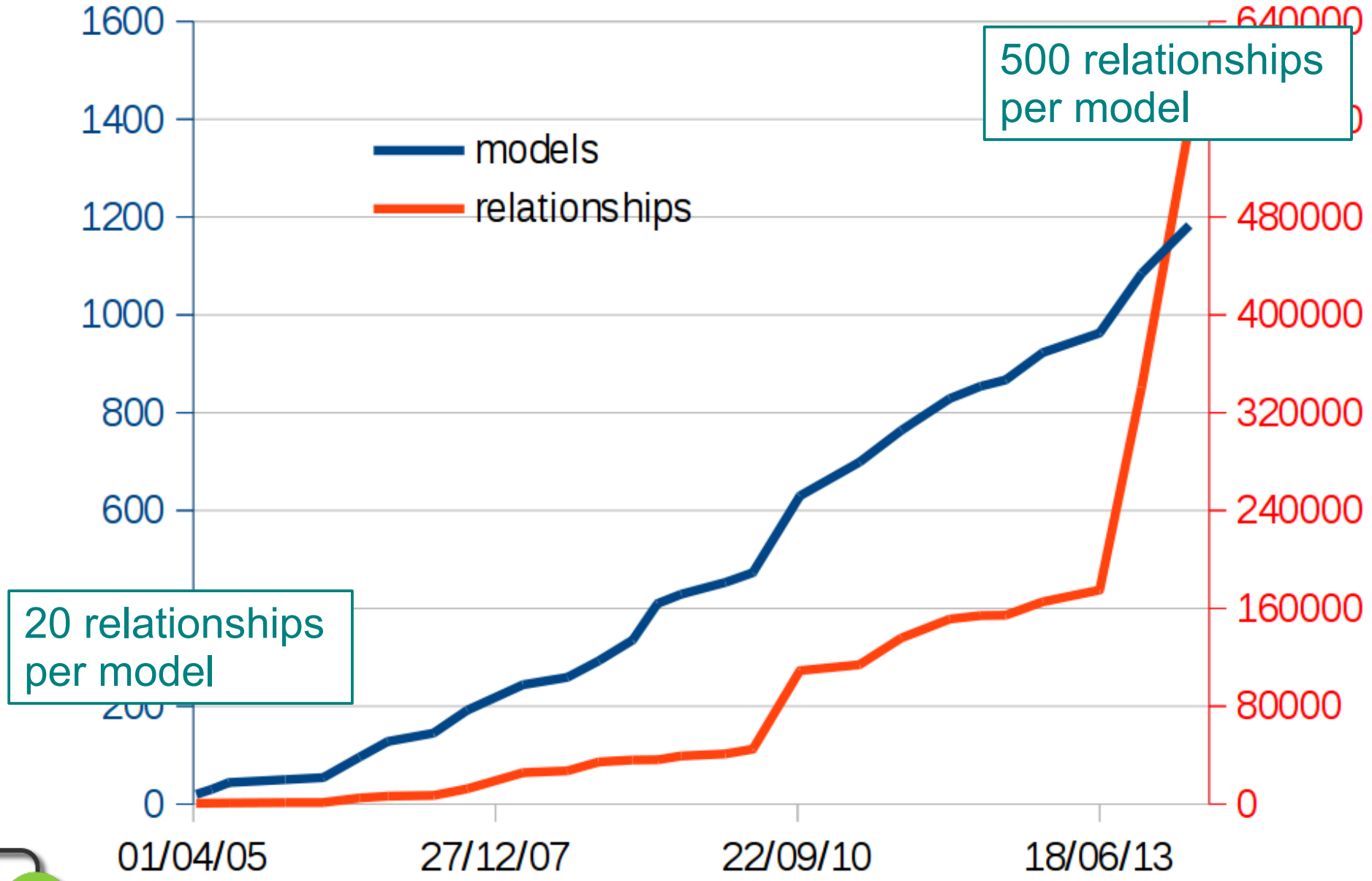
Interoperable Standards
For modelling in biology

Computational models on the rise



BioModels growth (published models branch) since creation

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

We need to

Verify

Re-use

Modify

Build upon

Integrate with

Therefore we need to share

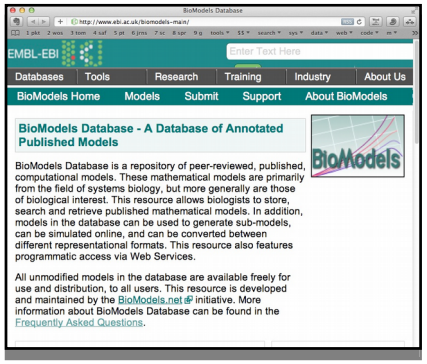
Model descriptions

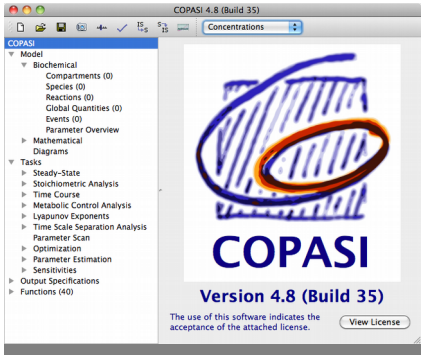
Simulation descriptions

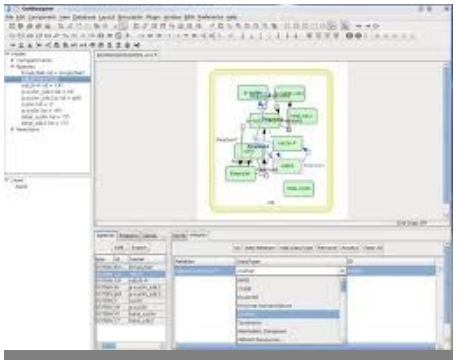
Parametrisations

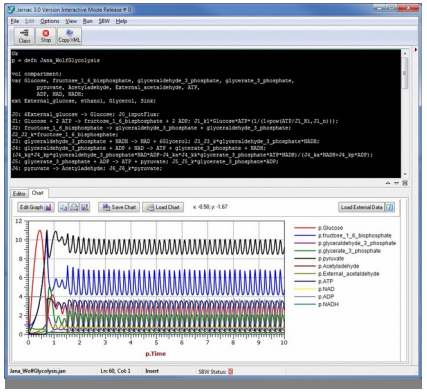
Biological meaning

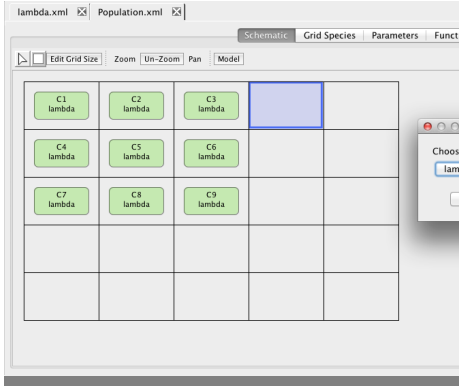
We need to use more than one software tool

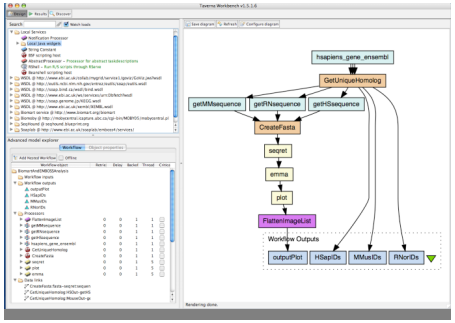


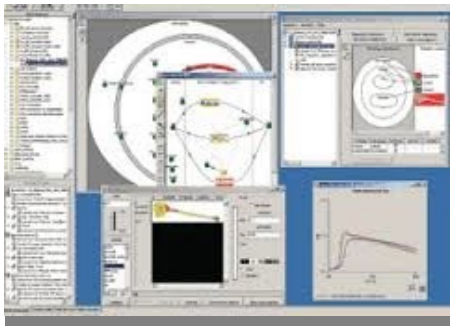




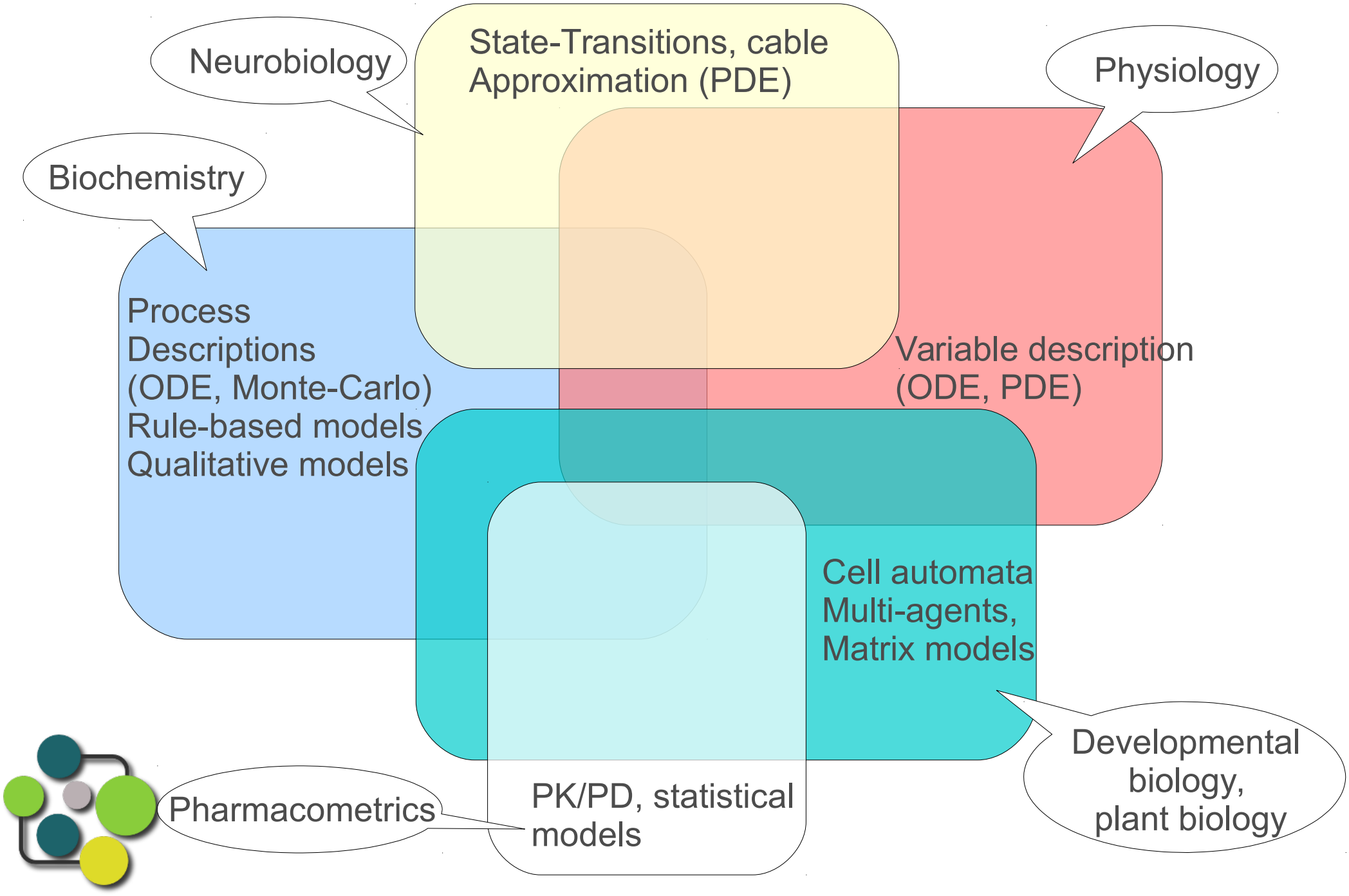




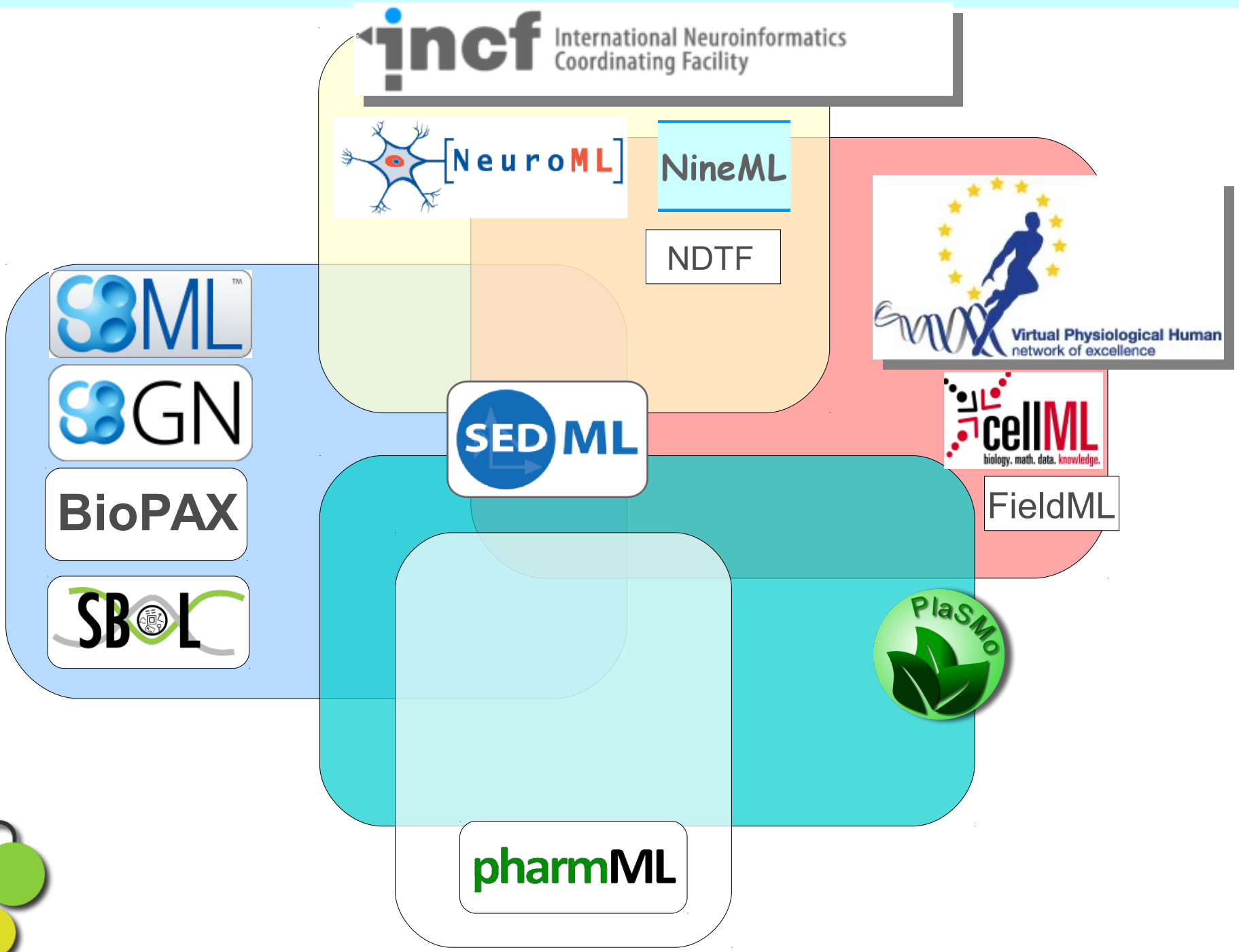




Many alternative modelling approaches



Parallel and redundant efforts

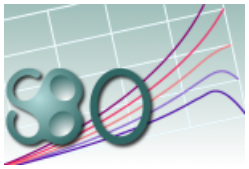


Overarching standardisation structure

http://co.mbine.org/

Mission 1: Coordinating development of standards

ASSOCIATED TOOLS




CORE STANDARDS

NineML
NuML
FieldML
PharmML
PSI-MI

RELATED EFFORTS

Format specification infrastructure

- Each format comes with many different flavors, described in many different specification documents.
- Format specifications are distributed in different ways, through different websites.
- The means of distribution for format specifications evolve over time, making hard to consistently refer to them.
- Trying to find reliable third parties proved difficult (e.g. Nature Precedings).
- We need a consistent way of naming specification documents

COMBINE specifications

View | Edit | Revisions | Access control

Name of the specification	Identifier	Location	node
Biological Pathway Exchange format	biopax	standards/biopax	86
BioPAX Level 1	biopax.level-1	standards/biopax/level-1	89
BioPAX Level 2	biopax.level-2	standards/biopax/level-2	88
BioPAX Level 3	biopax.level-3	standards/biopax/level-3	87
CellML 1.0	cellml.1.0	standards/cellml/1/0	93
CellML 1.1	cellml.1.1	standards/cellml/1/1	94
Systems Biology Graphical Notation	sbgn	standards/sbgn	52
SBGN Activity Flow language	sbgn.af	standards/sbgn/af	66
SBGN AF Level 1	sbgn.af.level-1	standards/sbgn/af/level-1/version-1/0	67
SBGN AF Level 1 Version 1	sbgn.af.level-1.version-1	standards/sbgn/af/level-1/version-1/0	67
SBGN AF Level 1 Version 1.0	sbgn.af.level-1.version-1.0	standards/sbgn/af/level-1/version-1/0	67
SBGN ER	sbgn.er	standards/sbgn/er	57
SBGN ER Level 1	sbgn.er.level-1	standards/sbgn/er/level-1/version-1/2	56
SBGN ER Level 1 Version 1	sbgn.er.level-1.version-1	standards/sbgn/er/level-1/version-1/2	56
SBGN ER Level 1 Version 1.0	sbgn.er.level-1.version-1.0	standards/sbgn/er/level-1/version-1/0	60
SBGN ER Level 1 Version 1.1	sbgn.er.level-1.version-1.1	standards/sbgn/er/level-1/version-1/1	59
SBGN ER Level 1 Version 1.2	sbgn.er.level-1.version-1.2	standards/sbgn/er/level-1/version-1/2	56
SBGN PD	sbgn.pd	standards/sbgn/pd	61
SBGN PD Level 1	sbgn.pd.level-1	standards/sbgn/pd/level-1/version-1/3	62
SBGN PD Level 1 Versio		3	62
SBGN PD Level 1 Versio		0	65
SBGN PD Level 1 Versio		1	64
SBGN PD Level 1 Version 1.2	sbgn.pd.level-1.version-1.2	standards/sbgn/pd/level-1/version-1/2	63
SBGN PD Level 1 Version 1.3	sbgn.pd.level-1.version-1.3	standards/sbgn/pd/level-1/version-1/3	62
Systems Biology Markup Language	sbml	standards/sbml	55
SBML Level 1	sbml.level-1	standards/sbml/level-1/version-2	78
SBML Level 1 Version 1	sbml.level-1.version-1	standards/sbml/level-1/version-1	79

http://co.mbine.org/standards/specifications/

Home › SBGN ER Level 1 Version 1.2

SBGN ER Level 1 Version 1.2

View | Edit | Revisions | Access control

Version 1.2 of Level 1 of the SBGN Entity Relationship Language was published on 14 April 2011.

The specification can be found at:

- http://co.mbine.org/specifications/sbgn.er.level-1.version-1.2.pdf
- http://dx.doi.org/10.1038/npre.2011.5902.1
- http://sbgn.svn.sourceforge.net/viewvc/sbgn/EntityRelationship/tags/Level1-Version1.2/sbgn_ER-level1.pdf

Identifier for this specification is: http://identifiers.org/combine.specifications/sbgn.er.level-1.version-1.2

To cite this document, please use:

Nicolas Le Novère, Emek Demir, Huaiyu Mi, Stuart Moodie, Alice Villéger. Systems Biology Graphical Notation: Entity Relationship language Level 1, Version 1.2. Available from COMBINE <http://identifiers.org/combine.specifications/sbgn.er.level-1.version-1.2> (2011)

http://identifiers.org/combine.specifications/sbgn.er.level-1.version-1.2

So many meetings ...

BioPAX face 2 face

SBML forum

SBGN meeting

SBML hackathon

BioModels training camp

SuperHackathon

CellML workshop

NeuroML workshop

Mission 2: Coordinating meetings

COMBINE coordinate the organisation of common meetings, where developers of all standards and related tools can gather together:

- Efficient collaboration and synergy
- Money saving
- Time saving

http://co.mbine.org/events

http://co.mbine.org/events/calendar

COMBINE Annual forum

Workshop-style event with oral presentations plus discussion, poster and breakout sessions. It is aimed at further developing the standards. The meetings cover the COMBINE standards and associated or related standardization efforts. The participants are everyone wishing to participate to the development of the standards.

- 2010 - Edinburgh, UK; 2011 - Heidelberg, DE; 2012 - Toronto, CA; 2013 - Paris, FR; 2014 - August 18-22, Los Angeles, USA; 2015 - Salt Lake City, USA
- COMBINE 2016 – 19-23 September, Newcastle, UK

HARMONY hackathons

Hackathon-type meetings, with a focus on development of the support for standards, their interoperability and software infrastructure. Focus is not on general discussions or oral presentations but hands-on hacking and interaction between people focused on practical development of standards and supporting software. The participants are generally developers.

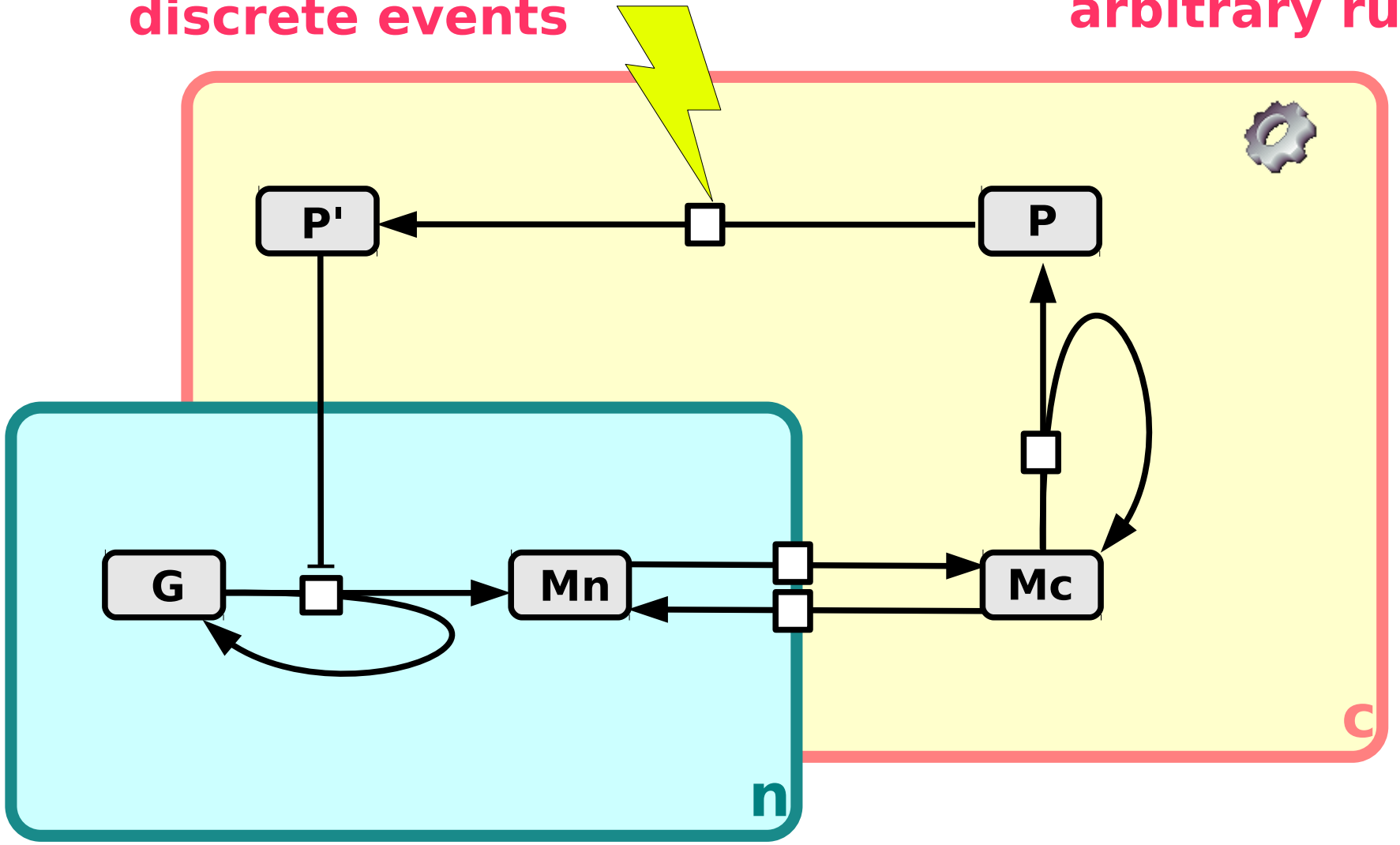
- 2011 - New-York City, USA; 2012 - Maastricht, NL; 2013 - Farmington, USA; 2014 - April 20-15, Manchester, UK; 2015 – Wittenberg, DE; 2016 – Auckland, NZ
- HARMONY 2017: June 26-30, Seattle, USA

End-user meetings

Attached to major scientific events such as the ICSB, COMBINE meetings are organised to communicate with scientists who benefit from our standards, primarily through their software tools. Those meetings are made up of tutorials, demo and non-technical presentations.

- Satellite of ICSB 2012 – Toronto; ICSB 2013 – Copenhagen; ICSB 2014 – Melbourne; ICSB 2015 – Singapore; ICSB 2016 – Barcelona!
- Satellite of ICSB 2017? ISMB 2017? Something else?

What can we encode in SBML (core)?

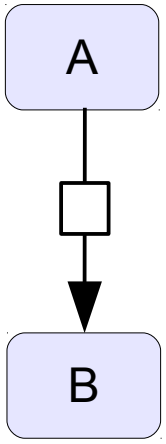


Structure of SBML

```
<?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

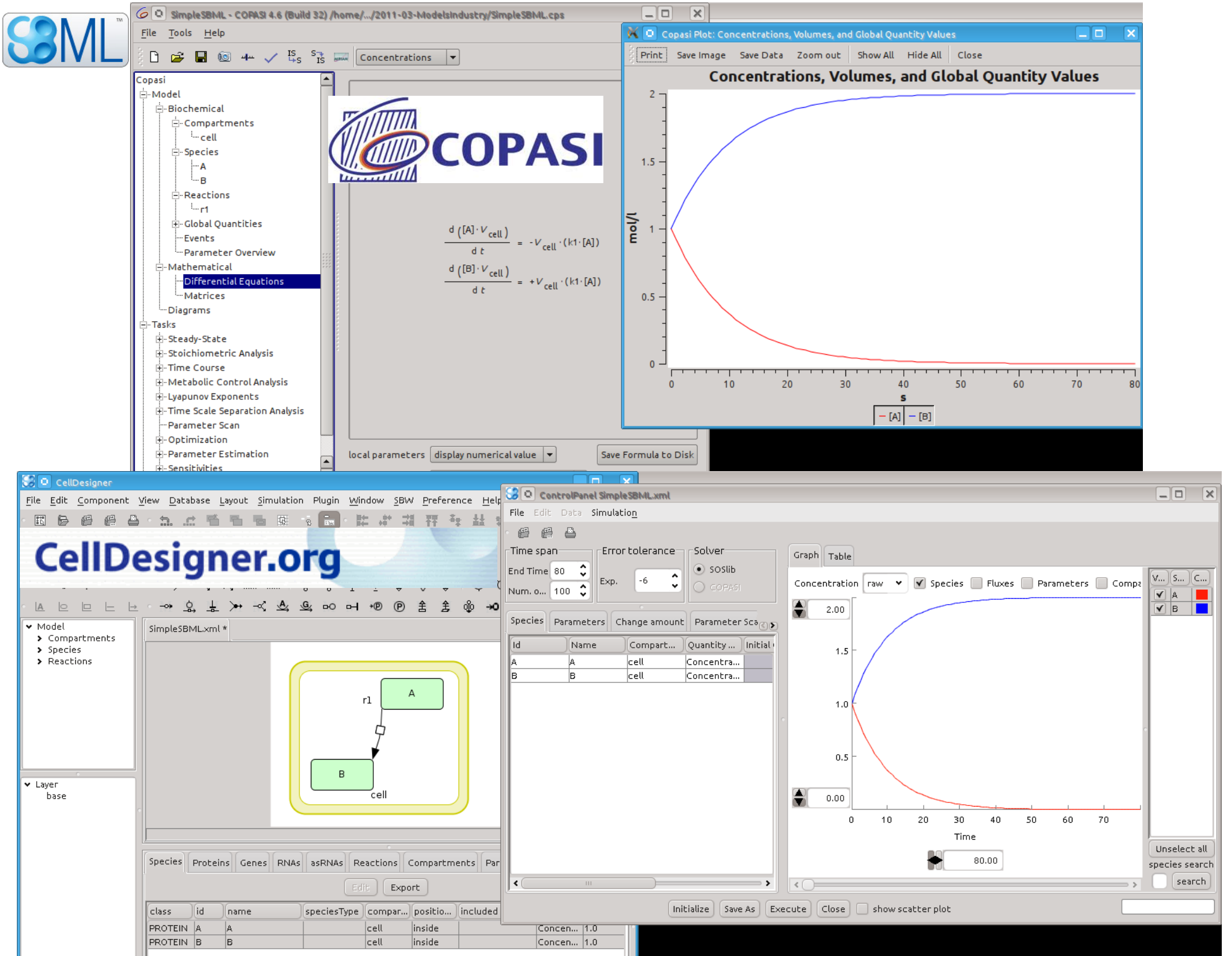
relationships



$$\frac{d[B]}{dt} = k1 \times [A]$$

A very simple SBML file

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level2/version4" level="2" version="4">
  <model name="Simple Model">
    <listOfCompartments>
      <compartment id="cell" size="1" />
    </listOfCompartments>
    <listOfSpecies>
      <species id="A" compartment="cell" initialConcentration="1"/>
      <species id="B" compartment="cell" initialConcentration="1"/>
    </listOfSpecies>
    <listOfParameters>
      <parameter id="k1" value="0.1"/>
    </listOfParameters>
    <listOfReactions>
      <reaction id="r1" reversible="false">
      <listOfReactants>
          <speciesReference species="A"/>
        </listOfReactants>
        <listOfProducts>
          <speciesReference species="B"/>
        </listOfProducts>
        <kineticLaw>
          <math xmlns="http://www.w3.org/1998/Math/MathML">
            <apply>
              <times/>
              <ci> cell </ci>
              <ci> k1 </ci>
              <ci> A </ci>
            </apply>
          </math>
        </kineticLaw>
      </reaction>
    </listOfReactions>
  </model>
</sbml>
```


SBML
SimpleSBML - COPASI 4.6 (Build 32) /home/.../2011-03-ModelsIndustry/SimpleSBML.cps
File Tools Help
Concentrations
Copasi
Model
Biochemical
Compartments
cell
Species
A
B
Reactions
r1
Global Quantities
Events
Parameter Overview
Mathematical
Differential Equations
Matrices
Diagrams
Tasks
Steady-State
Stoichiometric Analysis
Time Course
Metabolic Control Analysis
Lyapunov Exponents
Time Scale Separation Analysis
Parameter Scan
Optimization
Parameter Estimation
Sensitivities
COPASI
d([A]·V_cell)/dt = -V_cell·(k1·[A])
d([B]·V_cell)/dt = +V_cell·(k1·[A])
local parameters
display numerical value
Save Formula to Disk
Copasi Plot: Concentrations, Volumes, and Global Quantity Values
Print Save Image Save Data Zoom out Show All Hide All Close
Concentrations, Volumes, and Global Quantity Values
mol/l
s
[A] [B]
CellDesigner
File Edit Component View Database Layout Simulation Plugin Window SBW Preference Help
CellDesigner.org
Model
Compartments
Species
Reactions
Layer
base
SimpleSBML.xml *
r1
A
B
cell
Species Proteins Genes RNAs asRNAs Reactions Compartments
Edit Export
class id name speciesType compar... positio... included
PROTEIN A A cell inside Concen... 1.0
PROTEIN B B cell inside Concen... 1.0
ControlPanel SimpleSBML.xml
File Edit Data Simulation
Time span
End Time 80
Num. o... 100
Error tolerance
Exp. -6
Solver
SOSlib
COPASI
Species Parameters Change amount Parameter Sca
Id Name Compart... Quantity ... Initial
A A cell Concentra...
B B cell Concentra...
Graph Table
Concentration raw
Species Fluxes Parameters Compa
2.00
0.00
Time
80.00
V... S... C...
A
B
Unselect all
species search
search
Initialize Save As Execute Close show scatter plot

A community-driven global reconstruction of human metabolism

Ines Thiele[1,2,37], Neil Swainston[3,4,37], Ronan M T Fleming[1,5], Andreas Hoppe[6], Swagatika Sahoo[1], Maike K Aurich[1], Hulda Haraldsdottir[1], Monica L Mo[7], Ottar Rolfsson[1], Miranda D Stobbe[8,9], Stefan G Thorleifsson[1], Rasmus Agren[10], Christian Bölling[6], Sergio Bordel[10], Arvind K Chavali[11], Paul Dobson[12], Warwick B Dunn[3,13], Lukas Endler[14], David Hala[15], Michael Hucka[16], Duncan Hull[4], Daniel Jameson[3,4], Neema Jamshidi[7], Jon J Jonsson[5], Nick Juty[17], Sarah Keating[17], Intawat Nookaew[10], Nicolas Le Novère[17,18], Naglis Malys[3,19,20], Alexander Mazein[21], Jason A Papin[11], Nathan D Price[22], Evgeni Selkov, Sr[23], Martin I Sigurdsson[1], Evangelos Simeonidis[22,24], Nikolaus Sonnenschein[25], Kieran Smallbone[3,26], Anatoly Sorokin[21,27], Johannes H G M van Beek[28–30], Dieter Weichart[3,31], Igor Goryanin[21,32], Jens Nielsen[10], Hans V Westerhoff[3,28,33,34], Douglas B Kell[3,35], Pedro Mendes[3,4,36] & Bernhard Ø Palsson[1,7]

Multiple models of human metabolism have been reconstructed, but each represents only a subset of our knowledge. Here we describe Recon 2, a community-driven, consensus 'metabolic reconstruction', which is the most comprehensive representation of human metabolism that is applicable to computational modeling. Compared with its predecessors, the reconstruction has improved topological and functional features, including ~2× more reactions and ~1.7× more unique metabolites. Using Recon 2 we predicted changes in metabolite biomarkers for 49 inborn errors of metabolism with 77% accuracy when compared to experimental data. Mapping metabolomic data and drug information onto Recon 2 demonstrates its potential for integrating and analyzing diverse data types. Using protein expression data, we automatically generated a compendium of 65 cell type–specific models, providing a basis for manual curation or investigation of cell-specific metabolic properties. Recon 2 will facilitate many future biomedical studies and is freely available at http://humanmetabolism.org/.

An understanding of metabolism is fundamental to comprehending the phenotypic behavior of all living organisms, including humans, where metabolism is integral to health and is involved in much of human disease. High quality, genome-scale 'metabolic reconstructions' are at the heart of bottom-up systems biology analyses and represent the entire network of metabolic reactions that a given organism is known to exhibit[1]. The metabolic-network reconstruction procedure is now well-established[2] and has been applied to a growing number of model organisms[3]. Metabolic reconstructions allow for the conversion of biological knowledge into a mathematical format and the subsequent computation of physiological states[1,4,5] to address a variety of scientific and applied questions[3,6]. Reconstructions enable network-wide mechanistic investigations of the genotype-phenotype relationship. A high-quality reconstruction of the metabolic network is thus

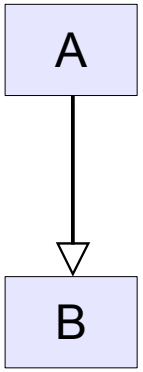
A not so simple SBML file (Recon2)

- 8 compartments
- 5 063 metabolites
- 2 194 proteins
- 7 440 reactions

MODEL1109130000

- Core package – public specification
- Flux balance constraint – public specification
- Qualitative models – public specification
- Model composition – public specification
- Graph Layout – public specification
- Groups – public specification
- Graph rendering – specification finalised
- Complex species – specification finalised
- Spatial diffusion – specification finalised
- Distributions and ranges – draft specification available
- Arrays and sets – draft specification available
- Dynamic structures – draft specification available

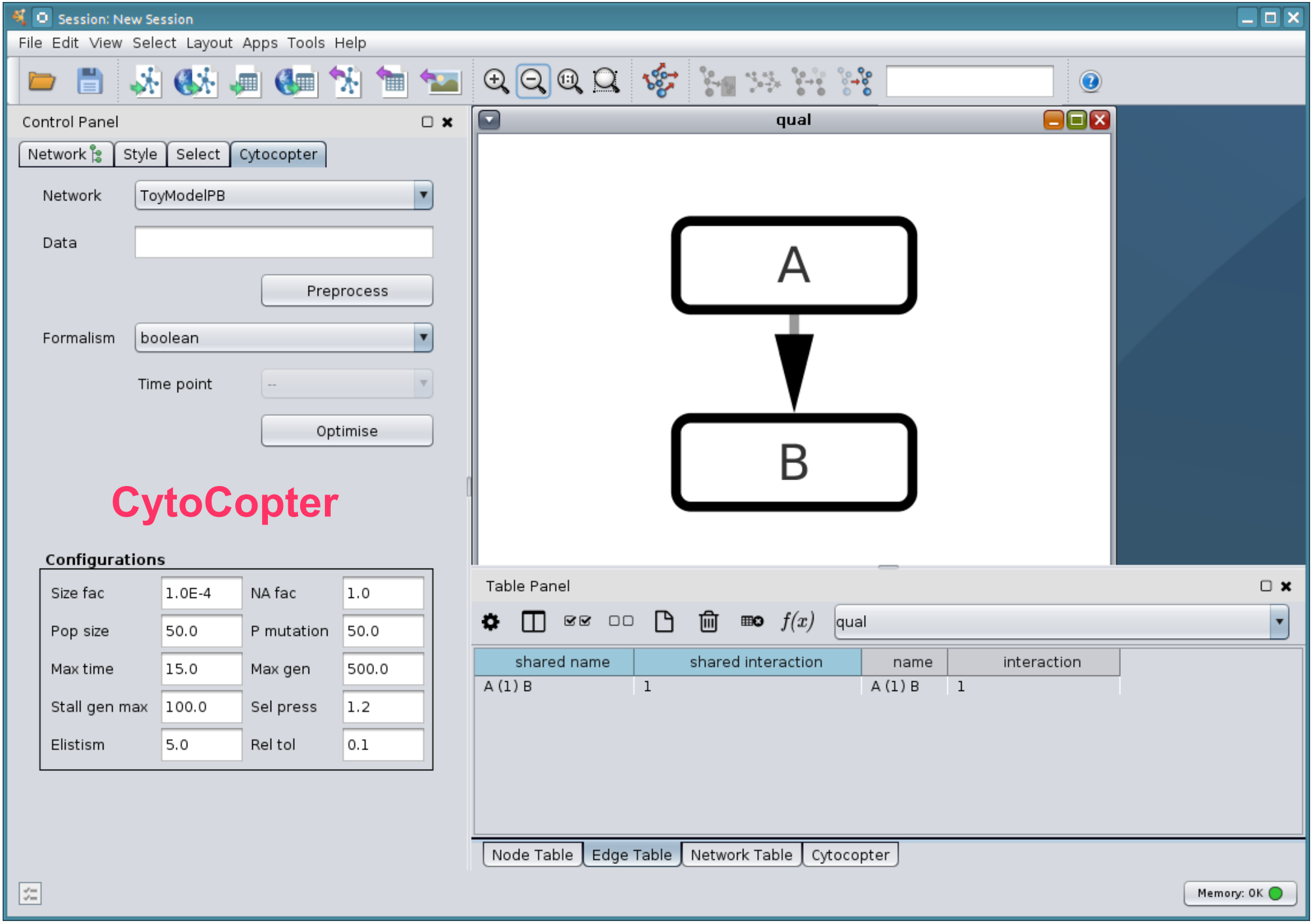
SBML Level 3 is modular

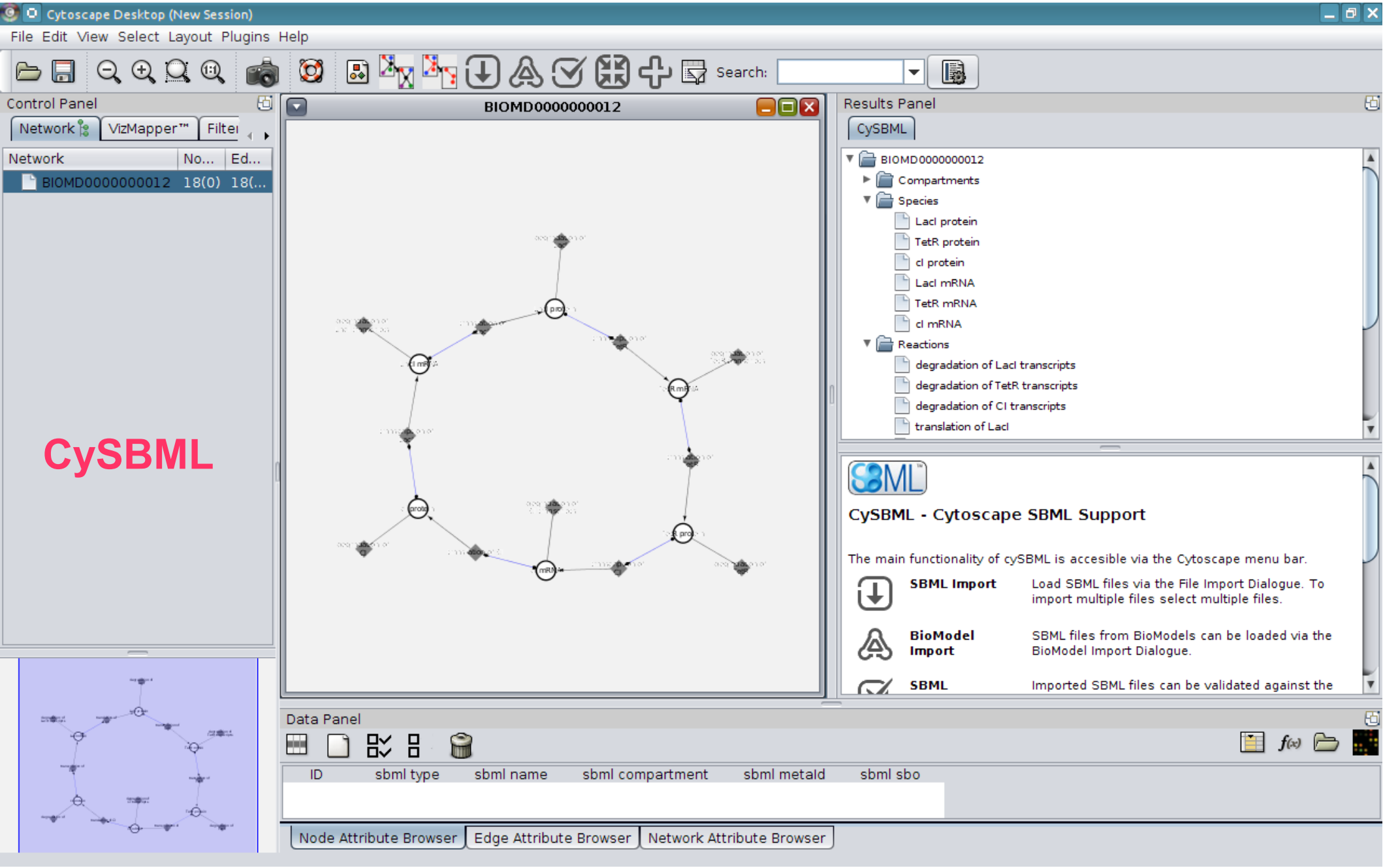


$$A \geqslant 1 \Rightarrow B = 1$$

Logical model with SBML Qual

```
<?xmlversion="1.0" encoding="UTF8"?>
<sbml xmlns="http://www.sbml.org/sbml/level3/version1/core" level="3" version="1"
      xmlns:qual="http://www.sbml.org/sbml/level3/version1/qual/version1" qual:required="true">
  <model id="example">
    <listOfCompartments>
      <compartment id="cytosol" name="cytosol" constant="true"/>
    </listOfCompartments>
    <qual:listOfQualitativeSpecies>
      <qual:qualitativeSpecies qual:compartment="cytosol" qual:constant="false"
                               qual:id="A" qual:maxLevel="2"/>
      <qual:qualitativeSpecies qual:compartment="cytosol" qual:constant="false"
                               qual:id="B" qual:maxLevel="1"/>
    </qual:listOfQualitativeSpecies>
    <qual:listOfTransitions>
      <qual:transition qual:id="tr_B">
        <qual:listOfInputs>
          <qual:input qual:id="theta_B_A" qual:qualitativeSpecies="A" qual:sign="positive"
                      qual:thresholdLevel="1" qual:transitionEffect="none"/>
        </qual:listOfInputs>
        <qual:listOfOutputs>
          <qual:output qual:transitionEffect="assignmentLevel" qual:qualitativeSpecies="B"/>
        </qual:listOfOutputs>
        <qual:listOfFunctionTerms>
          <qual:functionTerm qual:resultLevel="1">
            <math xmlns="http://www.w3.org/1998/Math/MathML">
              <apply>
                <geq/>
                <ci>A</ci>
                <ci>theta_B_A</ci>
              </apply>
            </math>
          </qual:functionTerm>
          <qual:defaultTerm qual:resultLevel="0"/>
        </qual:listOfFunctionTerms>
      </qual:transition>
    </qual:listOfTransitions>
  </model>
</sbml>
```


Session: New Session
File Edit View Select Layout Apps Tools Help
Control Panel
Network Style Select Cytocopter
Network
ToyModelPB
Data
Preprocess
Formalism
boolean
Time point
--
Optimise
CytoCopter
Configurations
Size fac
1.0E-4
NA fac
1.0
Pop size
50.0
P mutation
50.0
Max time
15.0
Max gen
500.0
Stall gen max
100.0
Sel press
1.2
Elistism
5.0
Rel tol
0.1
qual
A
B
Table Panel
qual
shared name
shared interaction
name
interaction
A (1) B
1
A (1) B
1
Node Table
Edge Table
Network Table
Cytocopter
Memory: OK


Cytoscape Desktop (New Session)
File Edit View Select Layout Plugins Help
Search:
Control Panel
Network
VizMapper™
Network
No...
Ed...
BIOMD0000000012 18(0) 18(...
CySBML
BIOMD0000000012
Results Panel
CySBML
BIOMD0000000012
Compartments
Species
LacI protein
TetR protein
cI protein
LacI mRNA
TetR mRNA
cI mRNA
Reactions
degradation of LacI transcripts
degradation of TetR transcripts
degradation of CI transcripts
translation of LacI
CySBML - Cytoscape SBML Support
The main functionality of cySBML is accesible via the Cytoscape menu bar.
SBML Import
Load SBML files via the File Import Dialogue. To import multiple files select multiple files.
BioModel Import
SBML files from BioModels can be loaded via the BioModel Import Dialogue.
SBML
Imported SBML files can be validated against the
Data Panel
ID
sbml type
sbml name
sbml compartment
sbml metaId
sbml sbo
Node Attribute Browser
Edge Attribute Browser
Network Attribute Browser

SBML Software Guide

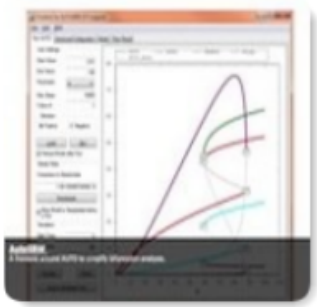
The following pages describe SBML-compatible software packages known to us. We offer different ways of viewing the information, all drawn from the same underlying data collected from the systems' developers via our **software survey**. The *Matrix* provides a table listing all known software and a variety of their features; the *Summary* provides general descriptions of most of the software; and the *Showcase* provides a sequential slideshow of a subset of the software.

Number of software packages listed in the matrix today: **283**.

Go to the SBML Software Matrix

Go to the SBML Software Summary

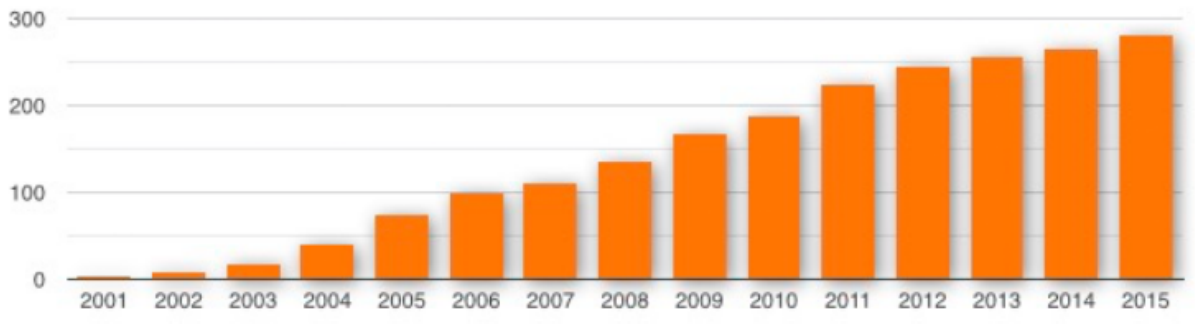
Go to the SBML Software Showcase



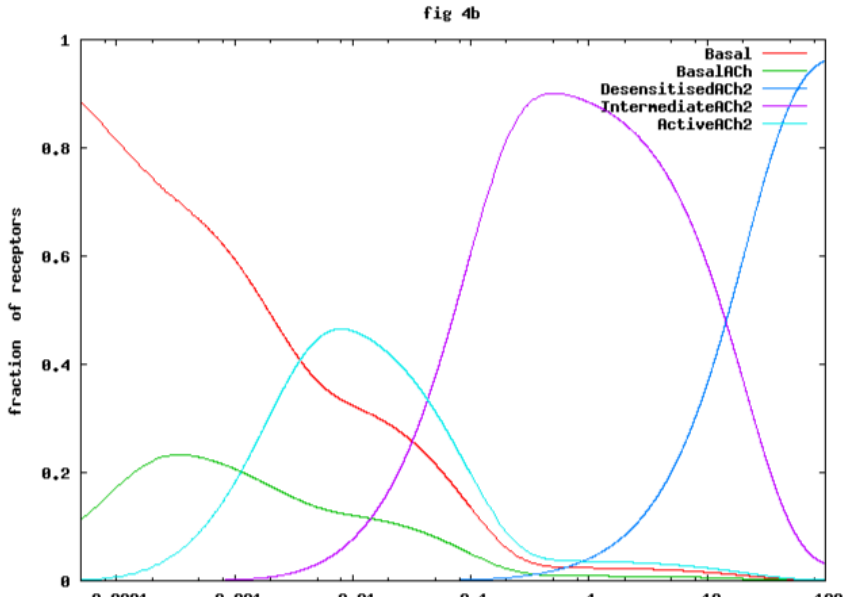
Please **tell us about additions and updates**.

Historical trend

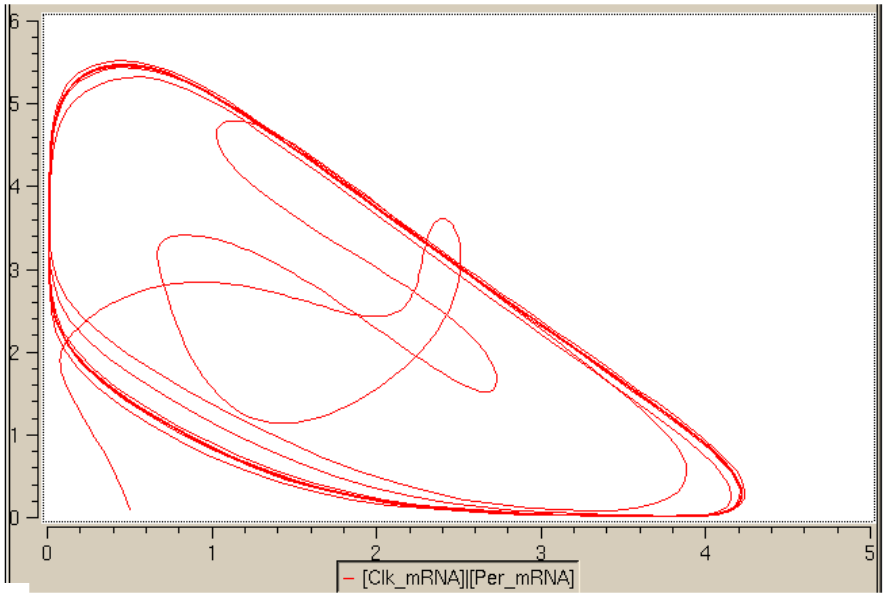
The following graph shows the total number of known SBML-compatible software packages each year, as counted by the SBML Team. The counts shown are for approximately the middle of each year.



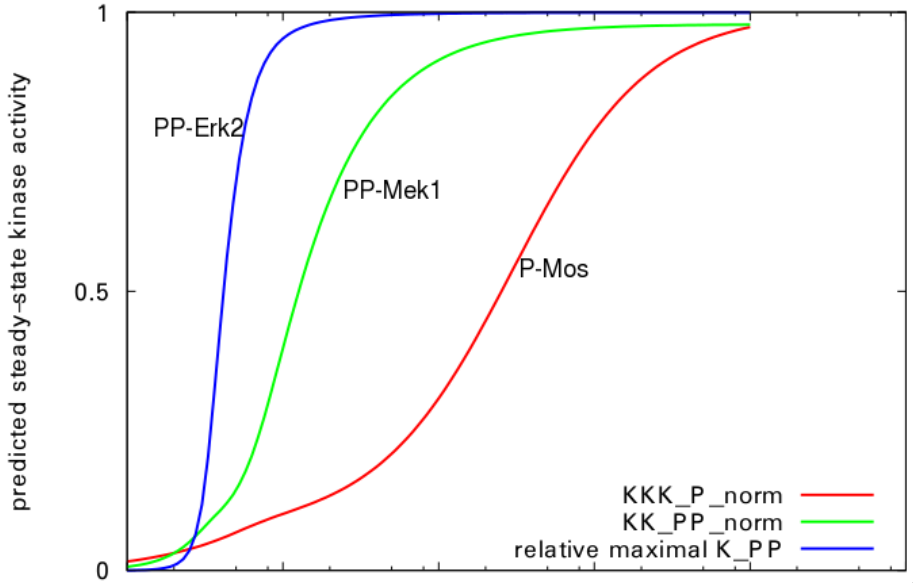
Reproduction of published simulation results



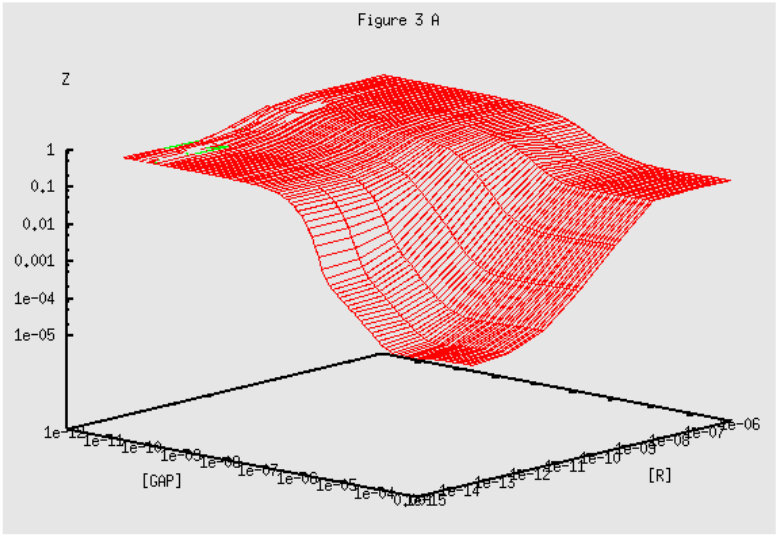
Edelstein et al 1996 (BIOMD0000000002)



Ueda, et al 2001 (BIOMD0000000022)

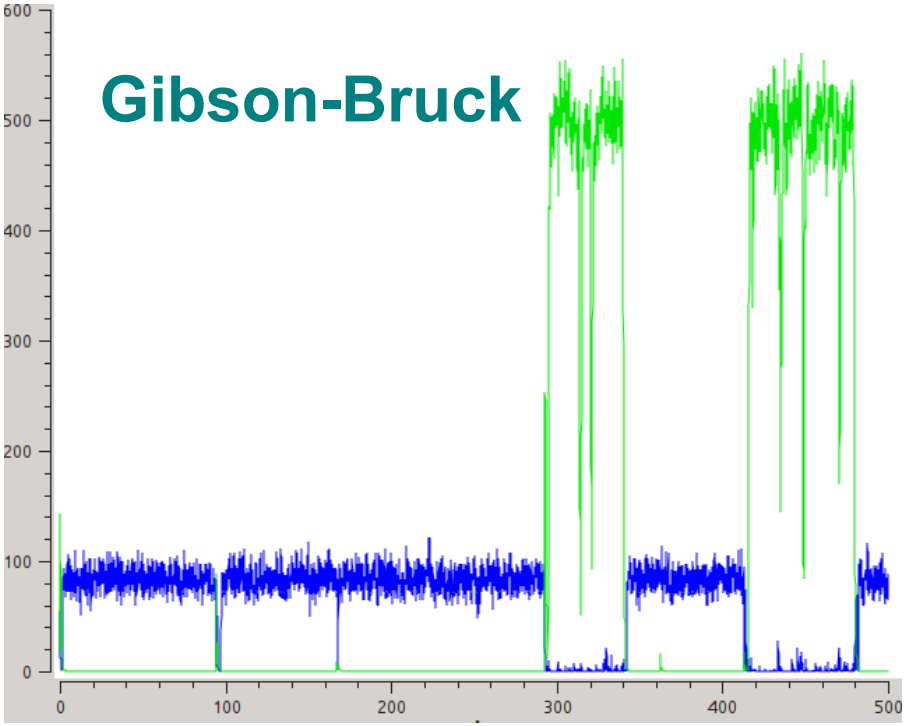


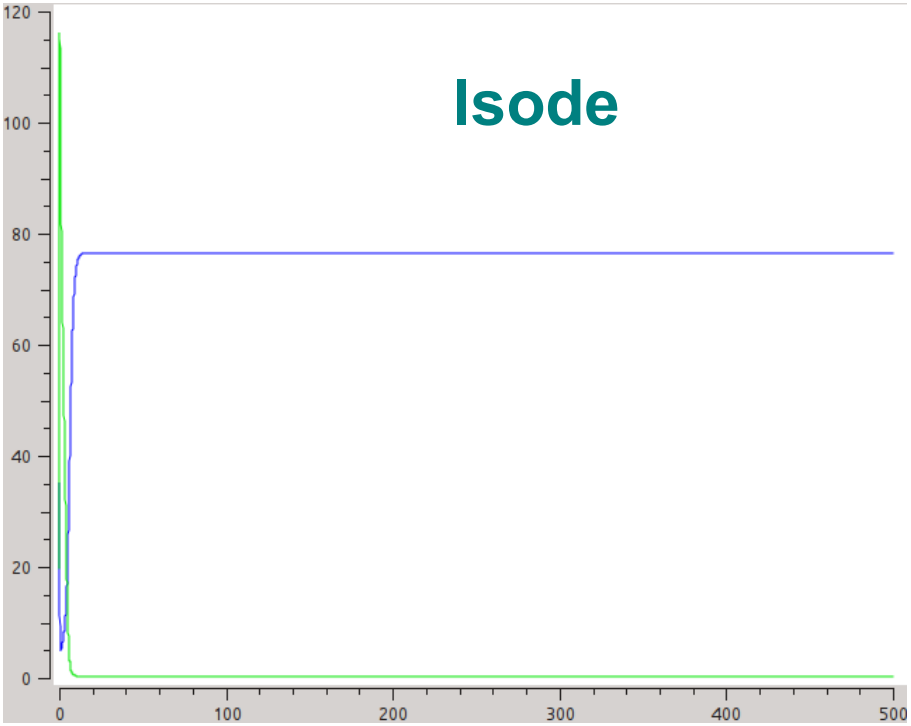
Huang & Ferrell (BIOMD0000000009)

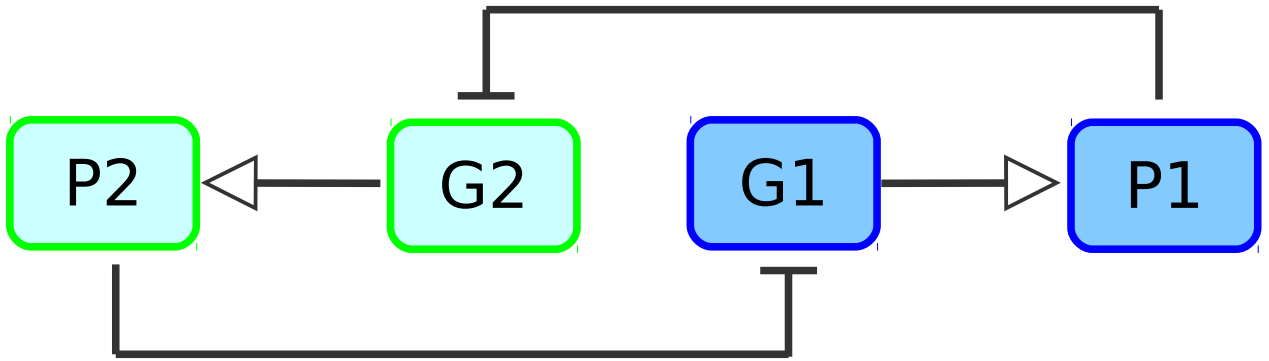


Bornheimer et al 2004 (BIOMD0000000086)

Algorithm choice and multistability







Simulation Experiment Description Markup Language

```
<?xml version="1.0" encoding="utf-8"?>
<sedML xmlns:math="http://www.w3.org/1998/Math/MathML"
       xmlns="http://sed-ml.org/"
       level="1" version="1">
  <listOfModels>
    <model id="model1" name="Repressilator-regular oscillations">
      <listOfChanges><!-- --></listOfChanges>
    </model>
  </listOfModels>
  <listOfSimulations><!-- --></listOfSimulations>
  <listOfTasks><!-- --></listOfTasks>
  <listOfDataGenerators><!-- --></listOfDataGenerators>
  <listOfOutputs><!-- --></listOfOutputs>
</sedML>
```

http://sed-ml.org

SED ML

Flexible model use in SED-ML

```
<listOfModels>
  <model id="model1" name="Repressilator-regular oscillations"
         language="urn:sedml:language:sbml.level-2.version-3"
         source="http://identifiers.org/biomodels.db/BIOMD0000000012" >
  </model>
  <model id="model2" name="Damped oscillations"
         language="urn:sedml:language:sbml.level-2.version-3"
         source="model1">
    <listOfChanges>
      <changeAttribute
        target="/sbml:sbml/sbml:model/sbml:listOfParameters/sbml:parameter[@name='tps
        newValue="1.3e-5">
      </changeAttribute>
      <changeAttribute
        target="/sbml:sbml/sbml:model/sbml:listOfParameters/sbml:parameter[@name='tps
        newValue="0.013">
      </changeAttribute>
    </listOfChanges>
  </model>
</listOfModels>
```

Any XML

Remote access

Modifications before simulations

Access to internal entities via XPath

Multiple simulations algorithms

```
<listOfSimulations>

  <uniformTimeCourse id="simulation1" initialTime="0"
                     outputStartTime="0" outputEndTime="1000" numberOfPoints="1000">
    <algorithm kisaoID="KISAO:0000088" />
  </uniformTimeCourse>

  <uniformTimeCourse id="simulation2" initialTime="0"
                     outputStartTime="0" outputEndTime="1000" numberOfPoints="1000">
    <algorithm kisaoID="KISAO:0000027" />
  </uniformTimeCourse>

</listOfSimulations>
```

LSODA

Gibson-Bruck method

Tasks: simulating models

```
<listOfTasks>

  <task id="task1" name="Oscillations using a deterministic simulator"
        modelReference="model1" simulationReference="simulation1" />

  <task id="task2" name="Damped oscillations using a deterministic simulator"
        modelReference="model2" simulationReference="simulation1" />

  <task id="task3" name="Oscillations using a stochastic simulator"
        modelReference="model1" simulationReference="simulation2" />

</listOfTasks>
```

Generating numerical results

```
<listOfDataGenerators>

  <dataGenerator id="timeDG" name="Time">
    <listOfVariables>
      <variable id="Time" taskReference="task1" symbol="urn:sedml:symbol:time" />
    </listOfVariables>
    <math:math>
      <math:ci> Time </math:ci>
    </math:math>
  </dataGenerator>

  <dataGenerator id="LacINormalizedDG" name=" NormalizedLaCI repressor">
    <listOfVariables>
      <variable id="LacI" taskReference="task1"
                target="/sbml:sbml/sbml:model/sbml:listOfSpecies/sbml:species[@id='PX']" />
    </listOfVariables>
    <math:math>
      <math:apply>
        <math:divide />
        <math:ci>LacI</math:ci>
        <math:apply>
          <math:max />
          <math:ci>LacI</math:ci>
        </math:apply>
      </math:apply>
    </math>
  </dataGenerator>

</listOfDataGenerators>
```

$$LacINormalizedDG(t) = \frac{LacI(t)}{max(LacI)}$$

Presenting results

```
<listOfOutputs>

  <plot2D id="plot_normalized" name="Normalized protein levels">
    <listOfCurves>

      <curve id="c7" logX="false" logY="false"
             xDataReference="timeDG"
             yDataReference="TetRNormalizedDG" />

      <curve id="c8" logX="false" logY="false"
             xDataReference="timeDG"
             yDataReference="CIb_normalizedDG" />

      <curve id="c9" logX="false" logY="false"
             xDataReference="timeDG"
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    </listOfCurves>
  </plot2D>

</listOfOutputs>
```
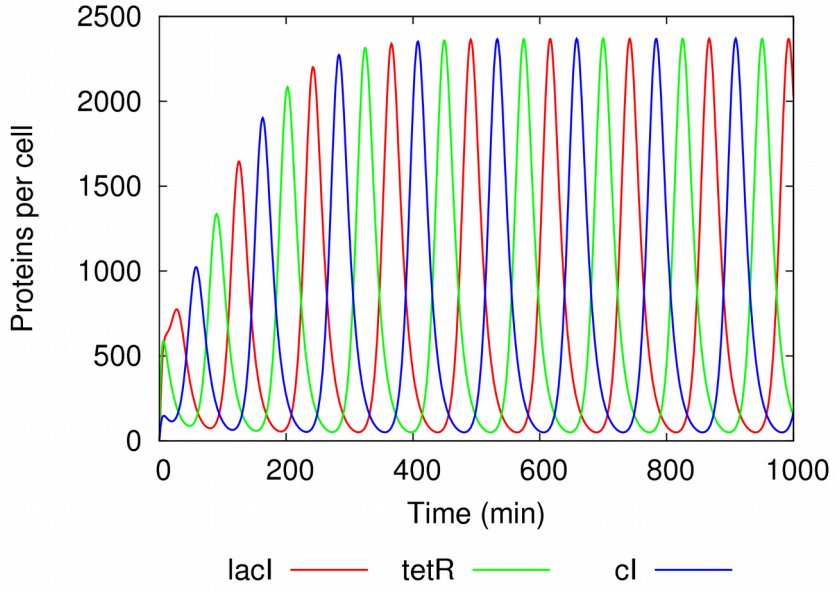
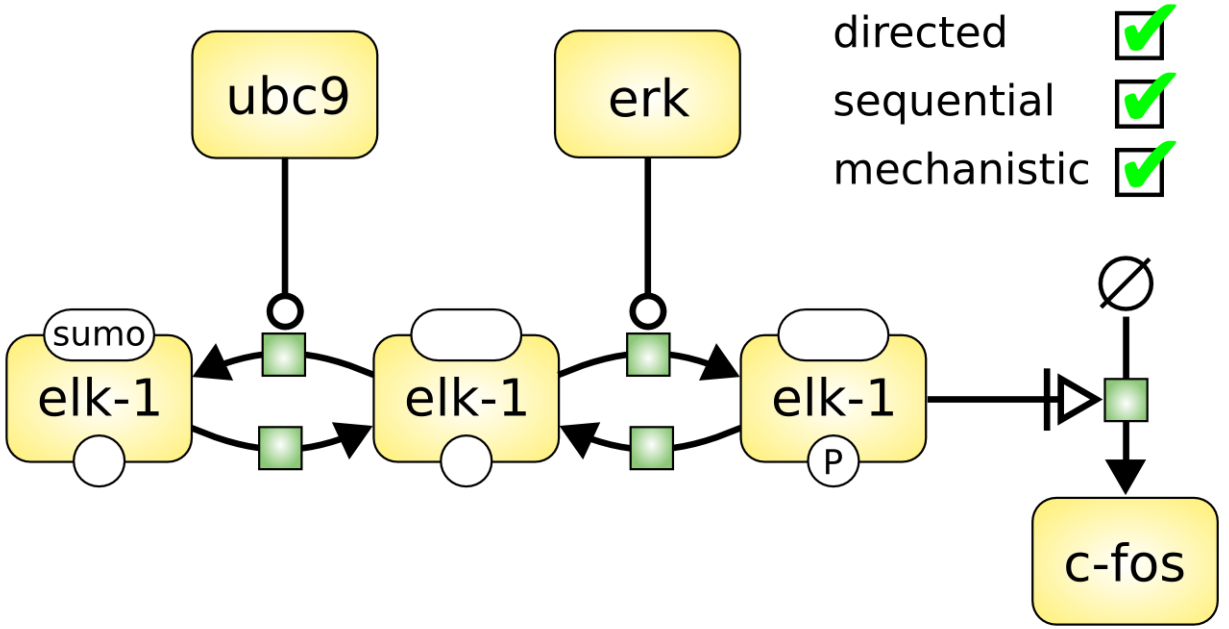



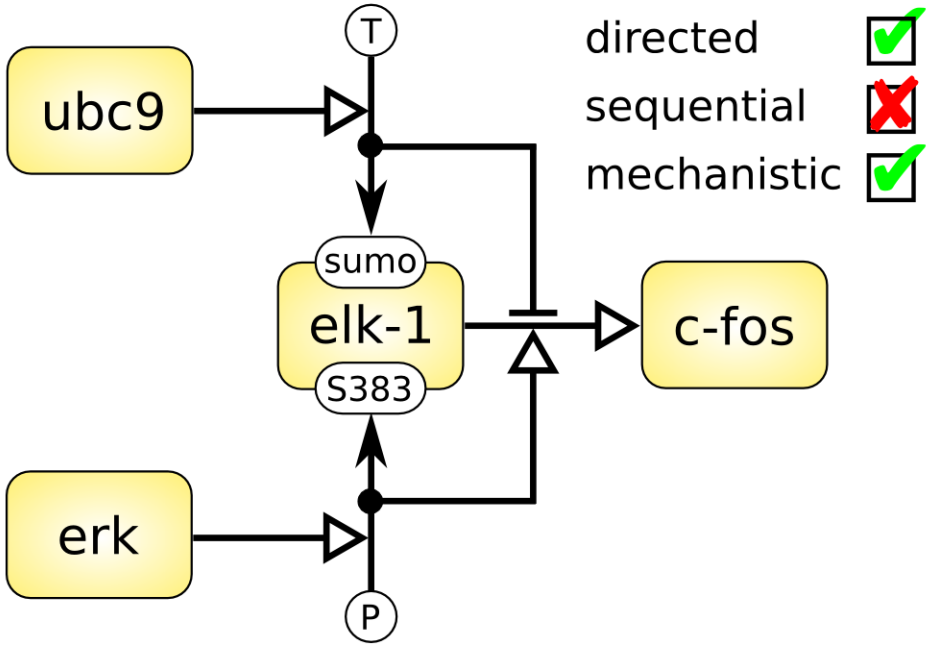
Unambiguous consensual visual notation

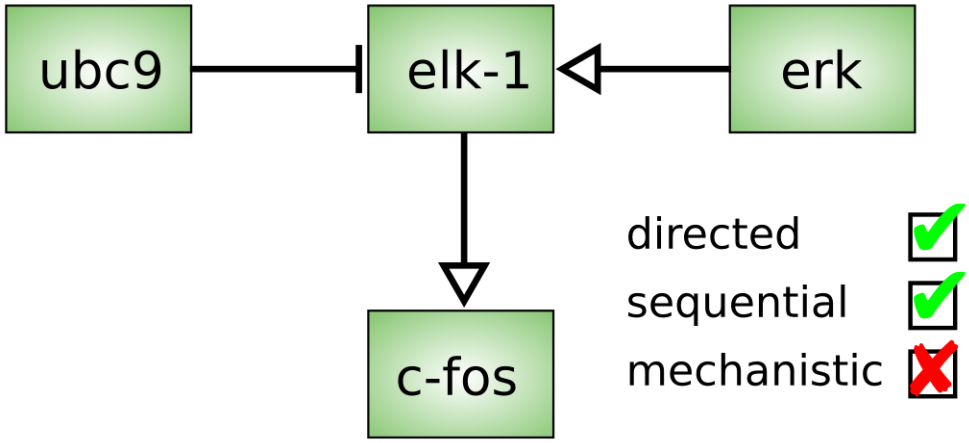
- An unambiguous way of graphically describing and interpreting biochemical and cellular events
- Limited amount of symbols
  Re-use existing symbols
  ☞ Smooth learning curve
- Can represent logical or mechanistic models, biochemical pathways, at different levels of granularity
- Detailed technical specification, precise data-models, standard API and growing software support
- Developed over ten years by a diverse community, including biologists, modellers, computer scientists etc.

http://sbgn.org/

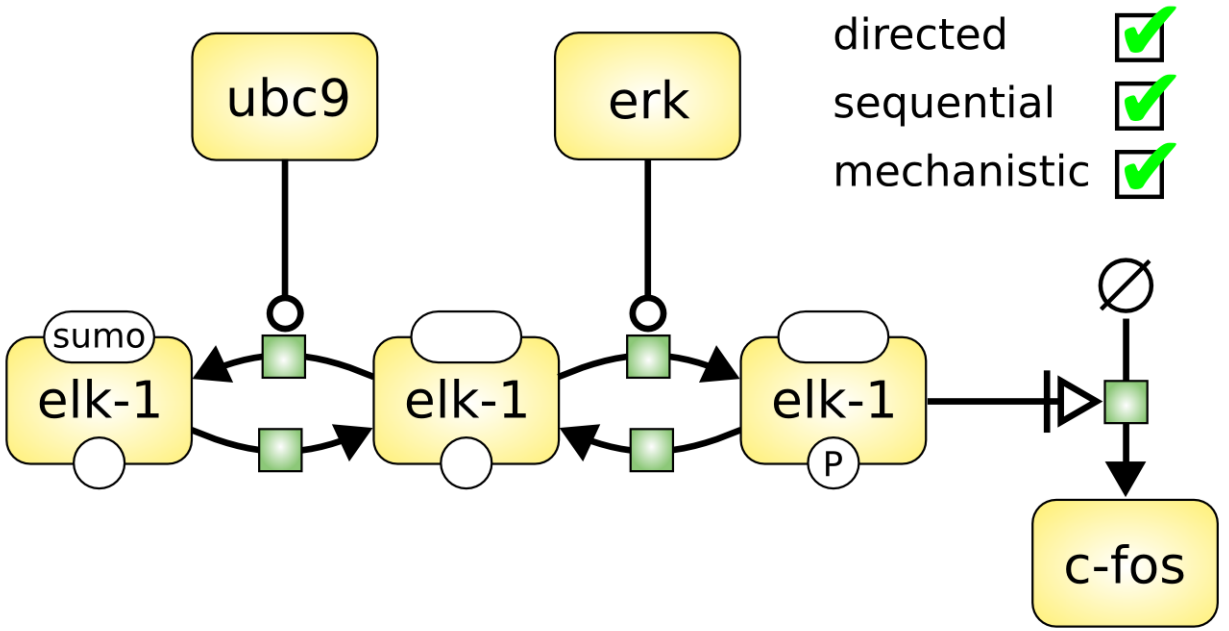
1 standard, 3 languages





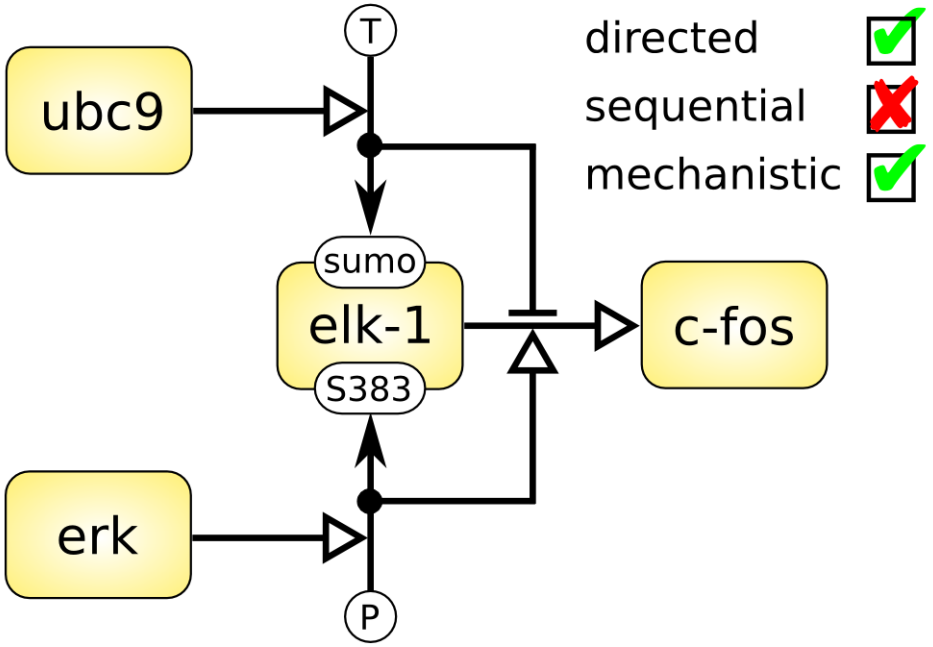


Process Descriptions



- Process modelling
- Biochemistry, Metabolic networks
- Generally within “closed world”
- Subjected to combinatorial explosion

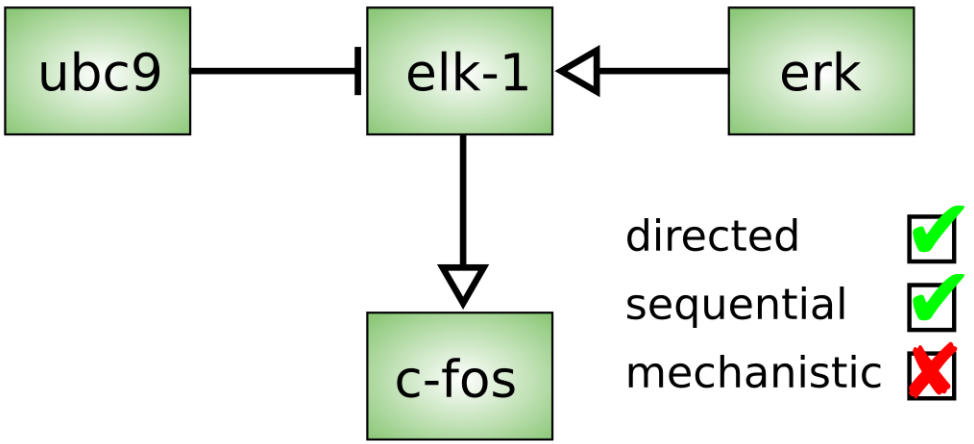
Entity Relationships



- Rule-based modelling
- Molecular Biology
- “Open world”
- Independent rules: no explosion

Activity Flows

- Logic modelling
- Signalling pathways, gene regulatory networks

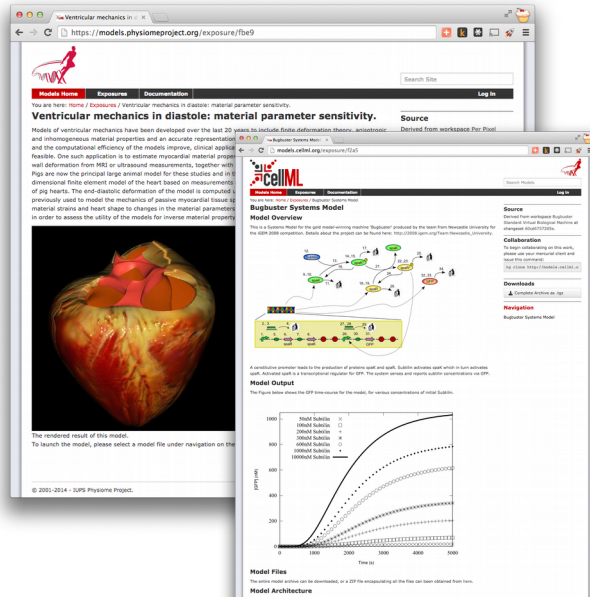


AUCKLAND BIOENGINEERING INSTITUTE
THE UNIVERSITY OF AUCKLAND
NEW ZEALAND

http://cellml.org/

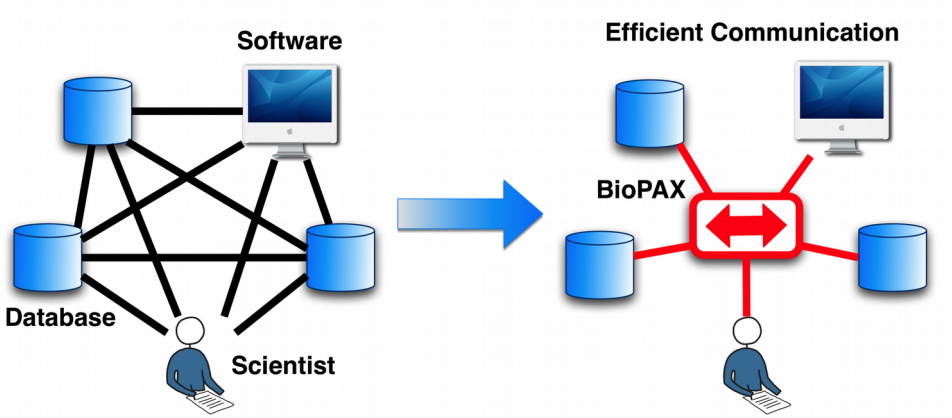
- Modular framework for encoding mathematical models:
  - differential algebraic equations using MathML
  - math is the primary data, biological context, provenance, etc., provided through annotations using RDF
- Units ensuring unambiguous conversion of numerical values

- Hierarchies of modules enable mathematical abstraction
- Hierarchical modules can be imported ⎵ reuse
- Free and open repository: http://models.physiomeproject.org/ supporting versioned model reuse, archiving, collaboration…

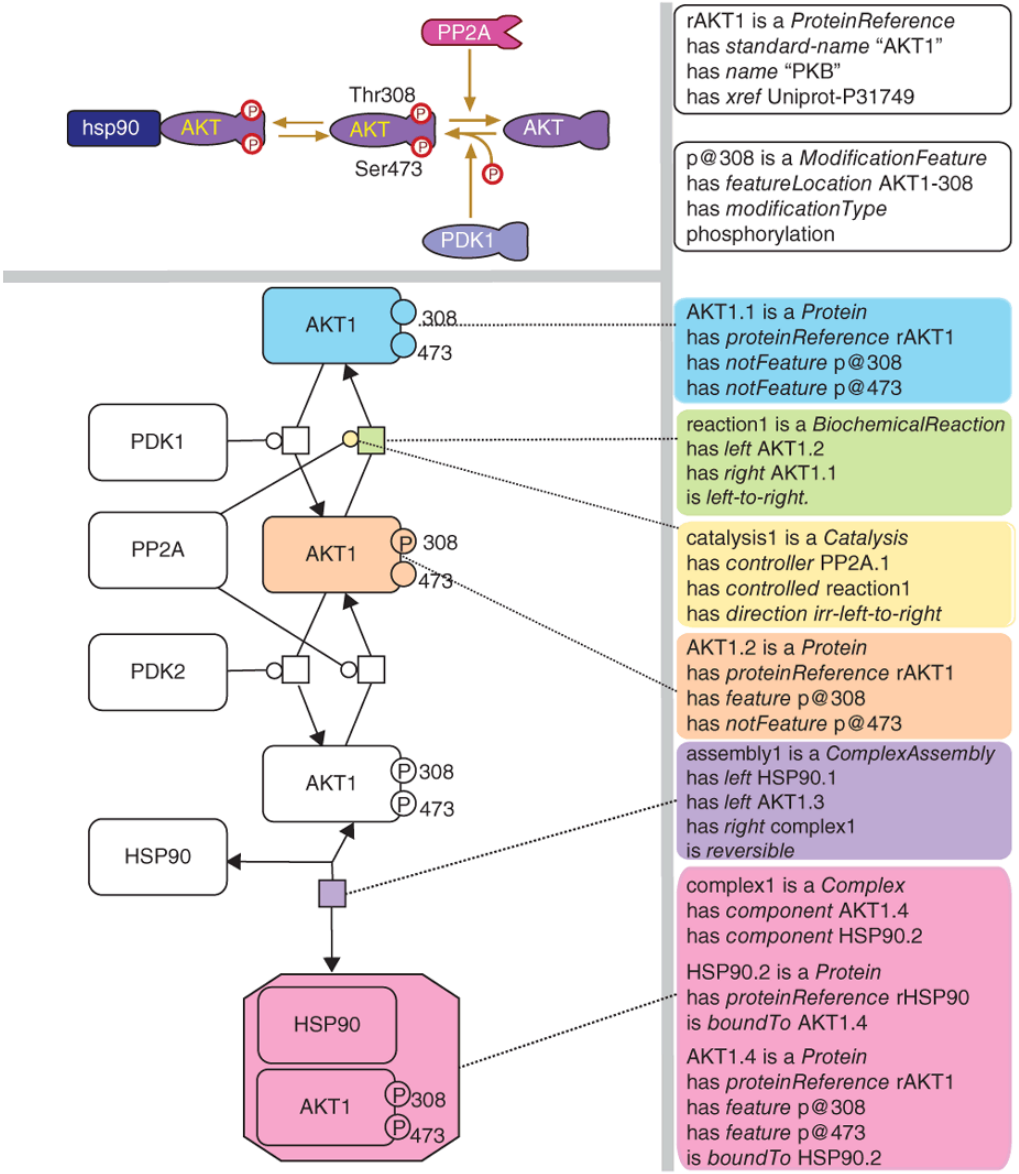


BioPAX Scope and Goals

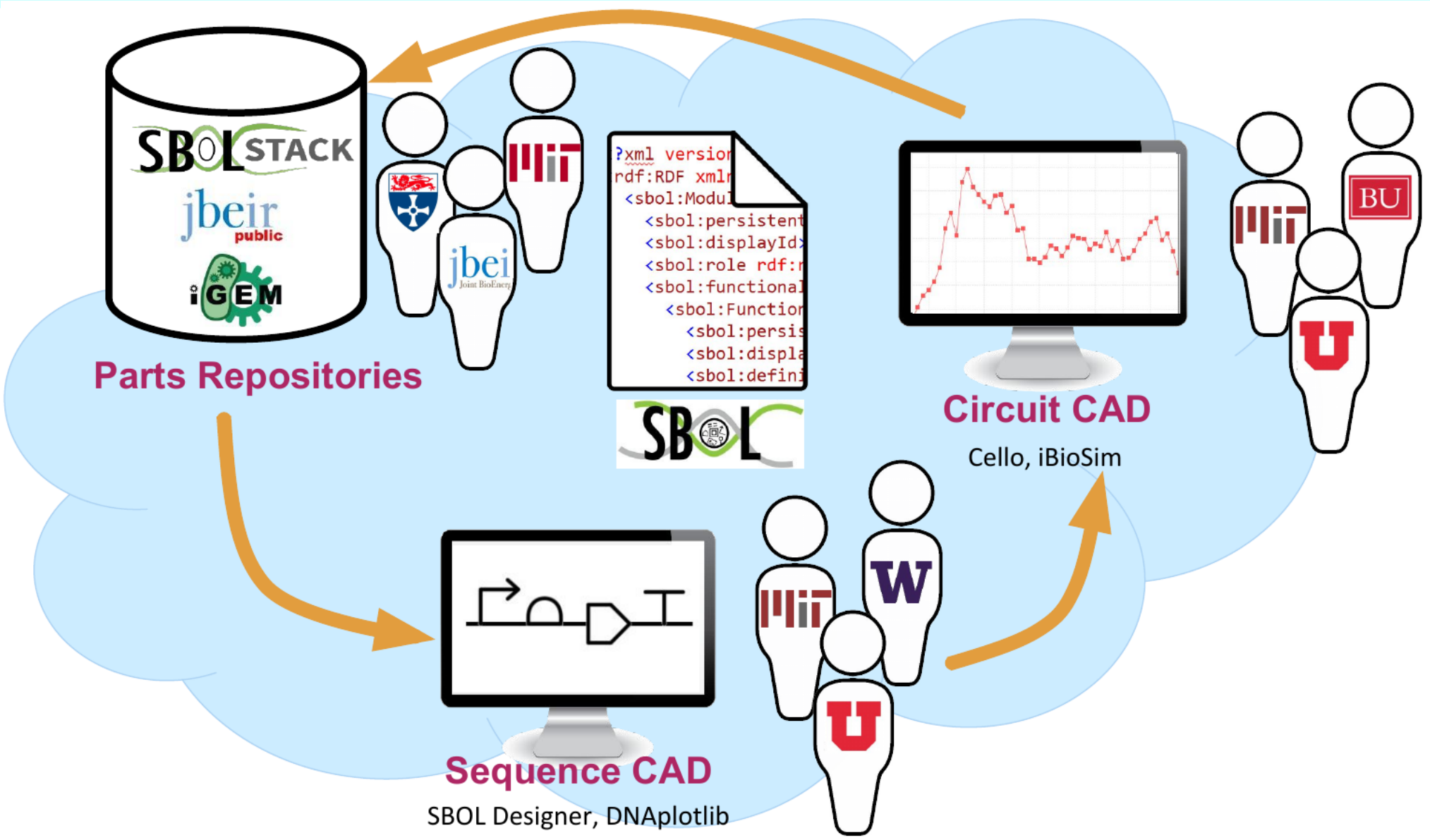
- To represent biological interactions and pathways
  - Pathways are collections of interactions that biologists have found useful to group together for organizational, historic, biophysical or other reasons
  - Types
    - Metabolic pathways
    - Signaling pathways
    - Protein-protein, molecular interactions
    - Gene regulatory pathways
- Encourage a community-wide effort to distribute pathway data in standard format; over 500 databases listed on pathguide.org



From Pathway Diagrams to BioPAX

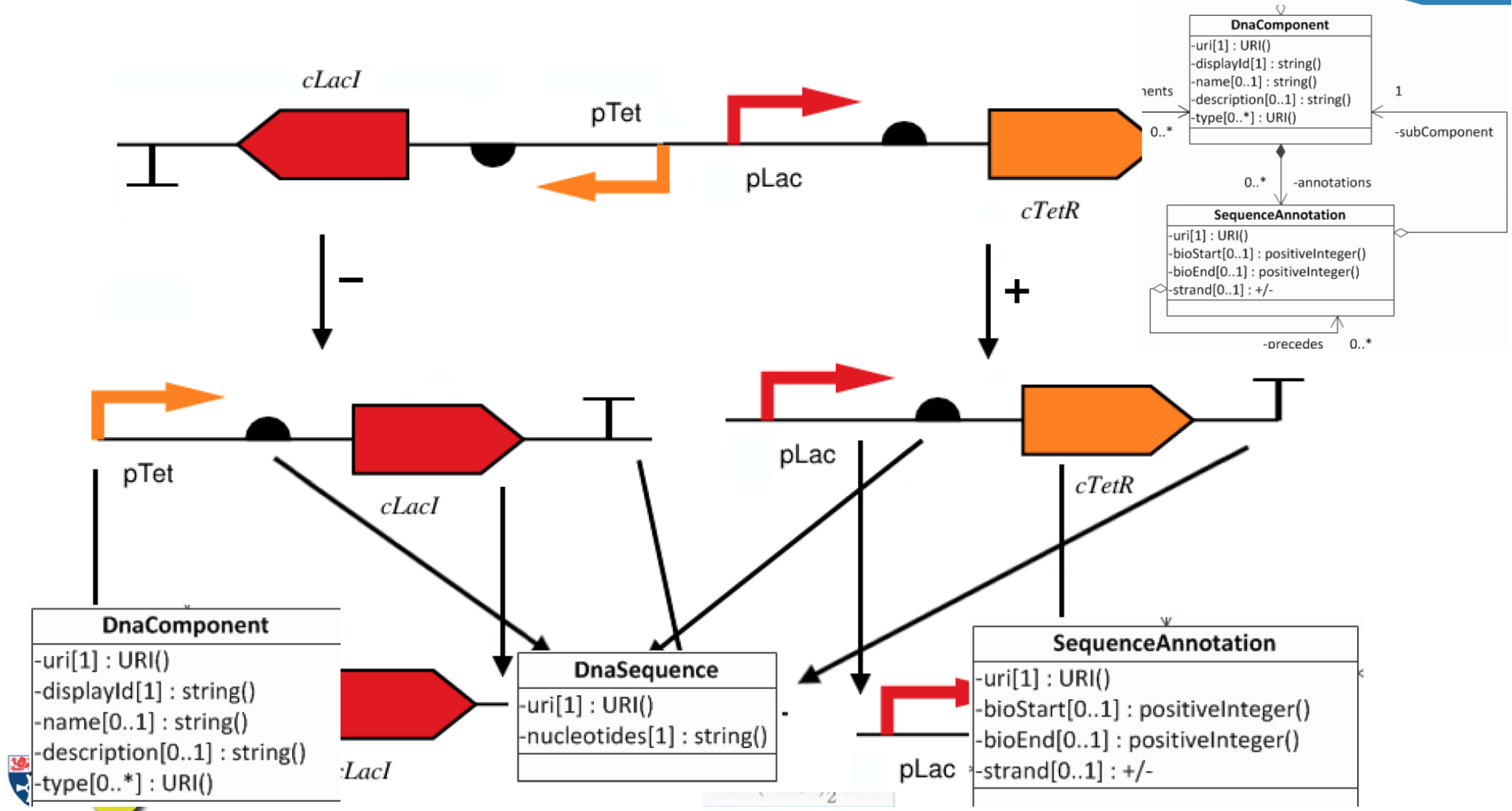


Synthetic Biology Open Language



http://sbolstandard.org/

Hierarchical Composition with SBOL v1



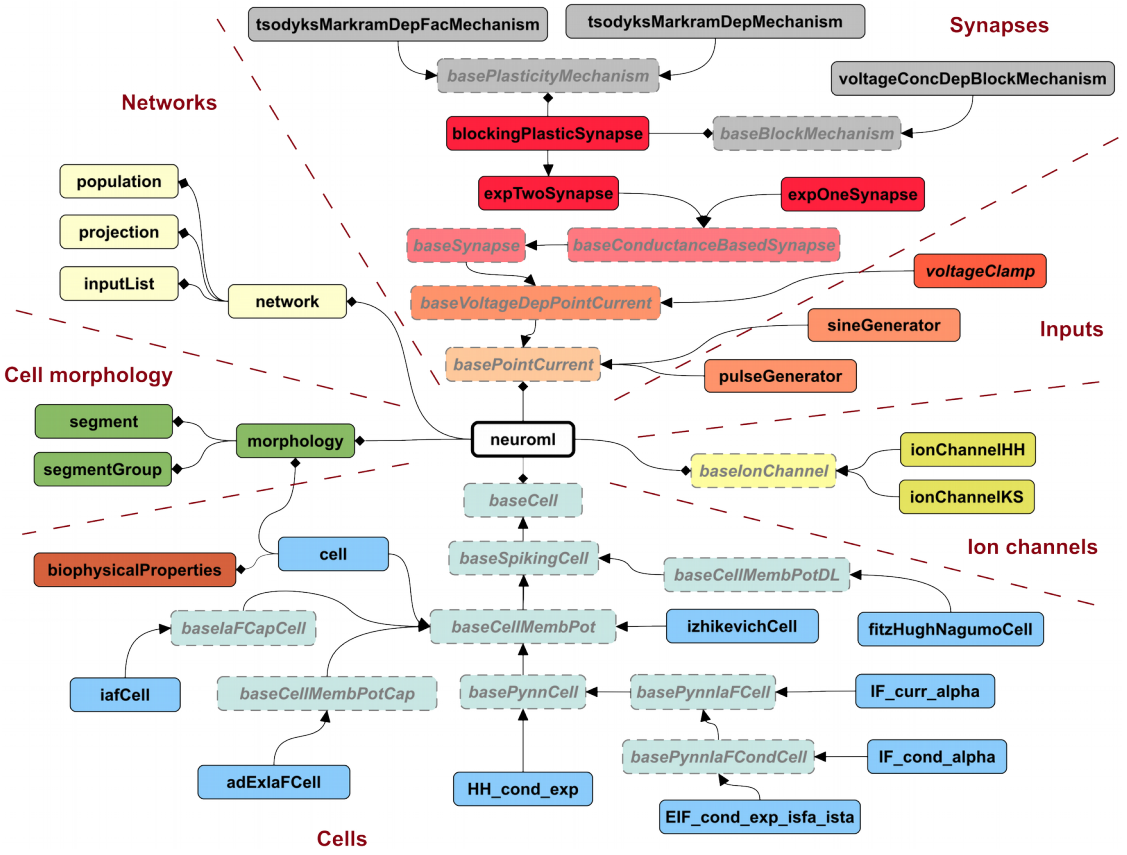
[NeuroML]

Standardised XML language for computational neuroscience

Models range from **point neuron networks** to **complex 3D multicompartmental cells**

Open source & contributors from around the world

Models from **Allen Institute, Blue Brain Project & Neuromorpho** converted to NeuroML



Cell, channel, synapse and network models supported by NeuroML

http://neuroml.org/

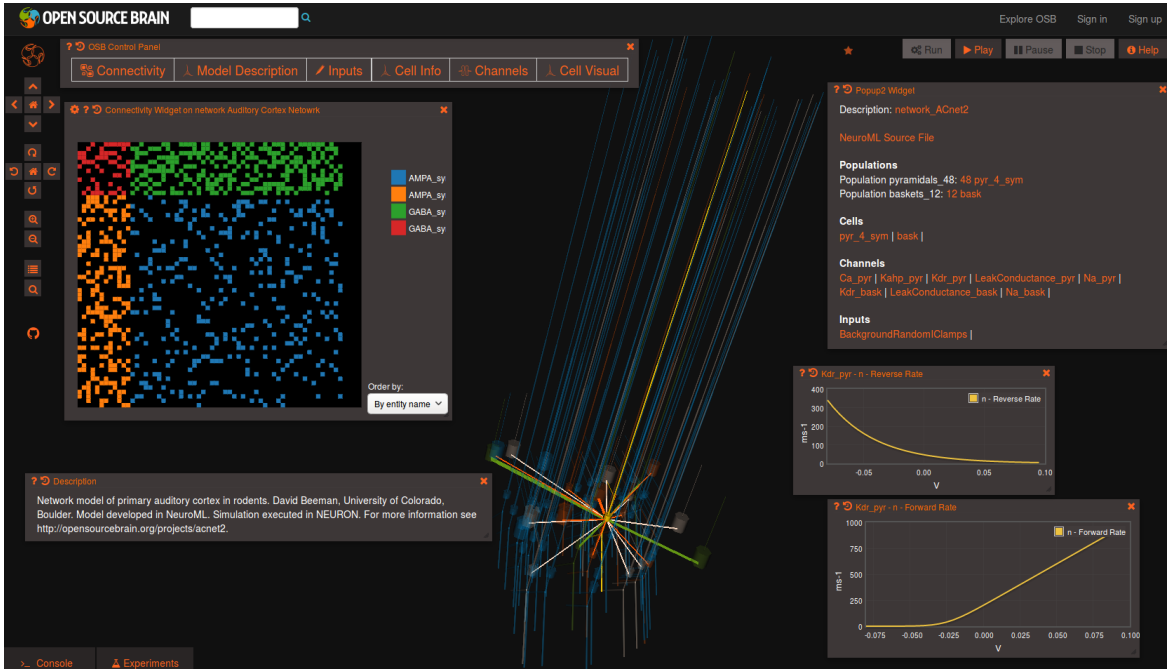
OPEN SOURCE BRAIN

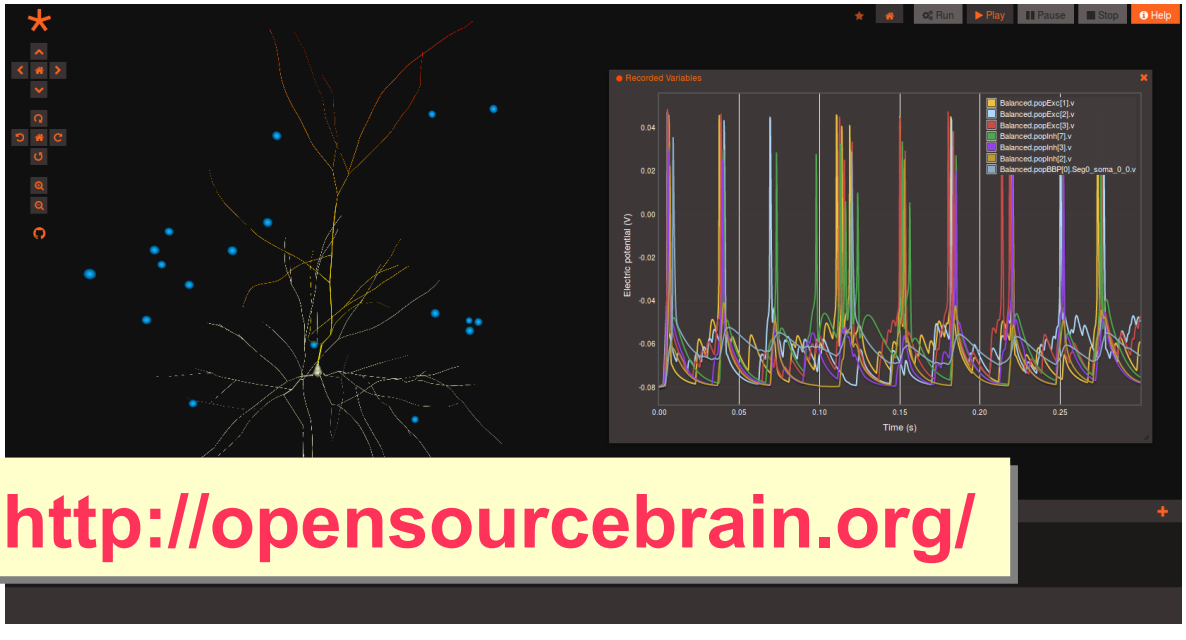
Models can be **visualised in 3D inside your browser**

Analyses performed on network connectivity, cell & channel properties

Models can be converted NeuroML→NEURON, executed on OSB servers & **replayed in browser**

Direct submission of simulations to the **Neuroscience Gateway Portal** in San Diego in development

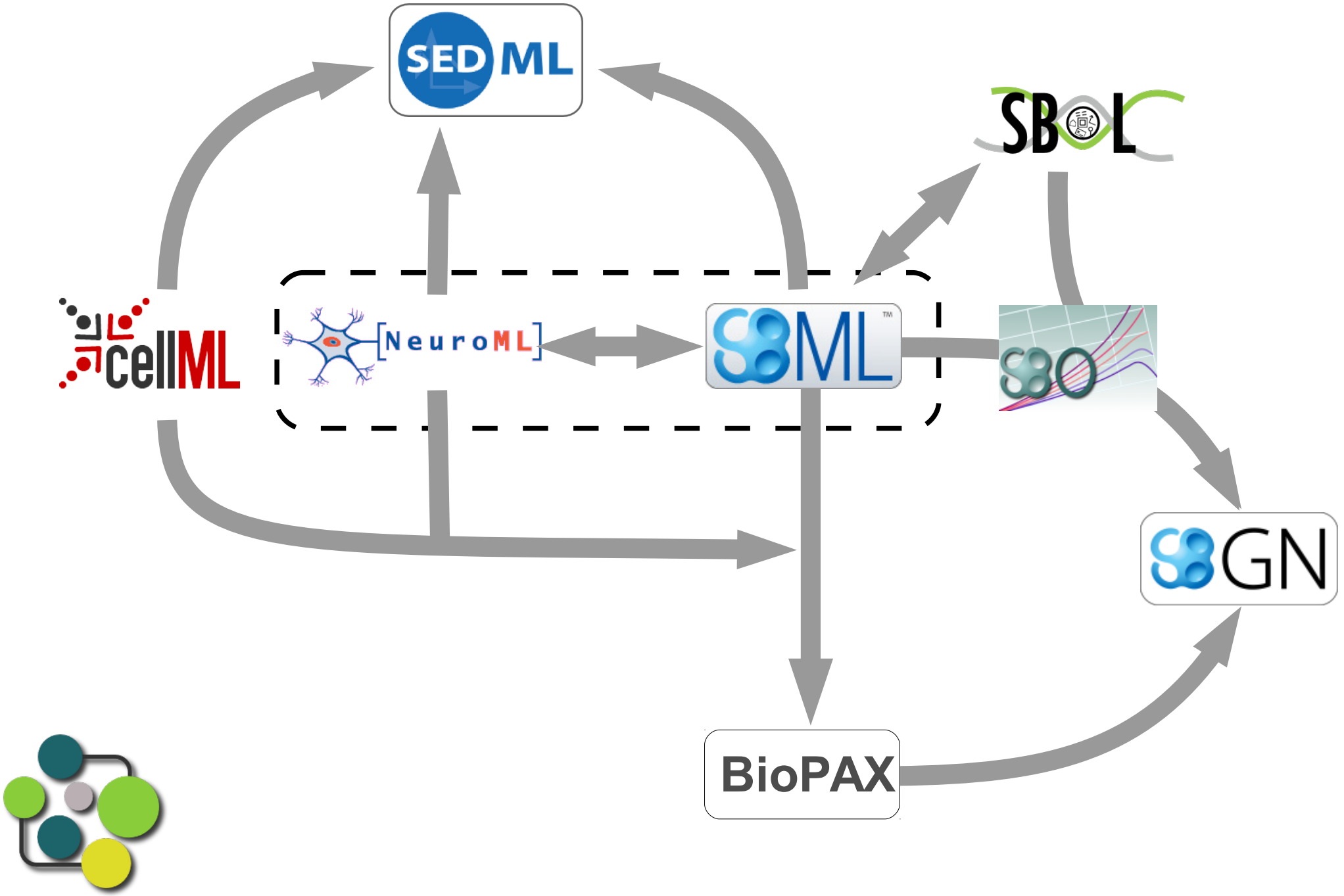




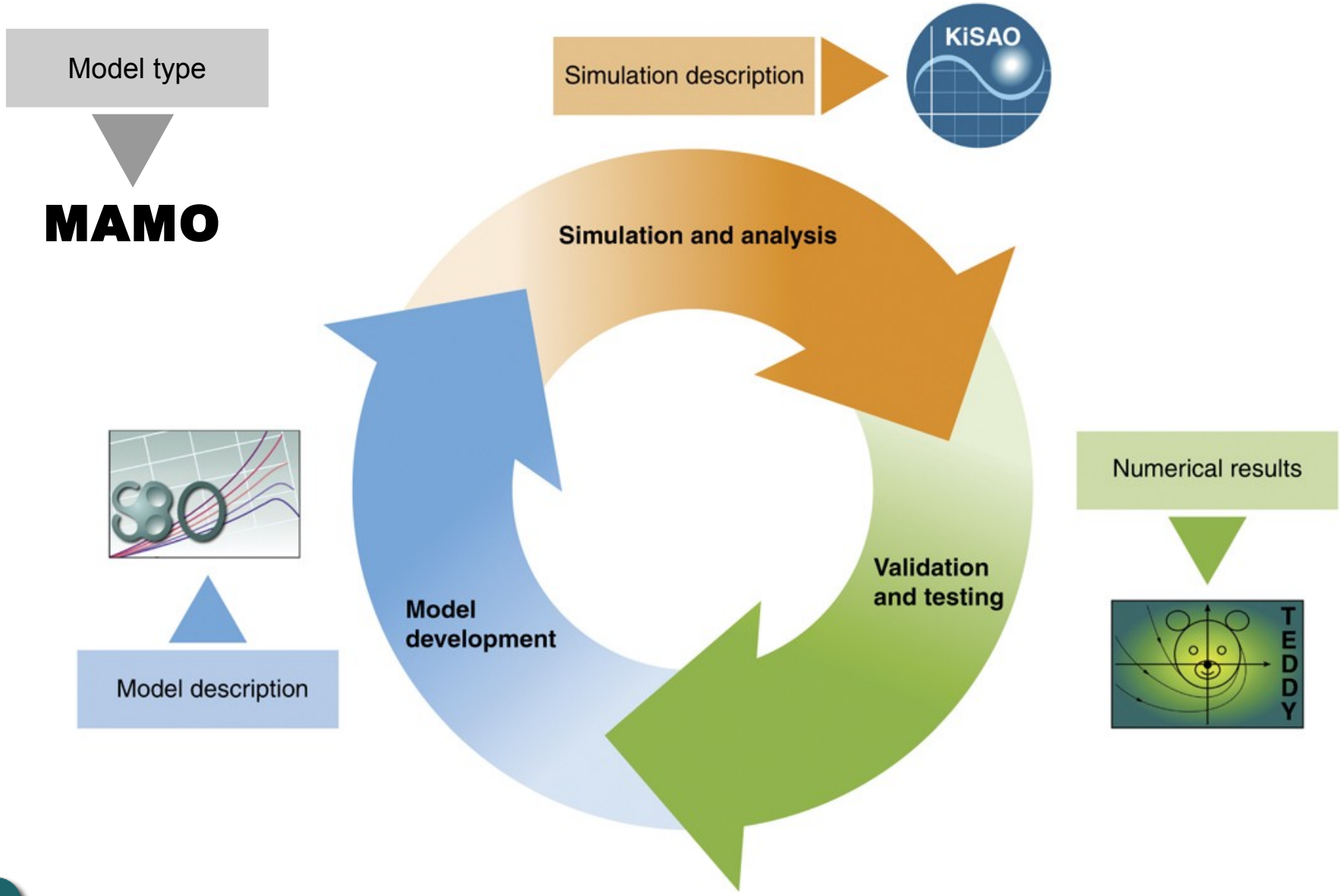
http://opensourcebrain.org/

COMBINE does NOT aim to take over the development of the standard formats, but to help coordinating and supporting this process

Interoperable standards = coupled development



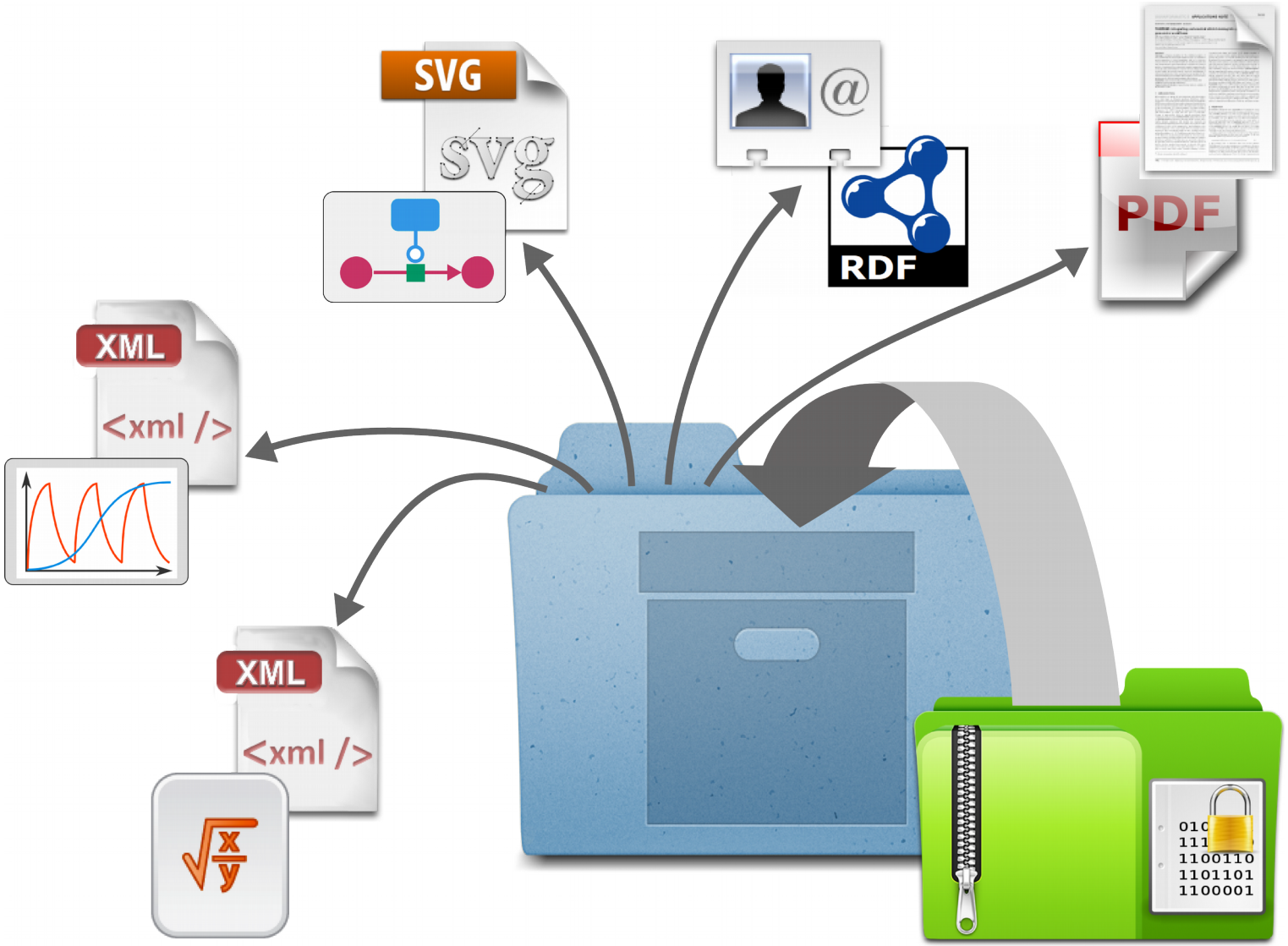
Terminologies



BioModels qualifiers

identifiers.org

combine archive



http://co.mbine.org/standards/omex

Want to join the conversation?

http://co.mbine.org/

@combine_coord

Mailing lists and forums of discussion

View | Edit | Revisions | Access control | Delete

list name	post address	aim
COMBINE news	@combine_coord	General announcement about COMBINE and its activities
COMBINE discuss	combine-discuss @ googlegroups.com	Main discussion forum of the COMBINE community, Feel free to use it to any aspect of the project, meetings, technology etc.
COMBINE archive	combine-archive @ googlegroups.com	Forum to discuss the OMEX format, the structure of the COMBINE archive, implementation issues, and all related questions. For more information about the COMBINE archive, please see the OMEX page.
COMBINE metadata	combine-meta @ googlegroups.com	Forum to discuss the structure and content of metadata to use together with COMBINE formars].
COMBINE site support	combine-support @ googlegroups.com	Use this address to report problems with the website.
COMBINE coordinators	combine-coord @ googlegroups.com	

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Thank-you

All editors of the formats

Developers of related ontologies and software

Organisers of meetings and efforts to support our standards

The community of Computational Systems Biology


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