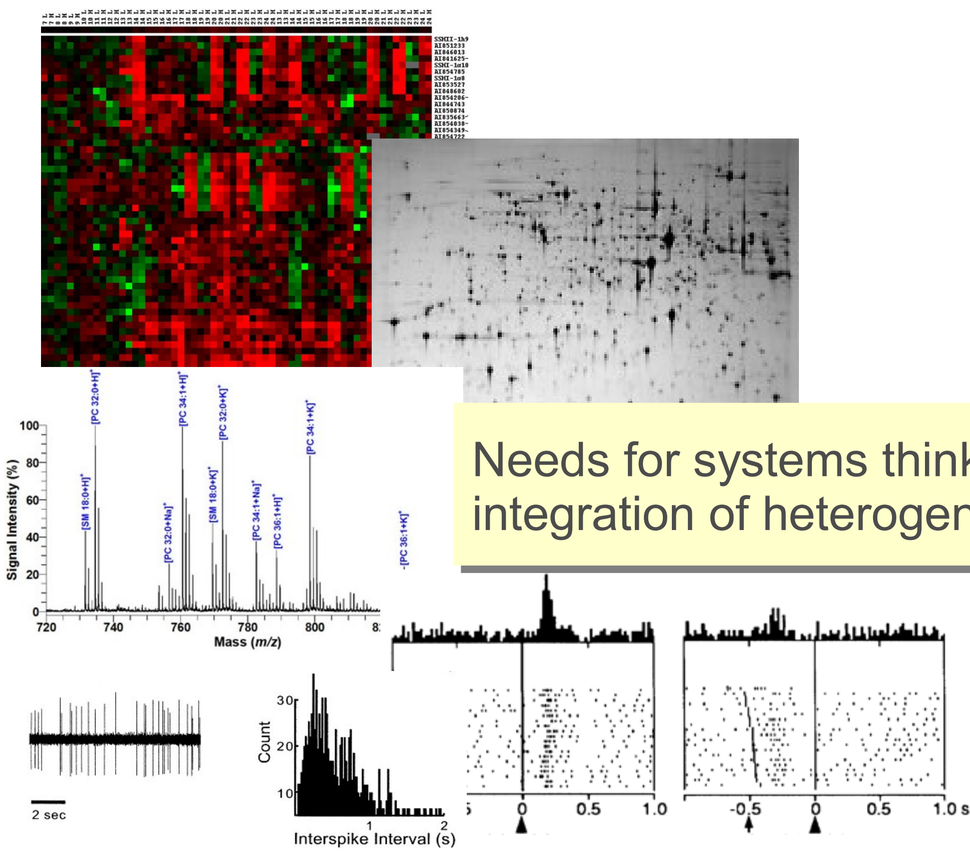
Nobel Symposium on Systems Biology (June 2009)



Consequences of this revolution on our activity

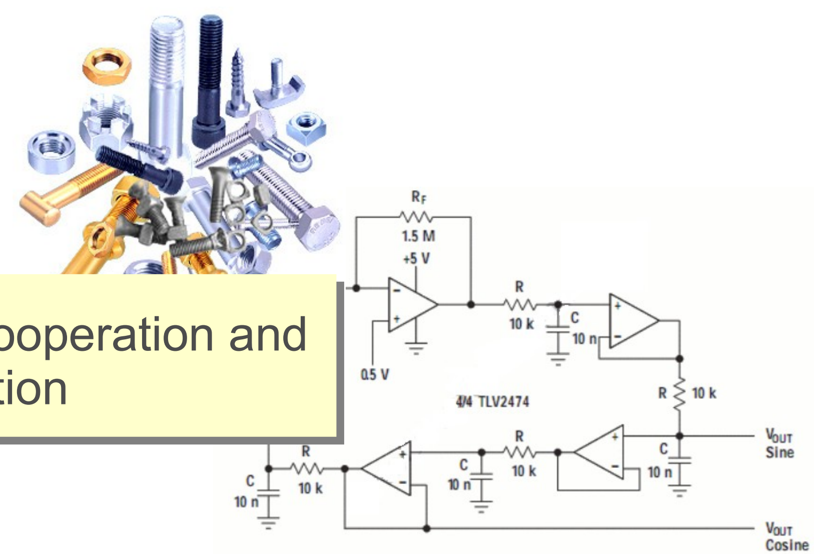
Needs for interplay between models and reality tests





Needs for systems thinking and integration of heterogeneous knowledge

Needs for cooperation and standardisation



Computational modelling for biology and medicine left the niches in the last decades

- 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)

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

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 pathways, controlled vocabularies, etc.

Search | Go to the model | Advanced search

Browse models

- Curated models (249)
- Browse models using GO
- Non-curated models (224)

Simulate in JWS Online

Submit a model

Mirror at California Institute of Technology http://biomodels.caltech.edu

BioModels AT SourceForge http://sourceforge.net/projects/biomodels/

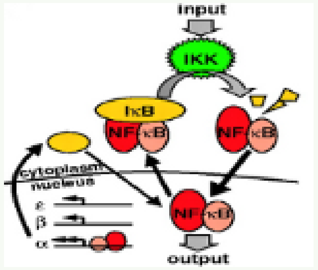
Web Services http://www.ebi.ac.uk/biomodels-main/webservices

Download archived models http://www.ebi.ac.uk/biomodels/models-main/tars/

Model of the month

July, 2010

The activity of the transcription factor NF-κB, is largely controlled by three IkB isoforms (IkBα, IkBβ, IkBε) which upon binding to NF-kB, prevents its association with DNA causing its localization to the cytoplasm. A computational model that describes the temporal control of NF-kB activation by IkB proteins is described here.



Read more...

News

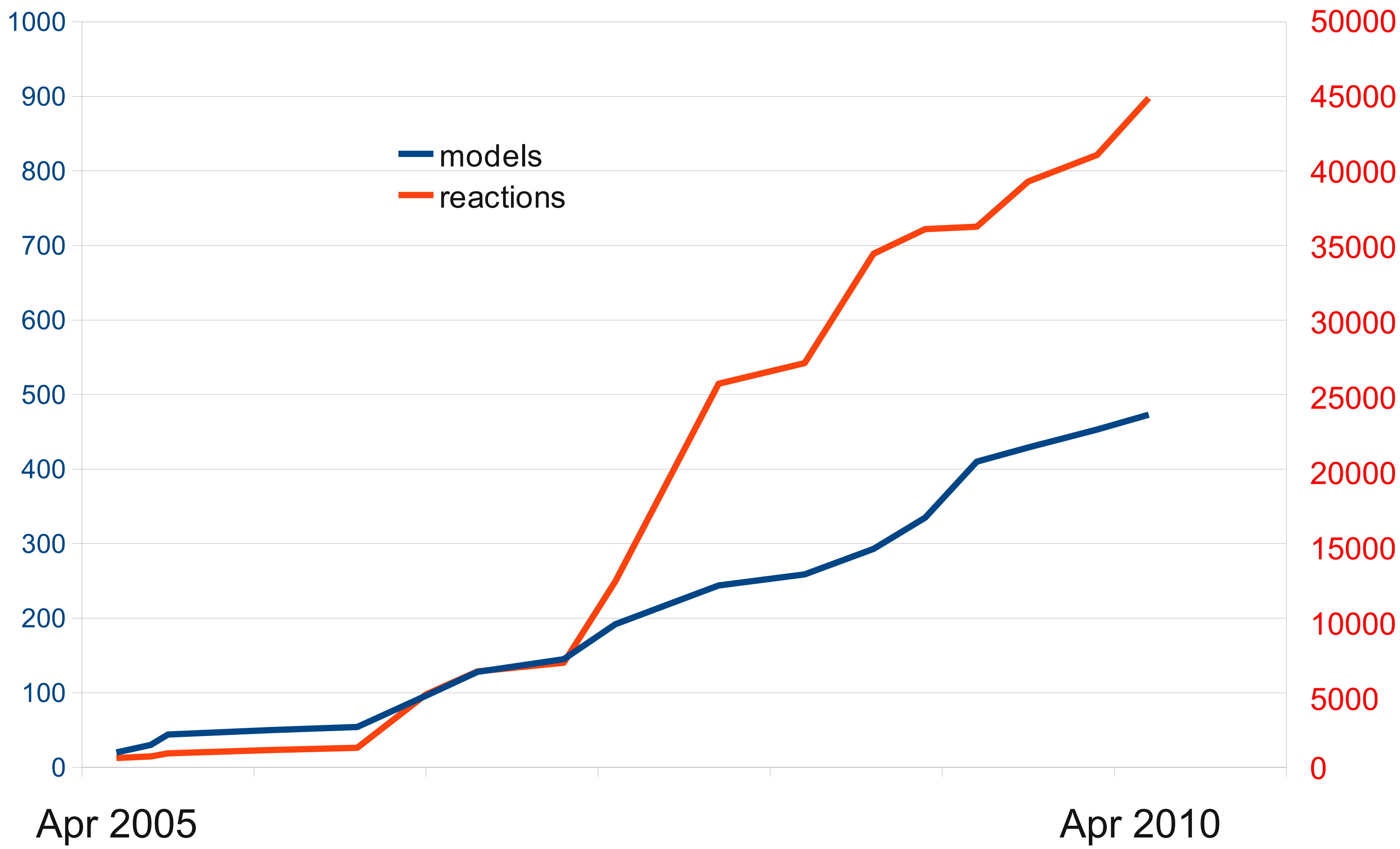
29 June 2010 **New BioModels Database publication**

New BioModels Database paper published in *BMC Systems Biology*: BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models.

2nd June 2010 **SBML to VCML converter updated**

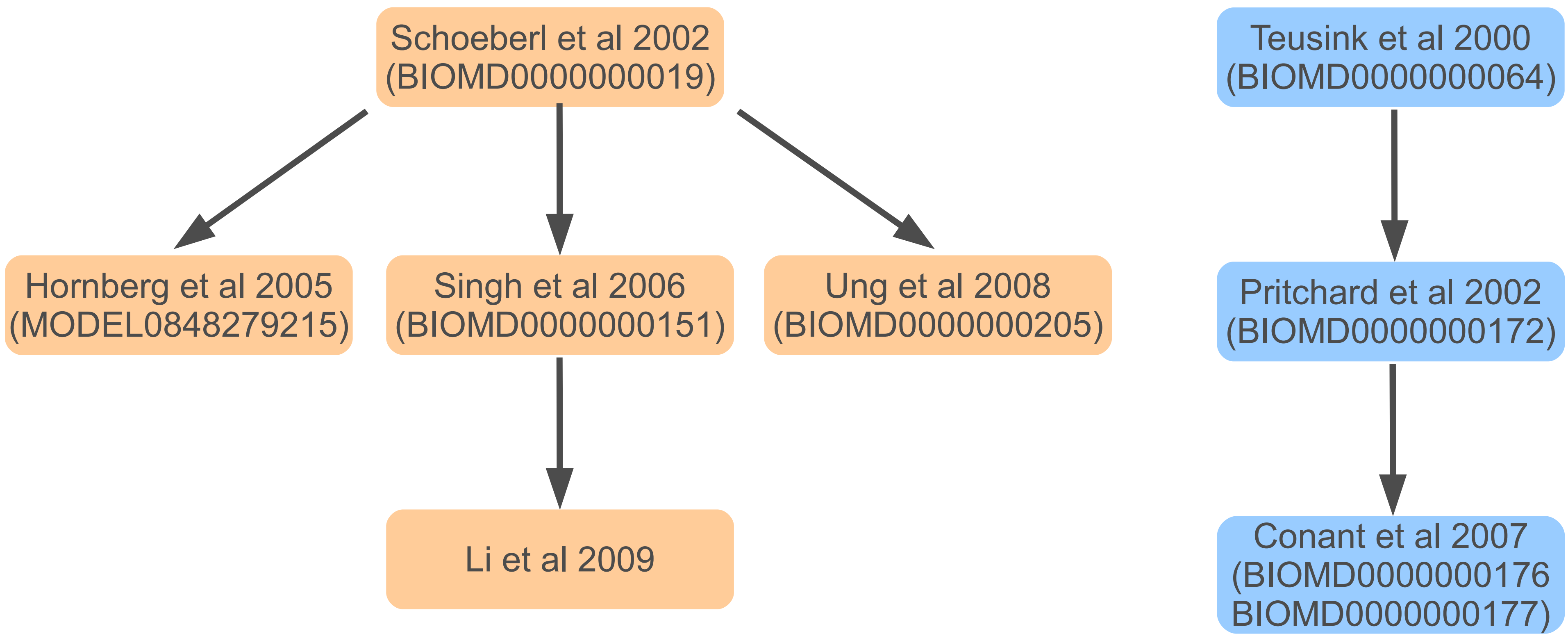
The Virtual Cell recently released a new version of

Computational models on the rise



Growth of BioModels Database between its creation and release 17

Direct model re-use: EGFR signalling and glycolysis



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	MIRIAM	MIASE	
Data-mode	SBML	ED ML	SBRML
Ontologies	SBO	KISAO	TEDDY

SBML is not limited to biochemistry!

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

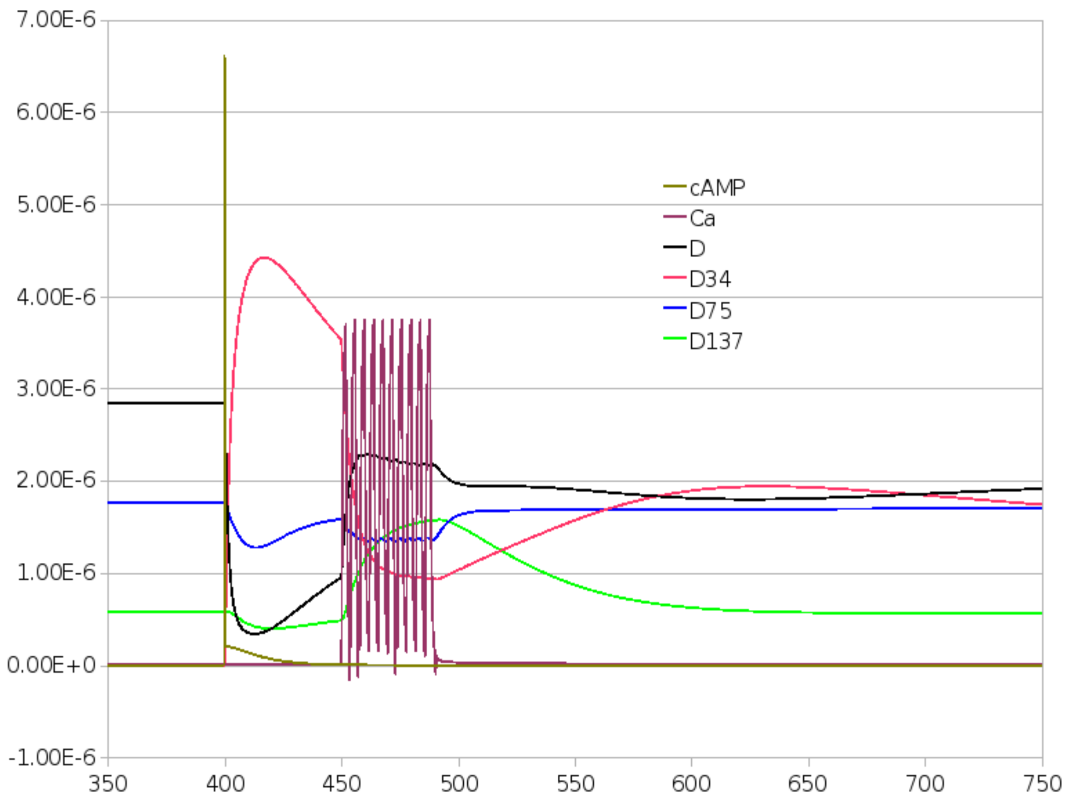
Events can describe any discontinuous change, e.g. neurotransmitter release or repolarisation;

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

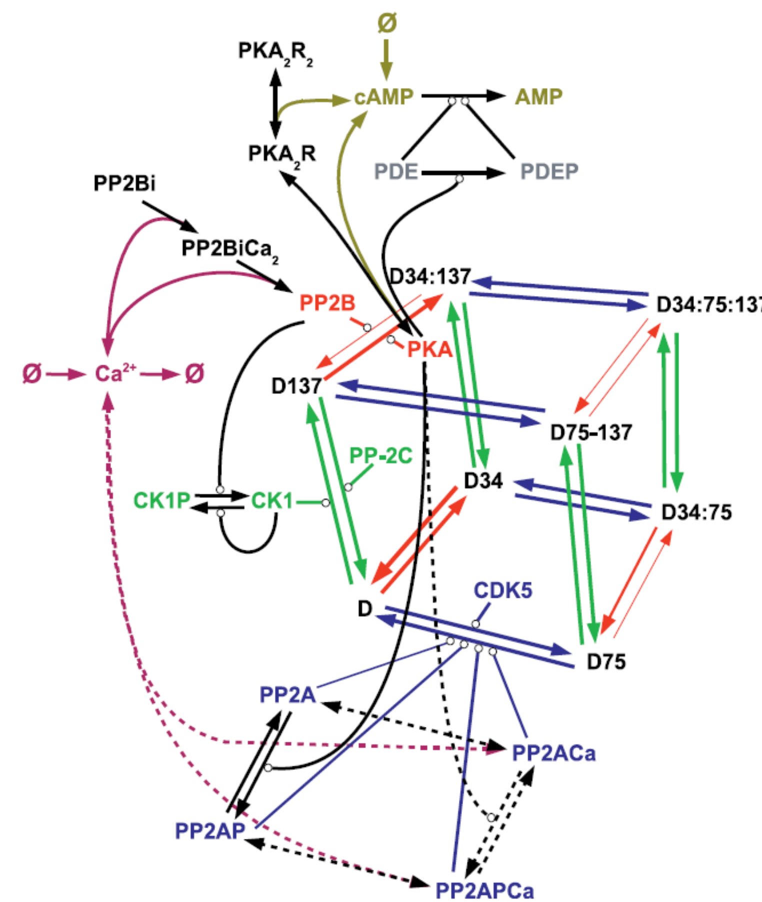
➔ SBML is about process descriptions

Model of signalling pathways



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

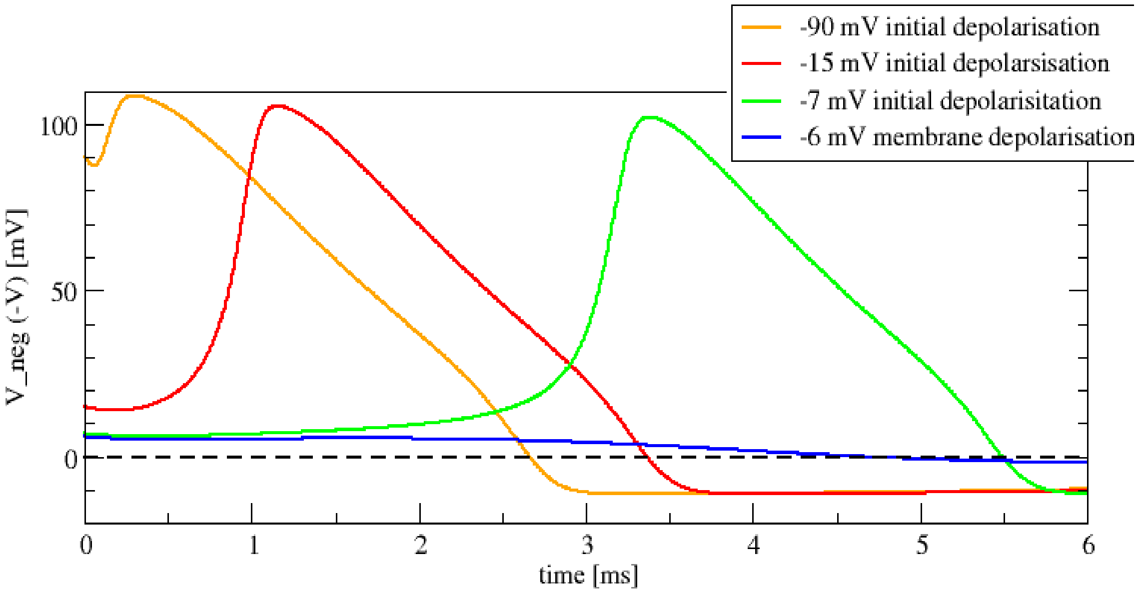
BIOMD0000000153



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.

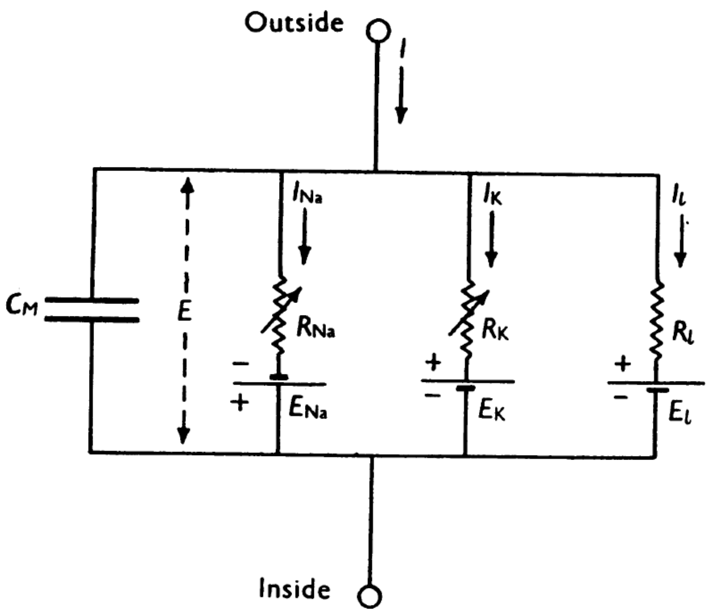
BIOMD0000000020

rate rule:

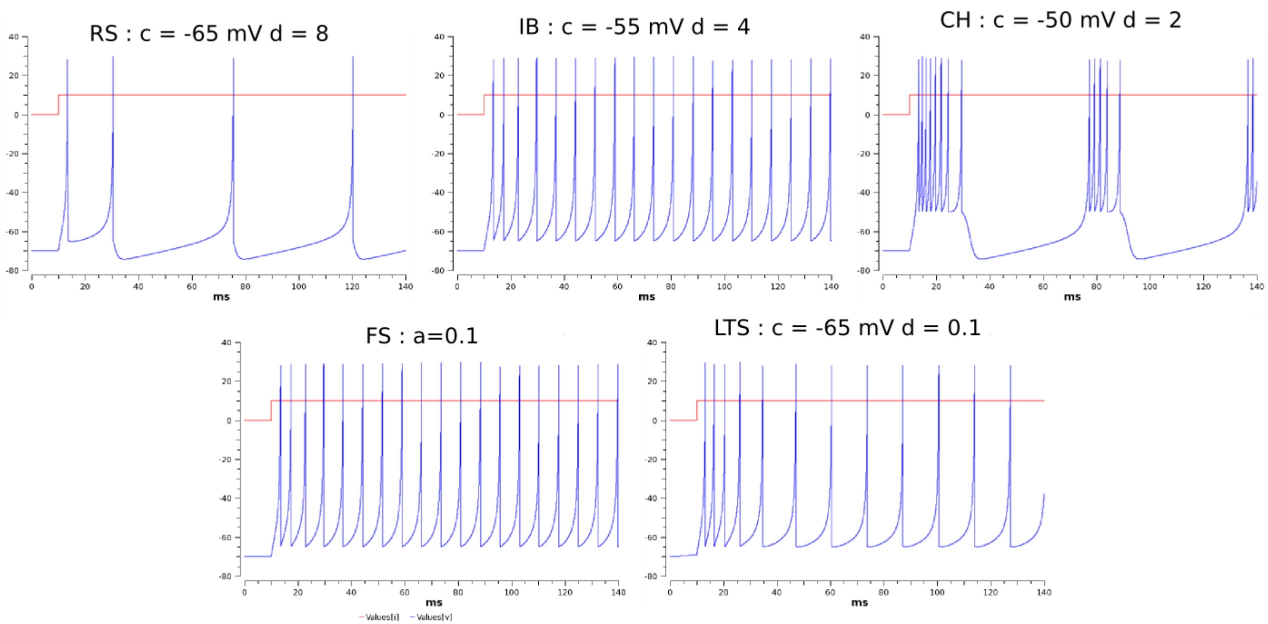
$$\frac{dv}{dt} = \frac{I - (i_{Na} + i_K + i_L)}{C_m}$$

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

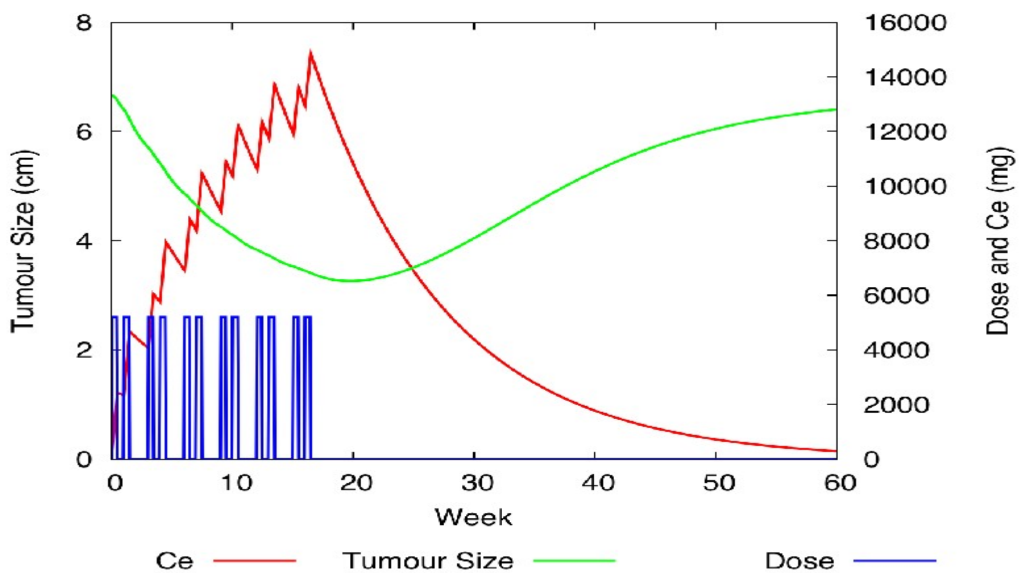
rate rule:

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

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

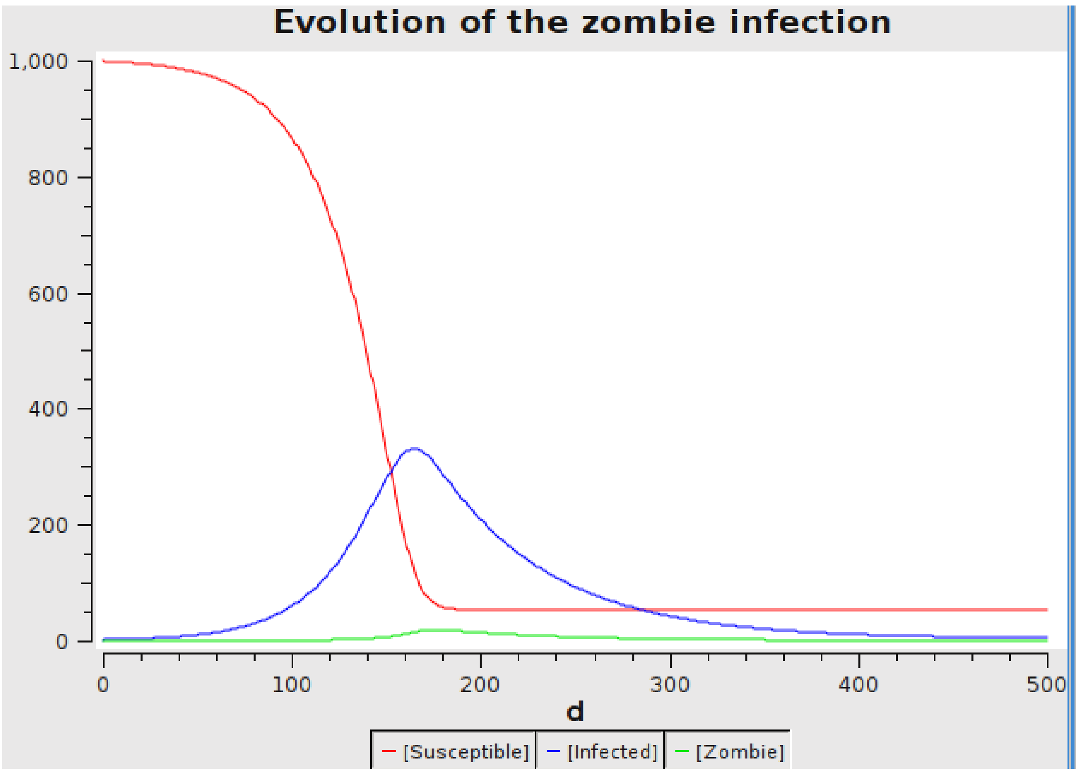
rate rule:

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

assignment rule:

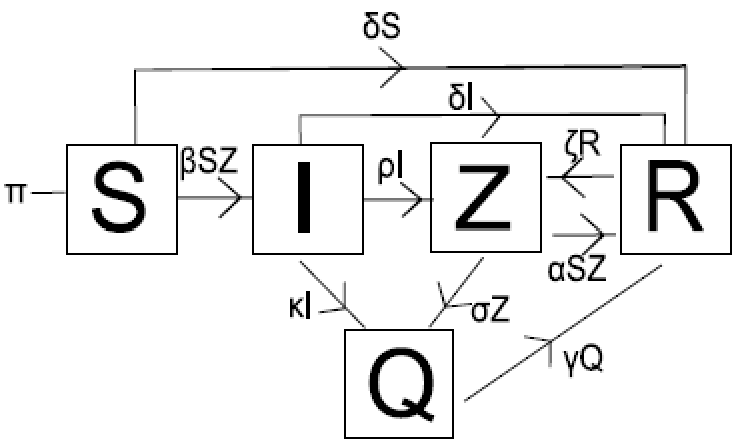
$$Effect = 1 - \frac{E_{max} - Ce}{Amt_{50} + Ce}$$

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



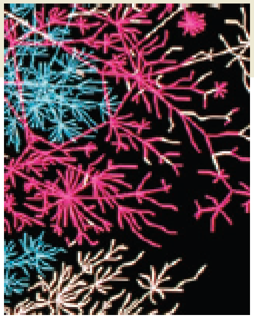
SBML Level 3 packages

- Core package – Release candidate
- 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

???

Model semantics

	Models	Simulation	Results
Minimal requiremen	MIRIAM	MIASE	
Data-models	SBML SBGN	SEDML	SBRML
Ontologies	SBO	KISAO	TEDDY



_computational BIOLOGY

PERSPECTIVE

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

Nicolas Le Novère[1,15], Andrew Finney[2,15], Michael Hucka[3], Upinder S Bhalla[4], Fabien Campagne[5], Julio Collado-Vides[6], Edmund J Crampin[7], Matt Halstead[7], Edda Klipp[8], Pedro Mendes[9], Poul Nielsen[7], Herbert Sauro[10], Bruce Shapiro[11], Jacky L Snoep[12], Hugh D Spence[13] & Barry L Wanner[14]

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

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

MIRIAM cross-references

Data-type identifier (required) ← URI

Not a URL, not a “Web-address”!

Data-set Identifier (required) ← text string

Format depends on the resource identified by the data-type

Annotation qualifier (optional) ← text string

Controlled vocabulary established by the community

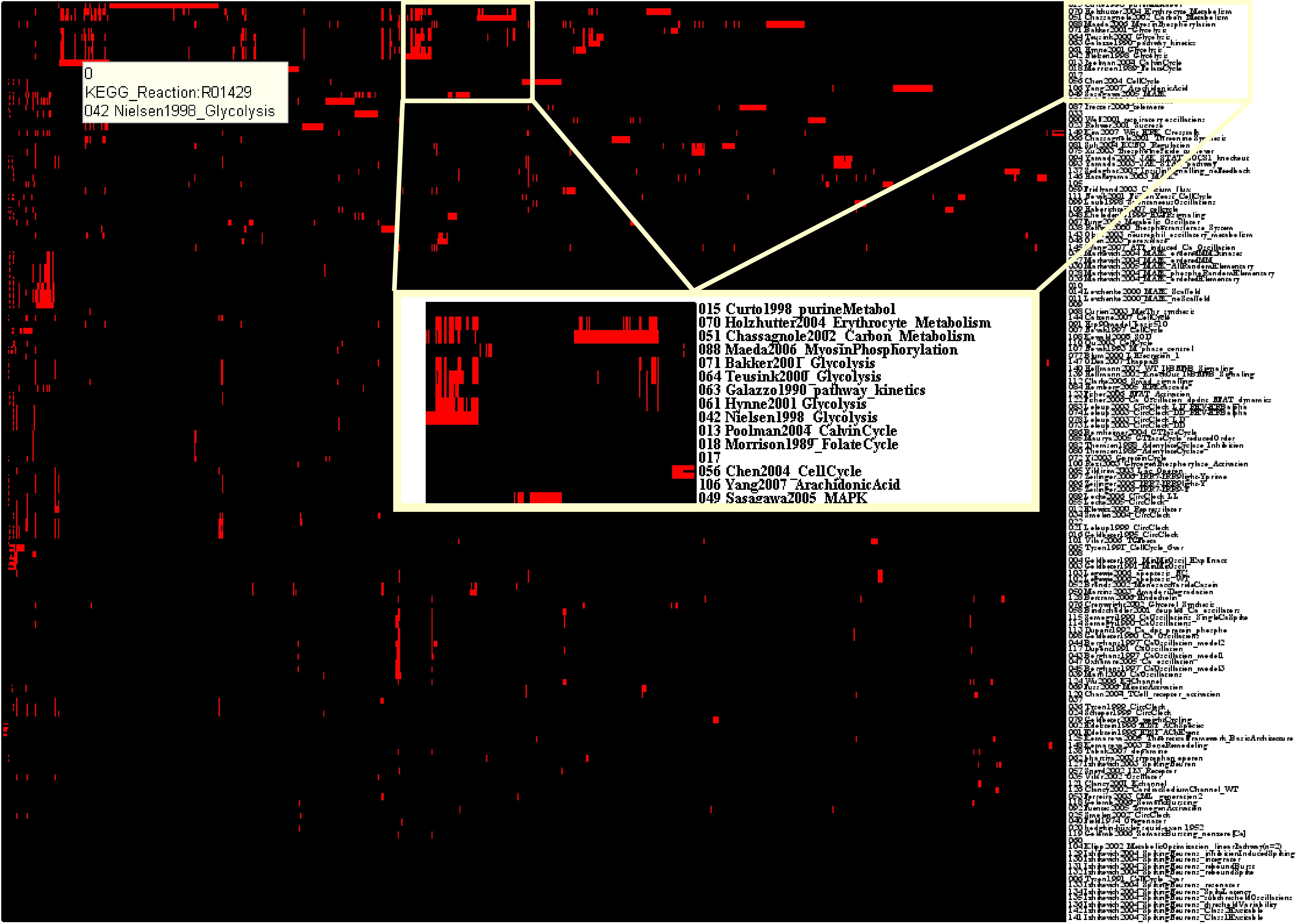
```
UniProt and P62158 (human calmodulin)
        → urn:miriam:uniprot:P62158
EC code and 1.1.1.1 (alcohol dehydrogenase)
        → urn:miriam:ec-code:1.1.1.1
Gene Ontology and GO:0000186 (activation of MAPKK activity)
        → urn:miriam:obo.go:GO%3A0000186
```

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)


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

http://www.semanticsbml.org/semanticSBML/default/cluster/0

Semantic SBML

- HOME
- REST API

Login

semanticSBML 2.0

BioModels Similar to BIOMD0000000009.xml

Model	BioModel	Score	Bar Chart
Huang1996_MAPK_ultrasens	BIOMD0000000009	1.0	
Levchenko2000_MAPK_noScaffold	BIOMD0000000011	0.925093068877	
Levchenko2000_MAPK_Scaffold	BIOMD0000000014	0.86507748228	
Kholodenko2000_MAPK_feedback	BIOMD0000000010	0.816212542046	
Markevich2004_MAPK_orderedElementary	BIOMD0000000026	0.737035170293	
Markevich2004_MAPK_phosphoRandomElementary	BIOMD0000000028	0.68757623681	
Markevich2004_MAPK_AllRandomElementary	BIOMD0000000030	0.68757623681	
Markevich2004_MAPK_orderedMM	BIOMD0000000027	0.67292654353	
Markevich2004_MAPK_orderedMM2kinases	BIOMD0000000031	0.67292654353	
Markevich2004_MAPK_phosphoRandomMM	BIOMD0000000029	0.614419563376	
Hornberg2005_ERKcascade	BIOMD0000000084	0.467502293047	
McClean2007_CrossTalk	BIOMD0000000116	0.396968852299	
Kofahl2004_pheromone	BIOMD0000000032	0.347654497489	
Kim2007_Wnt_ERK_Crosstalk	BIOMD0000000149	0.323862350322	
Brown2004_NGF_EGF_signaling	BIOMD0000000033	0.259659012885	
Goldbeter1995_CircClock	BIOMD0000000016	0.243985892215	
Sasagawa2005_MAPK	BIOMD0000000049	0.239991163172	
Ung2008_EGFR_Endocytosis	BIOMD0000000205	0.233723629425	
Leloup1999_CircClock	BIOMD0000000021	0.22918483858	
Goldbeter1991_MinMitOscil_ExplInact	BIOMD0000000004	0.222401483635	
Goldbeter1991_MinMitOscil	BIOMD0000000003	0.213676433868	
Leloup1998_CircClock_LD	BIOMD0000000171	0.201464719898	
Tyson1991_CellCycle_6var	BIOMD0000000005	0.199125864464	
Veening2008_DegU_Regulation	BIOMD0000000240	0.179667408207	
Neves2008_Cell_Shape	BIOMD0000000182	0.168237862604	
Fisher2006_Ca_Oscillation_dpdnt_NFAT_dynamics	BIOMD0000000122	0.163742528861	
Leloup2003_CircClock_DD	BIOMD0000000073	0.163249339887	
Leloup2003_CircClock_LD	BIOMD0000000078	0.163249339887	
Novak2001_FissionYeast_CellCycle	BIOMD0000000111	0.158121867453	
Kholodenko1999_EGFRsignaling	BIOMD0000000048	0.157261597224	
Swat2004_Mammalian_G1_S_Transition	BIOMD0000000228	0.153857976349	
Chen2004_CellCycle	BIOMD0000000056	0.153626692372	

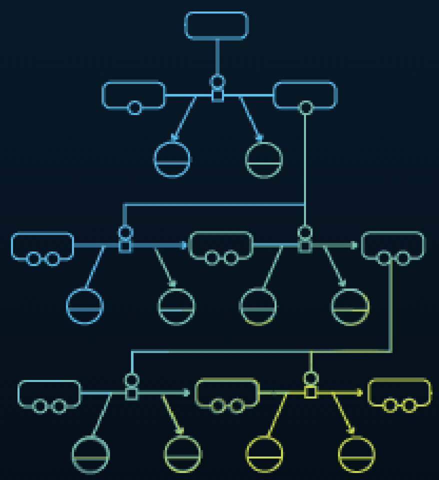
R. Henkel, L. Endler, A. Peters, N. Le Novère, D. Waltemath (2010) Ranked Retrieval of Computational Biology Models. *BMC Bioinformatics*, 11:423

M Schulz, F Krause, N Le Novère, E Klipp, and W Liebermeister: Comparison and clustering of biochemical network models based on semantic annotations. *submitted*

Visual representation of models

	Models	Simulation	Results
Minimal requirements	MIRIAM	MIASE	
Data-mode		ED ML	SBRML
Ontologies	SBO	KISAO	TEDDY

SBGN



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:

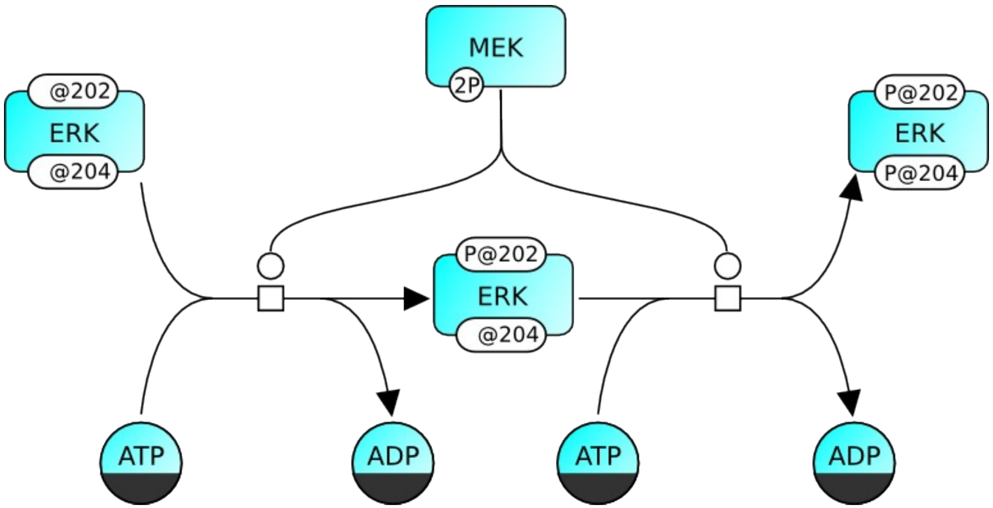
Le Novère N, Hucka M, Mi H, Moodie S, Schreiber F, Sorokin A, Demir E, Wegner K, Aladjem MI, Wimalaratne SM, Bergman FT, Gauges R, Ghazal P, Kawaji H, Li L, Matsuoka Y, Villéger A, Boyd SE, Calzone L, Courtot M, Dogrusoz U, Freeman TC, Funahashi A, Ghosh S, Jouraku A, Kim S, Kolpakov F, Luna A, Sahle 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.

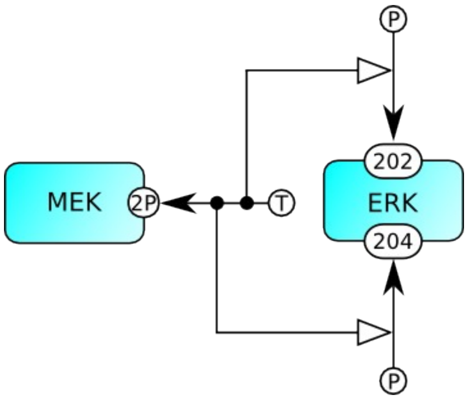
Graph trinity: three languages in one notation

Process Descriptions



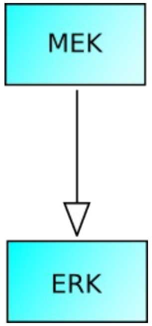
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships



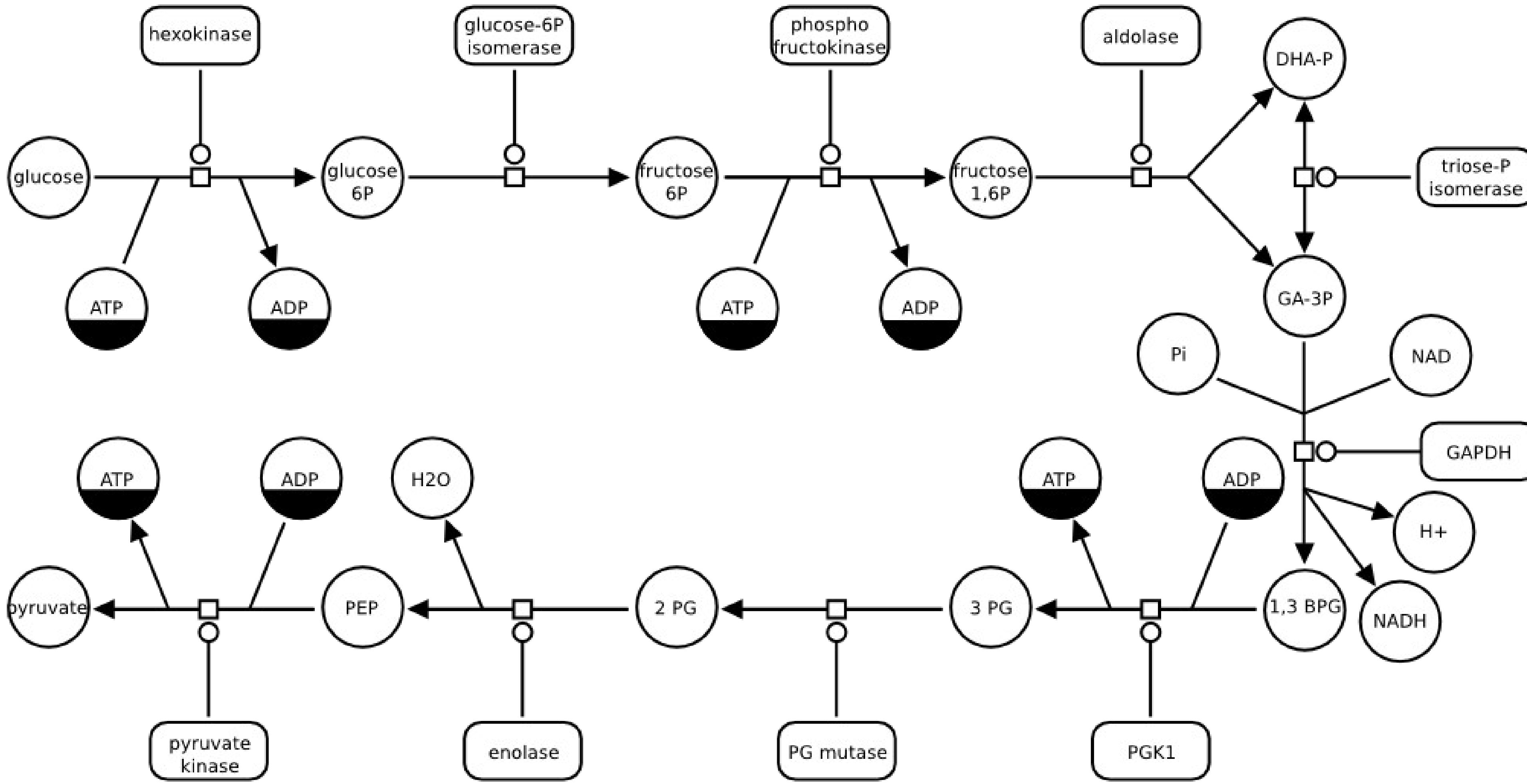
- Unambiguous
- Mechanistic
- Non-sequential
- Independence of relationships

Activity Flows

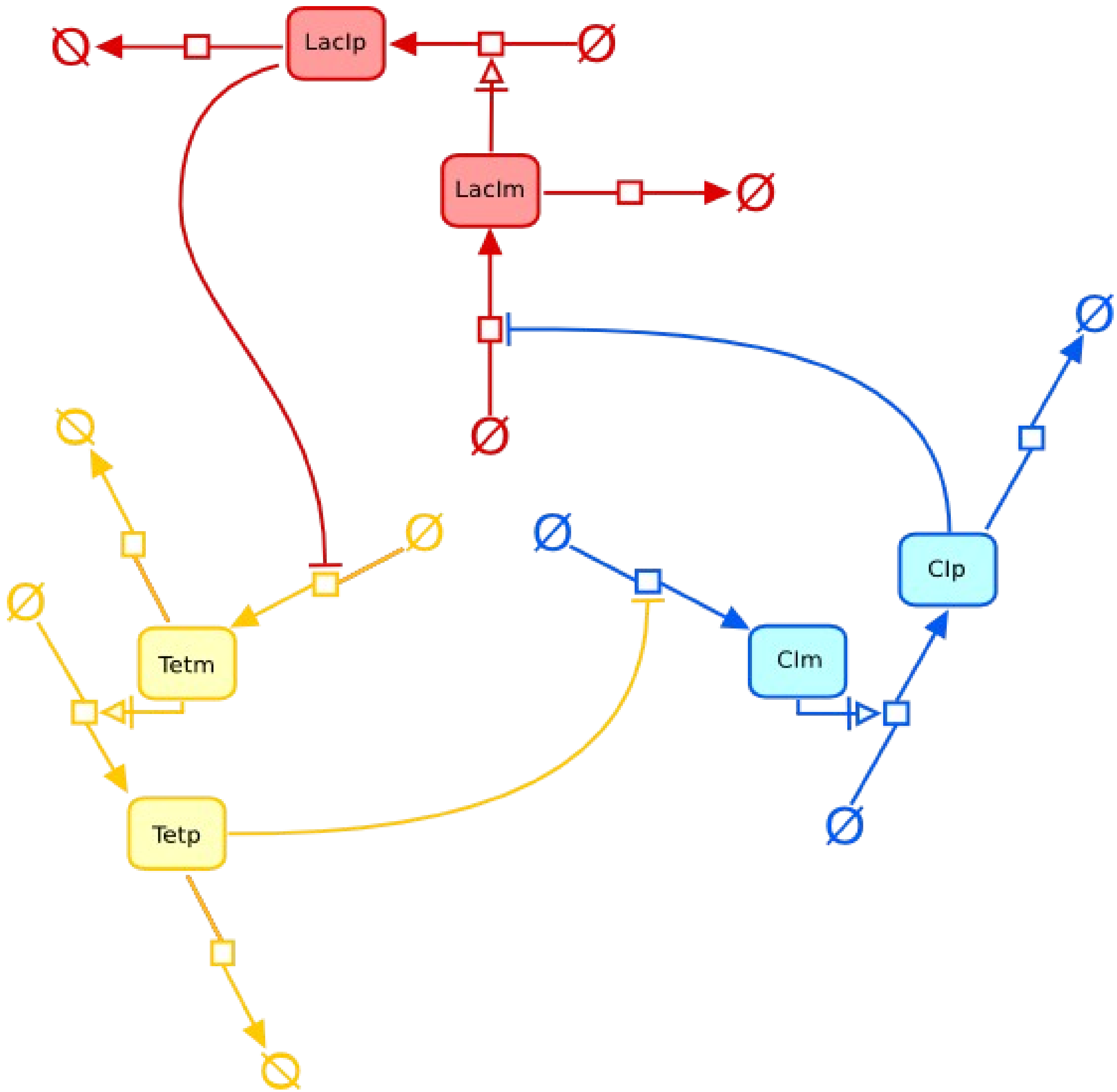


- Ambiguous
- Conceptual
- Sequential

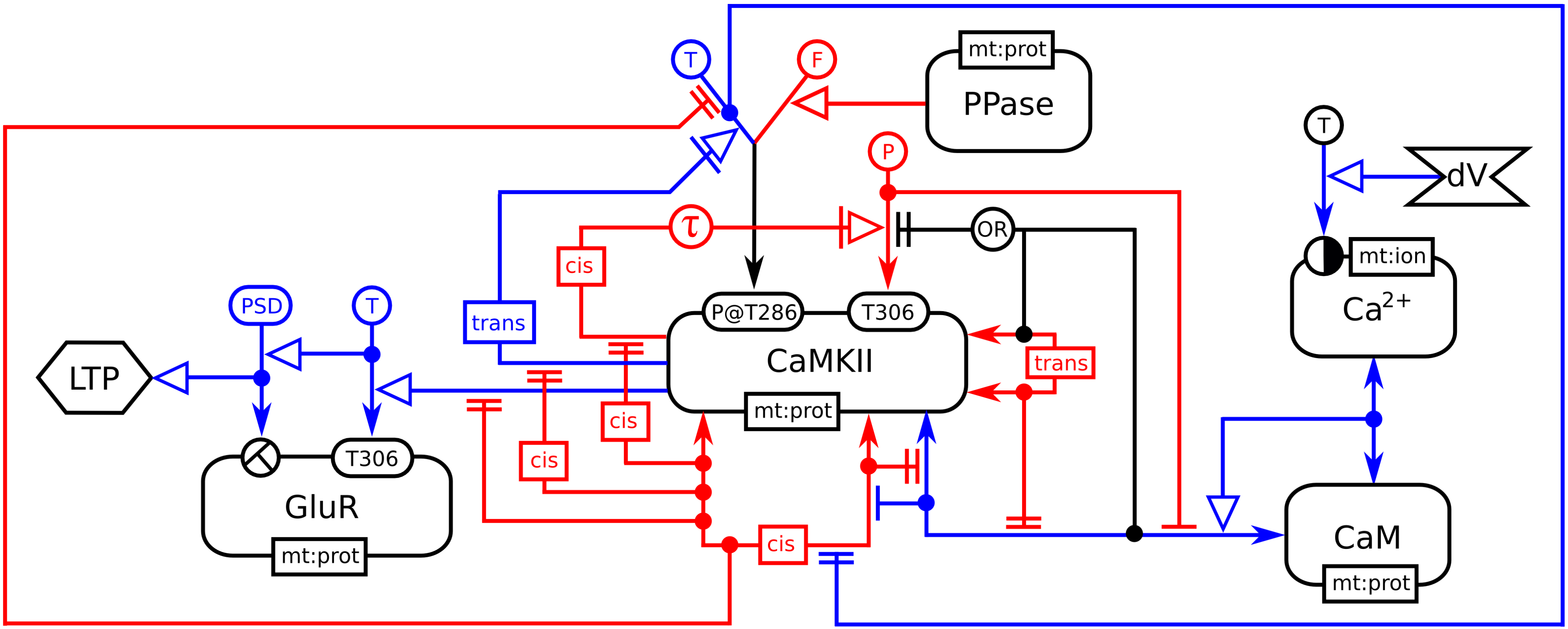
SBGN Metabolic network in Process Description Language



Repressilator in Process Description Language



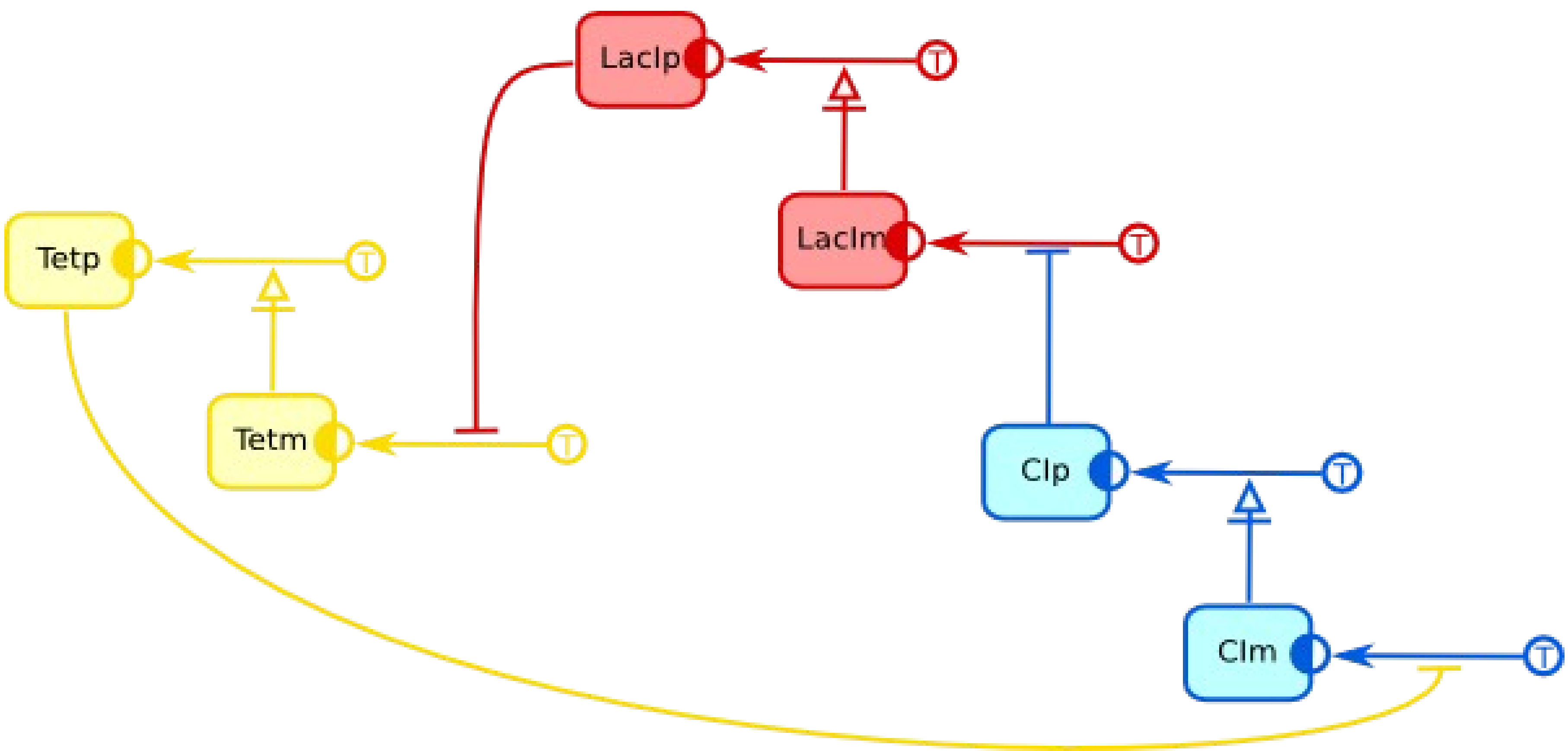
SBGN ER map of calcium-regulated synaptic plasticity



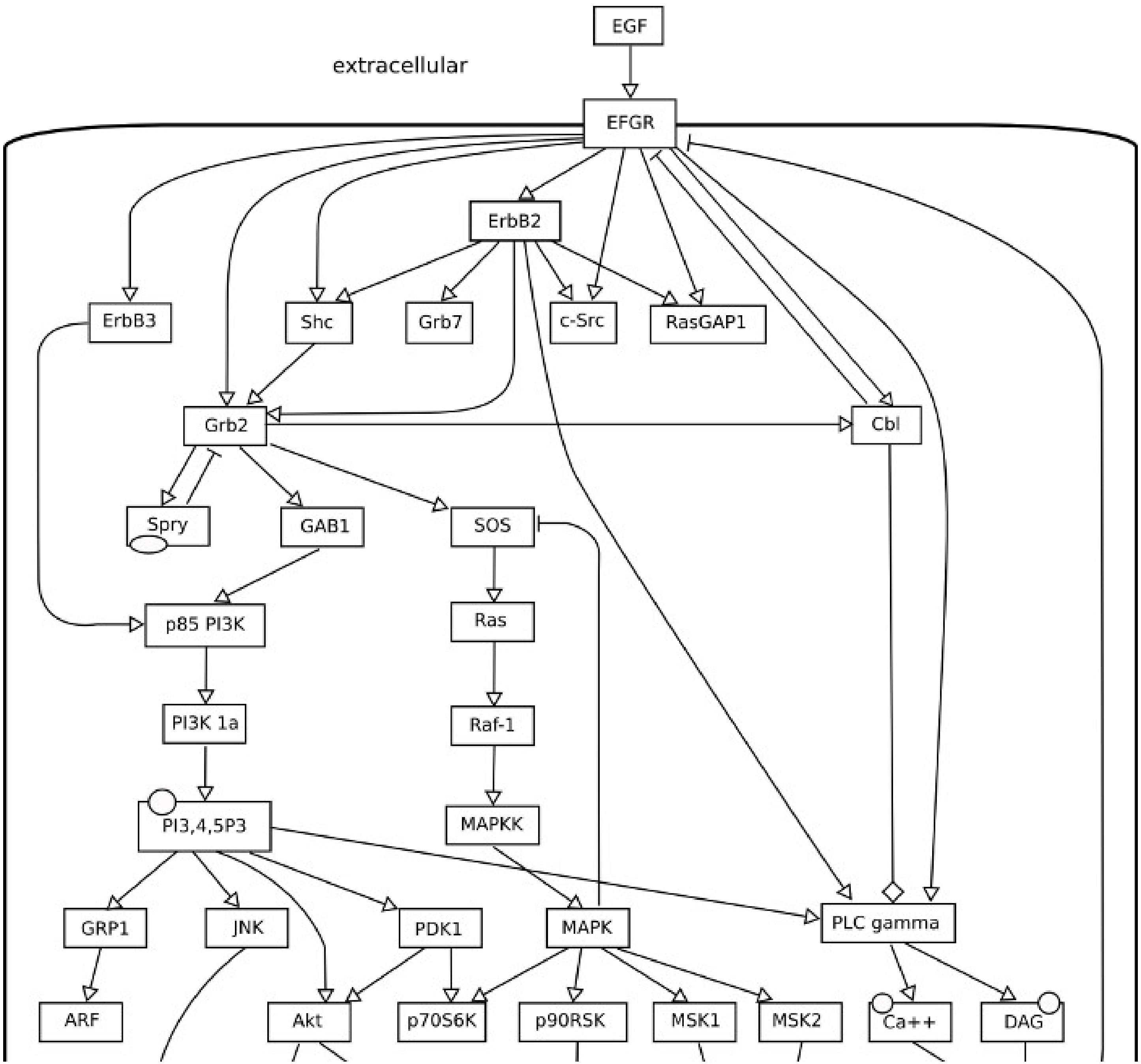
increases synaptic weight

decreases synaptic weight

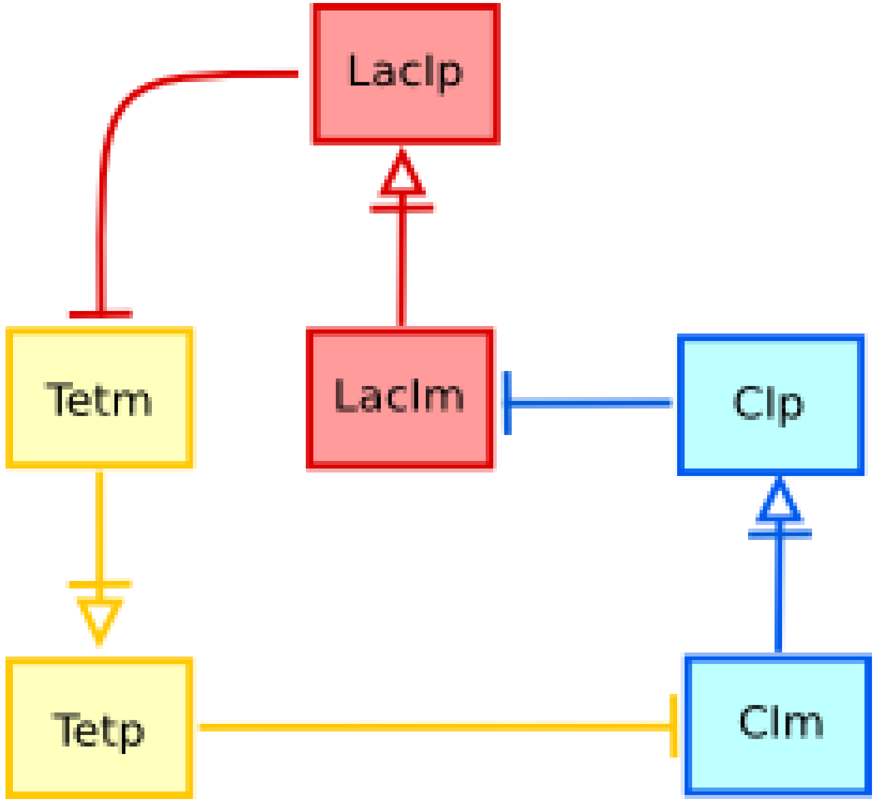
Repressilator in Entity Relationship Language



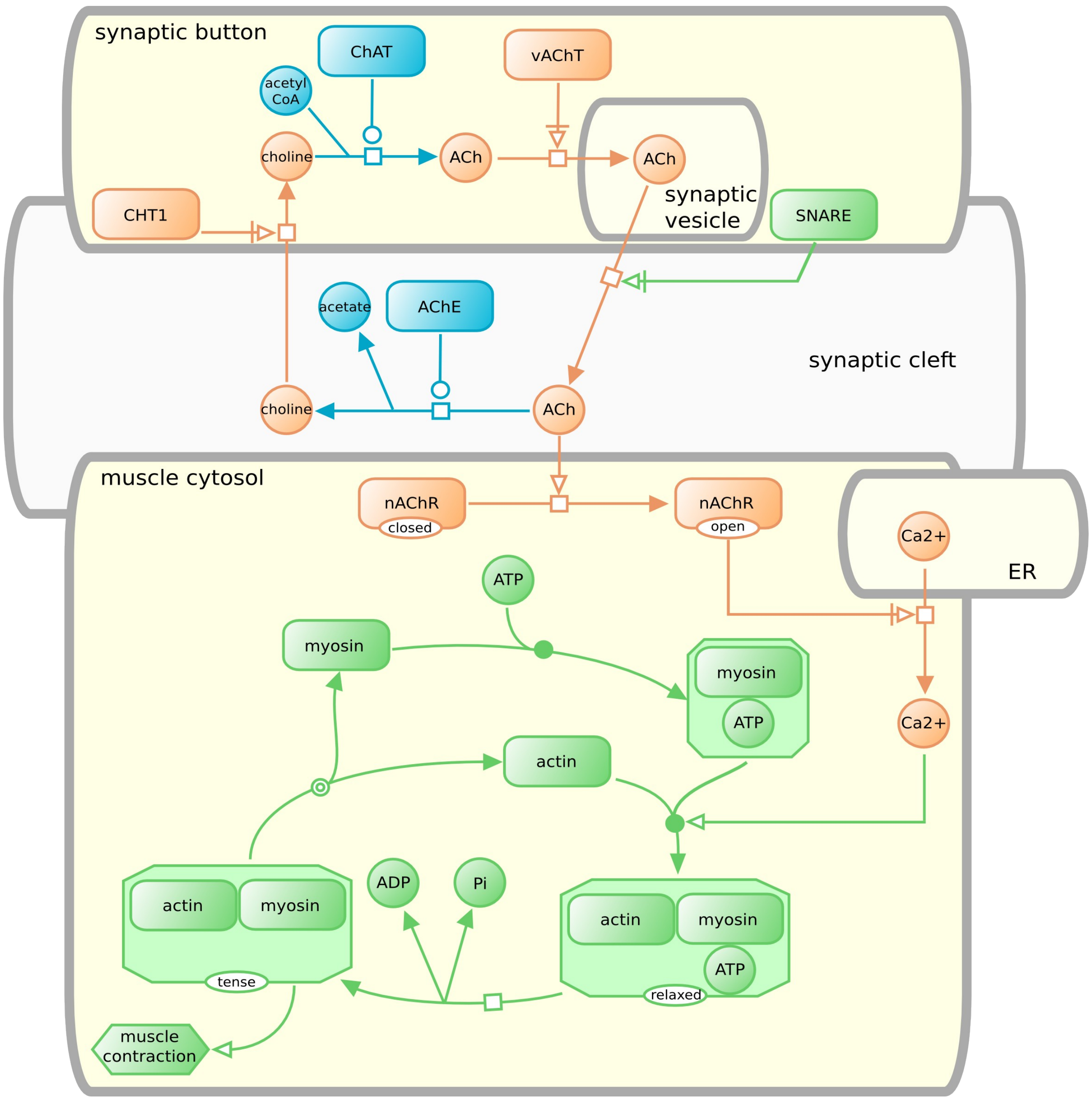
Example of Activity Flow map



Repressilator in Activity Flow Language



Linking SBGN maps to external information

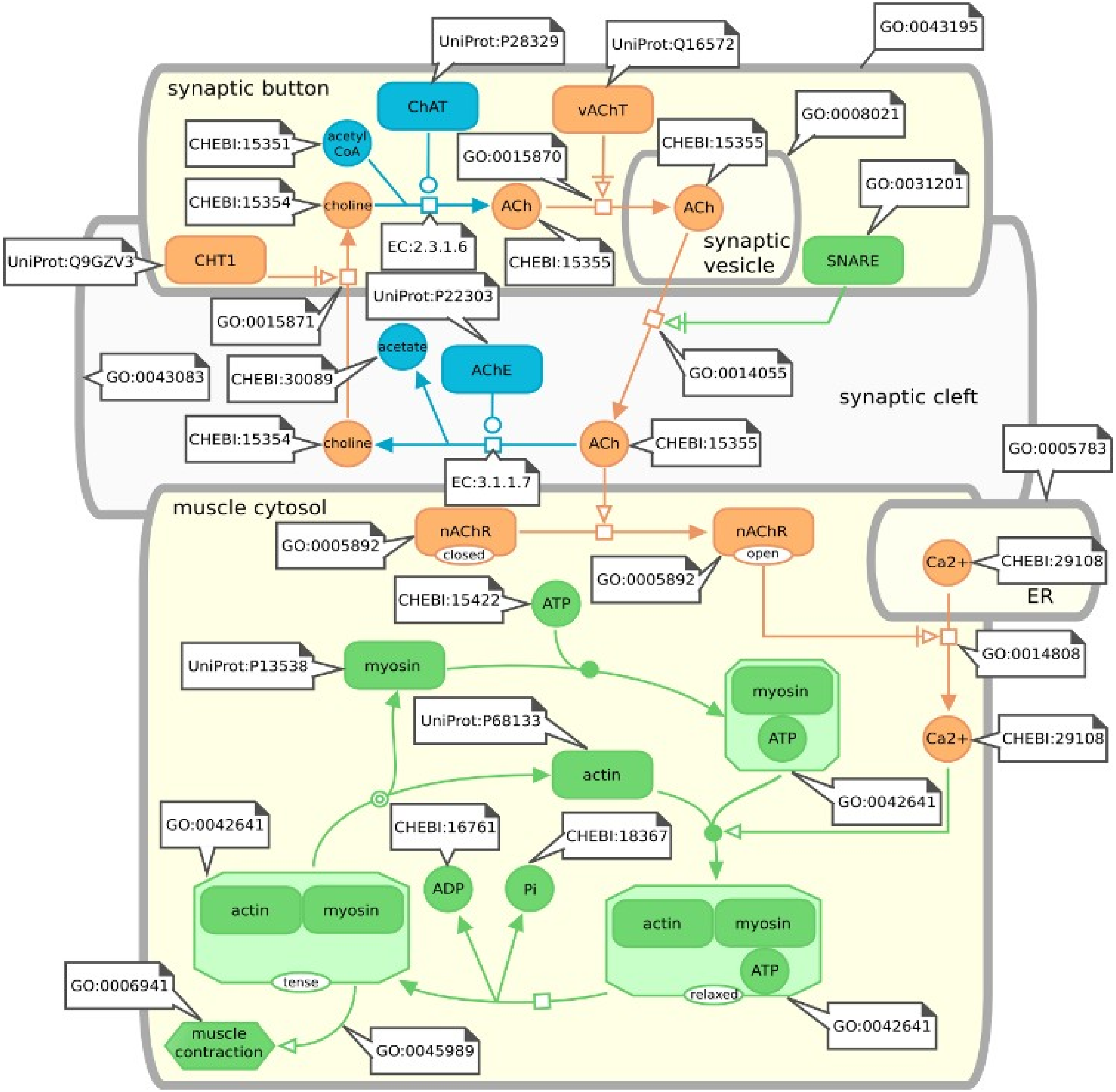


catalytic processes

transport processes

contractile proteins

Linking SBGN maps to external information



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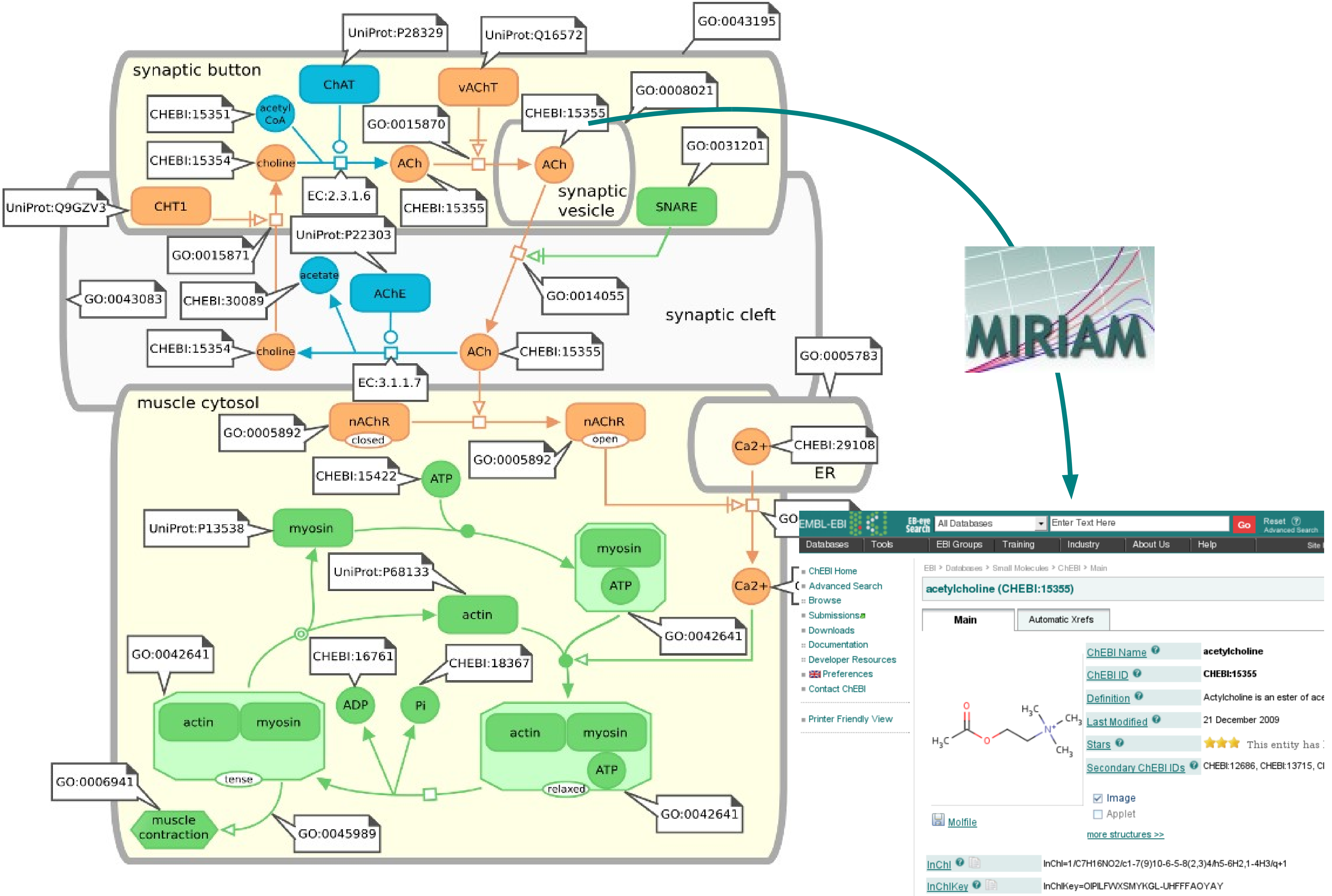

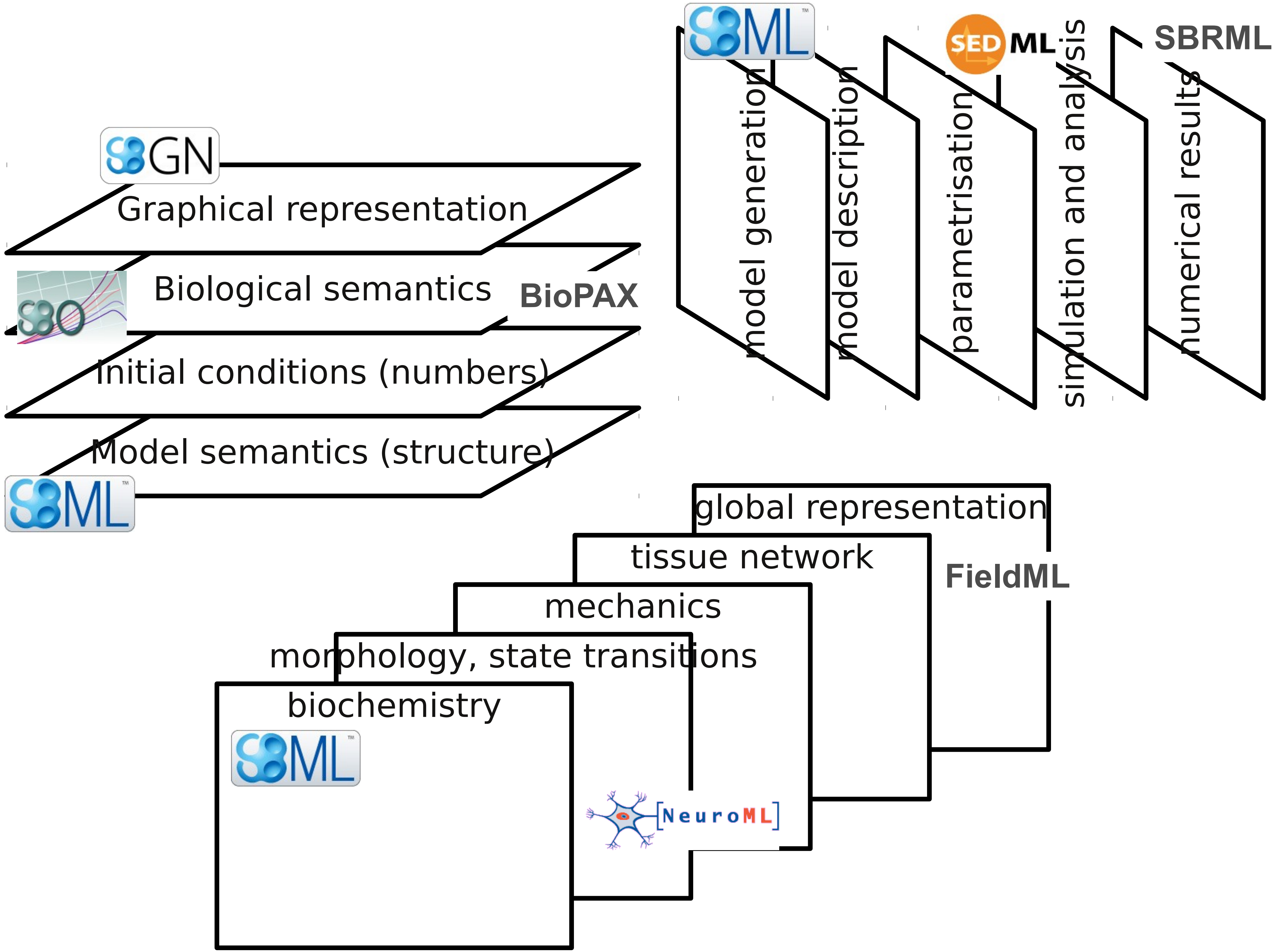

SBGN
Graphical representation
SBO
Biological semantics
BioPAX
Initial conditions (numbers)
Model semantics (structure)
SBML
SBML
SEDML
SBRML
model generation
model description
parametrisation
simulation and analysis
numerical results
global representation
tissue network
FieldML
mechanics
morphology, state transitions
biochemistry
SBML
NeuroML

Views: desktop mobile print

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W3C » About W3C

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W3C

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- Participate
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- Member H

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A "WorldWide Web consortium" for the modeling in life-sciences

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What is the difference between the Web and the Internet?

DRAFT

May 14, 2004

1 An Introduction

There are currently several project threads that have been floating around and I'd like to propose a project that I think would bring some of them together into a unique and globally useful resource. These threads include the following:

- People have been repeatedly voicing the desire for a better database of SBML models. The existing repository on `sbml.org` was never meant to be a full database, only a stop-gap collection until such time as we can find the resources to do better. It may be time to organize a real database.
- People want databases of models to connect to other databases, especially databases of molecular information, Medline, etc.
- We have connections now to EBI and other groups who have expertise in databases and an eagerness to connect them to computational modeling efforts in systems biology. The time is ripe for leveraging these connections.
- The SBML and CellML groups have a long-standing interest to connect not only to each other's efforts, but to others such as BioPAX.
- We have technology now to translate a substantial portion of models from CellML to SBML. Technology exists for translating SBML Level 1 to CellML, and although it doesn't exist for SBML Level 2, there is good reason to believe it could be implemented. It is therefore highly likely that a significant portion of models in practice can be cross-translated.
- The CellML group has been working on ontologies for models which may ultimately be an ideal basis for a unifying database schema that could serve as a master schema for storing models in format-independent manner. (It is worth remembering that SBML was never designed to be a database representation. It may not be suitable for that role. Ditto for CellML. Internal to a database, it may make sense to use a root schema from which projections of the contents of a model are then translated out to SBML, BioPAX, CellML, whatever.)

DRAFT

May 14, 2004

BioModels Database

1 An Introduction

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MIRIAM annotations

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COMBINE

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SBO

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Ruminations on Creating a Biomodels.net

Mike Hucka
mhucka@caltech.edu
The SBML Team
Control and Dynamical Systems, MC 107-81
California Institute of Technology, Pasadena, CA 91125, USA
http://www.sbml.org/

DRAFT

May 14, 2004

1 An Introduction

There are currently several project threads that have been floating around and I'd like to propose a project that I think would bring some of them together into a unique and globally useful resource. These threads include the following:

In the mist of time ...

Computation in Cells

An EPSRC Emergent Computing Workshop

17-18 April 2000

University of Hertfordshire, UK

Invited Speakers

Baltazar Aguda	Stephen Baigent	Upinder Bhalla	Maria Blair
Mark Borisuk	Dennis Bray	Jim Fleming	Igor Goryanin
Charles Hodgman	John Koza	Alan Robinson	Maria Samsonova
Denis Thieffry	Tau-Mu Yi		

Last Update: 23rd April 2000

Other participants included: Hamid Bolouri, Matthieu Louis, Herbert Sauro, Maria Schilstra, Tom Shimizu, Olaf Wolkenhauer ...

COMBINE Meetings

- COMBINE 2010: Edinburgh, 6-9 October 2010
- HARMONY 2011: New-York, April-May 2011
- COMBINE 2011: Somewhere, Sometimes between Aug and Oct 2011

COMBINE Meetings

- COMBINE 2010: Edinburgh, 6-9 October 2010

If you want to become powerful, famous and do interesting science, attend COMBINE meeting

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COMBINE Meetings

- COMBINE 2010: Edinburgh, 6-9 October 2010

See you in 10 years

- COMBINE 2011: Somewhere, Sometimes
  between Aug and Oct 2011

Acknowledgements

Visionary: **Hiroaki Kitano**

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

MIRIAM: Nick Juty, Camille Laibe

The whole community of Computational Systems Biology

The EBI group Computational Systems Neurobiology