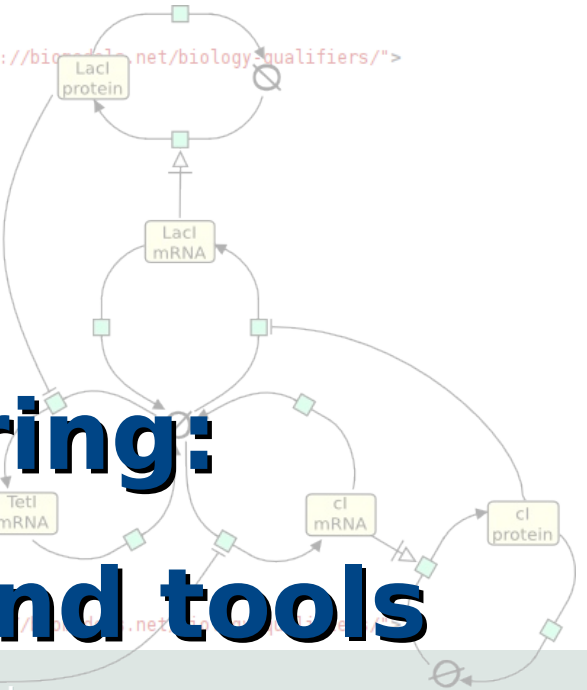
From art to engineering:

15 years of standards and tools towards digital organisms

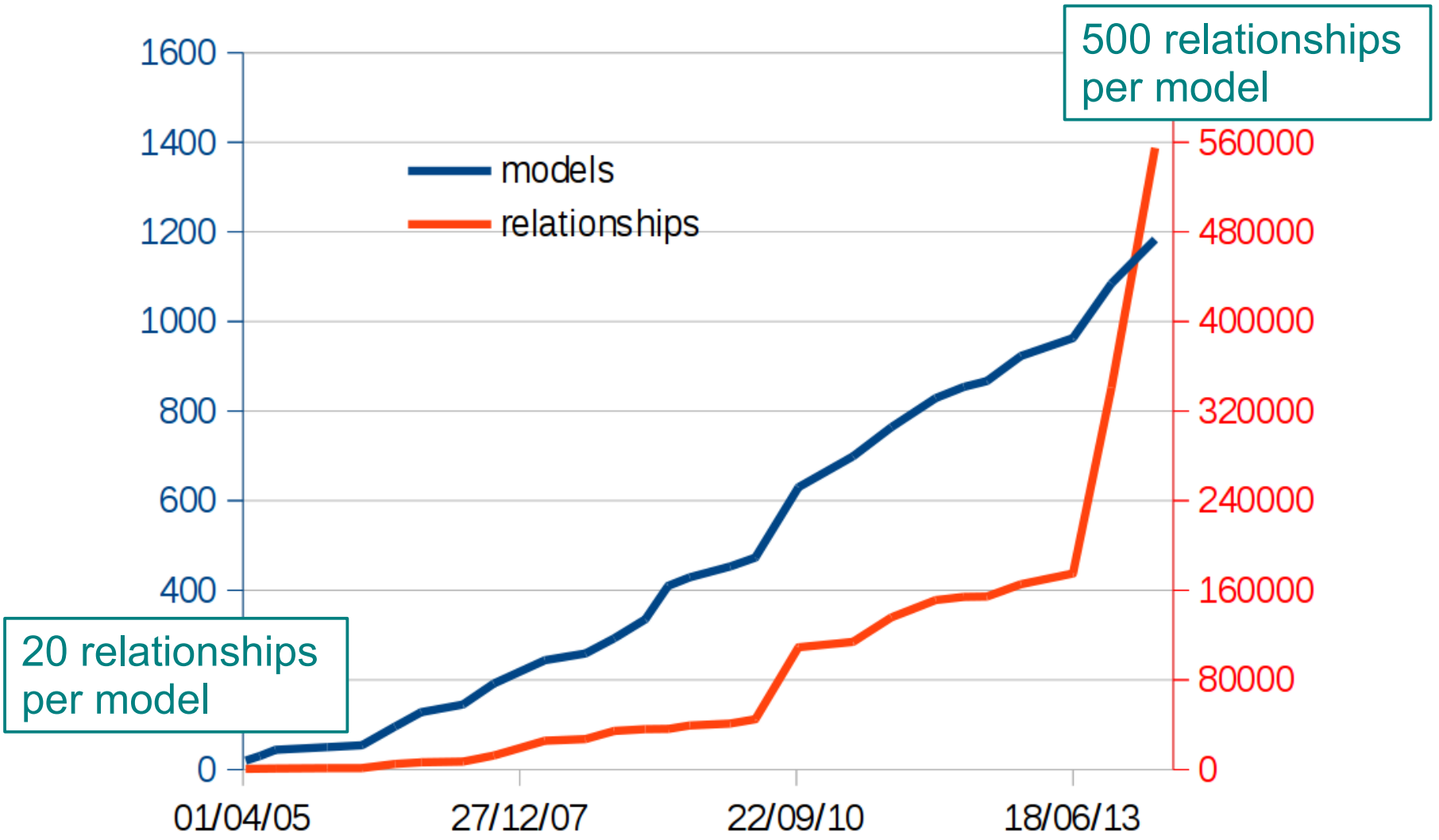
Nicolas Le Novère
Babraham Institute,
Cambridge, UK
n.lenovere@gmail.com



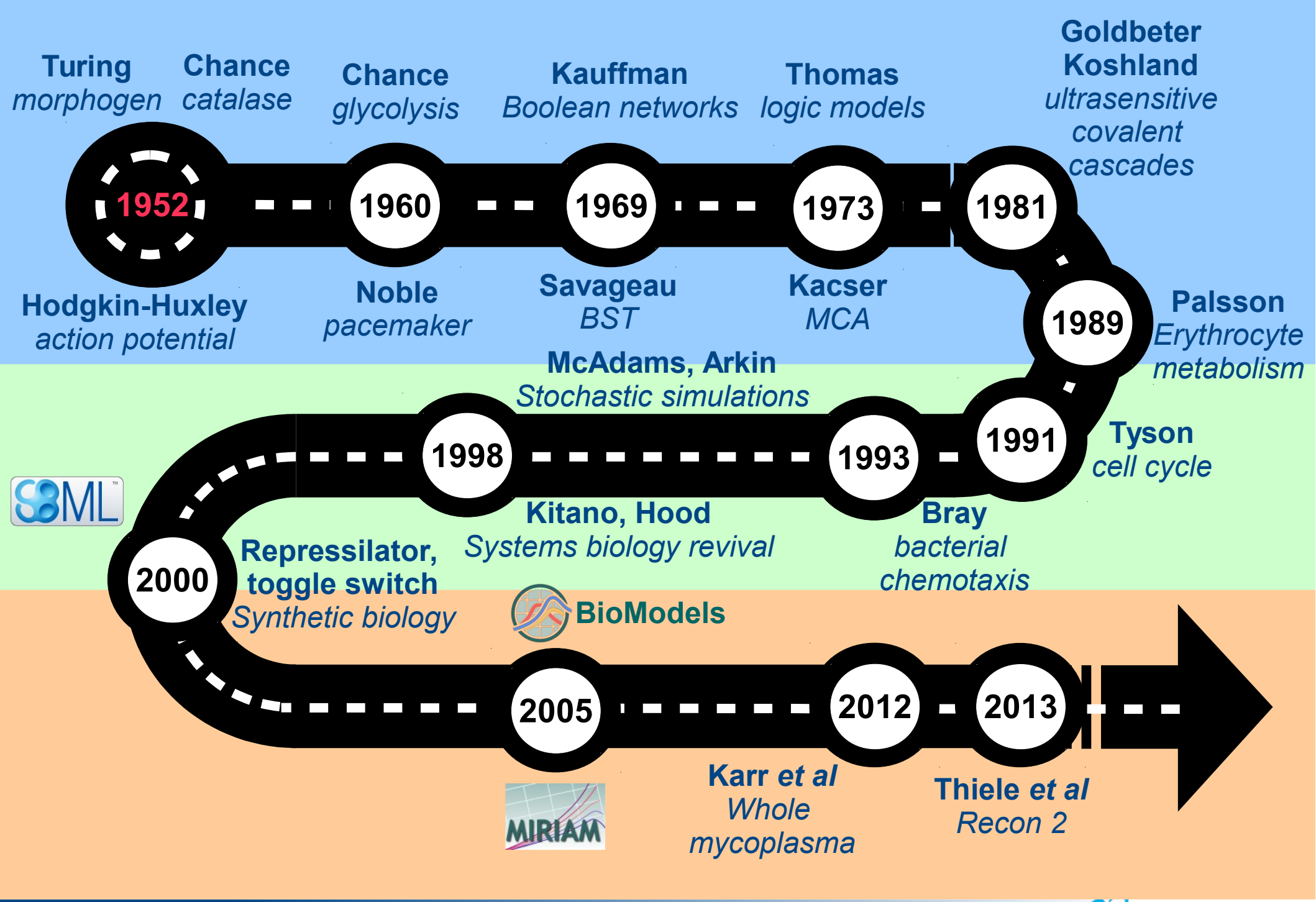
Babraham Institute

EMBL-EBI

Computational models on the rise



BioModels Database growth (published models branch) since its creation


Turing
morphogen
Chance
catalase
Chance
glycolysis
Kauffman
Boolean networks
Thomas
logic models
Goldbeter
Koshland
ultrasensitive
covalent
cascades
1952
1960
1969
1973
1981
Hodgkin-Huxley
action potential
Noble
pacemaker
Savageau
BST
Kacser
MCA
1989
Palsson
Erythrocyte
metabolism
McAdams, Arkin
Stochastic simulations
1998
1993
1991
Tyson
cell cycle
SBML
Kitano, Hood
Systems biology revival
Bray
bacterial
chemotaxis
2000
Repressilator,
toggle switch
Synthetic biology
BioModels
2005
2012
2013
MIRIAM
Karr et al
Whole
mycoplasma
Thiele et al
Recon 2

Improvised	Designed
One off	Many
Unique	Standard
Manually produced	Automated production
One or few artists	Collaboration
Produced in one go	Workflow
Fragile	Robust

Art.

Engineering

We need to

Verify

Re-use

Modify

Build upon

Integrate with

Therefore we need to share

Model descriptions

Simulation descriptions

Parametrisations

Biological meaning

Three types of standards

Minimal requirements **WHAT**	What to encode in order to share experiments and understand results MIBBI
Data-models **HOW**	How to encode the information defined above in a computer-readable manner combine
Terminologies	Structured representation of knowledge, with concept definitions and their relationships  OBO foundry

http://co.mbine.org

combine the computational modeling in biology network

HARMONY 2015 | Standards | Events | Documents | About | Forums | Search

COMBINE

- Home
- Help
- Sign-in

Coordinating standards for modeling in biology

The 'COmputational Modeling in BIology' NEtwork (COMBINE) is an initiative to coordinate the development of the various community standards and formats for computational models. By doing so, it is expected that the federated projects will develop a set of interoperable and non-overlapping standards covering all aspects of modeling in biology.

Building on the experience of mature projects, which already have stable specifications, software support, user-base and community governance, COMBINE will help foster or support fledgling efforts aimed at filling gaps or new needs. As those efforts mature, they may become part of the core set of COMBINE standards.

One of the initial activities of COMBINE is to coordinate the organization of scientific and technical events common to several standards. Those events, as others related to our field of research are gathered in a calendar.

To receive announcements from COMBINE, subscribe to combine-announce@ebi.ac.uk (Note that the main list of each of the COMBINE standards is already subscriber).

To discuss the goals, organization and operation of COMBINE, subscribe to combine-discuss@ebi.ac.uk.

To report issues about the co.mbine.org website, send a mail to combine-support @ googlegroups.com

Tweets

Follow

COMBINE @combine_coord 25 Feb
Short paper summarizing COMBINE activities
journal.frontiersin.org/article/10.338...
Expand

COMBINE @combine_coord 19 Dec
Publication of the OMEX format and the COMBINE archive
biomedcentral.com/1471-2105/15/3...
Expand

A language to describe computational models in biology

	Model descriptions
Data-models	SBML™

Born in Caltech 2000

John Doyle

Hiroaki Kitano

Hamid Bolouri

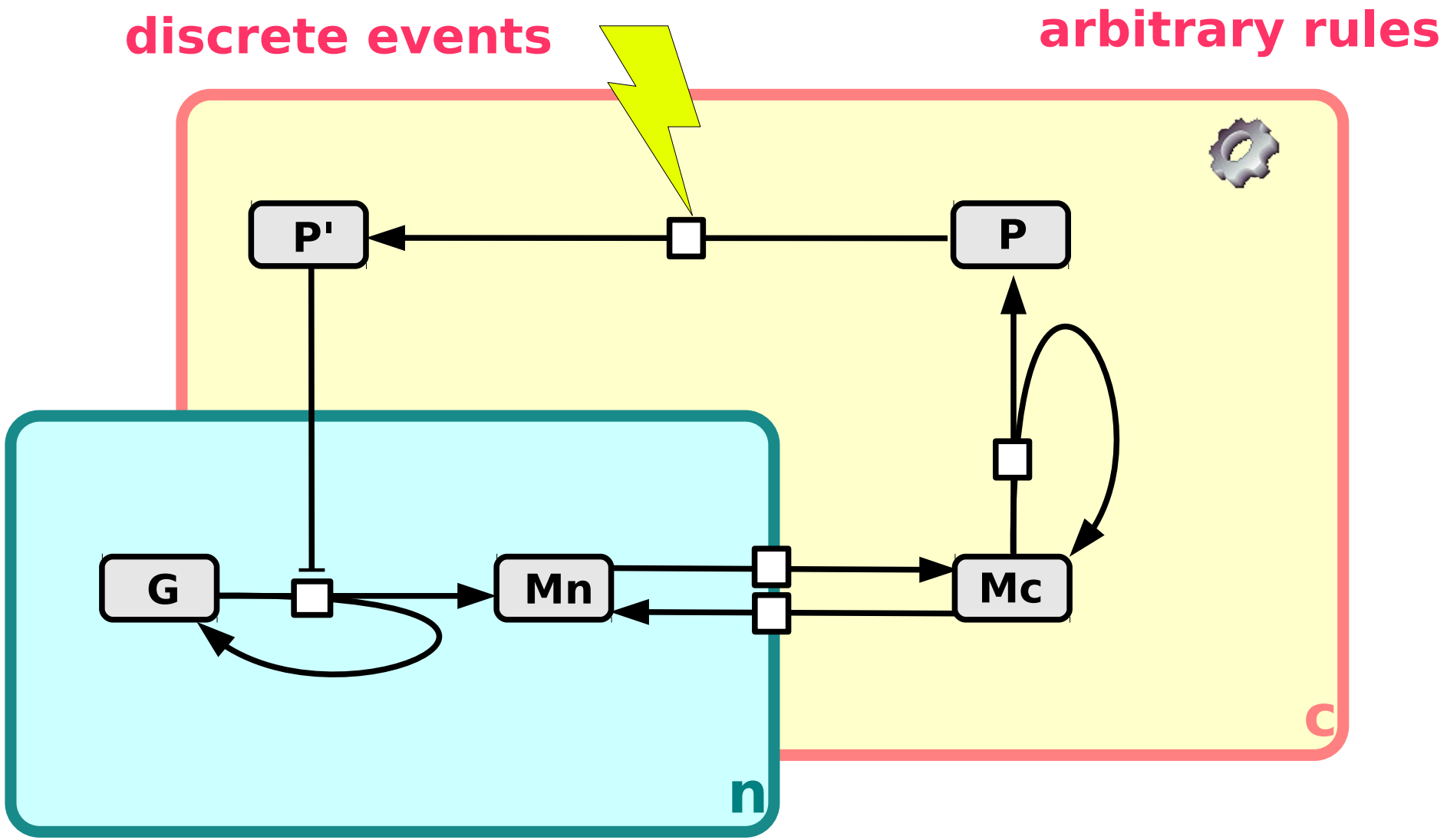
Mike Hucka

Andrew Finney

Herbert Sauro

Hucka et al. *Bioinformatics* (2003)

What can we encode in SBML (core)?

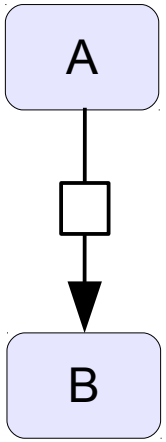


Structure of SBML

```
<?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

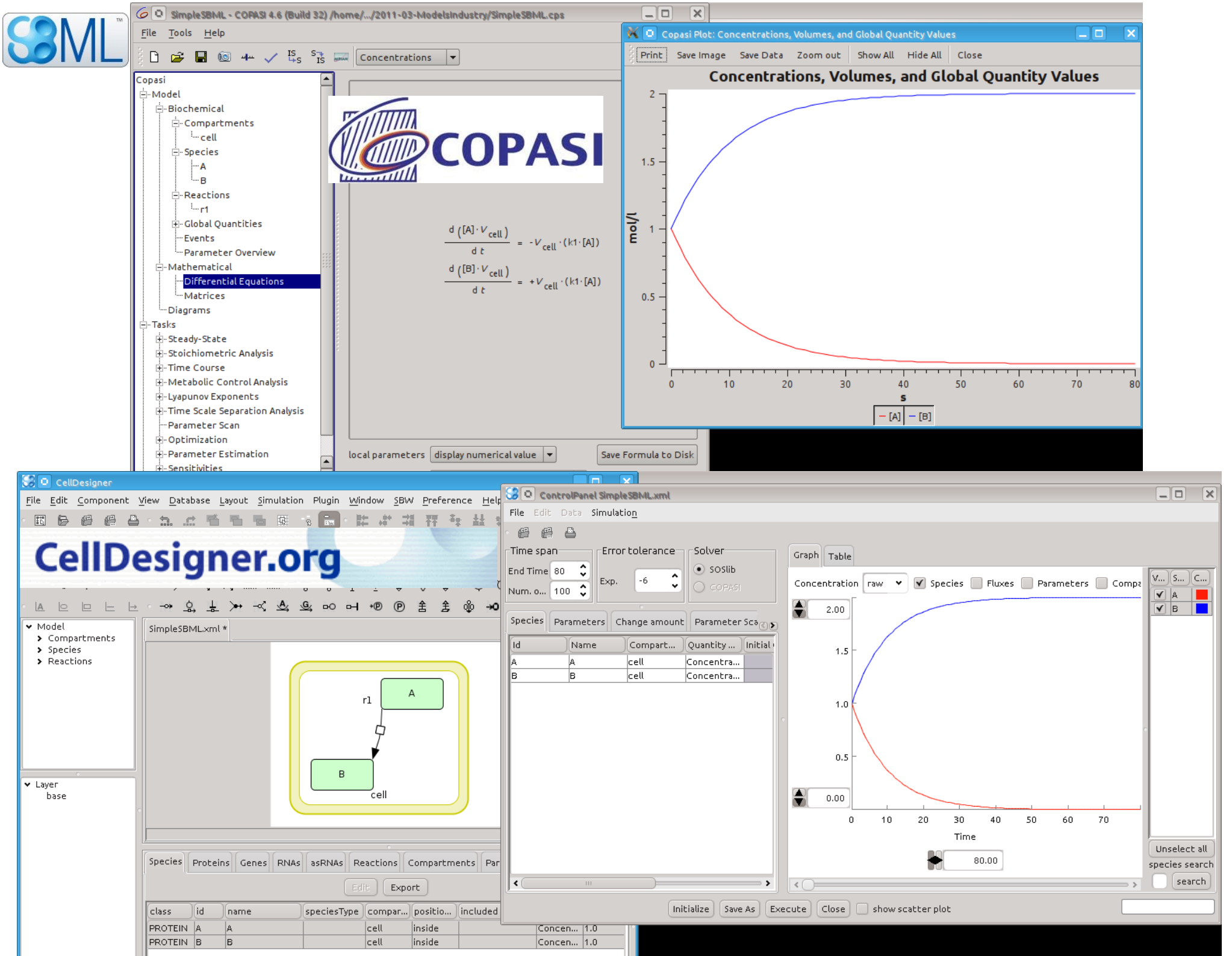


$$\frac{d[B]}{dt} = k1 \times [A]$$

```xml
<?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>
```

A very simple SBML file

http://sbml.org


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

_computational BIOLOGY

RESOURCE

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

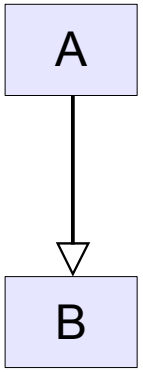
A not so simple SBML file (Recon2)

- 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
- Graph rendering – specification finalised
- Complex species – specification finalised
- Groups - specification finalised
- Distributions and ranges - specification under discussion
- Spatial diffusion – specification under discussion
- Enhanced metadata – specification proposed
- Arrays and sets – specification proposed
- Dynamic structures - discussed

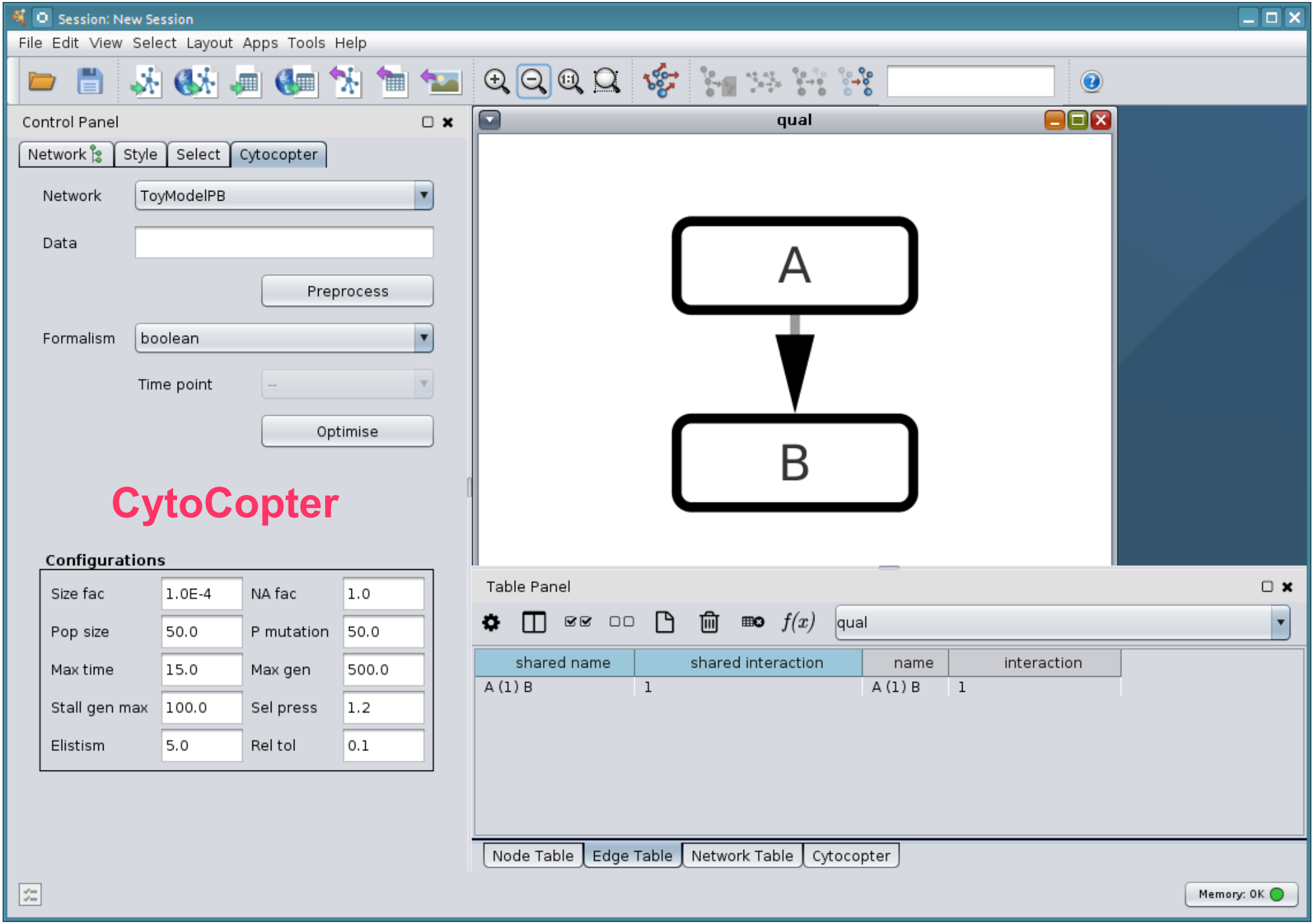
SBML Level 3 is modular

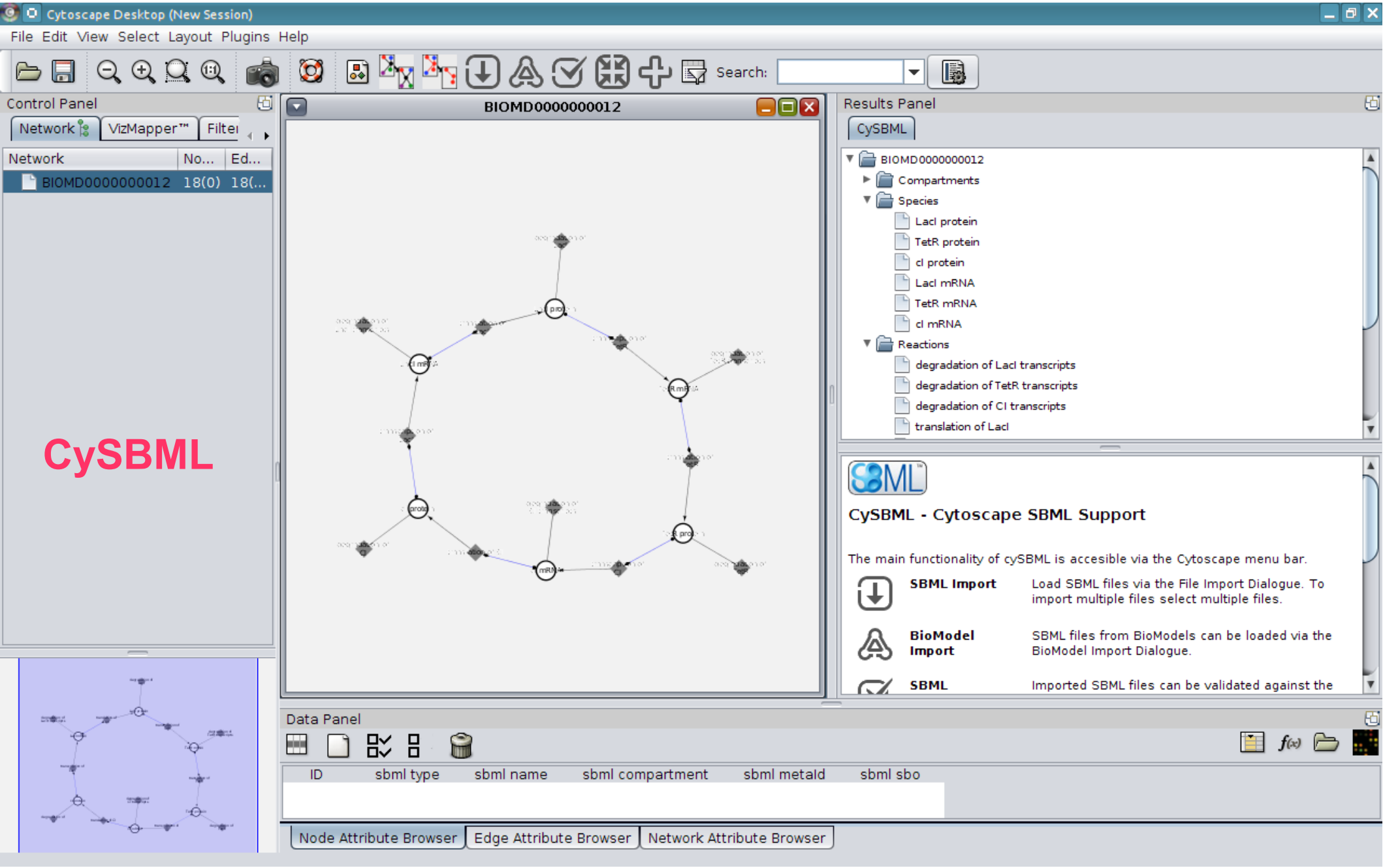


$$A \geqslant 1 \Rightarrow B = 1$$

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(...
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

CySBML

SBML Software Guide

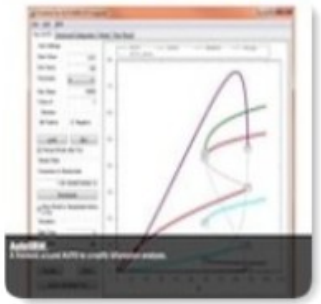
The following pages describe SBML-compatible software packages known to us. We offer different ways of viewing the information, all drawn from the same underlying data collected from the systems' developers via our **software survey**. The *Matrix* provides a table listing all known software and a variety 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: **263**.

Go to the SBML Software Matrix

Go to the SBML Software Summary

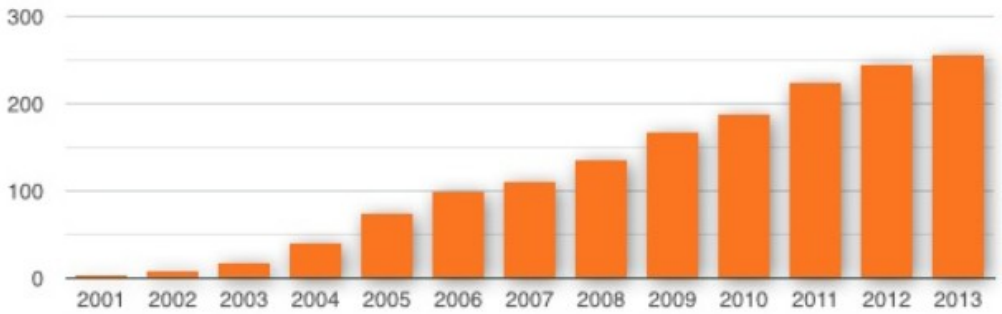
Go to the SBML Software Showcase



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.



Adding the semantics to the syntax

	Model descriptions
Minimal requirements	MIRIAM
Data-models	SBML
Terminologies	SBO

Born in Heidelberg 2004

Le Novère *et al. Nat Biotechnol* (2005), Courtot *et al. Mol Syst Biol*(2011)

Minimal Information Required In the Annotation of Models

Reference correspondence

1. In a public, standardized, machine-readable format
2. Comply with the standard in which it is encoded
3. Clearly related to a single reference description
4. Reflect biological processes
5. Instantiable in a simulation all numbers provided
6. Able to reproduce results

Attribution

1. Has to be named
2. Citation must be provided
3. Model creators details
4. Date and time of creation and last modification
5. Link to precise statement about terms of distribution

External resources

1. Annotation unambiguously model constituent to data
2. Link to external information as a triplet {collection, identifier, qualifier}
3. Annotation written as a Uniform Resource Identifier
4. Identifier considered within framework of the collection.
5. Collection namespace and record identifier in one URI
6. Qualifiers to refine the link between model constituent and external knowledge
7. Standard set of valid URIs agreed upon by community

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

Minimal Information Required In the Annotation of Models

Reference correspondence

1. In a public, standardized, machine-readable format
2. Comply with the standard in which it is encoded
3. Clearly related to a single reference description
4. Reflect biological processes
5. Instantiable in a simulation all numbers provided
6. Able to reproduce results

Attribution

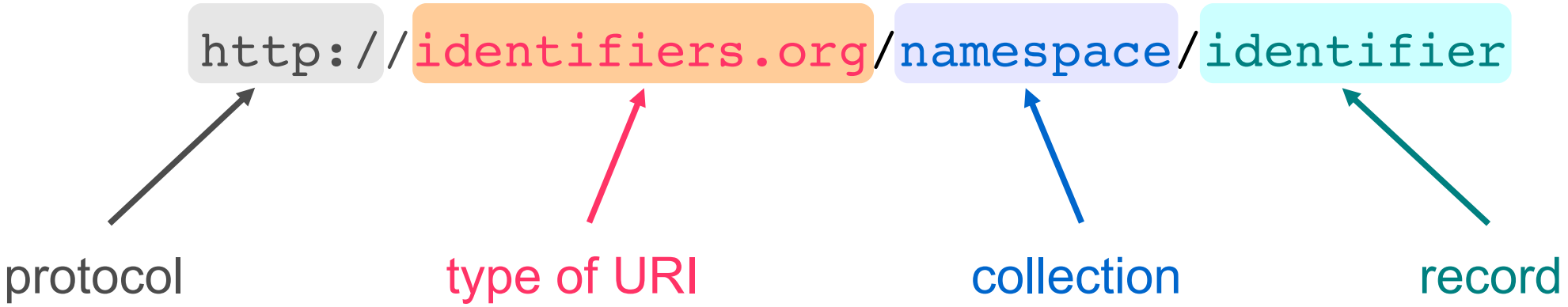
1. Has to be named
2. Citation must be provided
3. Model creators details
4. Date and time of creation and last modification
5. Link to precise statement about terms of distribution

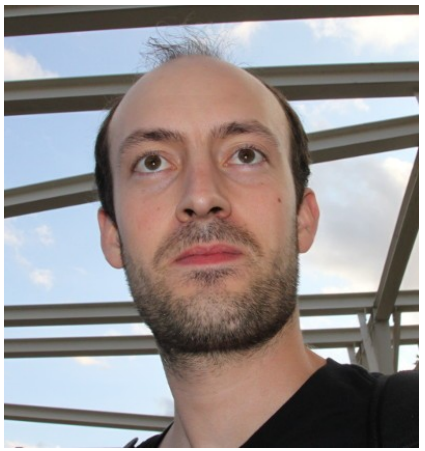
External resources

1. Annotation unambiguously model constituent to data
2. Link to external information as a triplet {collection, identifier, qualifier}
3. Annotation written as a Uniform Resource Identifier
4. Identifier considered within framework of the collection.
5. Collection namespace and record identifier in one URI
6. Qualifiers to refine the link between model constituent and external knowledge
7. Standard set of valid URIs agreed upon by community

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

identifiers.org (aka new MIRIAM URIs)





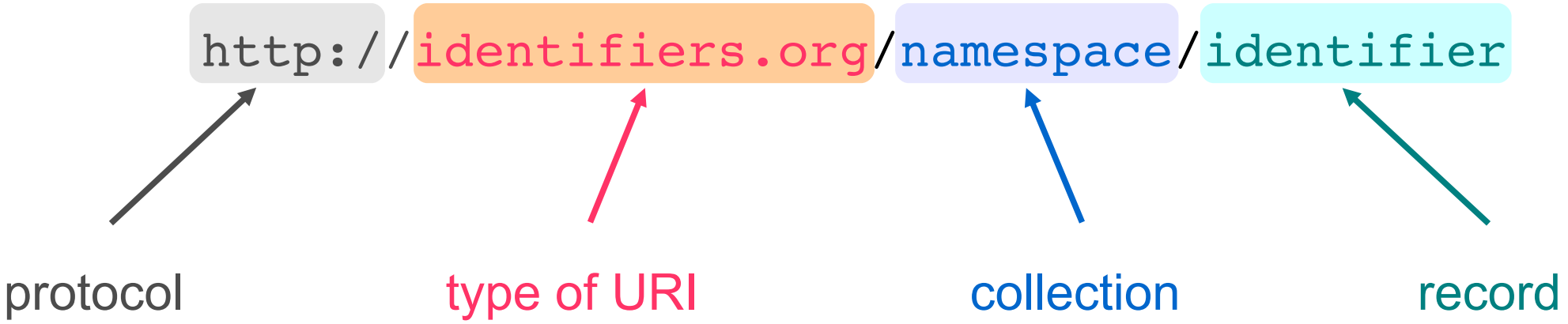
Camille Laibe

Nick Juty

Sarala Wimalaratne

Juty *et al. Nucleic Acid Res.* (2012)

identifiers.org (aka new MIRIAM URIs)



http://identifiers.org/pubmed/22140103

http://identifiers.org/ec-code/1.1.1.1

http://identifiers.org/go/GO:0000186

MIRIAM Registry

Search

Examples: ontology, enzyme, Japan, EMBL

Categories & tags

Home | Browse | Download | Web services | Documentation | Contribute | Identifiers.org | About | Feedback

Persistent identification for life science data

The MIRIAM **Registry** provides a set of online services for the generation of unique and perennial identifiers, in the form of URIs. It provides the core data which is used by Identifiers.org.

The core of the *Registry* is a catalogue of data collections (corresponding to controlled vocabularies, databases, ...), their URIs and the corresponding physical URLs (or resources). These resources are monitored daily to ensure data accessibility and the validity of the resolution mechanism.

Access to the Registry's dataset is made available via exports (XML and RDF) and Web Services (SOAP and REST).

All provided data and services are free for use by all.

Access data

- Browse by data collection name
- Browse by types of data (categories & tags)
- Web services
- Download complete dataset (XML)
- Identifiers.org

Contribute

- Contact the team and community
- Edit existing data collection
- Request new data collection(s)
- Provide feedback

Learn & discover

- Getting started with the Registry
- Frequently Asked Questions
- Publications, presentations, posters, ...
- Review of URI based identification systems
- Documentation
- About the Registry

Latest publication

Identifiers.org and MIRIAM Registry: community resources to provide persistent identification.

Juty N., Le Novère N., Laibe C.

Nucleic Acids Research. 2012; 40 (Database issue):

Registry statistics

Published

Data collections:	521 (531)
Resources:	651 (704)
Last update:	Aug 12, 2014

Under curation

Data collections:	409
Resources:	415
Last update:	Jun 30, 2014

News

Dataset descriptor and RDF representations

August 2013

The Registry now provides a dataset descriptor and RDF representations of the whole Registry and individual data collections (in RDF/XML and Turtle formats). Read more...

Primary resources

July 2013

Identifiers.org and its Registry now highlight the "primary resource" for data collections. Read more...

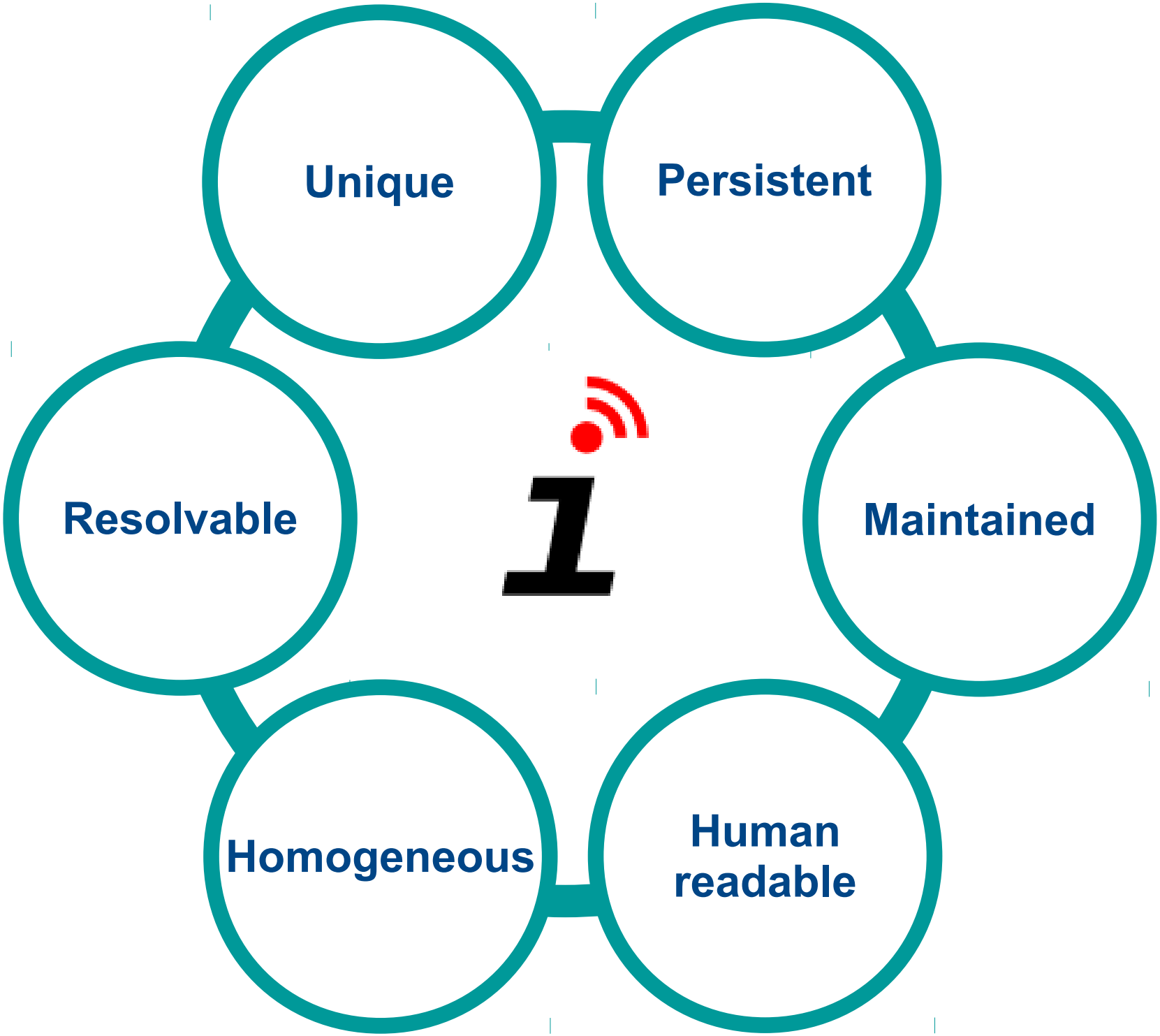
Presentation at BioHackathon 2013

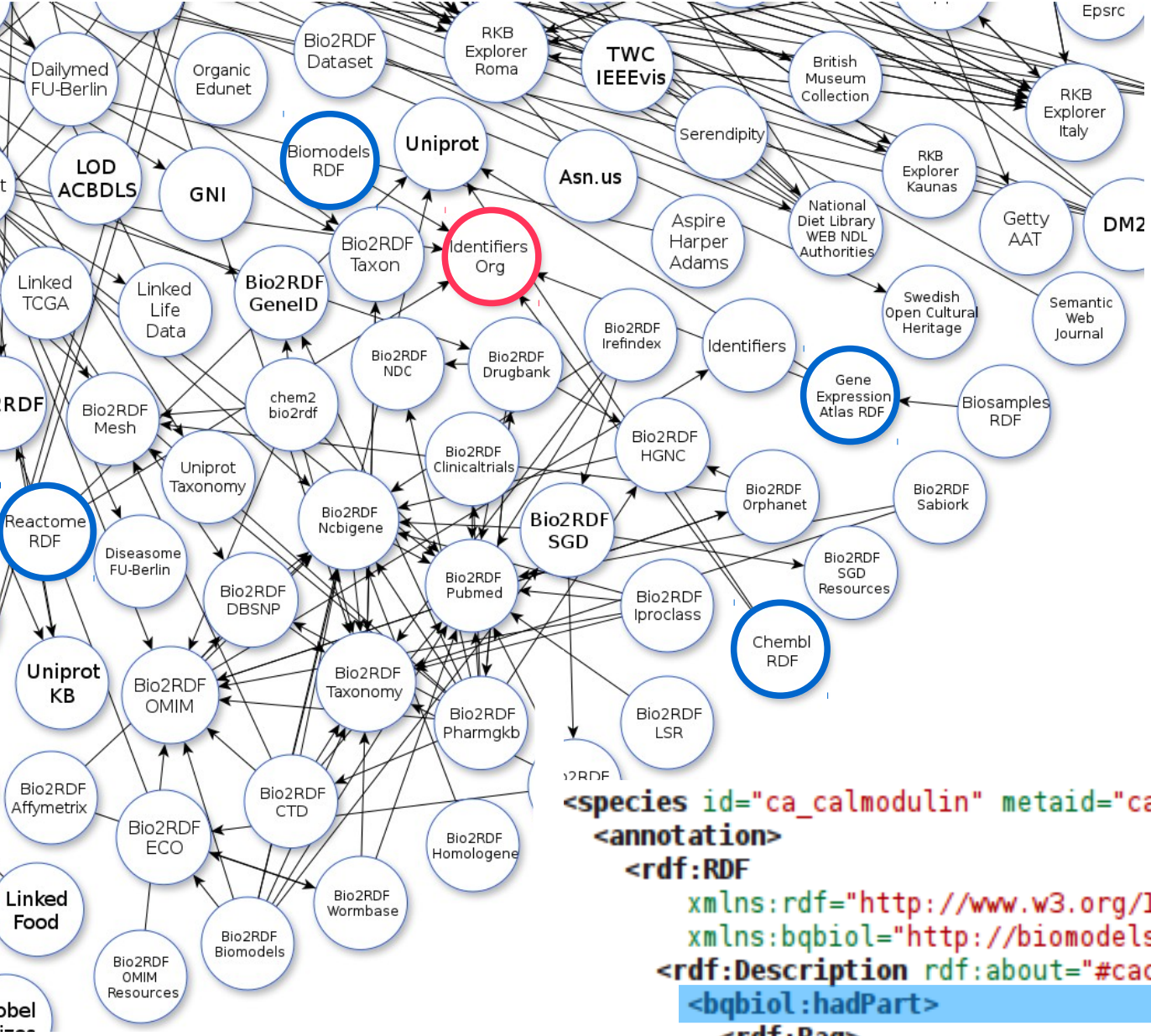
June 2013

Presentation "Identifiers.org: practical integration tool for heterogeneous datasets" Hackathon 2013 Symposium in an (slides, PDF)

Laibe *et al. BMC Syst Biol* (2007)

http://www.ebi.ac.uk/miriam/
http://identifiers.org/registry


Unique
Persistent
Resolvable
Maintained
Homogeneous
Human readable



W3C Semantic Web

```
<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:hadPart>
          <rdf:Bag>
            <rdf:li rdf:resource="http://identifiers.org/uniprot/62158"/>
            <rdf:li rdf:resource="http://identifiers.org/chebi/CHEBI:29108"/>
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
```

The Systems Biology Graphical Notation

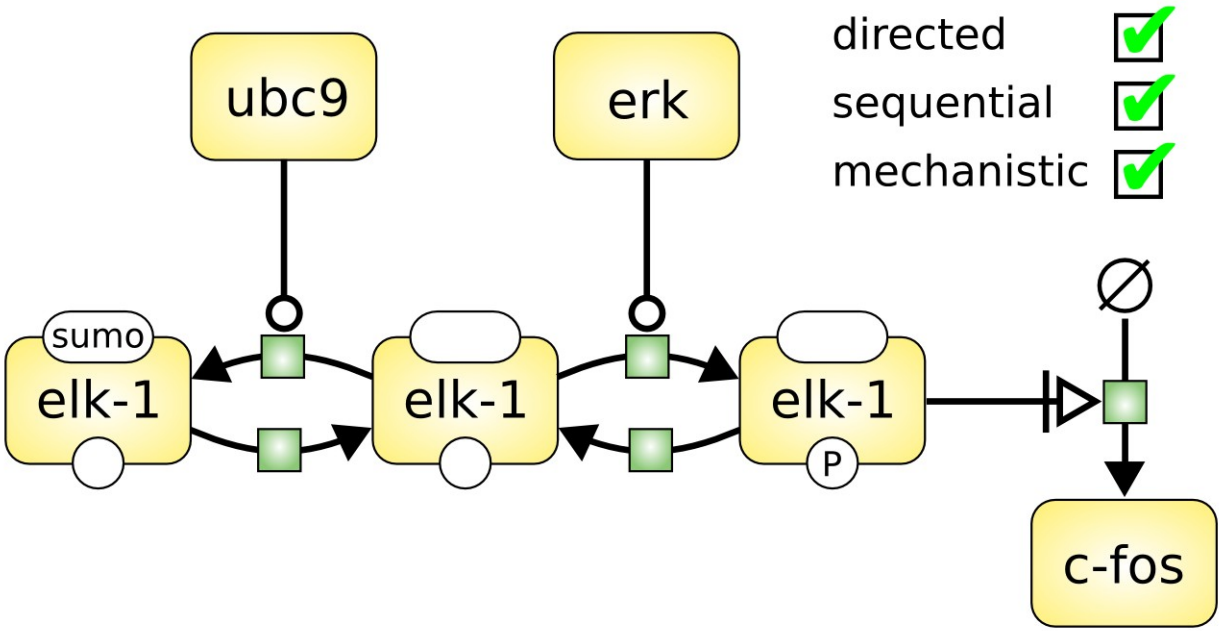
http://sbgn.org/

Le Novère et al (2009)

Unambiguous consensual visual notation

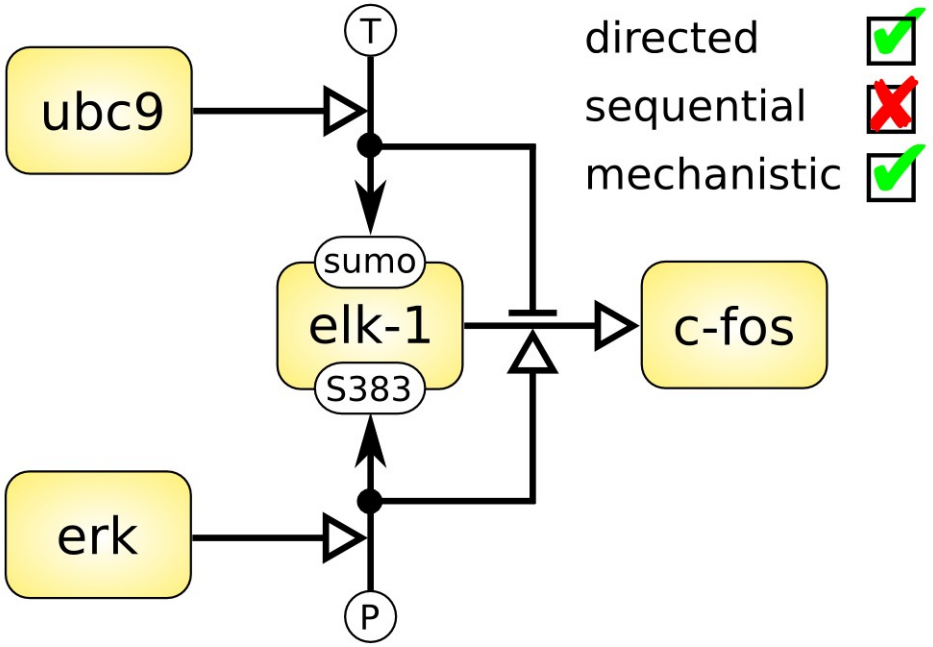
- An unambiguous way of graphically describing and interpreting biochemical and cellular events
- Limited amount of symbols
  Re-use existing symbols
  ☞ Smooth learning curve
- Can represent logical or mechanistic models, biochemical pathways, at different levels of granularity
- Detailed technical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

Process Descriptions



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

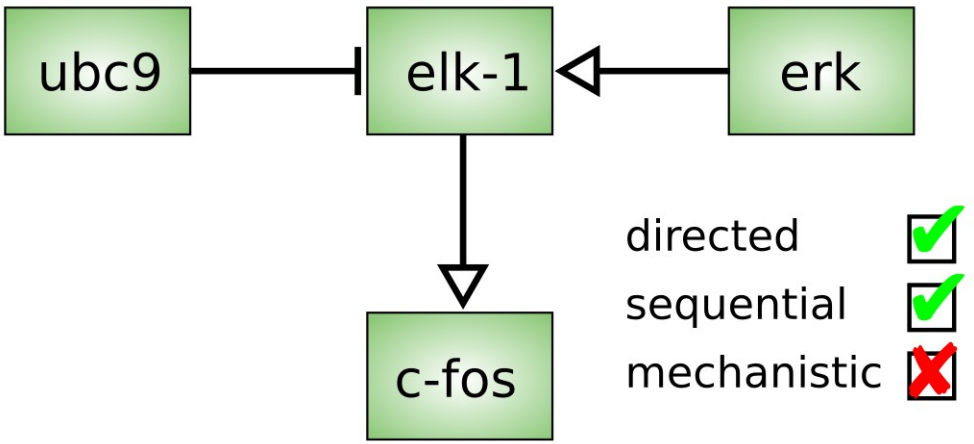
Entity Relationships



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

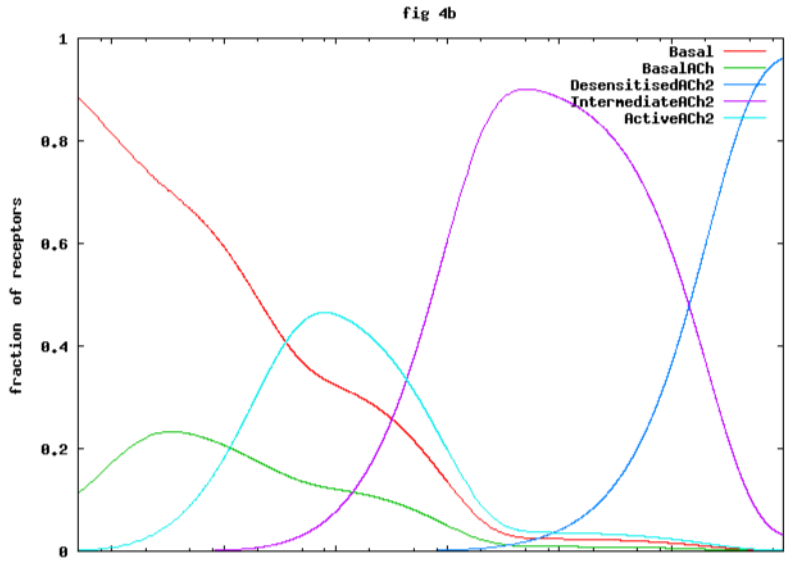
Activity Flows

- Logical modelling
- Signalling pathways, gene regulatory networks

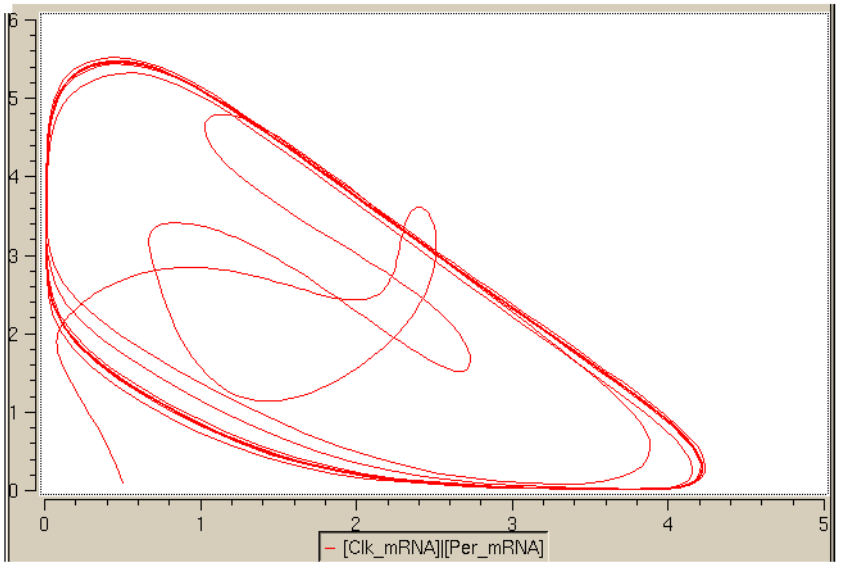


Surely, this is enough?

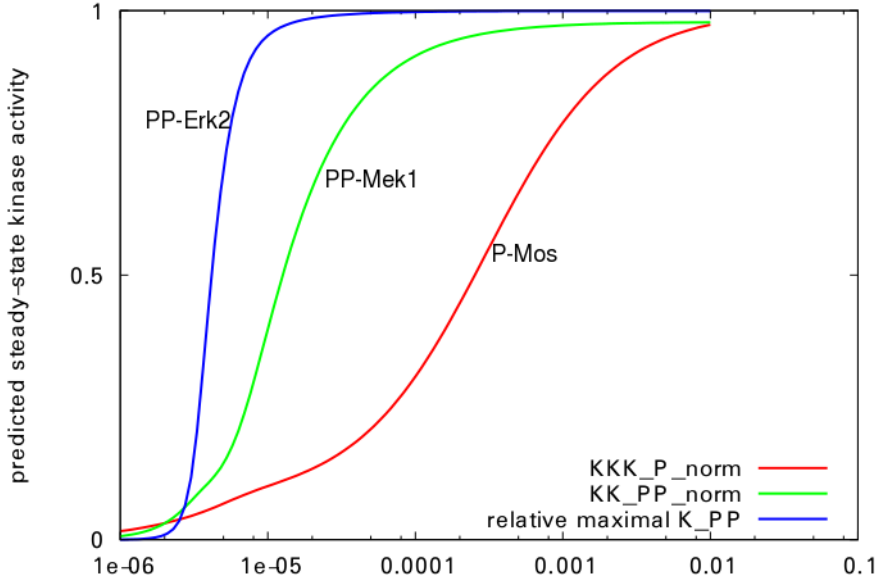
Simulation experiment = model + what to do with it



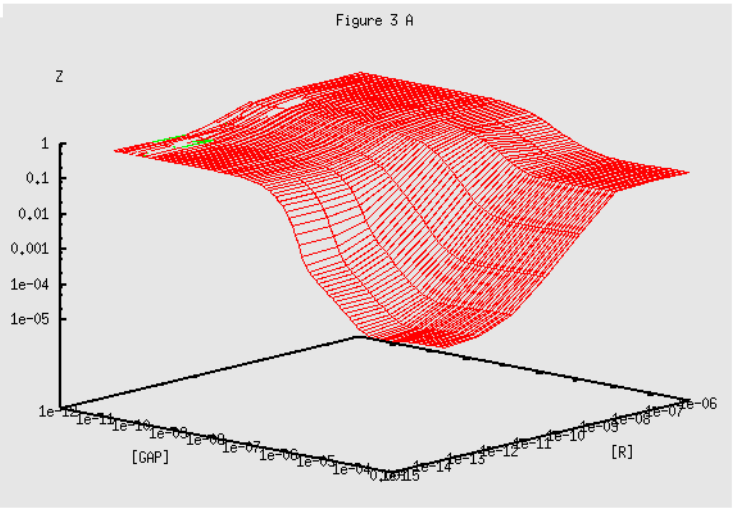
Edelstein et al 1996 (BIOMD0000000002)



Ueda, Hagiwara, Kitano 2001 (BIOMD0000000022)

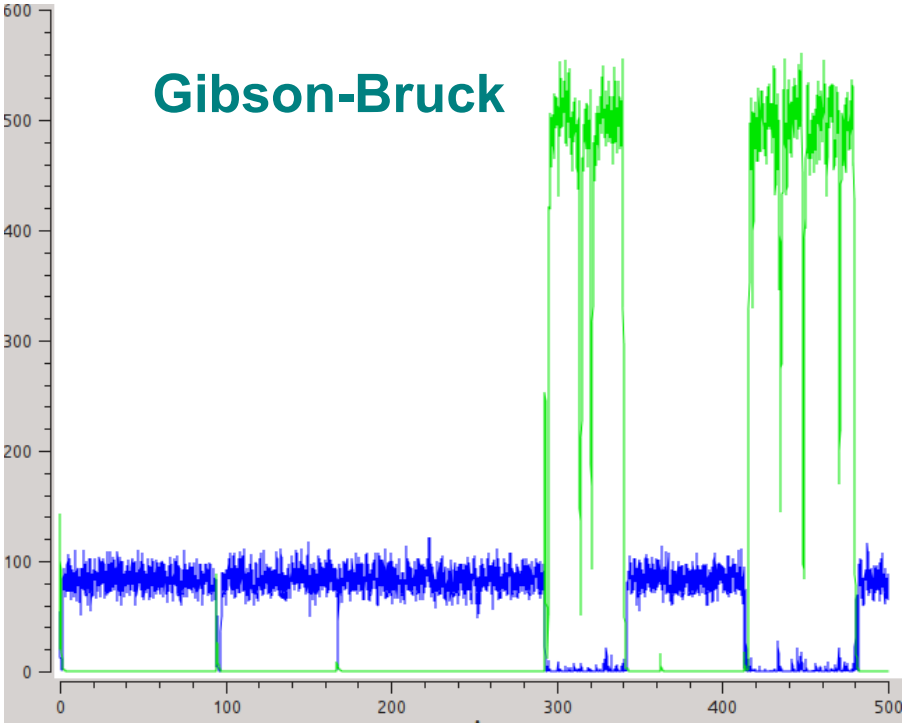


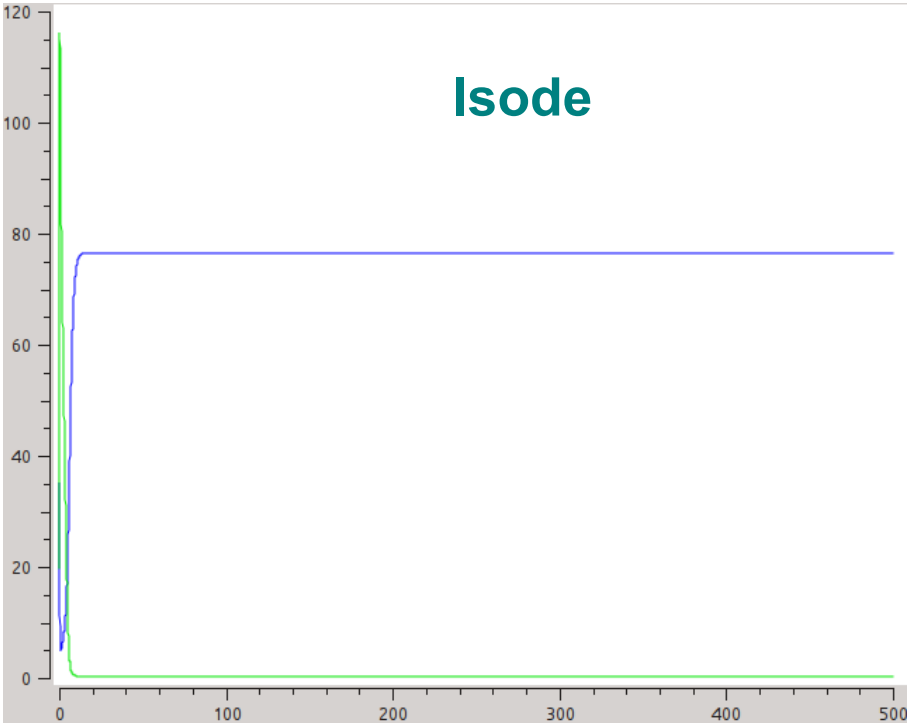
Huang & Ferrell (BIOMD0000000009)

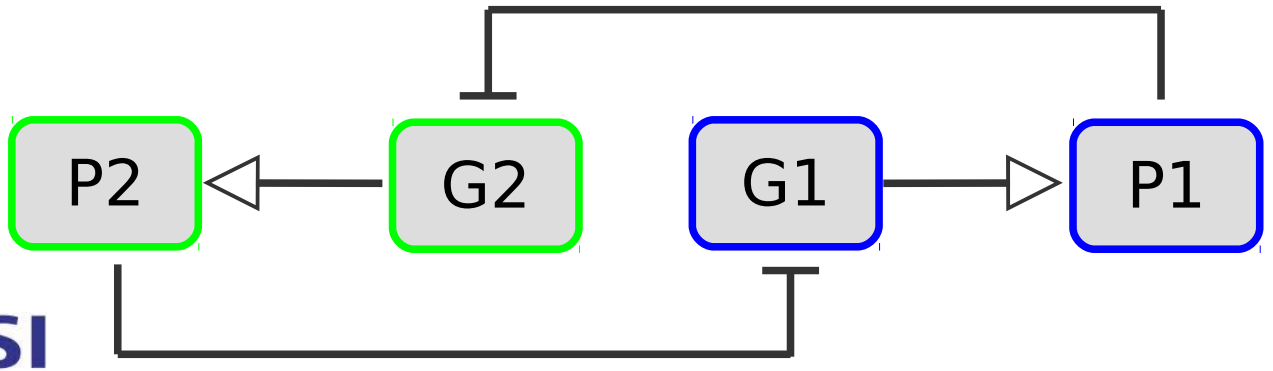


Bornheimer et al 2004 (BIOMD0000000086)

Choice of algorithm affects behaviour





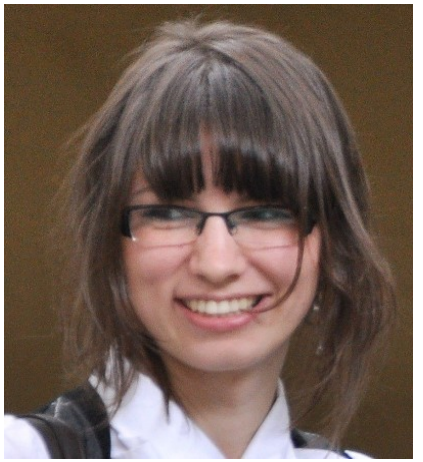


COPASI

Description of simulations and analyses

	Model descriptions	Simulations and analysis
Minimal requirements	MIRIAM	MIASE
Data-models	SBML, SBGN	SED-ML
Terminologies	SBO	KISAO

Dagmar Waltemath



Anna Zhukova

Born in Hinxton 2007

Waltemath *et al. PloS Comput Biol* (2011), *BMC Syst Biol* (2011), Courtot *et al. Mol Syst Biol* (2011)

Minimal Information About a Simulation Experiment

Models to use

1. Models provided, or precise mean of access
2. Model with all governing equations, parameter values and necessary conditions
3. Standard formats, otherwise code available. If not open code, full description provided
4. Description of modifications required before the execution of the simulation experiment

Simulation steps

1. Simulation steps described, with simulation algorithms, models, order of steps, data processing between steps
2. Information needed for correct implementation of necessary steps
3. If software source-code not available, information needed to reproduce the simulation, and not only repeat it, with algorithms and necessary info (e.g. discretization meth)
4. If divergence are known in different environments or platforms, explanation on how to be run with the specified environment/platform to achieve experiment's purpose

Output specification

1. Post-processing steps applied on the raw results to generate the final results, with identification of data to process, nature and order of changes to apply
2. If insights depend on relation between different results, (e.g. plot of one against another), the results to be compared must be specified.

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

Simulation Experiment Description Markup Language

```
<?xml version="1.0" encoding="utf-8"?>
<sedML xmlns="http://sed-ml.org/"
       xmlns:math="http://www.w3.org/1998/Math/MathML"
       level="1" version="1">
  <listOfSimulations><!-- --> </listOfSimulations>
  <listOfModels>
    <model id="" source="">
      <listOfChanges><!-- --></listOfChanges>
    </model>
  </listOfModels>
  <listOfTasks><!-- --></listOfTasks>
  <listOfDataGenerators><!-- --></listOfDataGenerators>
  <listOfOutputs>
    <plot2D />
    <plot3D />
    <report />
  </listOfOutputs>
</sedML>
```

http://sed-ml.org

Flexible model use in SED-ML

Any XML

Remote access

Modifications before simulations

```
<listOfModels>
  <model id="model1"
         name="Regular_Spiking"
         language="http://identifiers.org/combine.specifications/sbml.level-2.version-4.release-1"
         source="http://identifiers.org/biomodels.db/BIOMD0000000127" />
  <model id="model2"
         name="chattering"
         source="model1">
    <listOfChanges>
      <changeAttribute target=
           "/sbml/model/listOfParameters/parameter[@id='c']/@value" newValue="-50">
      </changeAttribute>
      <changeAttribute target=
           "/sbml/model/listOfParameters/parameter[@id='d']/@value" newValue="42">
      </changeAttribute>
    </listOfChanges>
  </model>
</listOfModels>
```

Etc.

	Model descriptions	Simulations and analysis	Numerical
Minimal requirements	MIRIAM	MIASE	 Christian Knüpfer
Data-models	SBML, SBGN	SED ML	NuML
Terminologies	SBO	KISAO	TEDDY

That looks very useful. Where can I find those?

BioModels Database

Search

Advanced

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

BioModels Database is a repository of computational models of biological processes. Models described from literature are manually curated and enriched with cross-references. All models are provided in the Public Domain. More information about BioModels Database can be found in the FAQ.

Models published in the literature

Browse

Manually curated
(530 models)

Non curated
(655 models)

Alternative access

Gene Ontology classification (new)

Gene Ontology tree

Advanced search

Models automatically generated from pathway resources (Path2Models)

Browse

Metabolic (112,898 models)
Non-metabolic (27,531 models)
Whole genome metabolism (2,641 models)

Alternative access

Taxonomy

Ded

Contact us | Main instance at EMBL-EBI, UK | Mirror at Caltech, USA | Mode

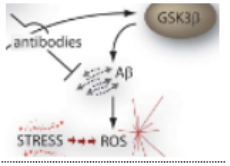
Acknowledgements: EMBL BBSRC bioscience for the future

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

Model of the month

August, 2014

A mathematical model describing the molecular mechanisms involved in AD and the effect of immunisation against Aβ on soluble Aβ,



Marco Donizelli

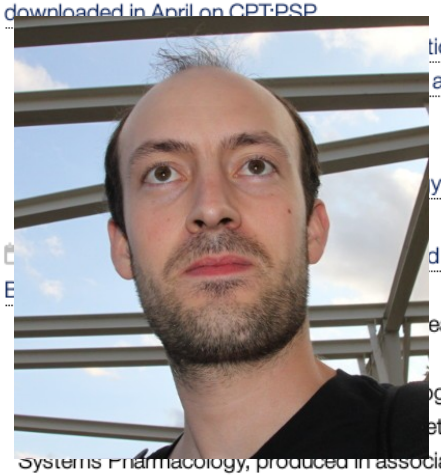
el access

o provide a
. Also, a
r models
ave been

25 April 2014 Our recent diabetes review most downloaded in April on CPT:PSP

Viji Chelliah

Camille Laibe



tical
and
y website
d curator of
ead
ogy
etrics &

Systems Pharmacology, produced in association with Nature Publishing Group (PSPod) is now online. Listen it.

Le Novère *et al. Nucleic Acid Res* (2006), Li *et al BMC Syst Biol* (2010), Juty *et al. Nucleic Acid Res (2015)*

>140 000 models

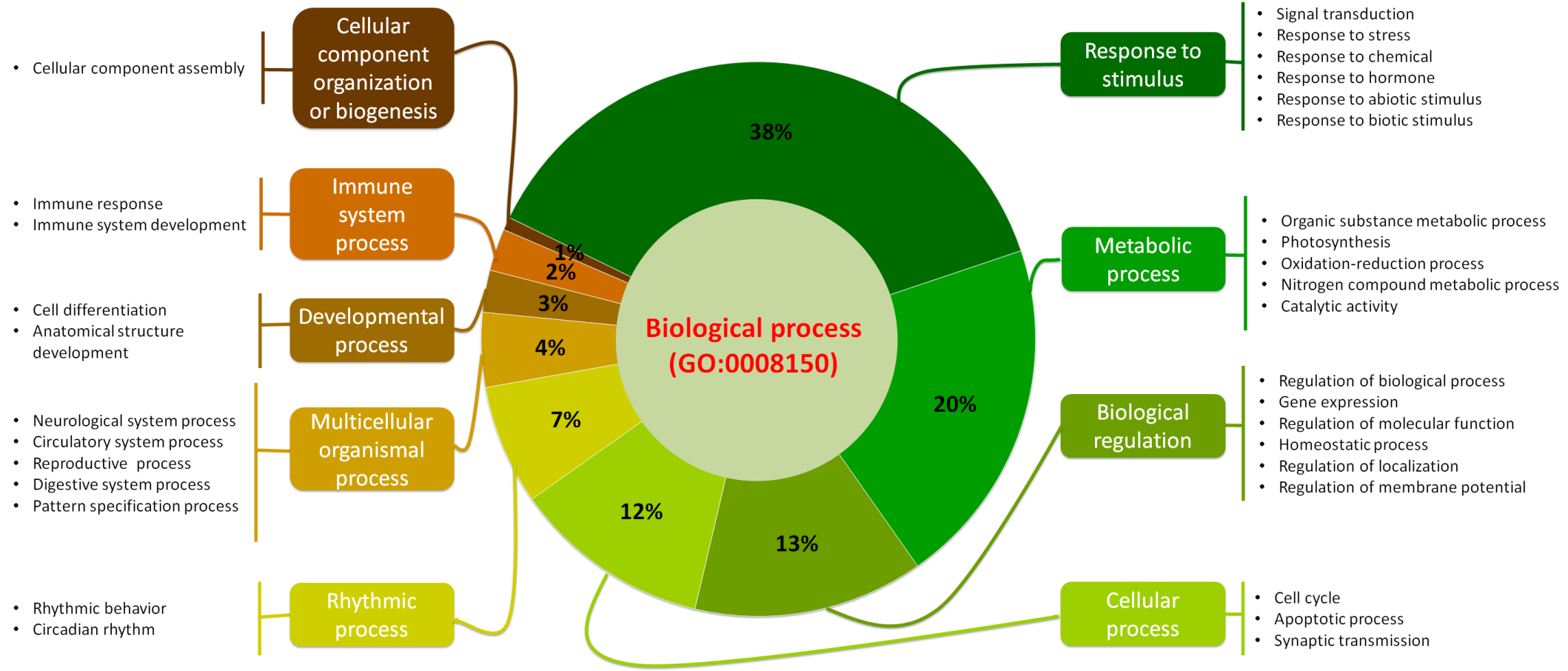
>10 millions math relations

~ 200 millions cross-refs

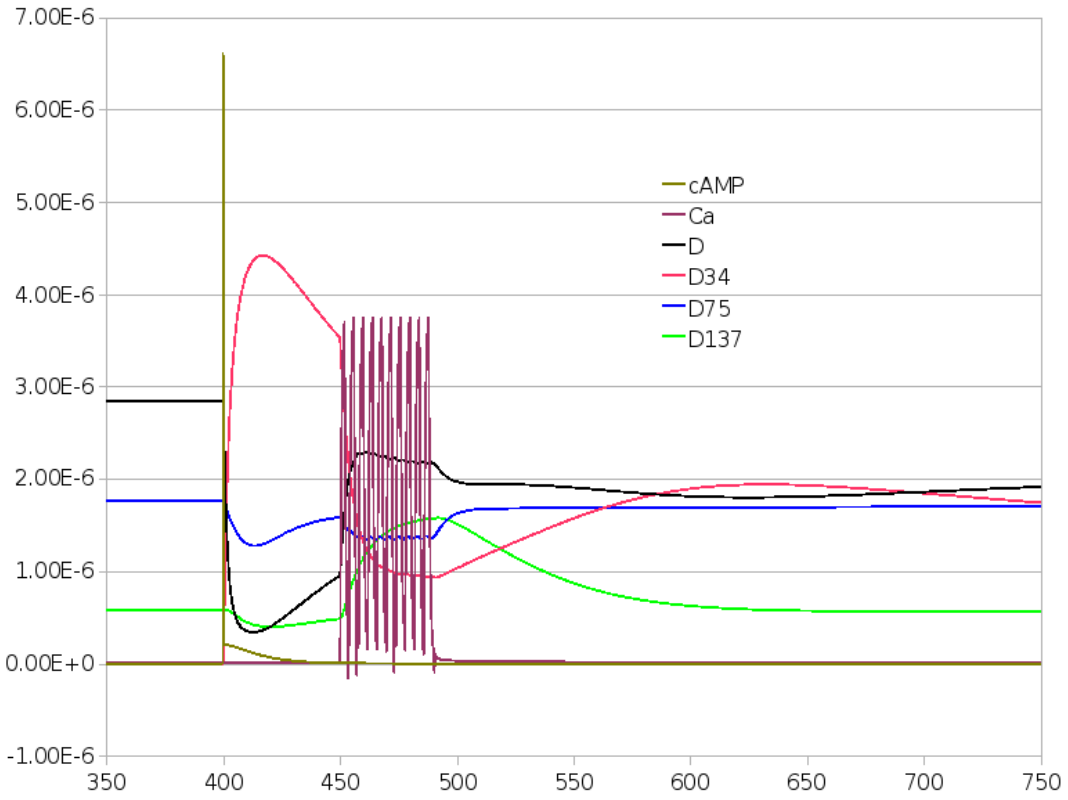
> 300 journals advise deposition

~ 1000 citations

1 million page requests per year

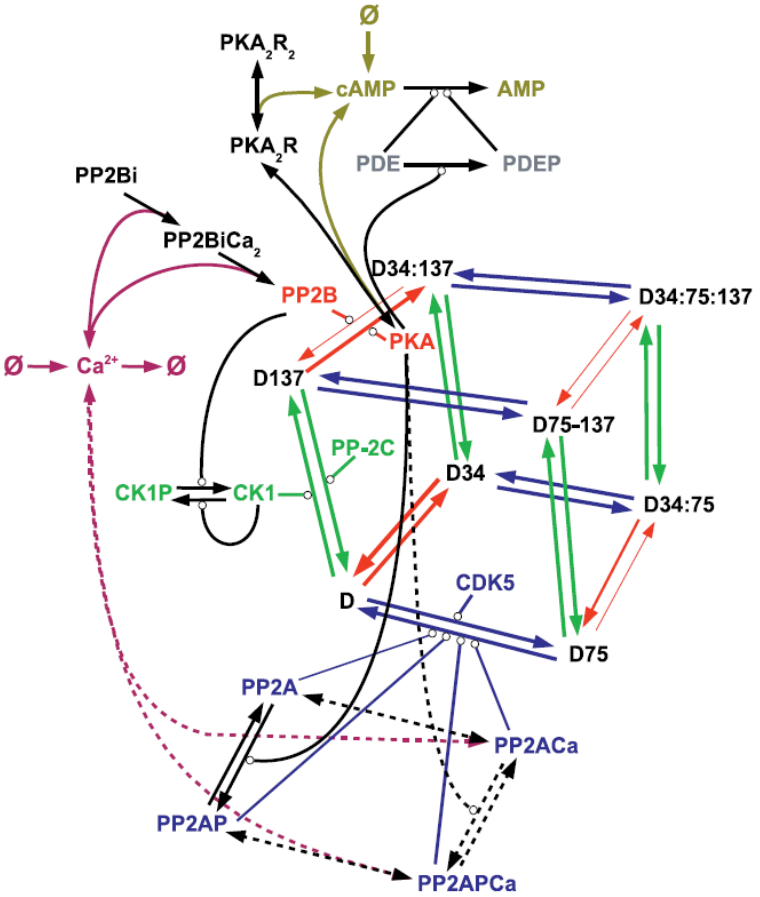

Biological process
(GO:0008150)
38%
20%
13%
12%
7%
4%
3%
2%
1%
Response to stimulus
Signal transduction
Response to stress
Response to chemical
Response to hormone
Response to abiotic stimulus
Response to biotic stimulus
Metabolic process
Organic substance metabolic process
Photosynthesis
Oxidation-reduction process
Nitrogen compound metabolic process
Catalytic activity
Biological regulation
Regulation of biological process
Gene expression
Regulation of molecular function
Homeostatic process
Regulation of localization
Regulation of membrane potential
Cellular process
Cell cycle
Apoptotic process
Synaptic transmission
Cellular component organization or biogenesis
Cellular component assembly
Immune system process
Immune response
Immune system development
Developmental process
Cell differentiation
Anatomical structure development
Multicellular organismal process
Neurological system process
Circulatory system process
Reproductive process
Digestive system process
Pattern specification process
Rhythmic process
Rhythmic behavior
Circadian rhythm

Biochemical models



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

BIOMD0000000153



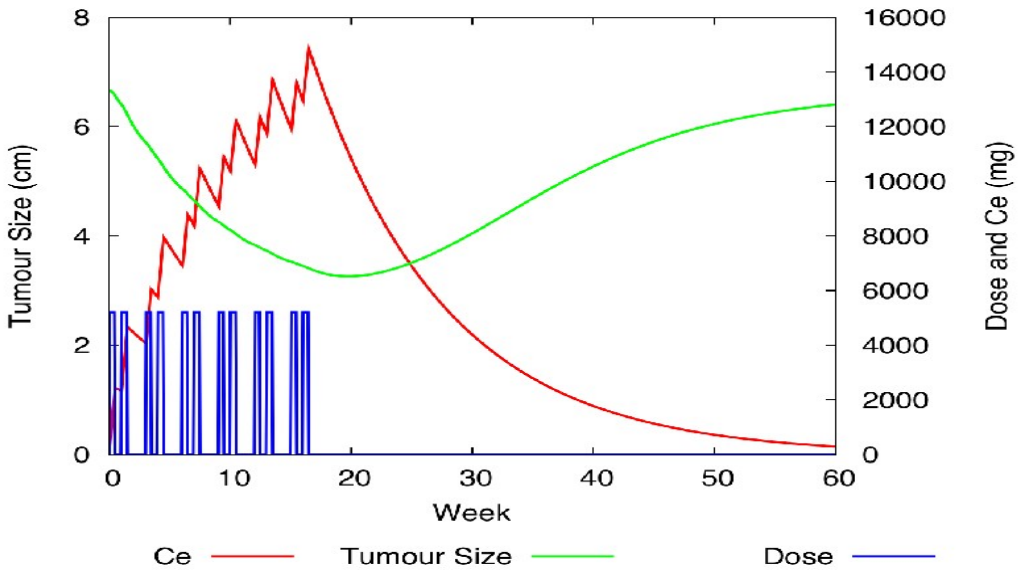
reaction:

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

Babraham Institute

EMBL-EBI

Pharmacometrics models



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

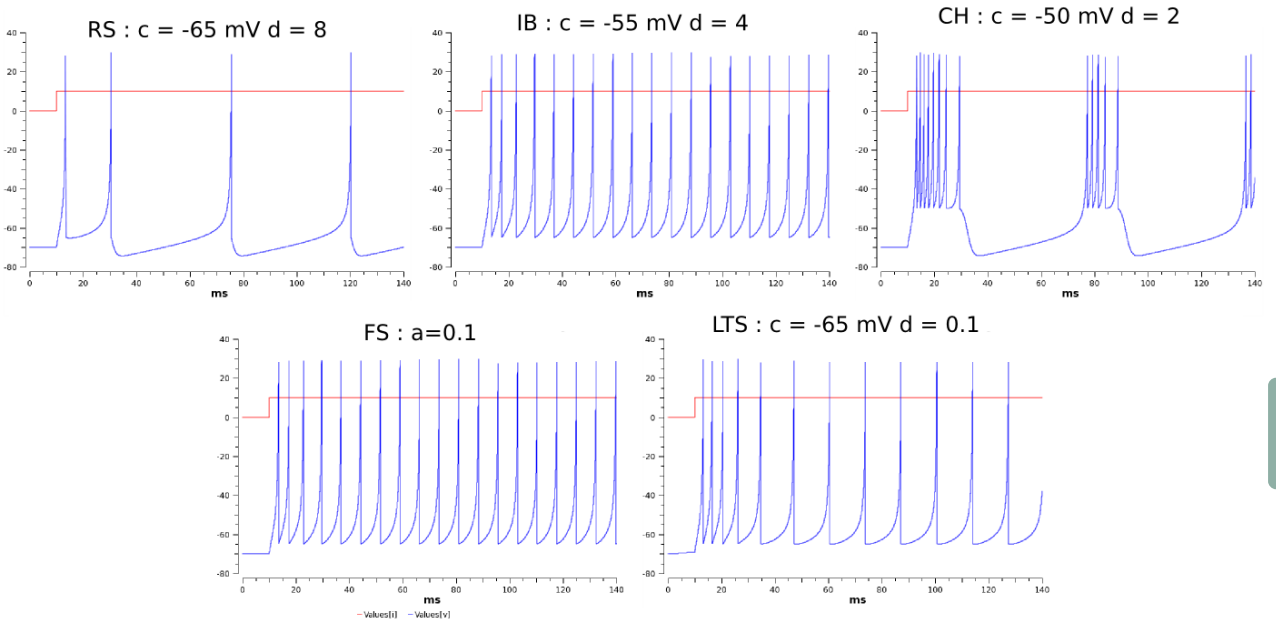
rate rule:

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

assignment rule:

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

Neuroscience models



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

BIOMD0000000127

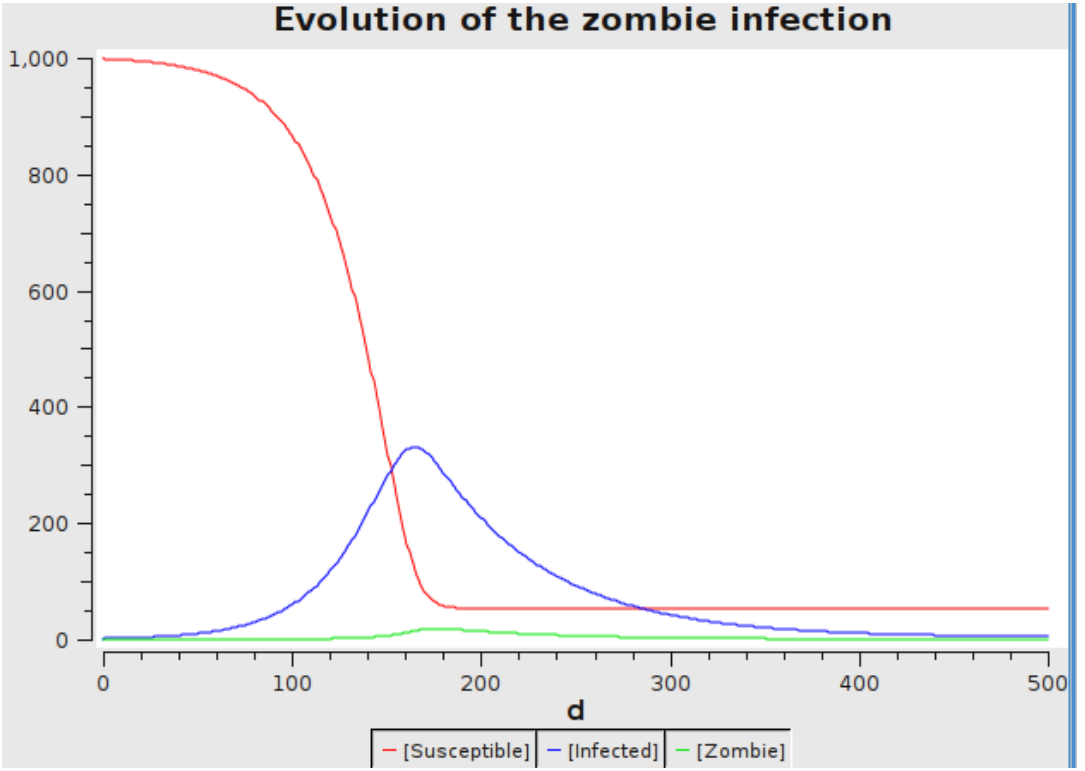
rate rule:

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

event:

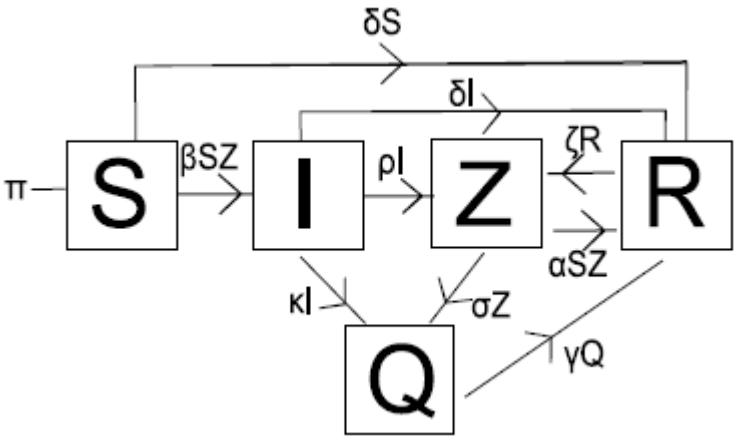
$$\text{when } v > V_{\text{thresh}} \begin{cases} v = c \\ U = U + d \end{cases}$$

Epidemiology models



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



Babraham Institute

EMBL-EBI

Was it worth it?

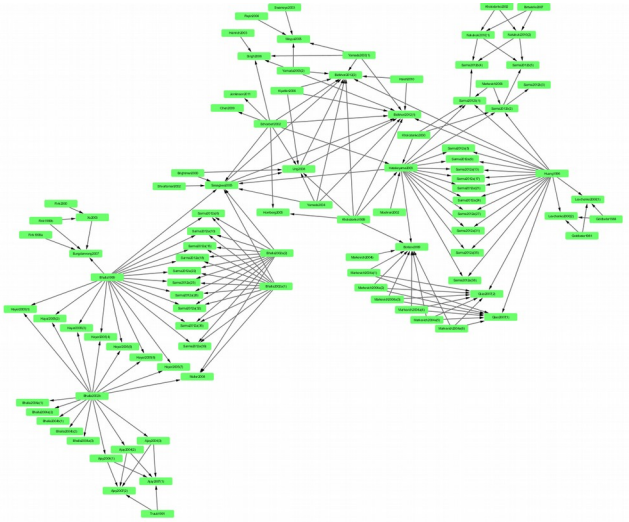
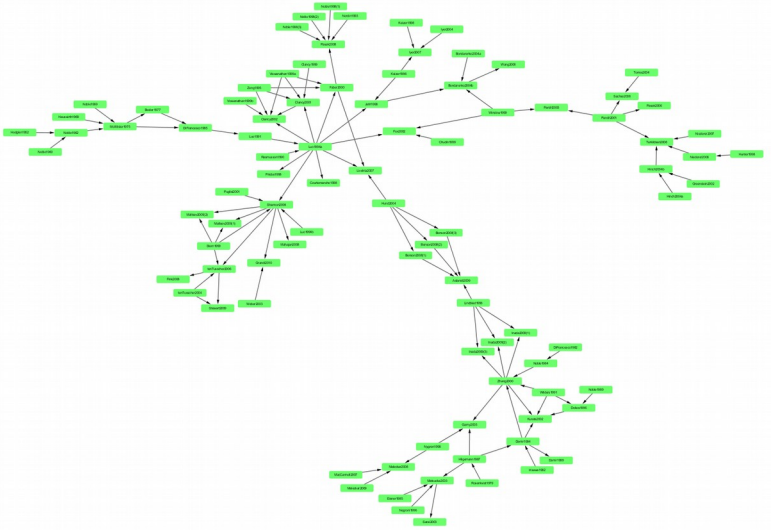
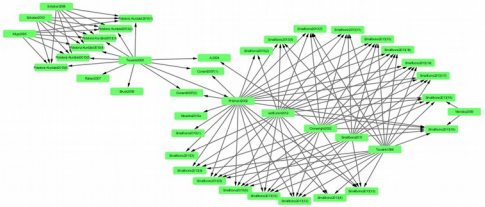
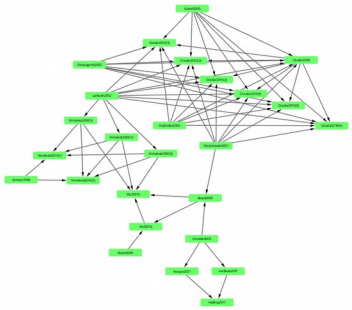
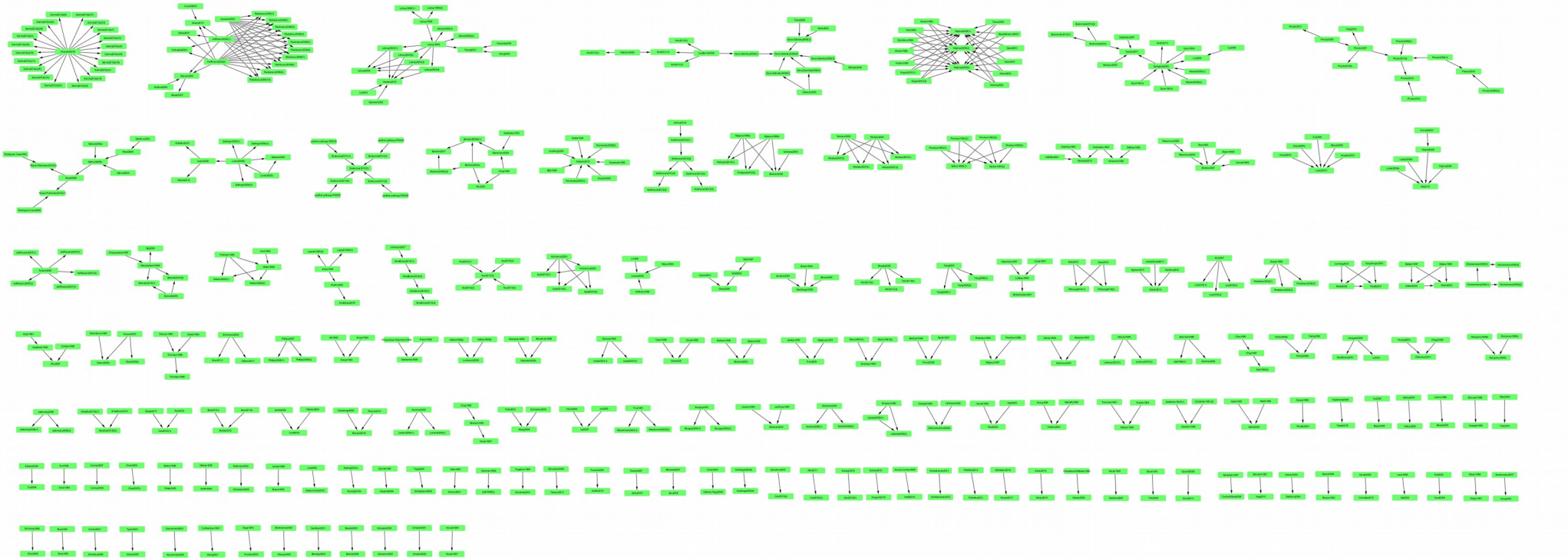
"You should not develop standards and easy to use modelling software. This allows biologists to write models, and they don't know how to do it properly."

Biomathematician, 2007

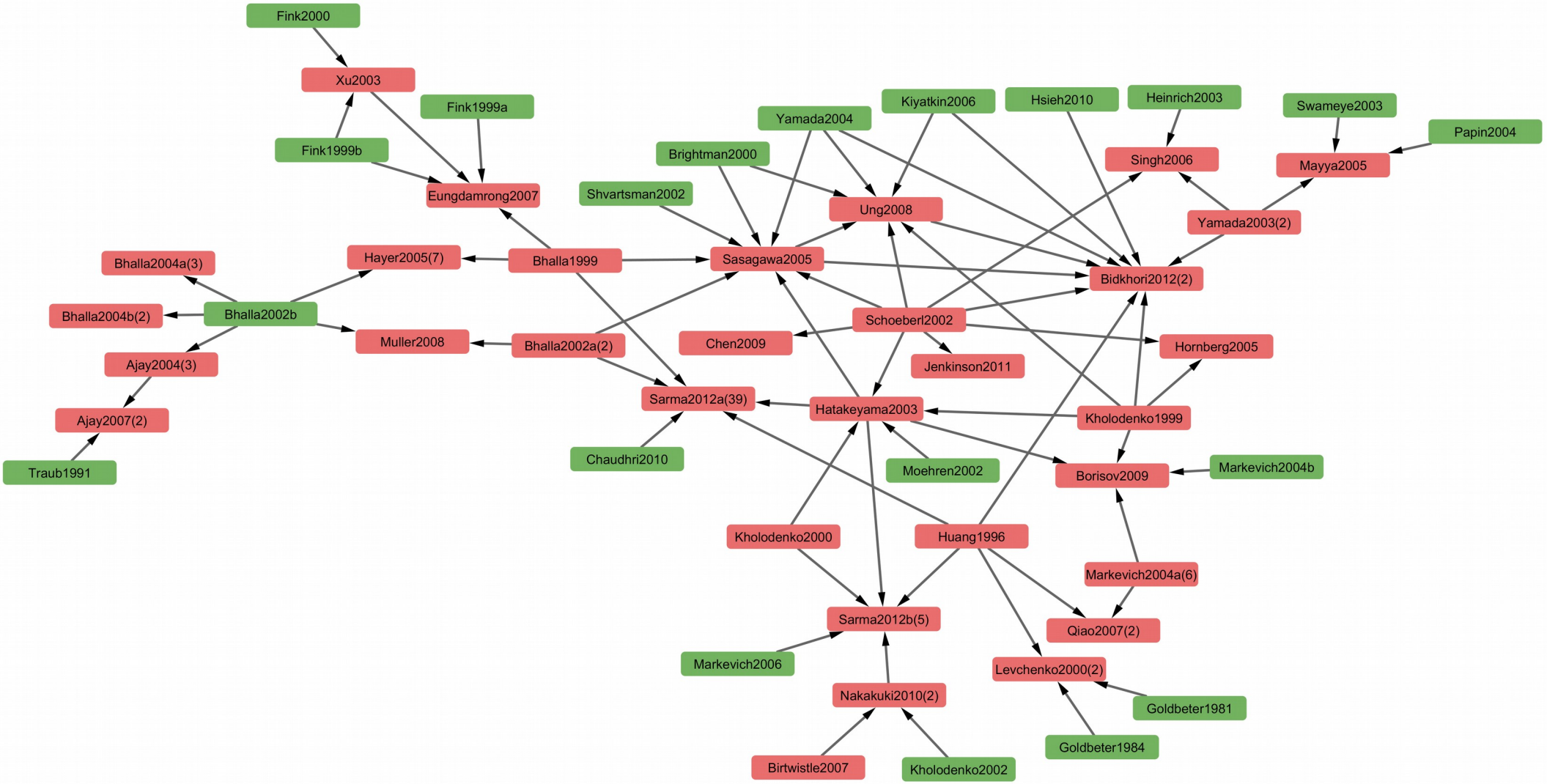
"By developing BioModels you harmed the cause of modelling in biology. My students do not learn how to make a model any more, instead, they download it ready to use."

Theoretical biologist, 2006

REUSE

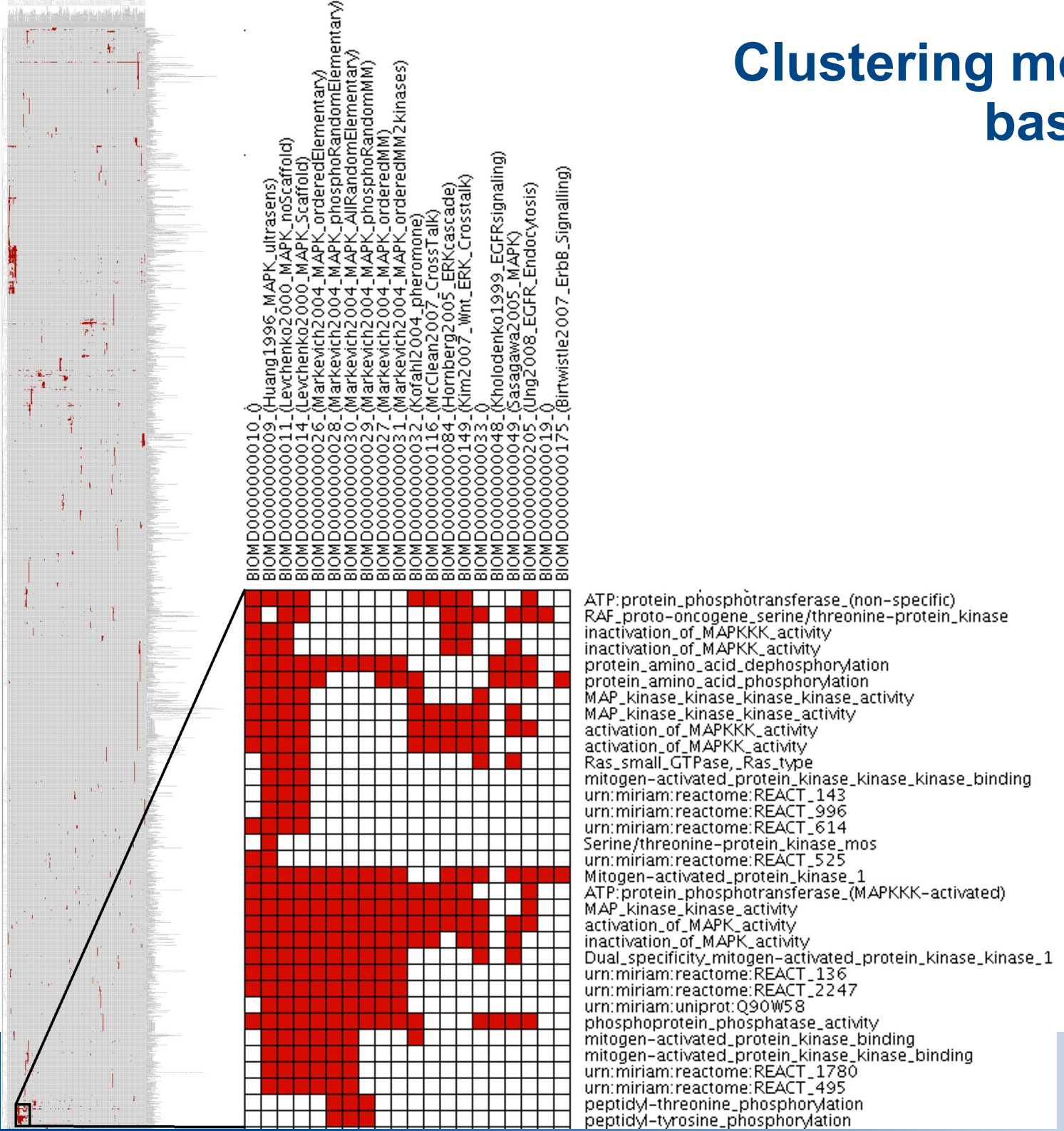






Erb receptor signalling



DISCOVER

Clustering models (and data) based on metadata



Schulz *et al.*
Mol Syst Biol (2011)

Babraham Institute

EMBL-EBI

Ranking and retrieval of models

Model	BioModel	Similarity	*P*-value	Overlap	*P*-value
Huang1996_MAPK_ultrasens	BIOMD0000000009	1.000	<=1e-3	30	0.0e+00
Levchenko2000_MAPK_noScaffold	BIOMD0000000011	0.930	<=1e-3	28	0.0e+00
Levchenko2000_MAPK_Scaffold	BIOMD0000000014	0.874	<=1e-3	26	0.0e+00
Kholodenko2000_MAPK_feedback	BIOMD0000000010	0.830	<=1e-3	20	0.0e+00
Markevich2004_MAPK_orderedElementary	BIOMD0000000026	0.749	<=1e-3	16	2.9e-15
Markevich2004_MAPK_phosphoRandomElementary	BIOMD0000000028	0.692	<=1e-3	15	9.1e-14
Markevich2004_MAPK_AllRandomElementary	BIOMD0000000030	0.692	<=1e-3	15	9.1e-14
Markevich2004_MAPK_orderedMM	BIOMD0000000027	0.691	<=1e-3	12	9.8e-10
Markevich2004_MAPK_orderedMM2kinases	BIOMD0000000031	0.691	<=1e-3	12	9.8e-10
Markevich2004_MAPK_phosphoRandomMM	BIOMD0000000029	0.626	<=1e-3	11	1.6e-08
Hornberg2005_ERKcascade	BIOMD0000000084	0.523	<=1e-3	9	2.7e-06
McClean2007_CrossTalk	BIOMD0000000116	0.453	<=1e-3	8	2.7e-05
Kofahl2004_pheromone	BIOMD0000000032	0.441	<=1e-3	12	9.8e-10
Goldbeter1991_MinMitOscil_ExplInact	BIOMD0000000004	0.389	<=1e-3	3	1.5e-01
Brown2004_NGF_EGF_signaling	BIOMD0000000033	0.371	<=1e-3	9	2.7e-06
Ung2008_EGFR_Endocytosis	BIOMD0000000205	0.363	<=1e-3	8	2.7e-05
Kim2007_Wnt_ERK_Crosstalk	BIOMD0000000149	0.355	<=1e-3	10	2.2e-07
Goldbeter1991_MinMitOscil	BIOMD0000000003	0.349	<=1e-3	3	1.5e-01
Sasagawa2005_MAPK	BIOMD0000000049	0.339	<=1e-3	9	2.7e-06
Swat2004_Mammalian_G1_S_Transition	BIOMD0000000228	0.317	<=1e-3	2	4.0e-01
Tyson1991_CellCycle_6var	BIOMD0000000005	0.304	<=1e-3	4	4.2e-02
Goldbeter1995_CircClock	BIOMD0000000016	0.274	<=1e-3	4	4.2e-02
Novak1997_CellCycle	BIOMD0000000007	0.259	<=1e-3	1	7.6e-01
Novak2001_FissionYeast_CellCycle	BIOMD0000000111	0.255	<=1e-3	2	4.0e-01
Leloup1999_CircClock	BIOMD0000000021	0.246	<=1e-3	4	4.2e-02
Birtwistle2007_ErbB_Signalling	BIOMD0000000175	0.236	<=1e-3	1	7.6e-01
Neves2008_Cell_Shape	BIOMD0000000182	0.222	<=1e-3	6	1.6e-03
Leloup1998_CircClock_LD	BIOMD0000000171	0.219	<=1e-3	4	4.2e-02
Veening2008_DegU_Regulation	BIOMD0000000240	0.211	4.0e-03	2	4.0e-01
Chen2004_CellCycle	BIOMD0000000056	0.209	4.0e-03	4	4.2e-02
Fernandez2006_ModelA	BIOMD0000000152	0.207	5.0e-03	2	4.0e-01
Fisher2006_NFAT_Activation	BIOMD0000000123	0.199	7.0e-03	2	4.0e-01
Hatakeyama2003_MAPK	BIOMD0000000146	0.198	7.0e-03	1	7.6e-01

MAPK

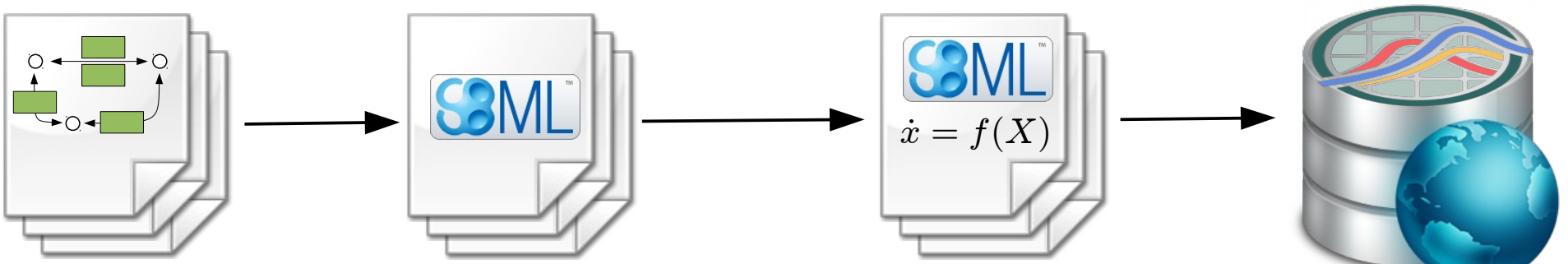
Retrieval of models using gene expression

Model	BioModel	Similarity	*P*-value	Overlap	*P*-value
Wolf2001 respiratory oscillations	BIOMD0000000090	0.207	<=1e-3	6	6.6e-09
Chassagnole2001_Threonine Synthesis	BIOMD0000000066	0.184	<=1e-3	4	1.5e-05
Curien2009_Aspartate_Metabolism	BIOMD0000000212	0.170	<=1e-3	5	3.6e-07
Curien2003_MetThr_synthesis	BIOMD0000000068	0.141	<=1e-3	2	1.0e-02
Proctor2007_ubiquitine	BIOMD0000000105	0.098	2.0e-03	1	1.4e-01
Curto1998_purineMetabol	BIOMD0000000015	0.063	1.1e-02	2	1.0e-02
Ibrahim2008_Spindle_Assembly_Checkpoint_dissociation	BIOMD0000000186	0.057	1.8e-02	0	1.0e+00
Ibrahim2008_Spindle_Assembly_Checkpoint_convey	BIOMD0000000187	0.057	1.8e-02	0	1.0e+00
Rodriguez-Caso2006_Polyamine_Metabolism	BIOMD0000000190	0.040	7.1e-02	1	1.4e-01
Nijhout2004_Folate_Cycle	BIOMD0000000213	0.032	1.1e-01	1	1.4e-01
Morrison1989_FolateCycle	BIOMD0000000018	0.030	1.3e-01	1	1.4e-01
Zatorsky2006_p53_Model3	BIOMD0000000154	0.023	2.5e-01	0	1.0e+00
Zatorsky2006_p53_Model6	BIOMD0000000155	0.023	2.5e-01	0	1.0e+00
Hunziker2010_p53_StressSpecificResponse	BIOMD0000000252	0.023	2.5e-01	0	1.0e+00
Zatorsky2006_p53_Model5	BIOMD0000000156	0.022	2.7e-01	0	1.0e+00
Zatorsky2006_p53_Model4	BIOMD0000000157	0.022	2.7e-01	0	1.0e+00
Zatorsky2006_p53_Model2	BIOMD0000000158	0.022	2.7e-01	0	1.0e+00
Zatorsky2006_p53_Model1	BIOMD0000000159	0.022	2.7e-01	0	1.0e+00
Proctor2008_p53_Mdm2_ATM	BIOMD0000000188	0.013	4.3e-01	0	1.0e+00
McClean2007_CrossTalk	BIOMD0000000116	0.012	4.7e-01	0	1.0e+00
Proctor2008_p53_Mdm2_ARF	BIOMD0000000189	0.012	4.9e-01	0	1.0e+00
Haberichter2007_cellcycle	BIOMD0000000109	0.011	5.0e-01	0	1.0e+00
Sasagawa2005_MAPK	BIOMD0000000049	0.006	5.5e-01	0	1.0e+00

BUILD

From pathways to models … path2models

- Provide pathways in a standard format
- Re-use existing pathway data to generate biochemically based models
- Provide starting points to build more quantitative models



Büchel *et al.* (2013)

Signalling Pathways

+

Logical models
of individual signalling pathways

Signalling Pathways

+

Logical models
of individual signalling pathways

Metabolic Networks

Chemical kinetics models
of individual metabolic pathways

Signalling Pathways

+

Logical models
of individual signalling pathways

Metabolic Networks

Chemical kinetics models
of individual metabolic pathways

Metabolic Networks

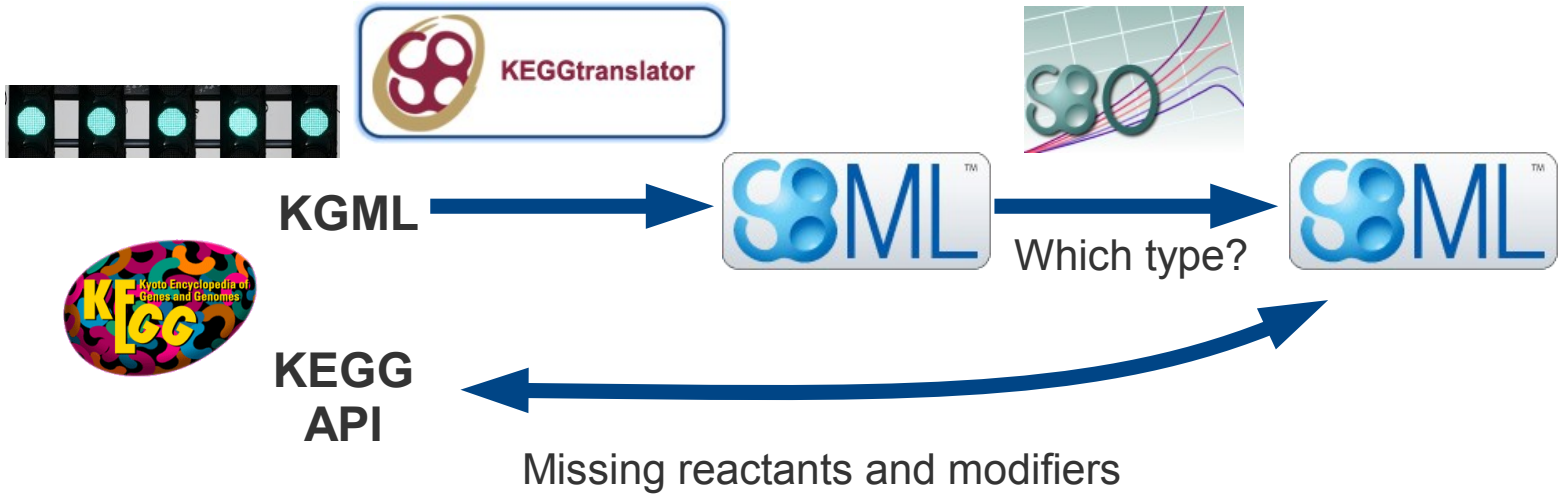
+

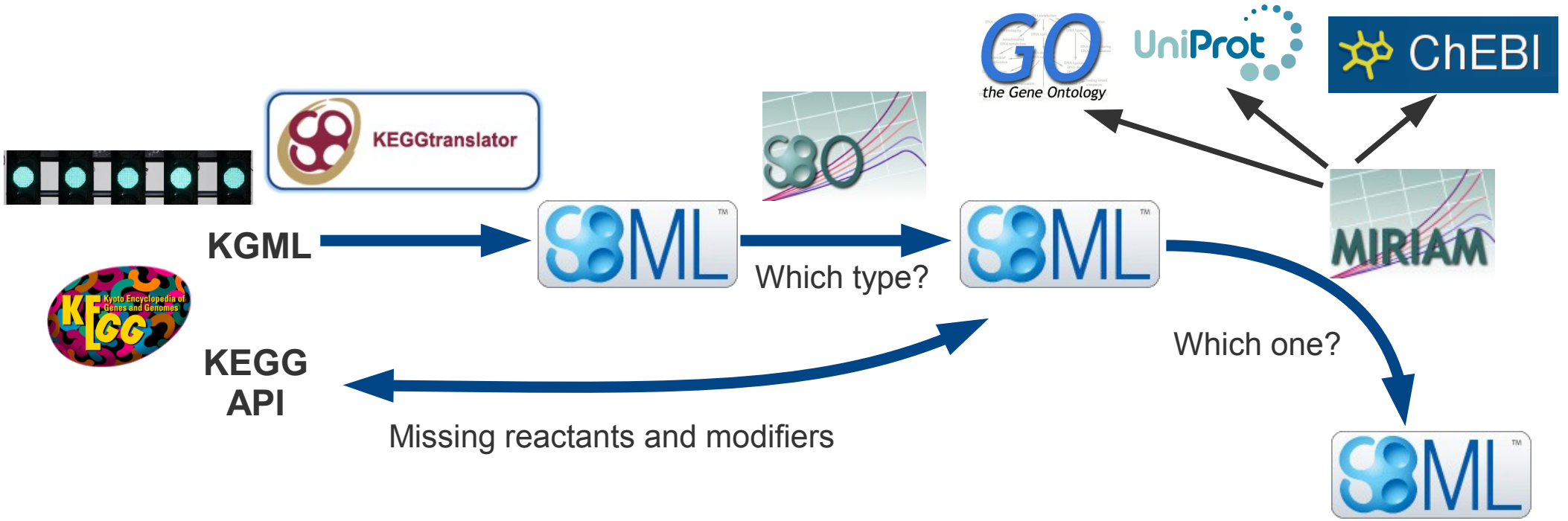
Flux Balance Analysis
of whole genome reconstructions

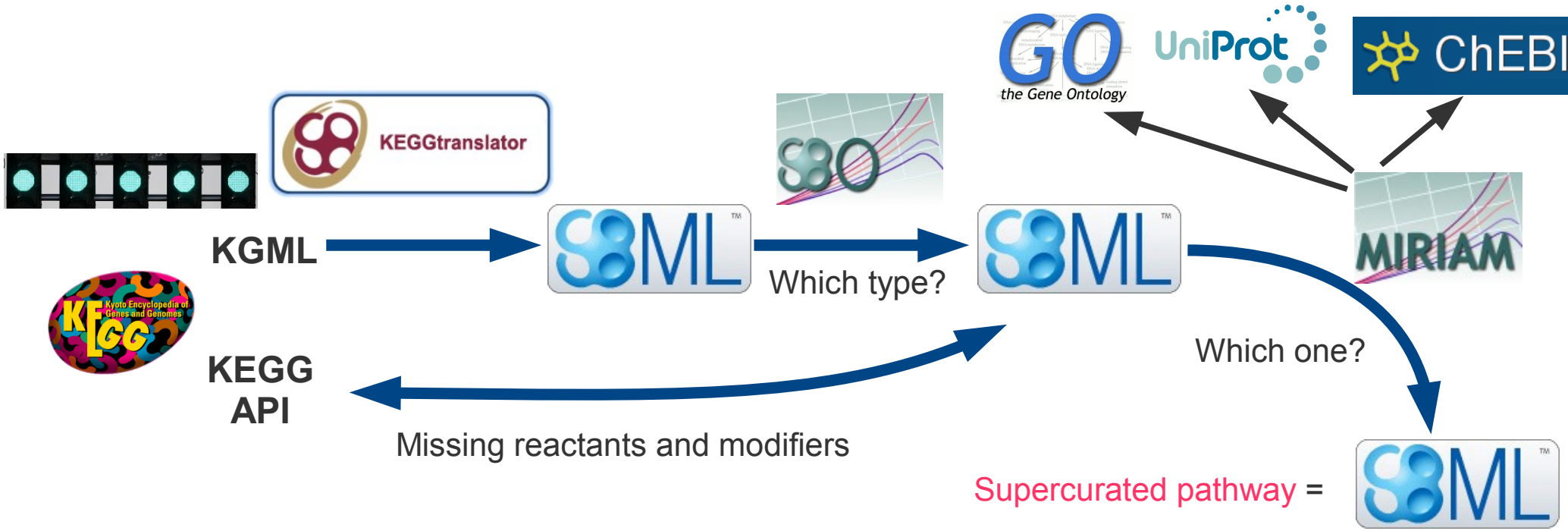
KEGGtranslator

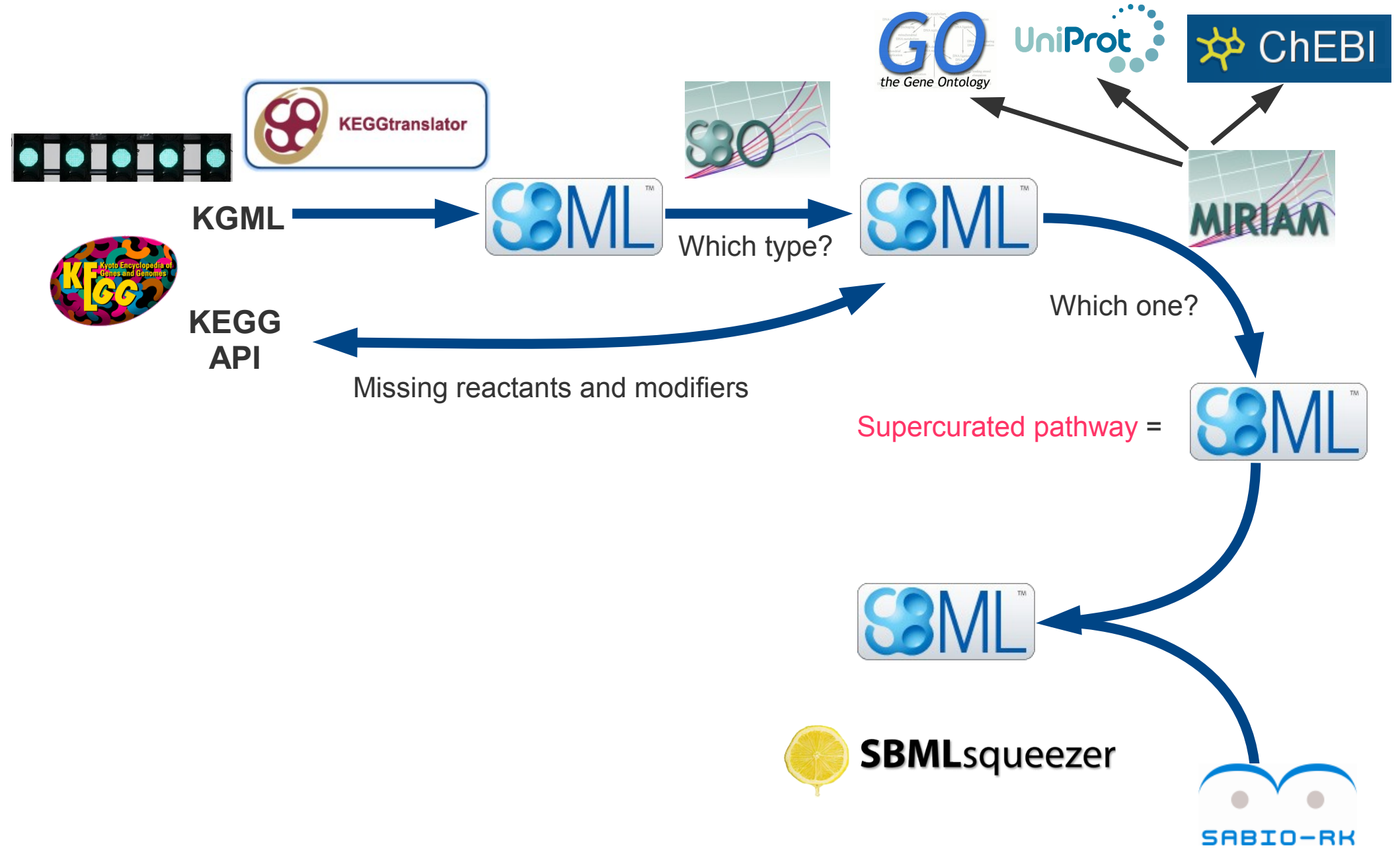
KGML → SBML

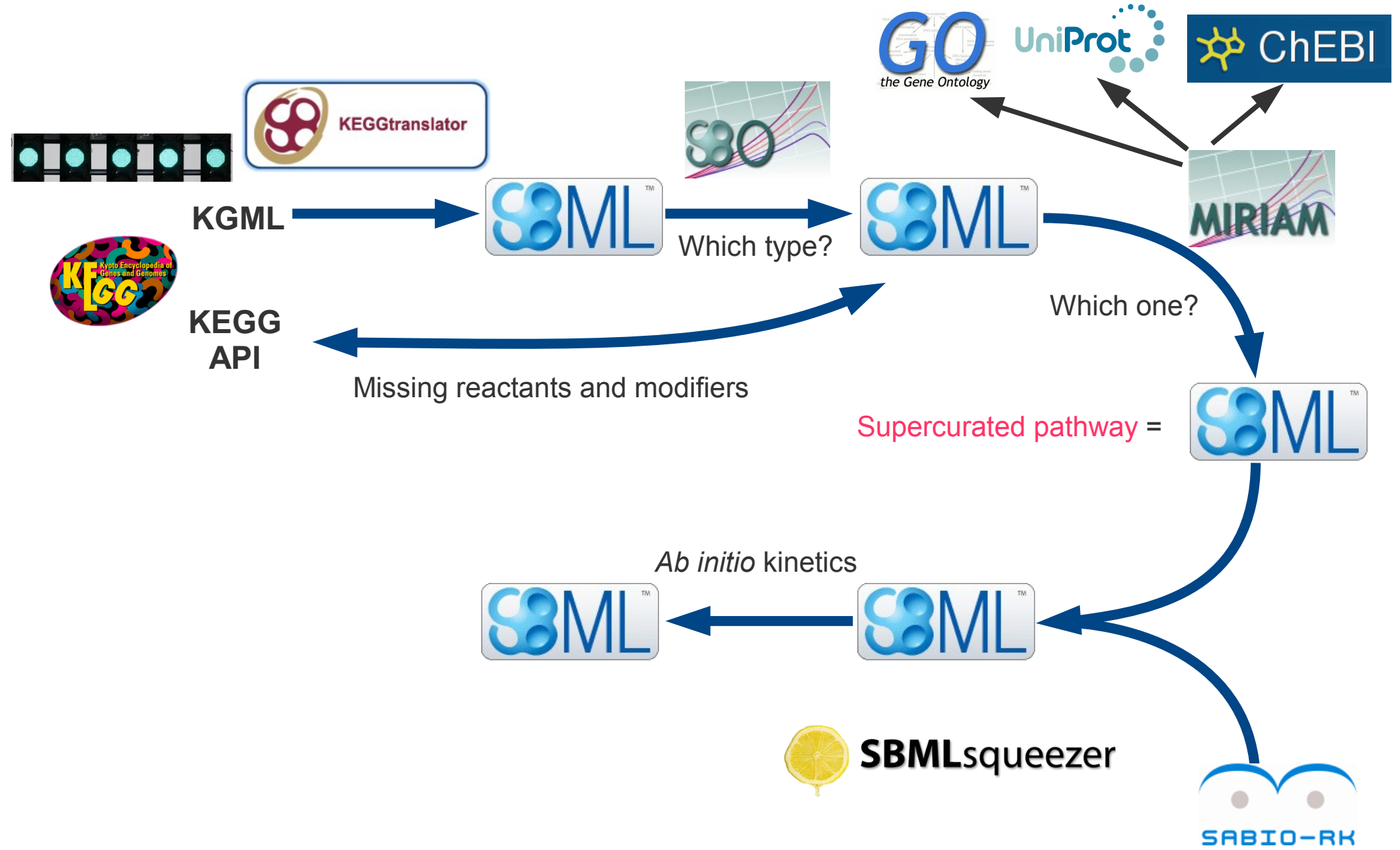

KEGGtranslator
KGML
SBML
Which type?
SBML
Kyoto Encyclopedia of Genes and Genomes

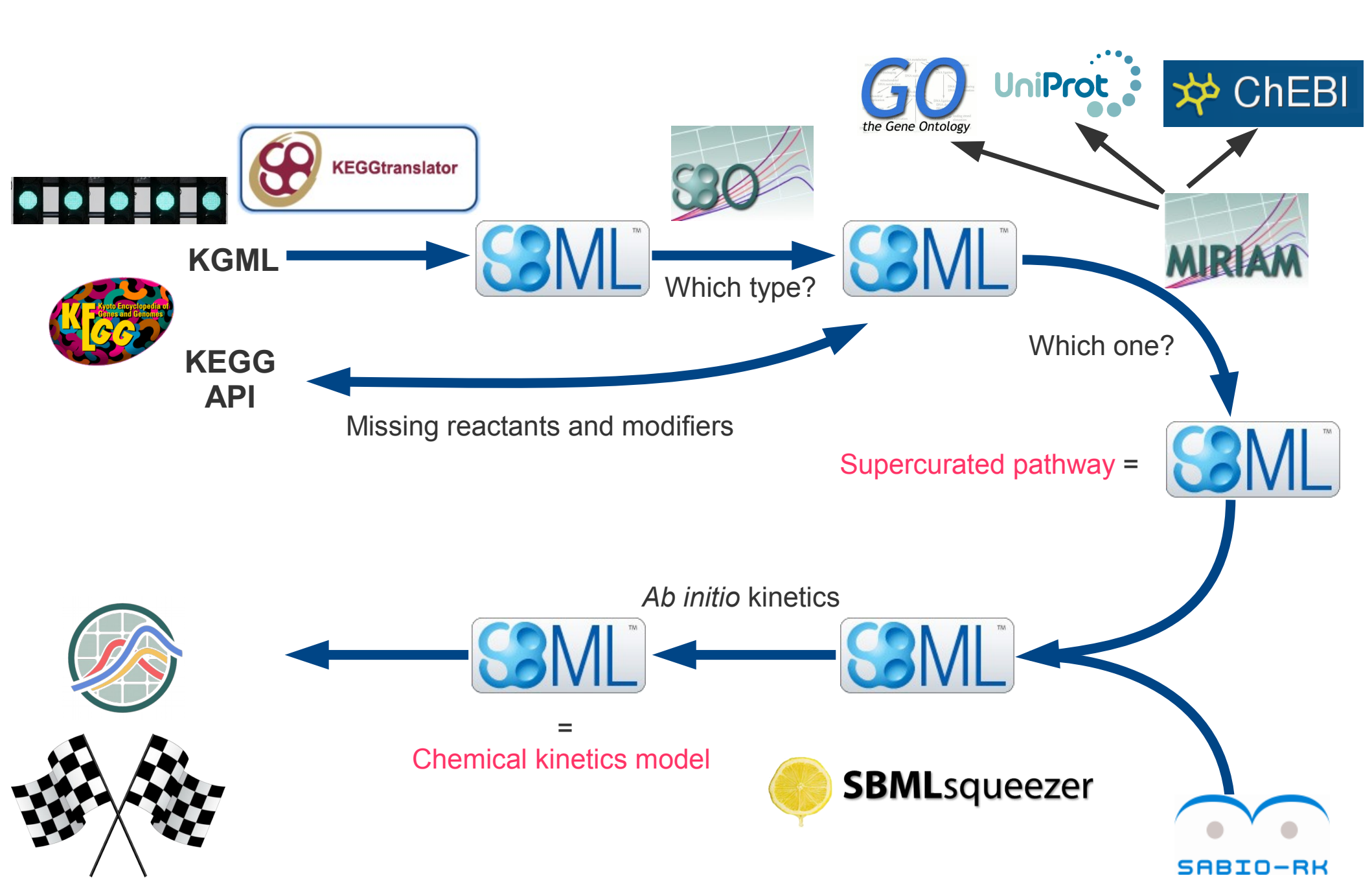

KEGGtranslator
KGML
SBML
Which type?
SBML
KEGG
API
Missing reactants and modifiers


GO
the Gene Ontology
UniProt
ChEBI
KEGGtranslator
SBO
KGML
SBML
Which type?
SBML
MIRIAM
KEGG
Kyoto Encyclopedia of Genes and Genomes
KEGG API
Missing reactants and modifiers
Which one?
SBML

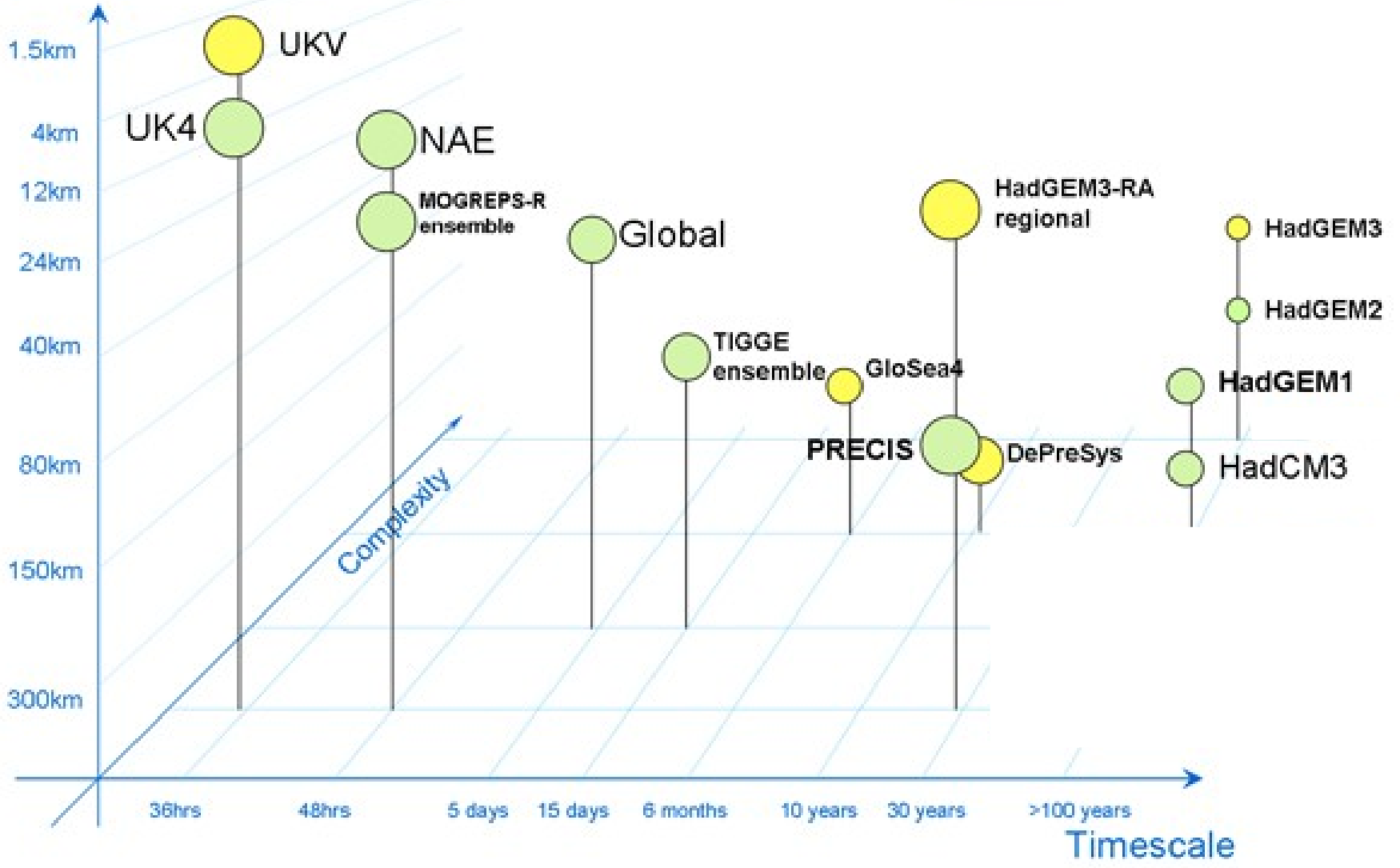

GO
the Gene Ontology
UniProt
ChEBI
KEGGtranslator
SBO
KGML
SBML
Which type?
SBML
MIRIAM
KEGG
Kyoto Encyclopedia of Genes and Genomes
KEGG API
Which one?
Missing reactants and modifiers
Supercurated pathway =
SBML


GO
the Gene Ontology
UniProt
ChEBI
KEGGtranslator
SBO
KGML
SBML
Which type?
SBML
MIRIAM
KEGG
API
Which one?
Missing reactants and modifiers
Supercurated pathway =
SBML
SBML
SBMLsqueezer
SABIO-RK

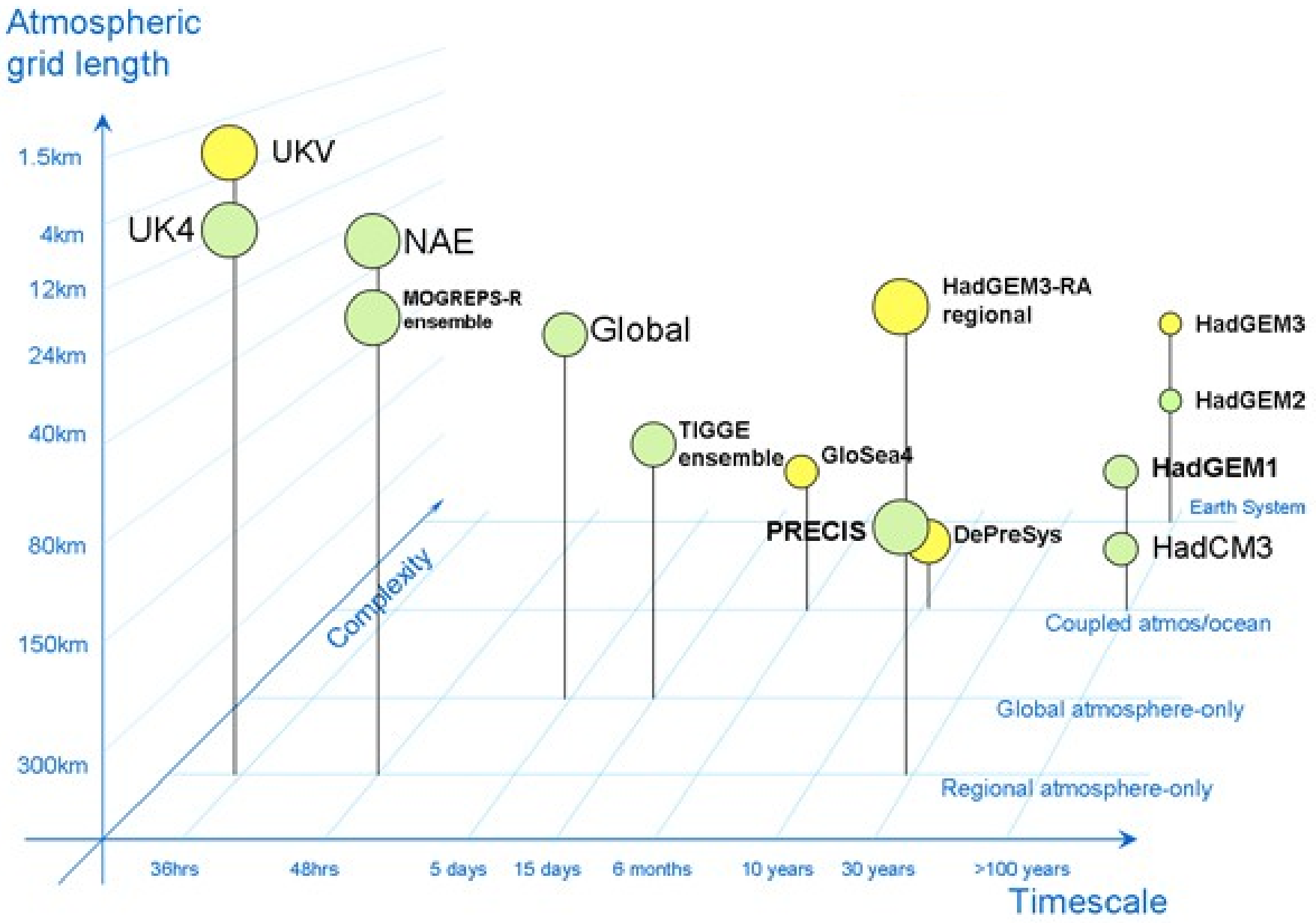

KEGGtranslator
KGML
Which type?
Which one?
KEGG API
Missing reactants and modifiers
Supercurated pathway =
Ab initio kinetics
SBMLsqueezer
SABIO-RK
MIRIAM
ChEBI
UniProt
the Gene Ontology


KEGGtranslator
KGML
Which type?
Which one?
KEGG API
Missing reactants and modifiers
Supercurated pathway =
Ab initio kinetics
=
Chemical kinetics model
SBMLsqueezer
MIRIAM
ChEBI
UniProt
the Gene Ontology
SABIO-RK

Are-we ready to develop comprehensive models of whole cells, organs and organisms?


1.5km
4km
12km
24km
40km
80km
150km
300km
UKV
UK4
NAE
MOGREPS-R ensemble
Global
TIGGE ensemble
GloSea4
PRECIS
HadGEM3-RA regional
DePreSys
HadGEM3
HadGEM2
HadGEM1
HadCM3
Complexity
36hrs
48hrs
5 days
15 days
6 months
10 years
30 years
>100 years
Timescale

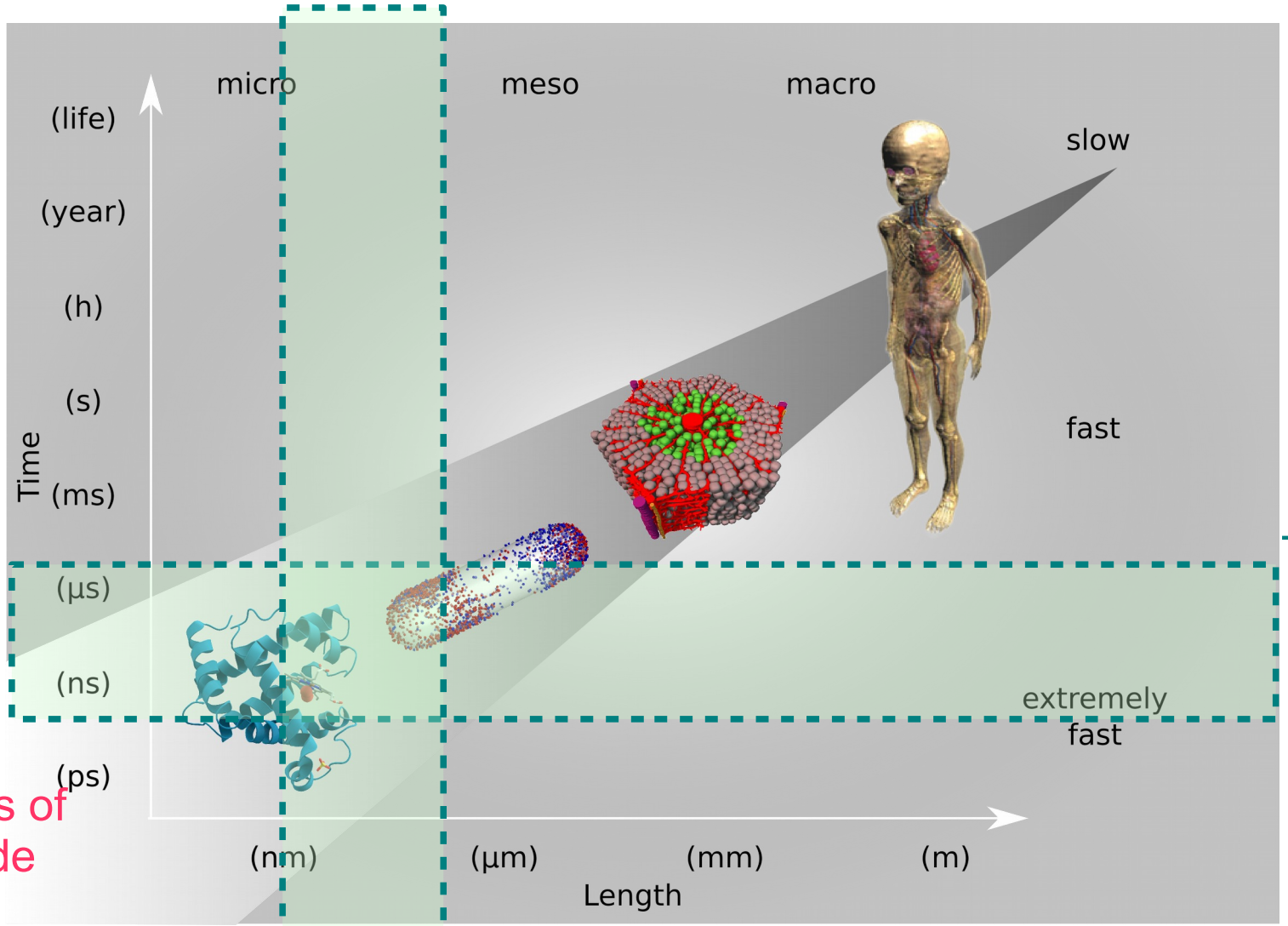
Met Office Seamless Unified Model



Babraham Institute

EMBL-EBI

Challenge 1: scales



Coupled multi-scale models

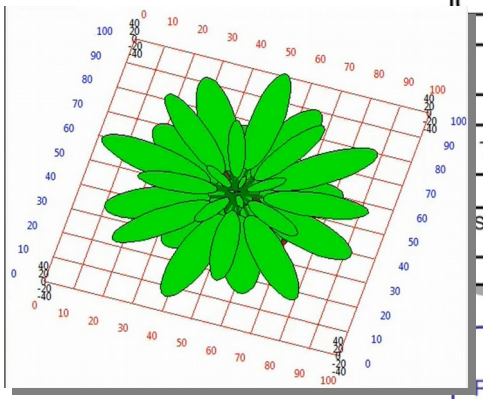
Theoretical and Computational roadblockers

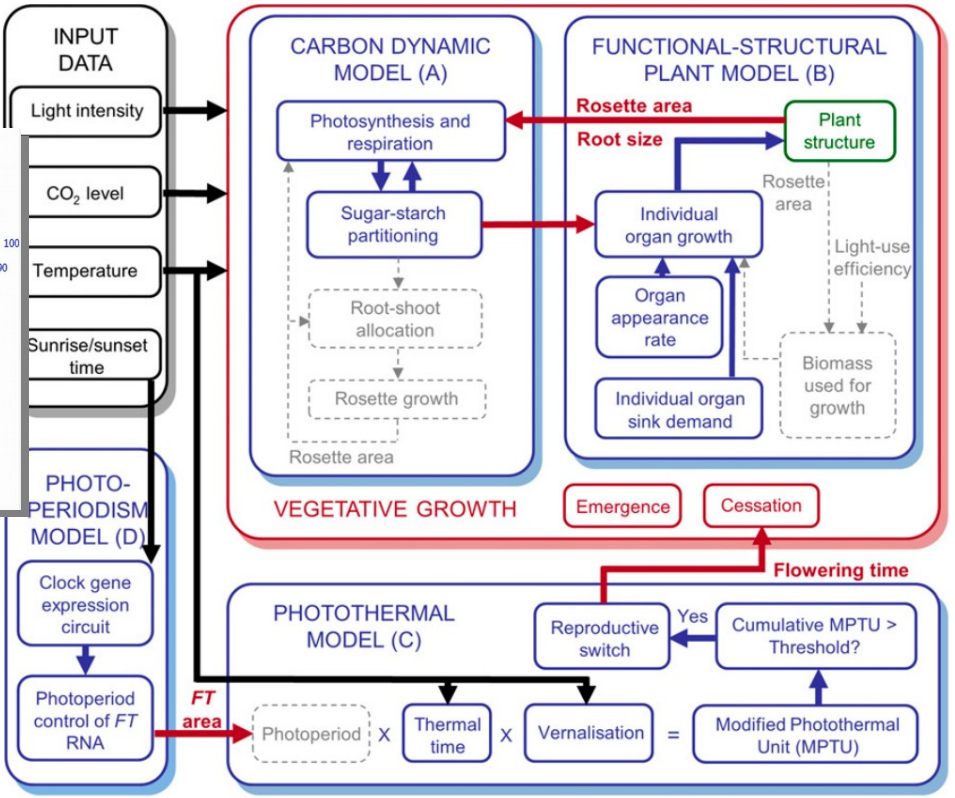
24 orders of magnitude

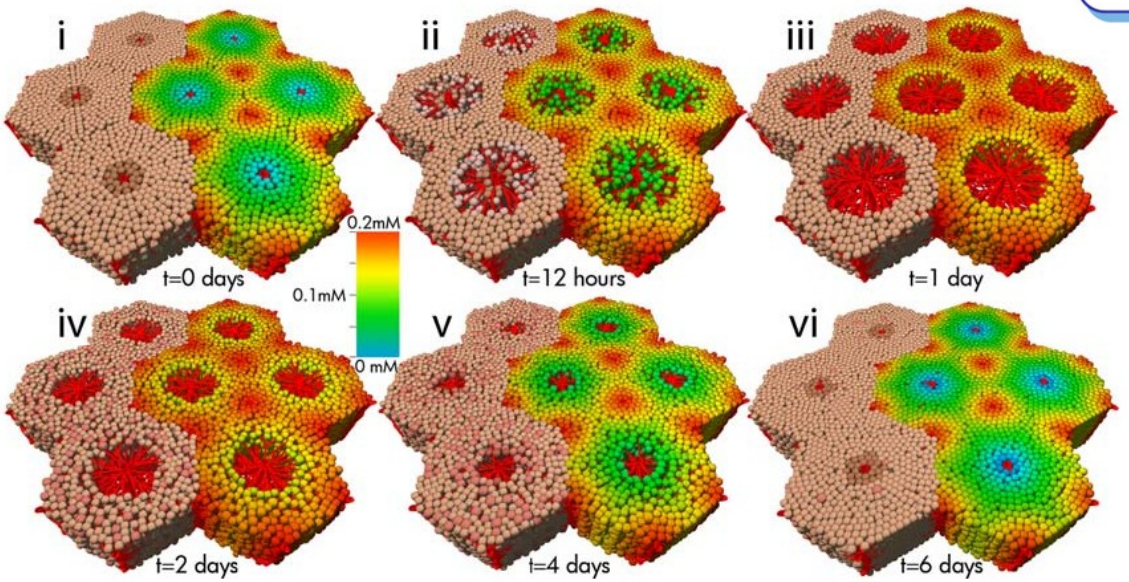
9 orders of magnitude

Adapted from Castiglione *et al.* (2014)

Chew *et al.* (2014)

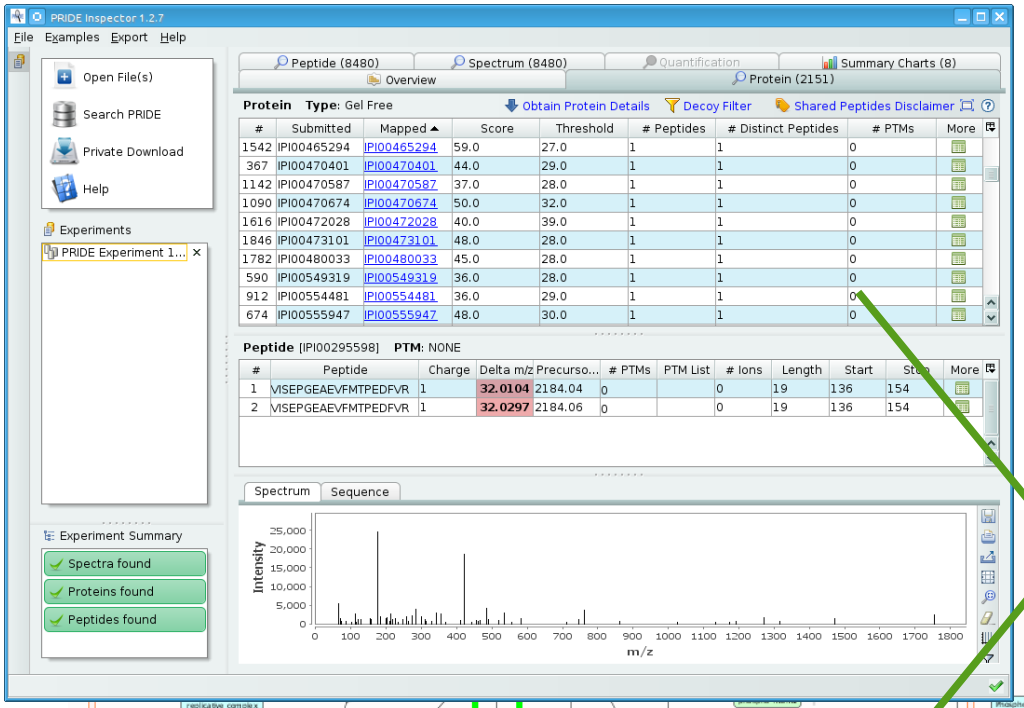


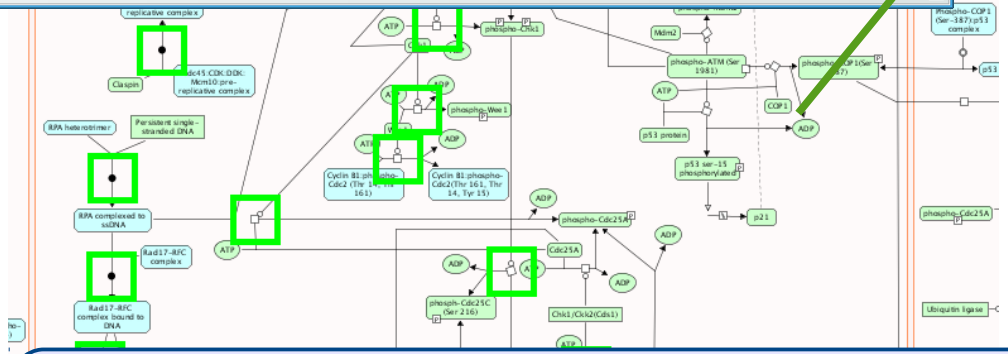




Schliess *et al.* (2014)

Challenge 2: automatic generation





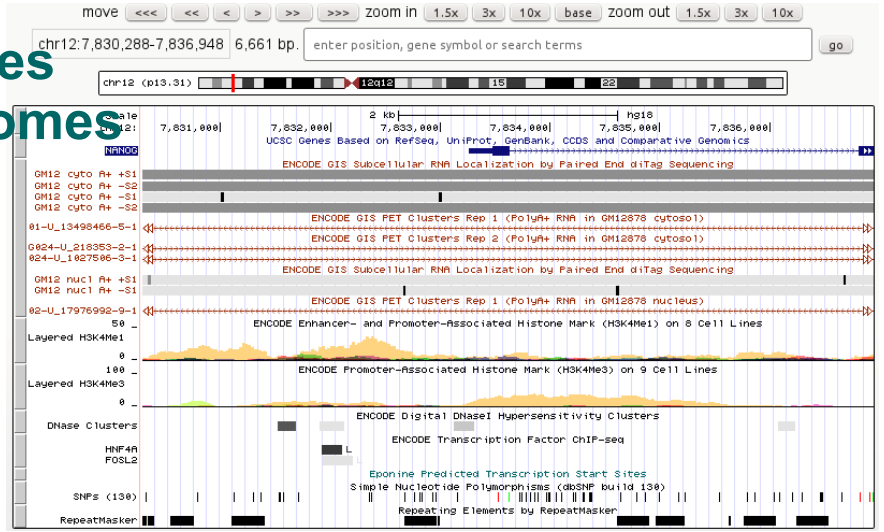
```
<assignmentRule metaid="metaid_0000023" variable="CT">
  <math xmlns="http://www.w3.org/1998/Math/MathML">
    <apply>
      <plus/>
      <ci> C2 </ci>
      <ci> CP </ci>
      <ci> M </ci>
      <ci> pM </ci>
    </apply>
  </math>
</assignmentRule>
</listOfRules>
<listOfReactions>
  <reaction id="Reaction1" name="cyclin_cdc2k dissociation" metaid="_000010" reversible="false">
    <annotation>
      <rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:bqmodel="http://biom
        <rdf:Description rdf:about="#_000010">
          <bqbiol:hasVersion>
            <rdf:Bag>
              <rdf:li rdf:resource="http://identifiers.org/reactome/REACT_6308"/>
            </rdf:Bag>
          </bqbiol:hasVersion>
          <bqbiol:isVersionOf>
            <rdf:Bag>
              <rdf:li rdf:resource="http://identif                    000079"/>
            </rdf:Bag>
          </bqbiol:isVersionOf>
        </rdf:Description>
      </rdf:RDF>
    </annotation>
        <listOfReactants>
      <speciesReference species="M" metaid="_712369"/>
    </listOfReactants>
    <listOfProducts>
      <speciesReference species="C2" metaid="_712382"/>
      <speciesReference species="YP" metaid="_712394"/>
    </listOfProducts>
    <kineticLaw metaid="_712406">
      <math xmlns="http://www.w3.org/1998/Math/MathML">
        <apply>
          <times/>
          <ci> cell </ci>
          <ci> k6 </ci>
          <ci> M </ci>
```

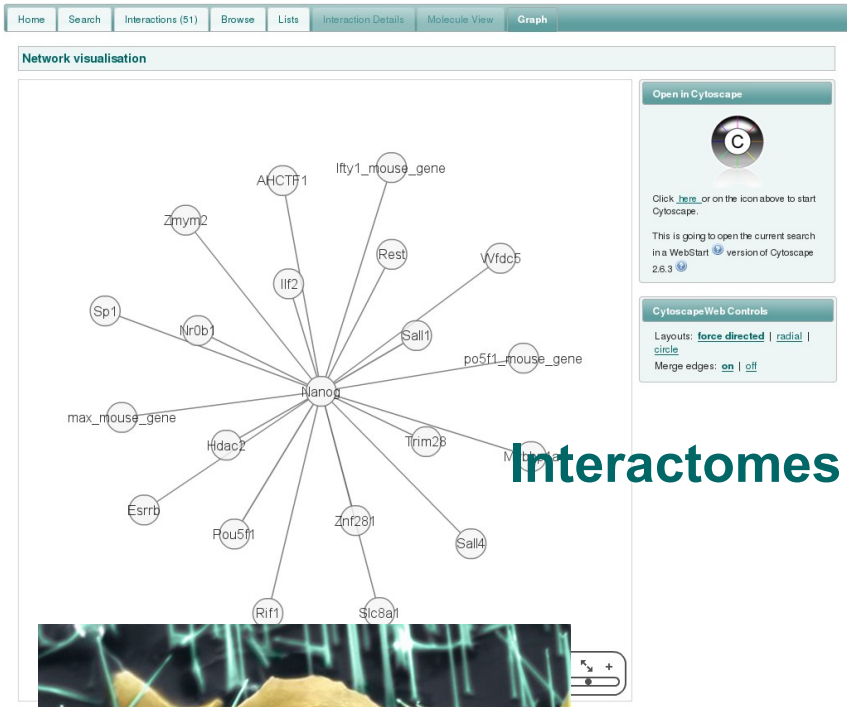
$$
\begin{aligned}
d[C2]/dt &= k_6[M] - k_8[{\sim}P][C2] + k_9[CP] \\
d[CP]/dt &= -k_3[CP][Y] + k_8[{\sim}P][C2] - k_9[CP] \\
d[pM]/dt &= k_3[CP][Y] - [pM]F([M]) + k_5[{\sim}P][M] \\
d[M]/dt &= [pM]F([M]) - k_5[{\sim}P][M] - k_6[M] \\
d[Y]/dt &= k_1[aa] - k_2[Y] - k_3[CP][Y] \\
d[YP]/dt &= k_6[M] - k_7[YP]
\end{aligned}
$$

Need to generate model automatically based on omics datasets. Known on small scale. The larger, the more human intervention needed.

Challenge 3: data heterogeneity

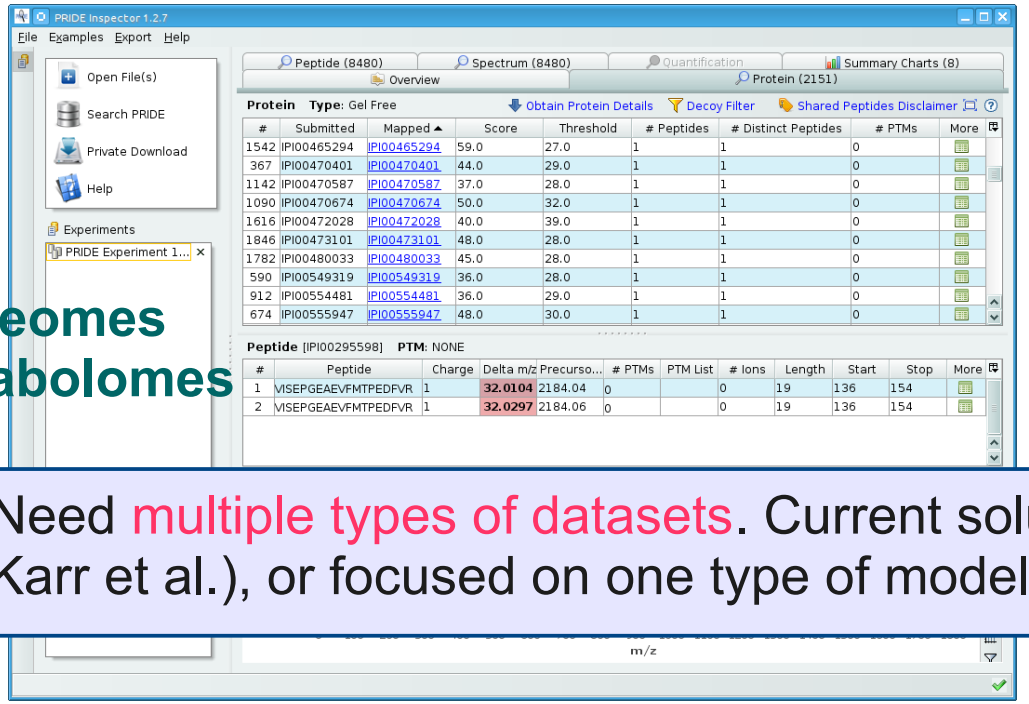
Genomes
epigenomes

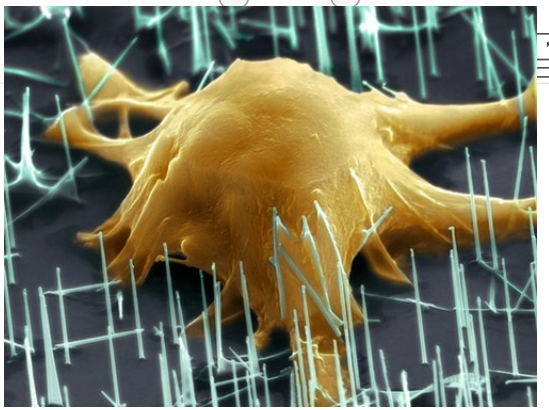




Interactomes

Proteomes
metabolomes

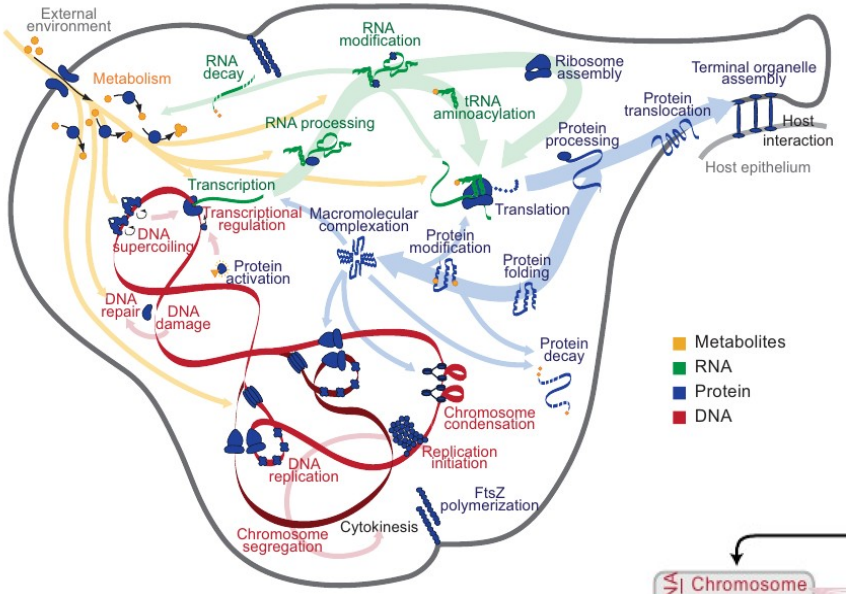




Imaging

Need multiple types of datasets. Current solutions either for small models (e.g Karr et al.), or focused on one type of model and data (e.g. metabolic models)

Modularity is mandatory



Theory

A Whole-Cell Computational Model Predicts Phenotype from Genotype

Jonathan R. Karr,[1,4] Jayodita C. Sanghvi,[2,4] Derek N. Macklin,[2] Miriam V. Gutschow,[2] Jared M. Jacobs,[2] Benjamin Bolival, Jr.,[2] Nacyra Assad-Garcia,[3] John I. Glass,[3] and Markus W. Covert[2,*]

[1]Graduate Program in Biophysics
[2]Department of Bioengineering
Stanford University, Stanford, CA 94305, USA
[3]J. Craig Venter Institute, Rockville, MD 20850, USA
[4]These authors contributed equally to this work
*Correspondence: mcovert@stanford.edu

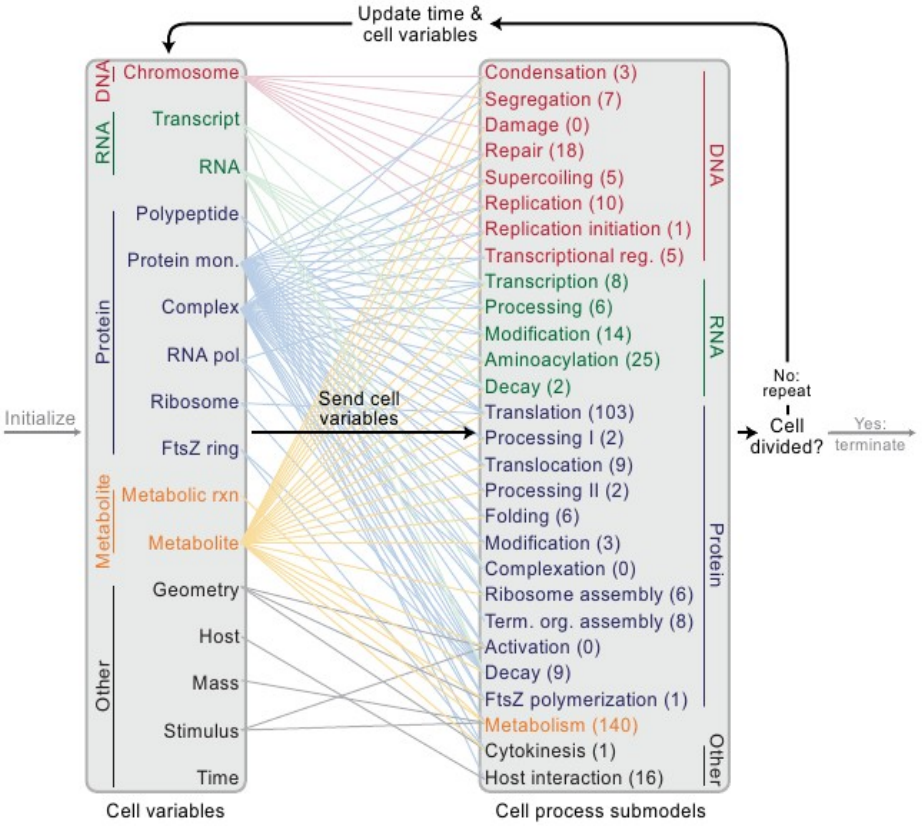
http://dx.doi.org/10.1016/j.cell.2012.05.044

SUMMARY

Understanding how complex phenotypes arise from individual molecules and their interactions is a primary challenge in biology that computational approaches are poised to tackle. We report a whole-cell computational model of the life cycle of the human pathogen *Mycoplasma genitalium* that includes all of its molecular components and their interactions. An integrative approach to modeling that combines diverse mathematics enabled the simultaneous inclusion of fundamentally different cellular processes and experimental measurements. Our whole-cell model accounts for all annotated gene functions and was validated against a broad range of data. The model provides insights into many previously unobserved cellular behaviors, including in vivo rates of protein-DNA association

First, until recently, not enough has been known about the individual molecules and their interactions to completely model any one organism. The advent of genomics and other high-throughput measurement techniques has accelerated the characterization of some organisms to the extent that comprehensive modeling is now possible. For example, the mycoplasmas, a genus of bacteria with relatively small genomes that includes several pathogens, have recently been the subject of an exhaustive experimental effort by a European consortium to determine the transcriptome (Güell et al., 2009), proteome (Kühner et al., 2009), and metabolome (Yus et al., 2009) of these organisms.

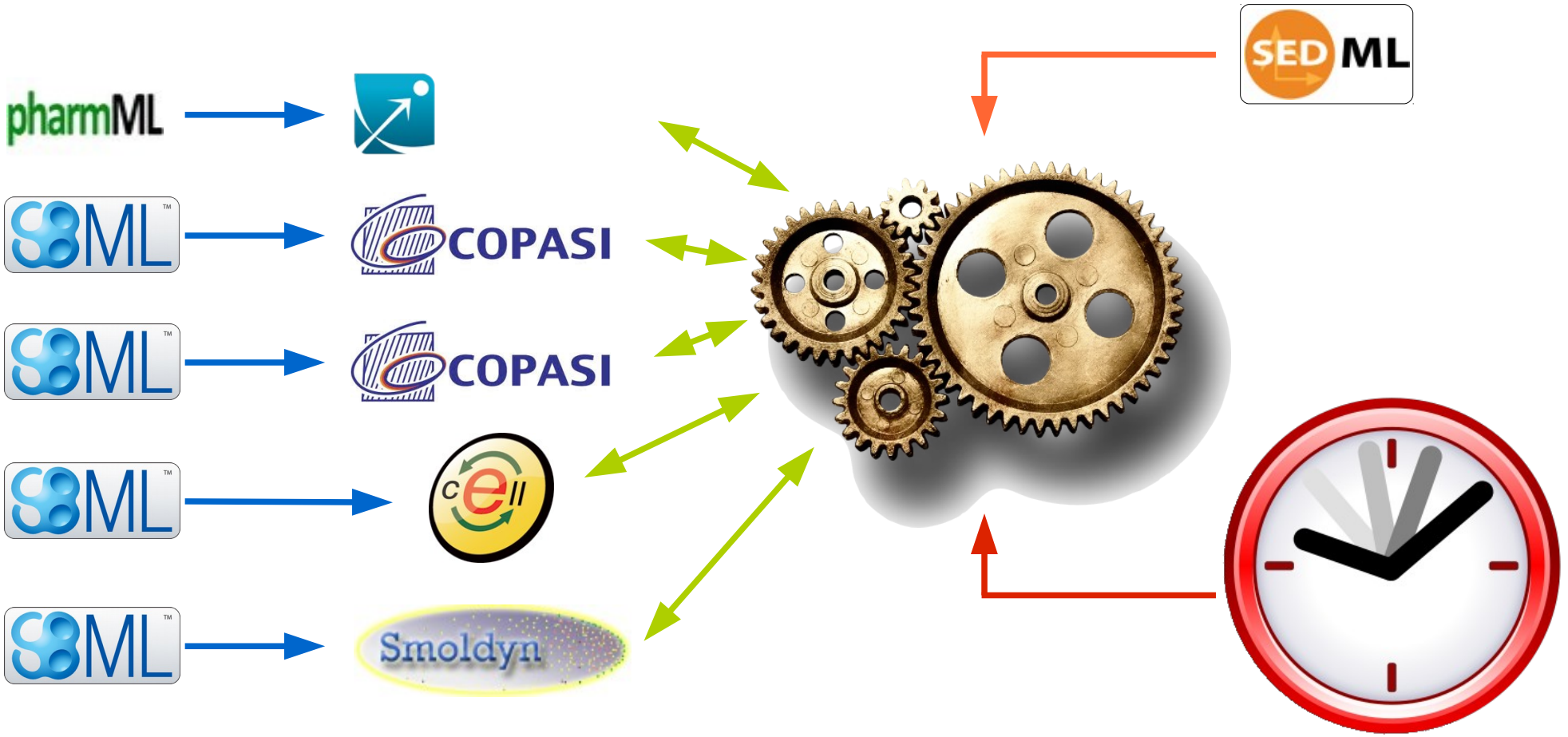
The second limiting factor has been that no single computational method is sufficient to explain complex phenotypes in terms of molecular components and their interactions. The first approaches to modeling cellular physiology, based on ordinary differential equations (ODEs) (Atlas et al., 2008; Browning et al., 2004; Castellanos et al., 2004, 2007; Domach et al., 1984; Tomita et al., 1999), were limited by the difficulty in obtaining the necessary model parameters. Subsequently, alternative



Why is modularity important?

- Different parts can be modelled with different approaches
- Alternative modules representing the same biological process with different granularities or different modelling approaches
- Model families with alternative parts: avoid combinatorial explosion
- Modules can be developed at their own pace; easier versioning
- Distributed maintenance. No single individual or group can master the entirety of the project.

Challenge 4: Single software not sufficient



modular model

hybrid simulation system

discrete event detection

adaptive synchronization

- model
  - 'domain model'
  - 'mathematical model'
    - 'Bayesian model'
    - 'computational model'
    - 'differential equation model'
    - 'interacting state machine'
    - 'logical model'
    - 'Markov model'
    - 'network model'
    - 'Petri net'
    - 'population model'
    - 'process algebra'
    - 'rule-based model'
    - 'statistical model'
    - 'steady-state model'
  - 'modelling entity feature'
  - readout
    - 'phase portrait'
    - 'steady state value'
    - timecourse
  - variable
    - 'dependent variable'
    - 'independent variable'
    - 'statistical data'

definition [language: en]

Description of a system using mathematical concepts and language. The model is composed of a set of variables and a set of equations that establish relationships between the variables.

example [language: en]

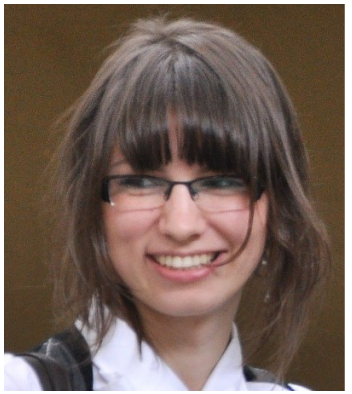
A set of ordinary differential equation describing a physical process.

'preferred label' [language: en]

mathematical model

seeAlso [type: anyURI]

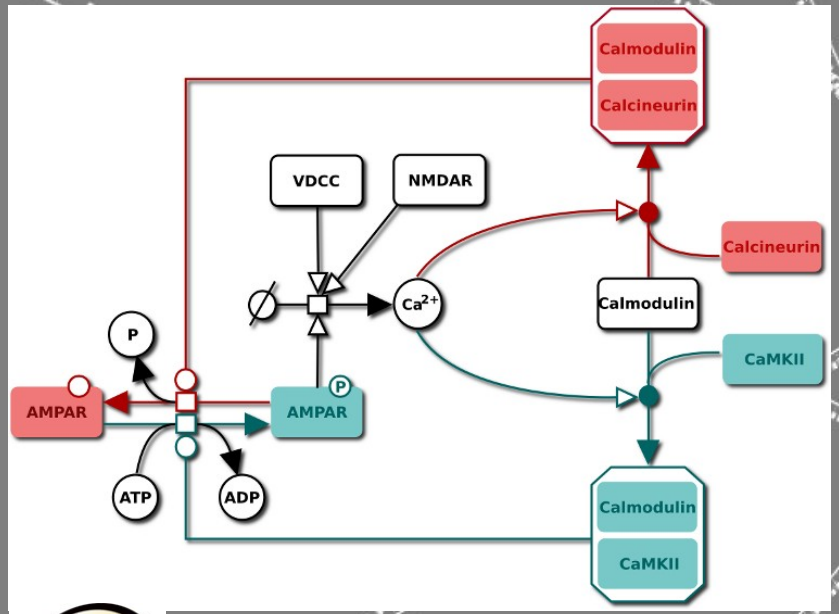
http://en.wikipedia.org/wiki/Mathematical_model

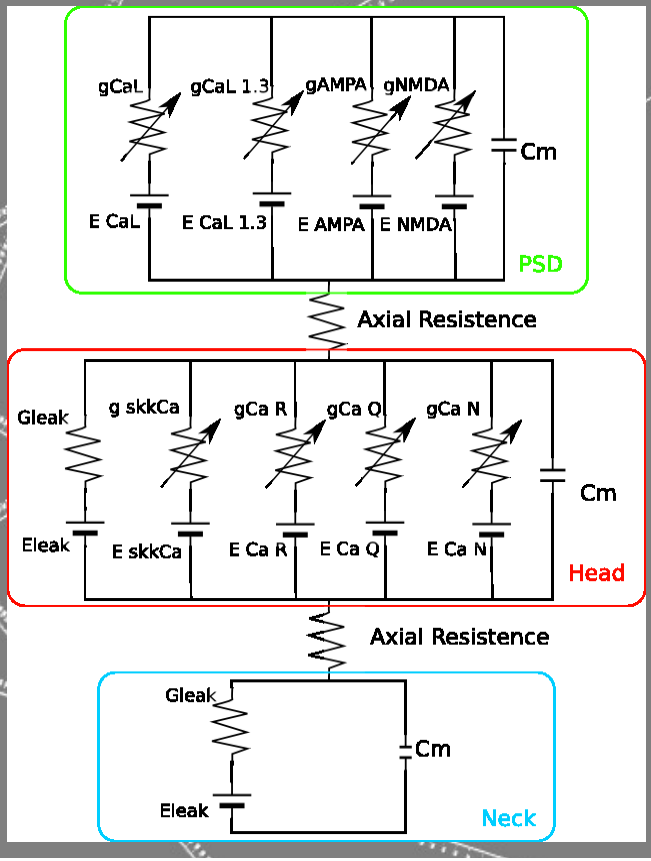


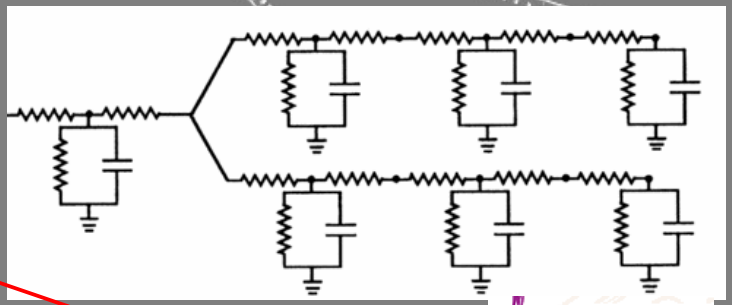
Mathematical Modelling Ontology

http://sourceforge.net/projects/mamo-ontology

Whole cell: electro-biochemical models



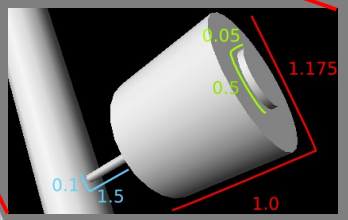




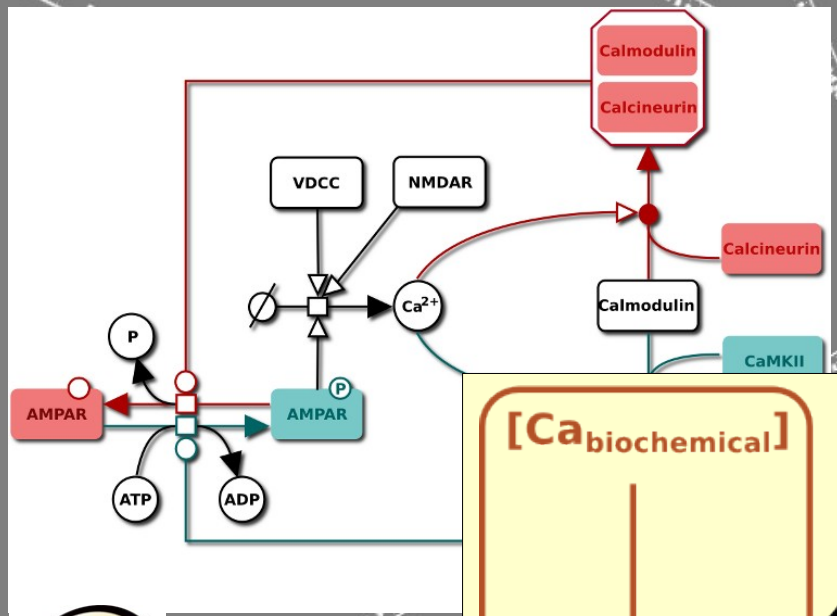
1504 spines

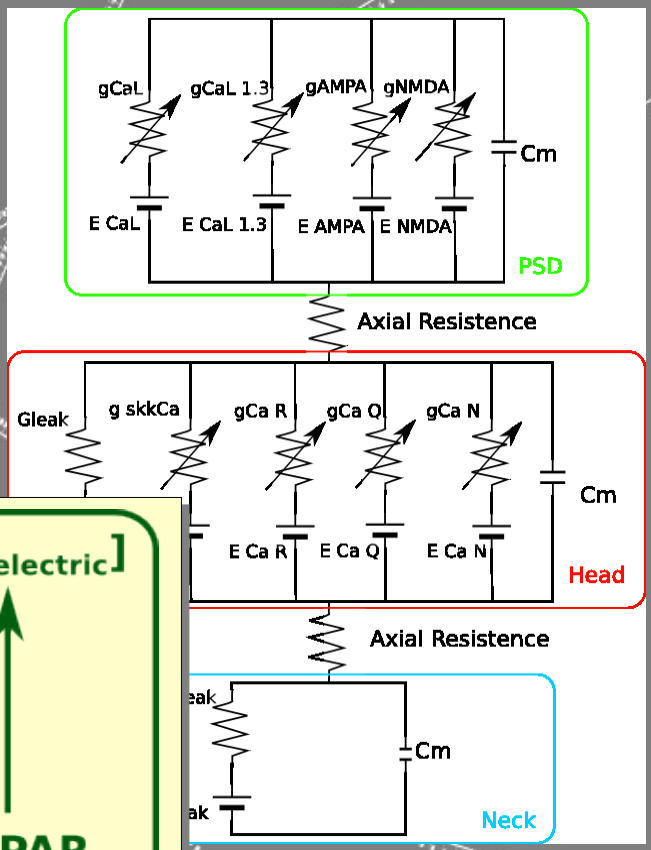
4761 compartments

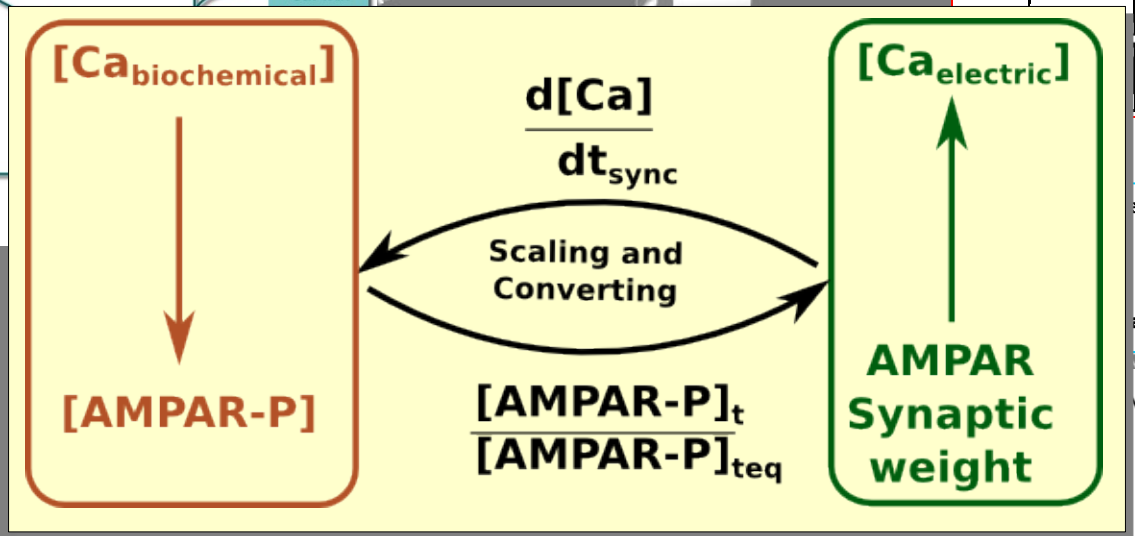
16362 channels



Mattioni *et al* (2012, 2013)



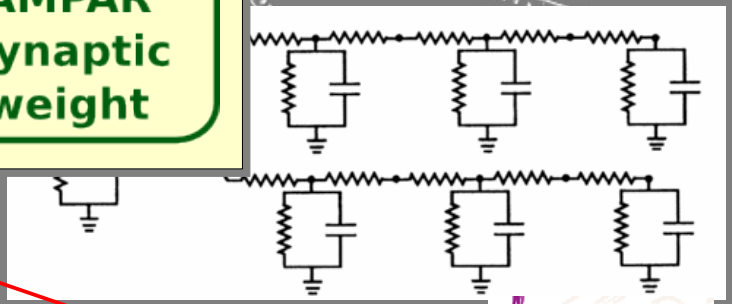


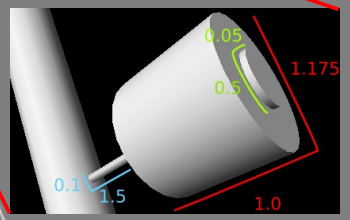


1504 spines

4761 compartments

16362 channels



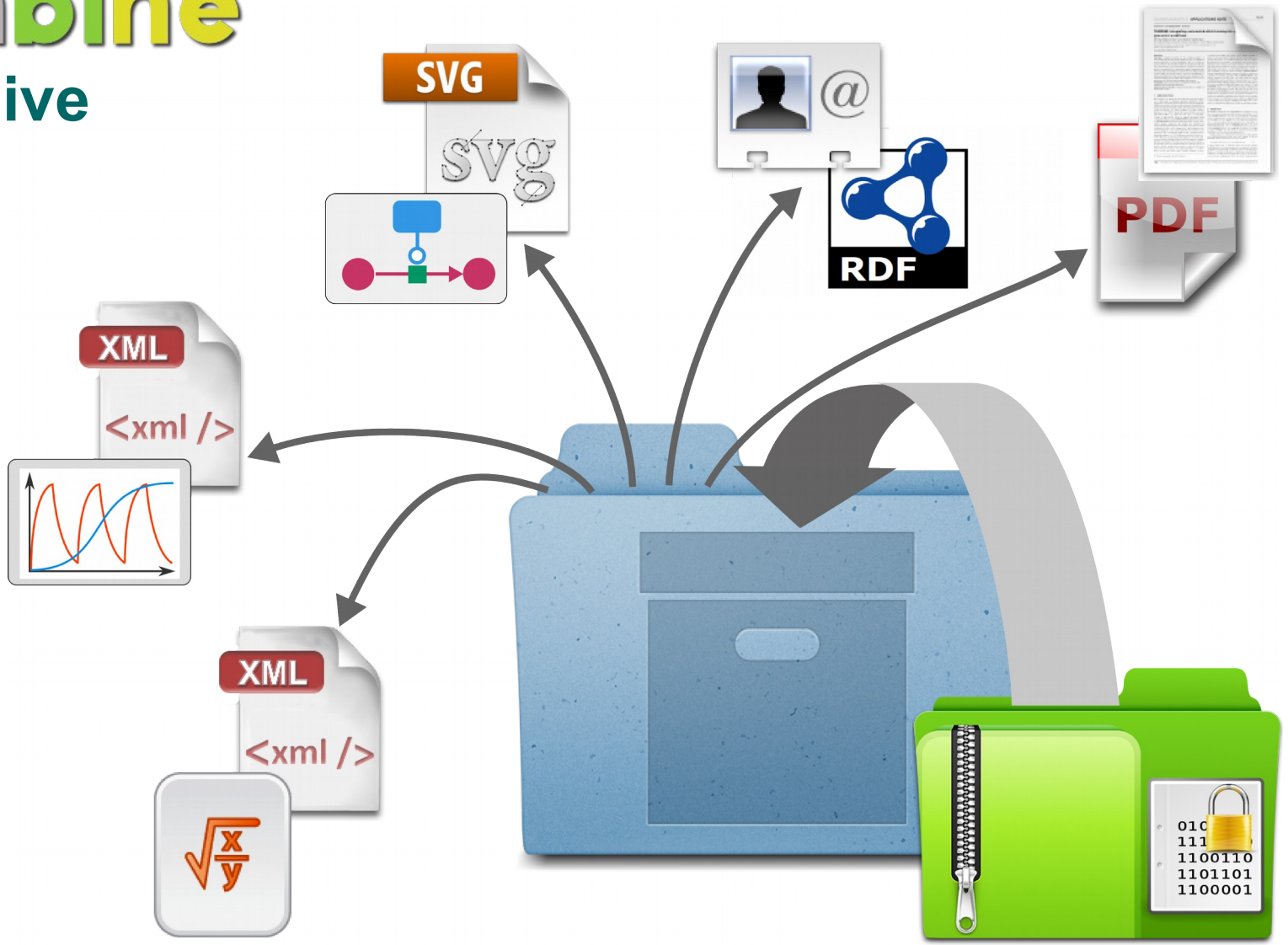


Mattioni *et al* (2012, 2013)

Challenge 5: reproducibility and virtualisation

Models must be self-contained and portable for everyone to reuse and customise → Virtual machines with models+tools

combine archive



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

Bergman *et al. BMC Syst Biol (2014)*

BioModels team

Ishan Ajmera
Raza Ali
Duncan Berenguier
Alexander Broicher
Vijayalakshmi Chelliah
Melanie Courtot
Marco Donizelli
Marine Dumousseau
Lukas Endler
Yvon Florent
Mihai Glont
Enuo He
Arnaud Henry
Henning Hermjakob
Gael Jalowicki
Nick Juty
Sarah Keating
Christian Knüpfer
Nicolas Le Novère
Chen Li
Camille Laibe
Stuart Moodie
Kedar Nath Natarajan
Jean-Baptiste Pettit
Michael Schubert
Maciej Swat
Karim Tazibt
Dagmar Waltemath
Sarala Wimalaratne
Anna Zhukova

Standards' editors

Richard Adams
Frank Bergman
Hamid Bolouri
Jonathan Cooper
Tobias Czauderna
Emek Demir
Andrew Finney
Stefan Hoops
Mike Hucka
Sarah Keating
Hiroaki Kitano
Nicolas Le Novère
Yukiko Matsuoka
Huaiyu Mi
Andrew Miller
Stuart Moodie
Ion Moraru
Chris Myers
David Nickerson
Brett Olivier
Sven Sahle
Herbert Sauro
Jim Schaff
Falk Schreiber
Lucian Smith
Anatoly Sorokin
Alice Villeger
Katja Wegner
Darren Wilkinson
Dagmar Waltemath

Path2Models

Finja Büchel
Claudine Chaouiya
Tobias Czauderna
Andreas Dräger
Mihai Glont
Martin Golebievski
Henning Hermjakob
Mike Hucka
Douglas Kell
Roland Keller
Camille Laibe
Nicolas Le Novère
Pedro Mendes
Florent Mittag
Wolfang Müller
Matthias Rall
Nicolas Rodriguez
Julio Saez-Rodriguez
Michael Schubert
Falk Schreiber
Neil Swainston
Martijn van Iersel
Clemens Wrzodek
Andreas Zell

The numerous scientists who participated to discussions

The community of Computational Systems Biology

cnrs

MEMORIAL SLOAN-KETTERING CANCER CENTER
ESTABLISHED 1884

ENFIN
Enabling Systems Biology

CAM

UCONN HEALTH CENTER

Netherlands Consortium for
Systems Biology

nbic
netherlands
bioinformatics
centre

Universiteitsfonds Limburg
| SWOL |

OICR
Ontario Institute
for Cancer Research

Maastricht
University

National
Human Genome
Research Institute

OntarioGenomicsInstitute

ERASysAPP
ERA-Net for Applied Systems Biology

INSTITUT DES SYSTEMES COMPLEXES
ISC
PARIS ÎLE DE FRANCE

HITS

virtual liver
network

DFG

FONDATION
PIERRE-GILLES
DE GENNES
POUR LA RECHERCHE