BioModels Database

Sharing and re-using computational models of biological processes

Nicolas Le Novère, Babraham Institute, EMBL-EBI

What happened to Biology at the end of XXth century?

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

A New Approach to Decoding Life:
Systems Biology

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

New Generation Computing, 18(2000)199-216
Ohmsha, Ltd. and Springer-Verlag

Invited Paper

Perspectives on Systems Biology

Hiroaki KITANO
Sony Computer Science Laboratories, Inc.

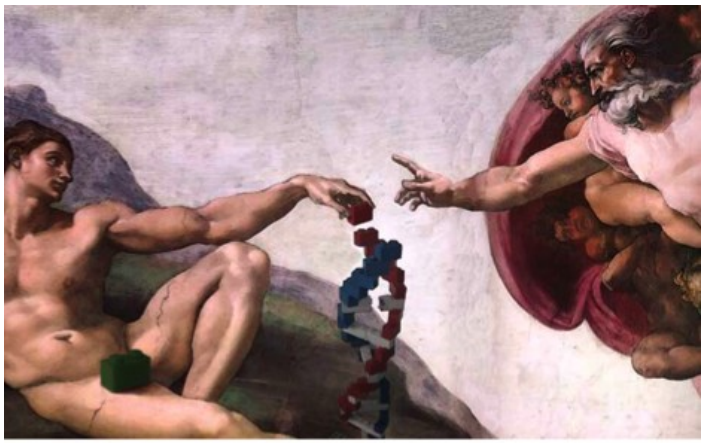
What happened to biology at the end of XXth century?

RESEARCH ARTICLE

Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome

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

2 JULY 2010 VOL 329 SCIENCE www.sciencemag.org



EXTREME GENETIC ENGINEERING

An Introduction to Synthetic Biology

etc group

January 2007

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

Cell

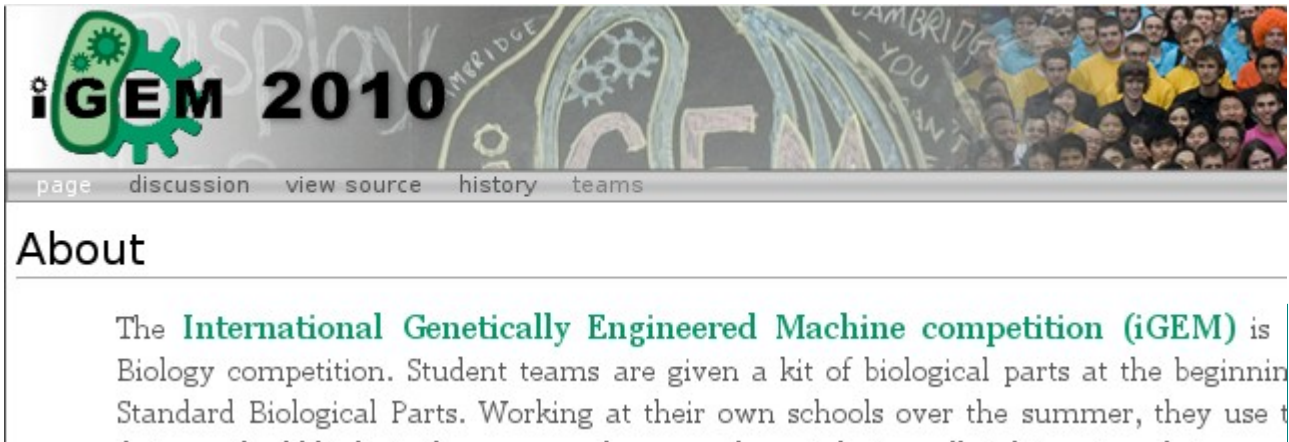
Kazutoshi Takahashi[1] and Shinya Yamanaka[1,2,*]
[1] Department of Stem Cell Biology, Institute for Frontier Medical Sciences, Kyoto University, Kyoto 606-8507, Japan
[2] CREST, Japan Science and Technology Agency, Kawaguchi 332-0012, Japan
*Contact: yamanaka@frontier.kyoto-u.ac.jp
DOI 10.1016/j.cell.2006.07.024

A synthetic oscillatory network of transcriptional regulators

Michael B. Elowitz & Stanislas Leibler

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

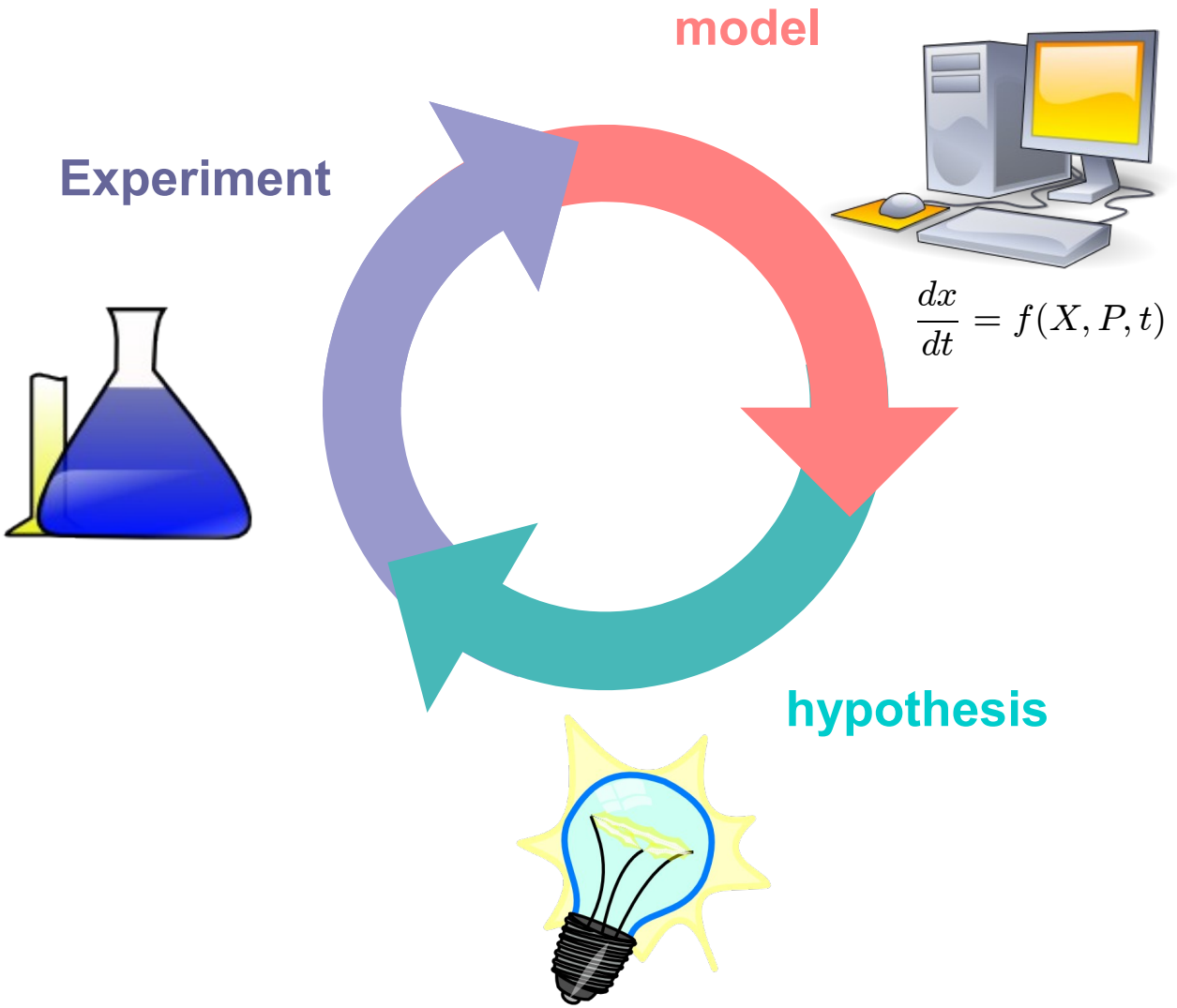
NATURE | VOL 403 | 20 JANUARY 2000 | www.nature.com



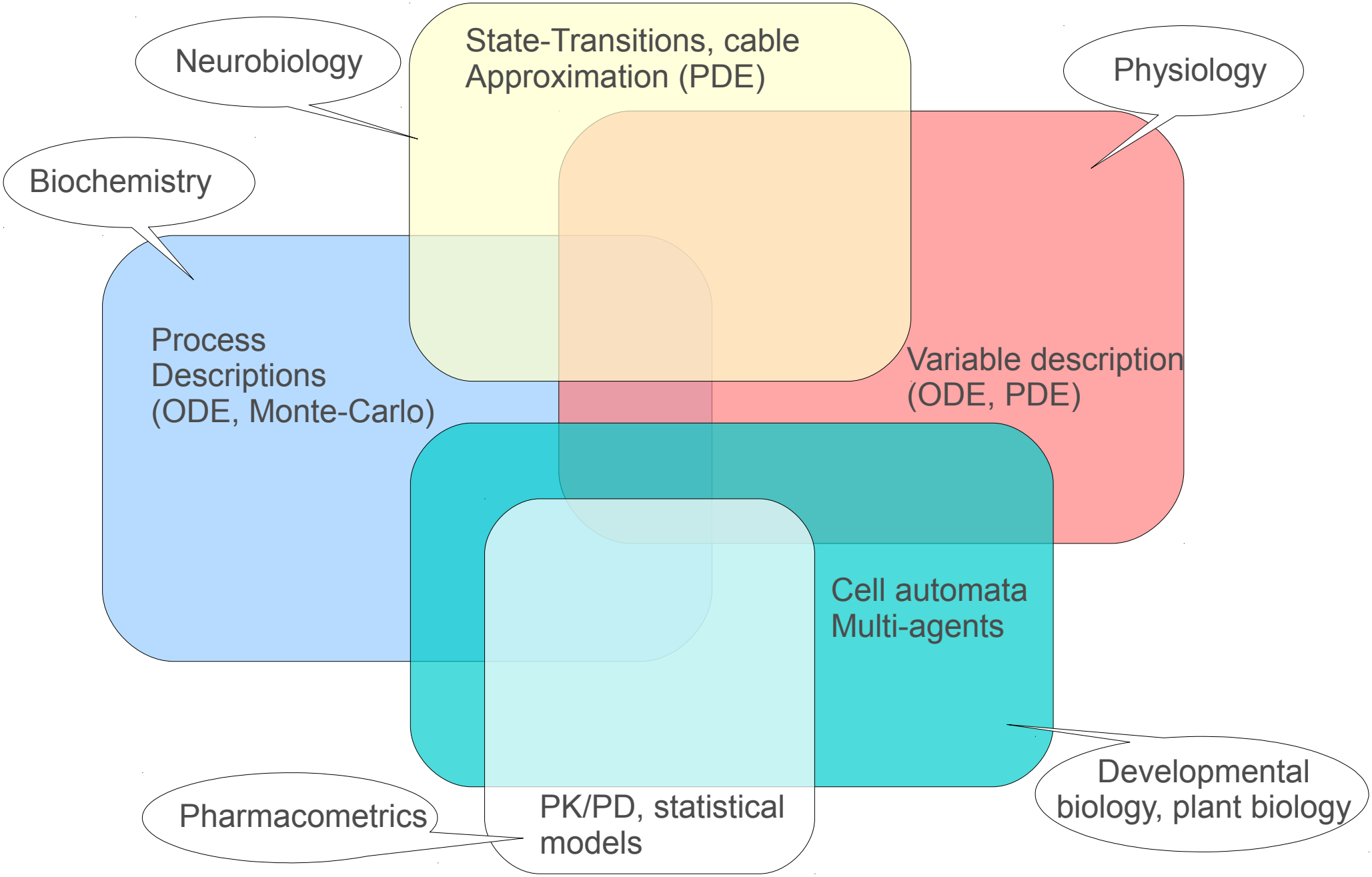
About

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

For all that we need models



Many complementary modelling approaches



Computational modelling left the niches

- Metabolic networks Fung et al. A synthetic gene-metabolic oscillator. ***Nature*** 2005; Herrgård et al. A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. ***Nat Biotechnol*** 2008
- Signalling pathways Bray et al. Receptor clustering as a cellular mechanism to control sensitivity. ***Nature*** 1998; Bhalla ad Iyengar. Emergent properties of signaling pathways. ***Science*** 1998; Schoeberl et al. Computational modeling of the dynamics of the MAP kinase cascade activated by surface and internalized EGF receptors. ***Nat Biotechnol*** 2002; Hoffmann et. The IκB-NF-κB signaling module: temporal control and selective gene activation. ***Science*** 2002; Smith et al. Systems analysis of Ran transport. ***Science*** 2002; Bhalla et al. MAP kinase phosphatase as a locus of flexibility in a mitogen-activated protein kinase signaling network. ***Science*** 2002; Nelson et al. Oscillations in NF-κB Signaling Control the Dynamics of Gene Expression. ***Science*** 2004; Werner et al. Stimulus specificity of gene expression programs determined by temporal control of IKK activity. ***Science*** 2005; Sasagawa et al. Prediction and validation of the distinct dynamics of transient and sustained ERK activation. ***Nat Cell Biol*** 2005; Basak et al. A fourth IkappaB protein within the NF-κB signaling module. ***Cell*** 2007; McLean et al. Cross-talk and decision making in MAP kinase pathways. ***Nat Genet*** 2007; Ashall et al. Pulsatile Stimulation Determines Timing and Specificity of NF-κB-Dependent Transcription. ***Science*** 2009; Becker et al. Covering a broad dynamic range: information processing at the erythropoietin receptor. ***Science*** 2010
- Gene regulatory networks McAdams and Shapiro. Circuit simulation of genetic networks. ***Science*** 1995; Yue et al. Genomic cis-regulatory logic: Experimental and computational analysis of a sea urchin gene. ***Science*** 1998; Von Dassow et al. The segment polarity network is a robust developmental module. ***Nature*** 2000; Elowitz and Leibler. A synthetic oscillatory network of transcriptional regulators. ***Nature*** 2000; Shen-Orr et al, Network motifs in the transcriptional regulation network of Escherichia coli. ***Nat Genet*** 2002; Yao et al. A bistable Rb-E2F switch underlies the restriction point. ***Nat Cell Biol*** 2008; Friedland. Synthetic gene networks that count. ***Science*** 2009
- Pharmacometrics models Labrijn et al. Therapeutic IgG4 antibodies engage in Fab-arm exchange with endogenous human IgG4 in vivo. ***Nat Biotechnol*** 2009
- Physiological models Noble. Modeling the heart from genes to cells to the whole organ. ***Science*** 2002; Izhikevich and Edelman. Large-scale model of mammalian thalamocortical systems. ***PNAS*** 2008
- Infectious diseases Perelson et al. HIV-1 dynamics in vivo: Virion clearance rate, infected cell life-span, and viral generation time. ***Science*** 1996; Nowak. Population dynamics of immune responses to persistent viruses. ***Science*** 1996; Neumann et al. Hepatitis C viral dynamics in vivo and the antiviral efficacy of interferon-alpha therapy. ***Science*** 1998

Cell

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,*]

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[4]These authors contributed equally to this work
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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

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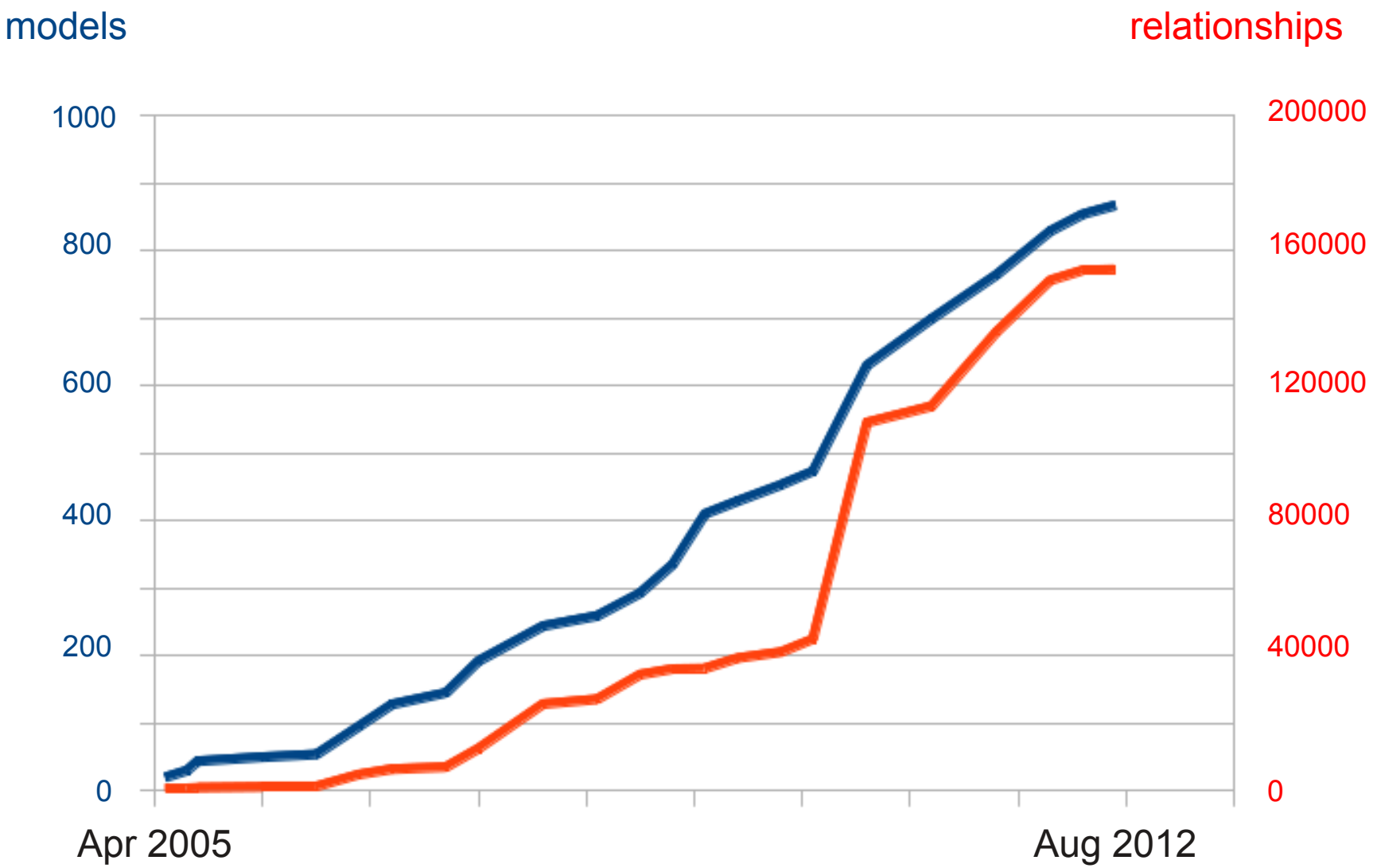
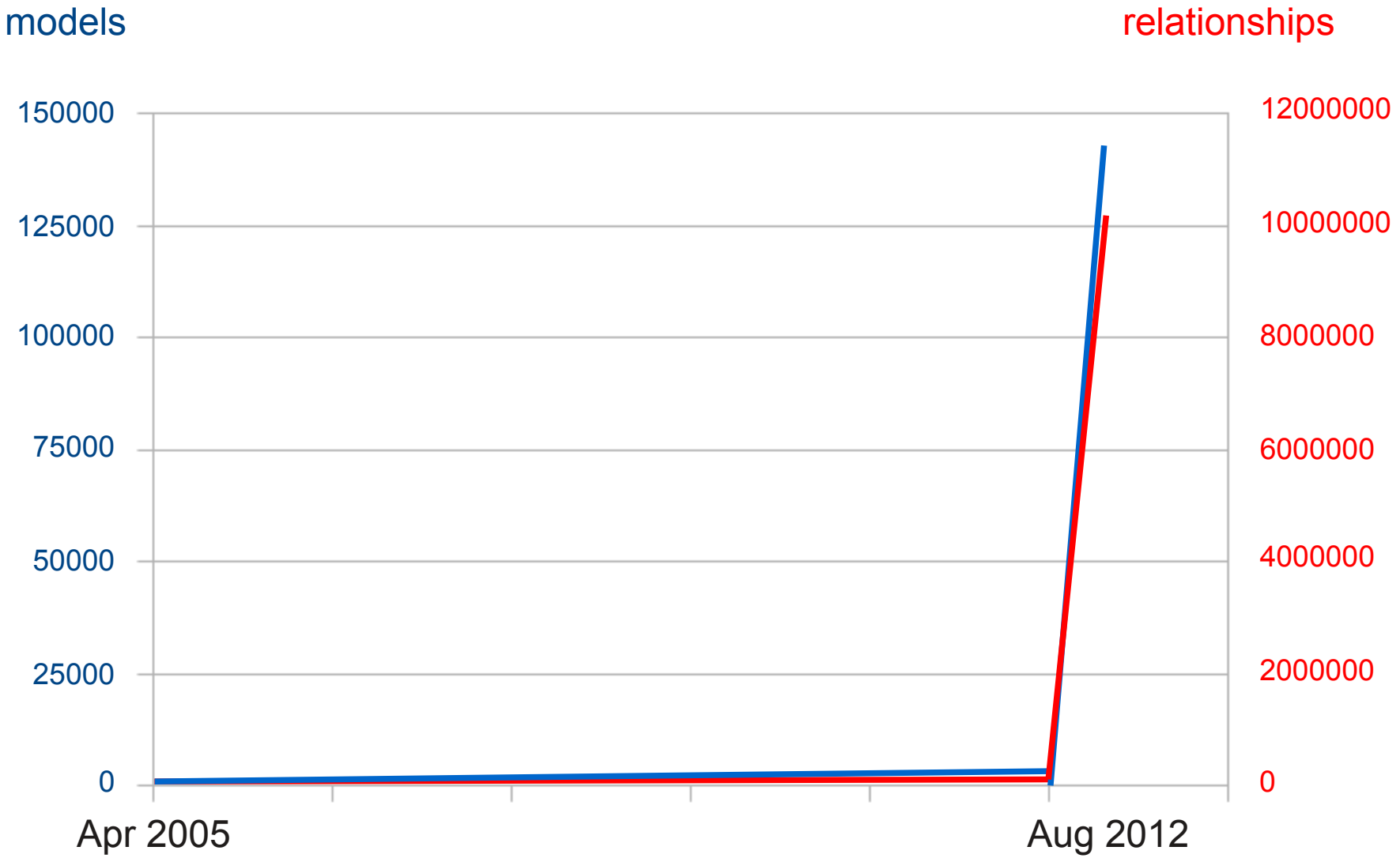
Computational models on the rise



BioModels Database growth since its creation, published models

Computational models on the rise



BioModels Database growth since its creation, with Path2Models

BioModels Database - A Database of Annotated Published Models

BioModels Database is a repository of peer-reviewed, published, computational models. These mathematical models are primarily from the field of systems biology, but more generally are those of biological interest. This resource allows biologists to store, search and retrieve published mathematical models. In addition, models in the database can be used to generate sub-models, can be simulated online, and can be converted between different representational formats. This resource also features programmatic access via Web Services.

All unmodified models in the database are available freely for use and distribution, to all users. This resource is developed and maintained by the BioModels.net initiative. More information about BioModels Database can be found in the Frequently Asked Questions.

Advanced Search

Search | Go to model

Models published in the literature

- Browse curated models
- Browse curated models
- Browse curated models using Taxonomy
- Browse non-curated models

Browse curated models

Browse the models in the curated branch. These models have been thoroughly curated, and model elements have been annotated with terms from controlled vocabularies as well as links to relevant data resources.

Path2Models *(new)*

Submit a model

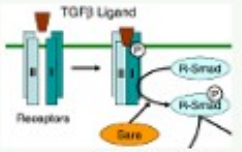
http://www.ebi.ac.uk/biomodels/

Links

- Main instance at EMBL-EBI, UK
- Mirror at Caltech, USA
- Project on SourceForge
- Web Services
- Download archived models

Model of the month

November 2012



Transforming growth factor β (TGF-β) ligands activate a signaling cascade with multiple cell context dependent outcomes. Disruption or disturbance leads to variant clinical disorders. A mathematical model to determine the relevance of feedback loops in the TGF-β signaling has been presented by Wegner et al. (2011).

Please read more...

News

7 November 2012 **Software developer position available**
We are seeking an experienced Software Developer to work on the software infrastructure behind BioModels Database. For more information and application instructions, please refer to the job description page (**closing date: 30 November 2012**).

6th September 2012 **Introduction to BioModels Database on Train online**
The EBI online training platform, Train online, now features an introduction to BioModels Database.

11th August 2012 **Twenty-third Release of BioModels Database!**
With this release, several new models have been published and numerous have been updated. Moreover new services are now available (for example related to the access to models from the Path2Models project) while others have been improved (such as the model browsing feature based on a tree of Gene Ontology terms or the BioPAX export). Please read the release notes for more information.
Download models archives

What is BioModels Database?

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

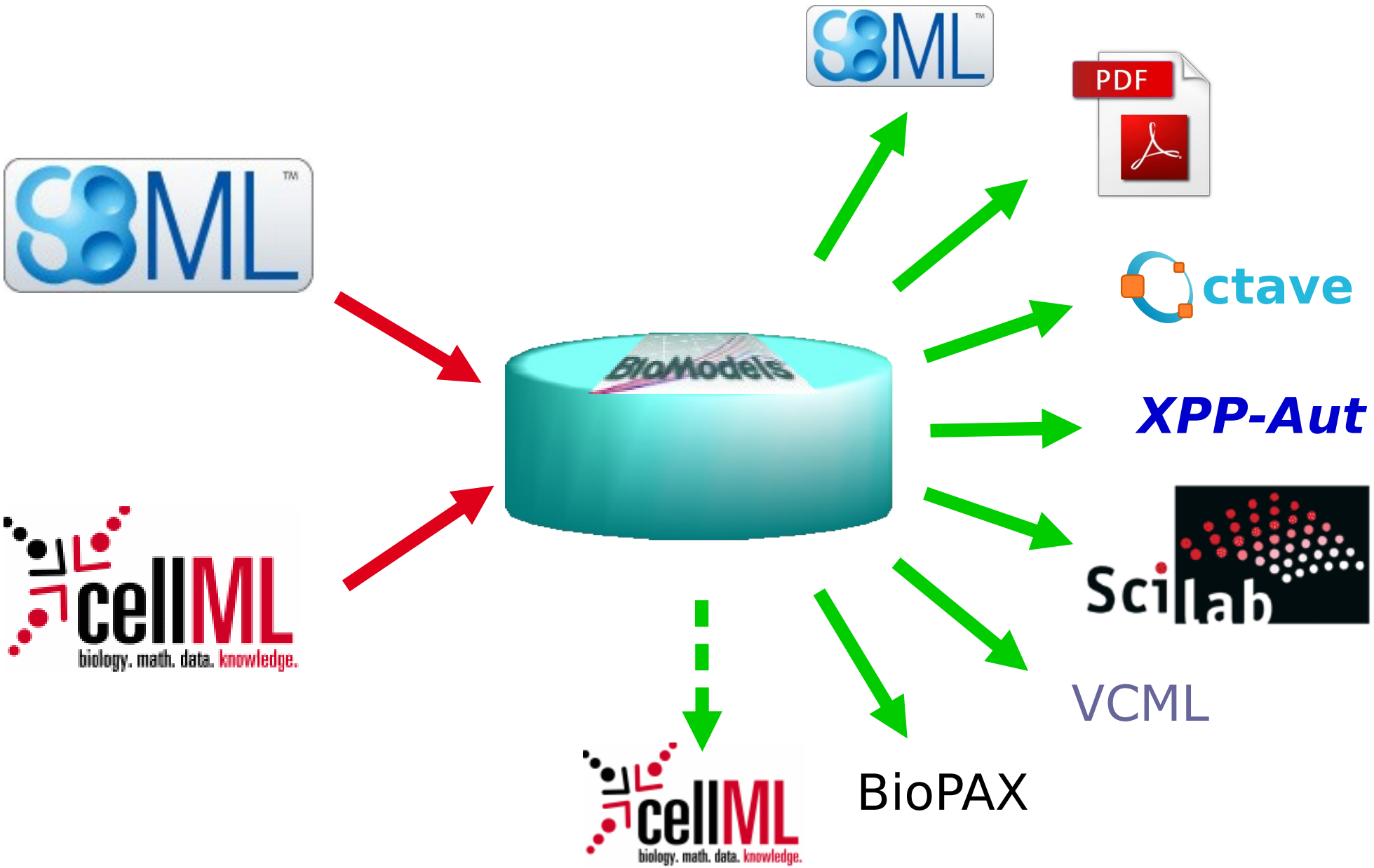
What can-we do with BioModels Database?

- Search and retrieve quantitative models of biomedical interest
- Explore the variables and the structure of the model
- Run timecourse simulations of the model
- Download the model in many formats
- Do all the above via Web Services
- Learn about significant models using the Model of the Month

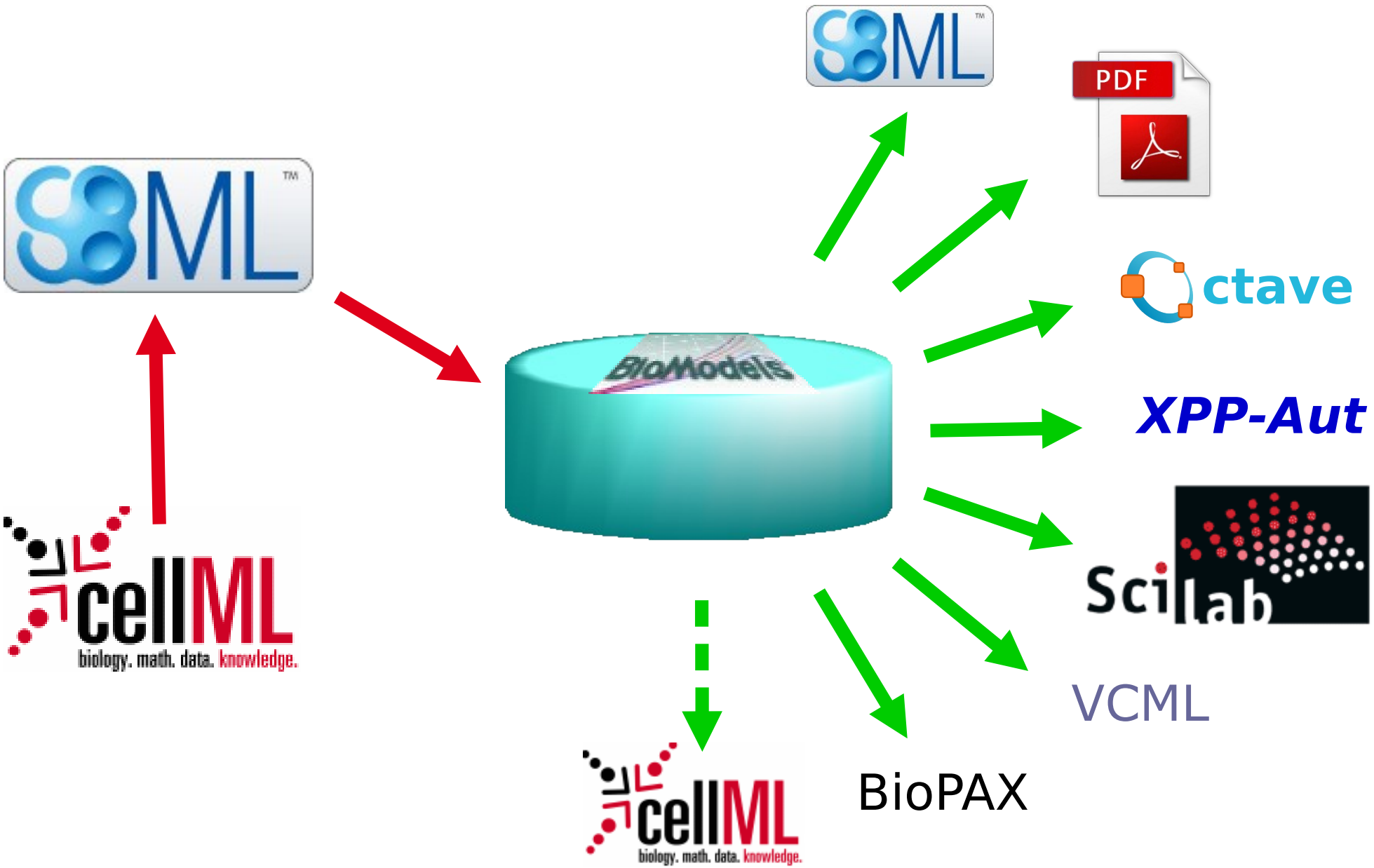
Where do models come from?

- From authors before grant applications or publications
- Over 300 scientific journals advise submission to BioModels Db:
  - Nature Molecular Systems Biology
  - Public Library of Science journals
  - BioMedCentral journals
  - Royal Society of Chemistry
- Various people curated models out of interest.
- Submitted by curators
  - imported from other repositories (DOQCS, CellML)
  - reimplemented from literature

Input and output formats



Input and output formats



SBML core is not limited to biochemistry!

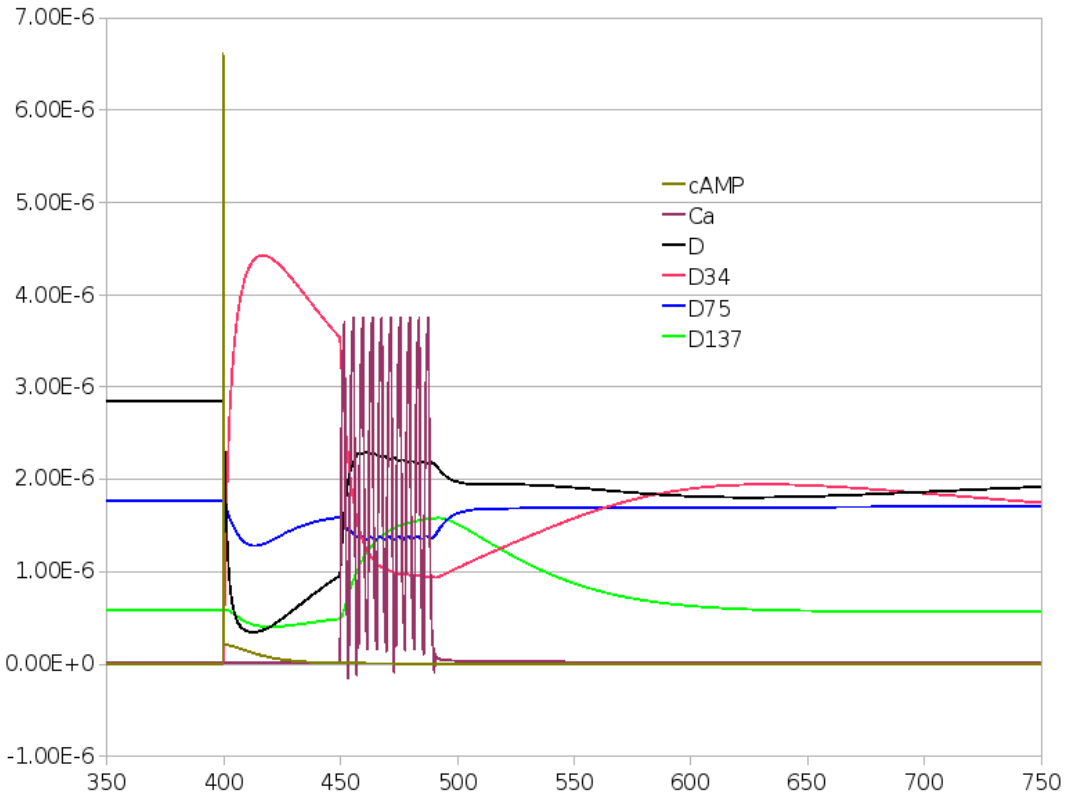
- A species is a pool of entities participating to a reaction, **not always** a **chemical** entity
  - It can be a pool of molecules
  - It can be a pool of cells
  - It can be a pool of organs
  - It can be a population of organi
- Rate Rules can describe the temporal evolution of any quantitative parameter, e.g. transmembrane voltage, tumour size etc.
- Events can describe any discontinuous change, e.g. neurotransmitter release, repolarisation, cell division etc.

➔ SBML core is about process descriptions

SBML supporting tools

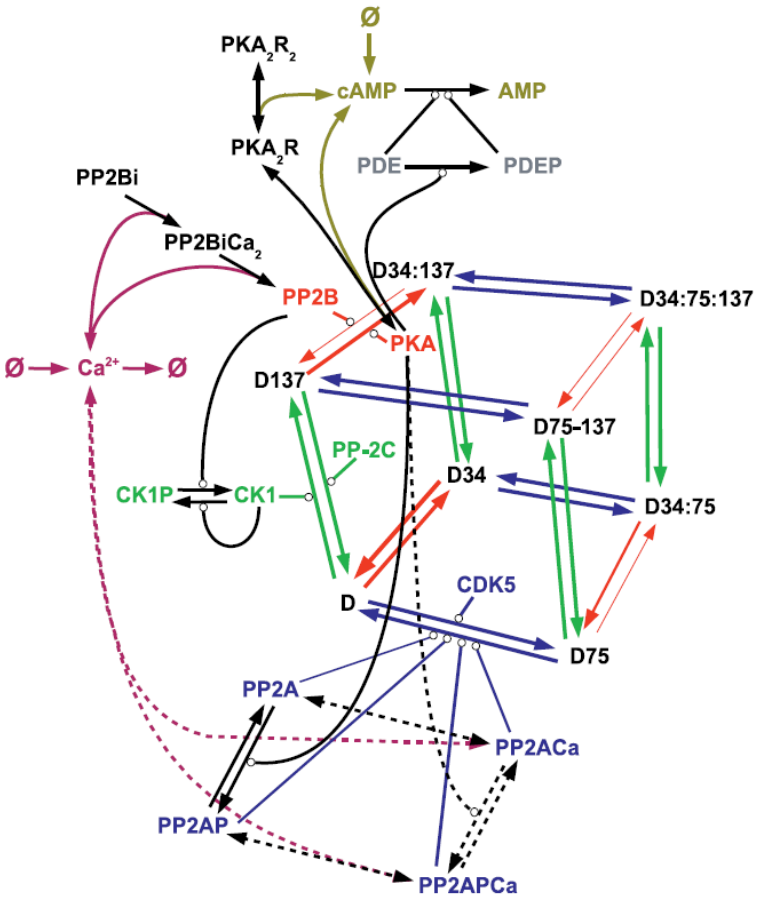
- Simulators
  - Discrete stochastic (25)
  - Continuous deterministic (42)
  - Spatial (4)
- Modelling and simulation environments (29)
  - Based on Mathematica (3)
  - Based on Matlab (12)
  - Based on Python/SciPy (9)
  - Based on R (3)
- Flux/metabolic analysis (16)
- Integrated framework (3)
- Libraries (3)
- Model Management, Data Integration, and Analysis (12)
- Model development tools (18)
- Model visualisation (7)
- Model Repositories, Test Suites, and Databases (16)
- Converters (7)
- Analysis and utility (12)

Process based biochemical models



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

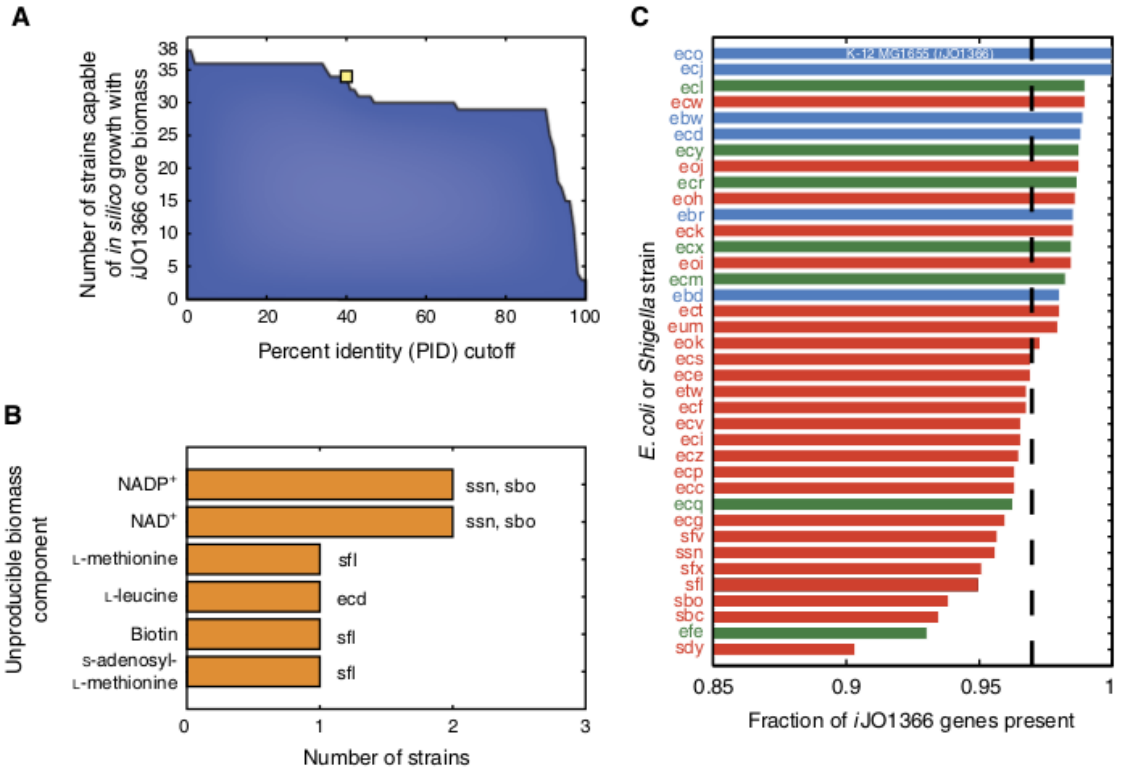
BioModels **BIOMD0000000153**



reaction:

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

Flux Balance Analysis models

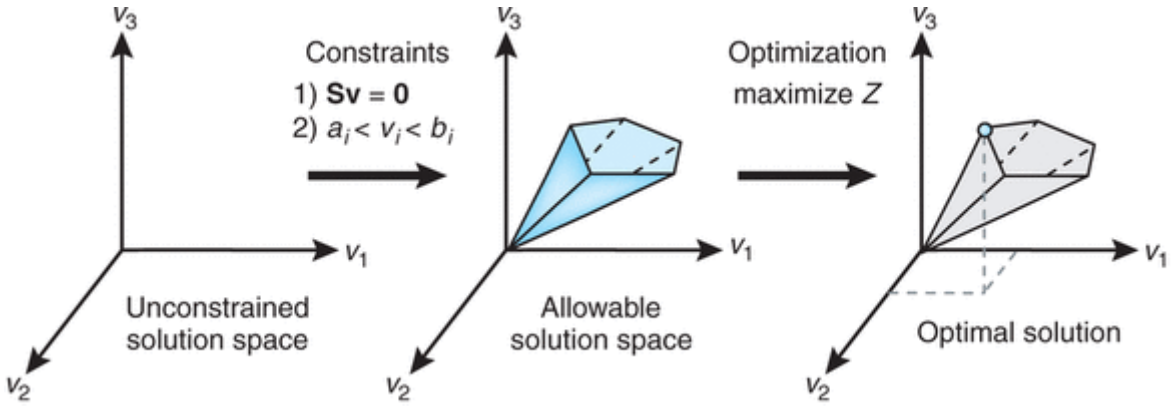


Orth et al. A comprehensive genome-scale reconstruction of Escherichia coli metabolism - 2011
Mol Syst Biol (2011);7:535

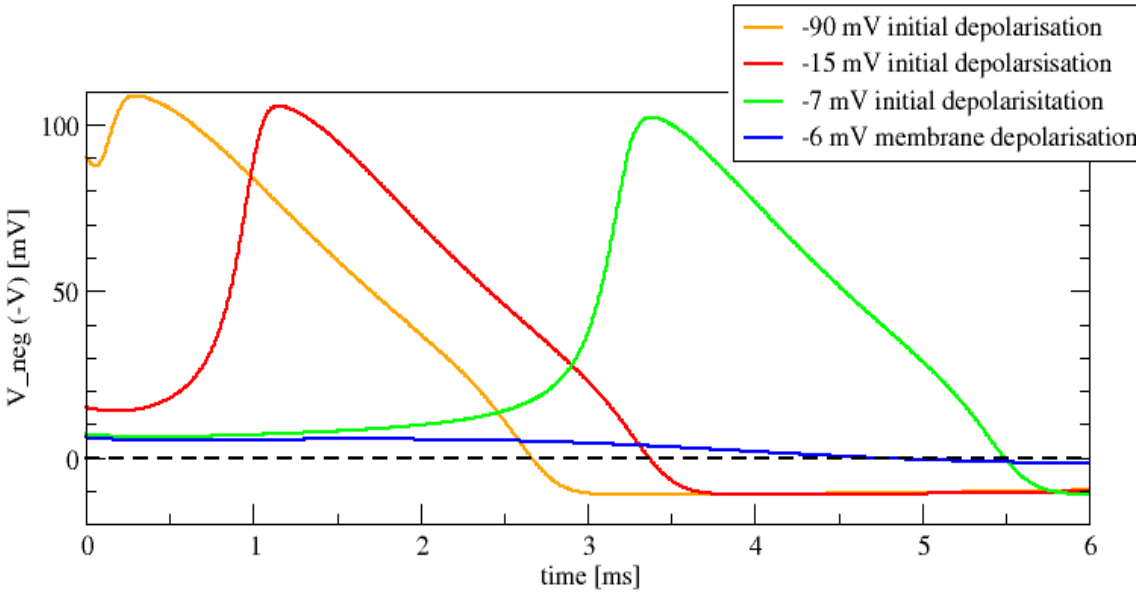
BioModels **MODEL1108160000**

reaction:

$$v_i = flux_i$$



Conductance-based model



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

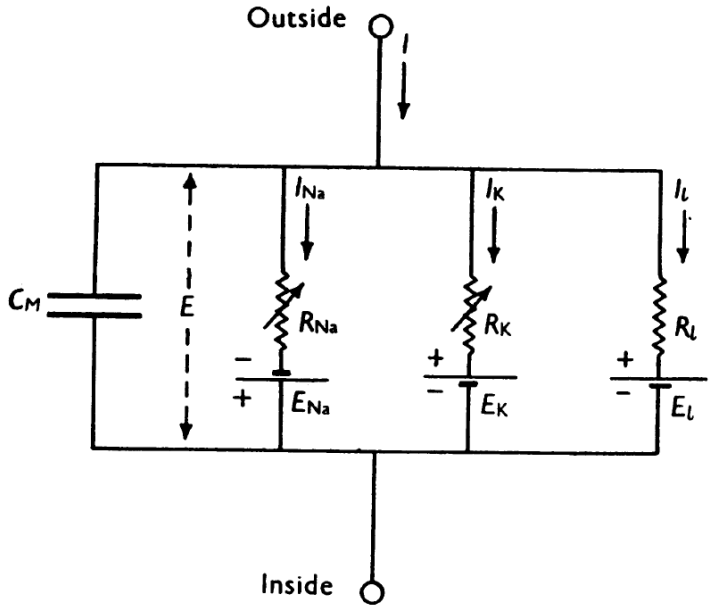
BIOMD0000000020

rate rule:

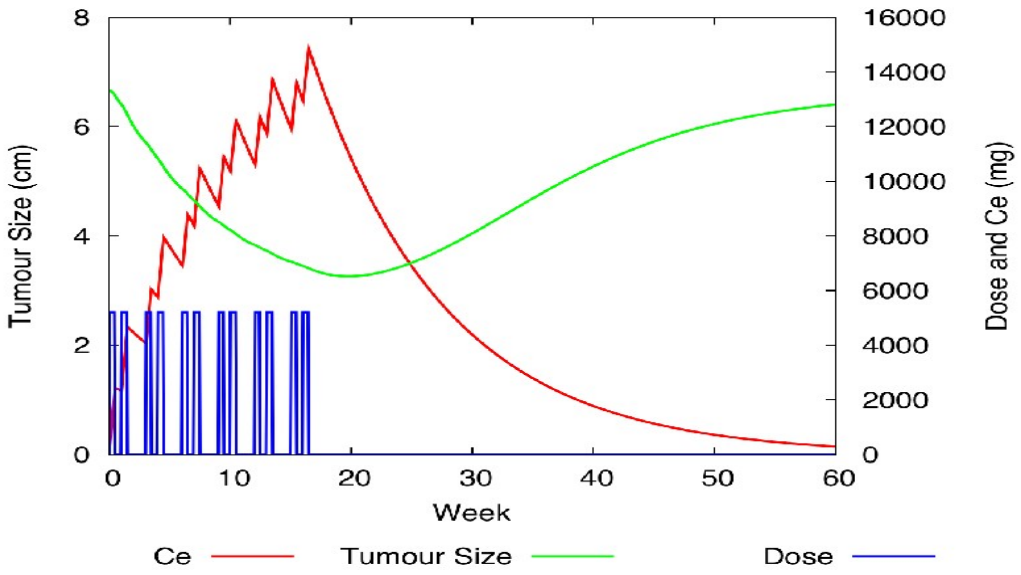
$$\frac{dv}{dt} = \frac{I - (i_{Na} + i_K + i_L)}{C_m}$$

assignment rule:

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



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

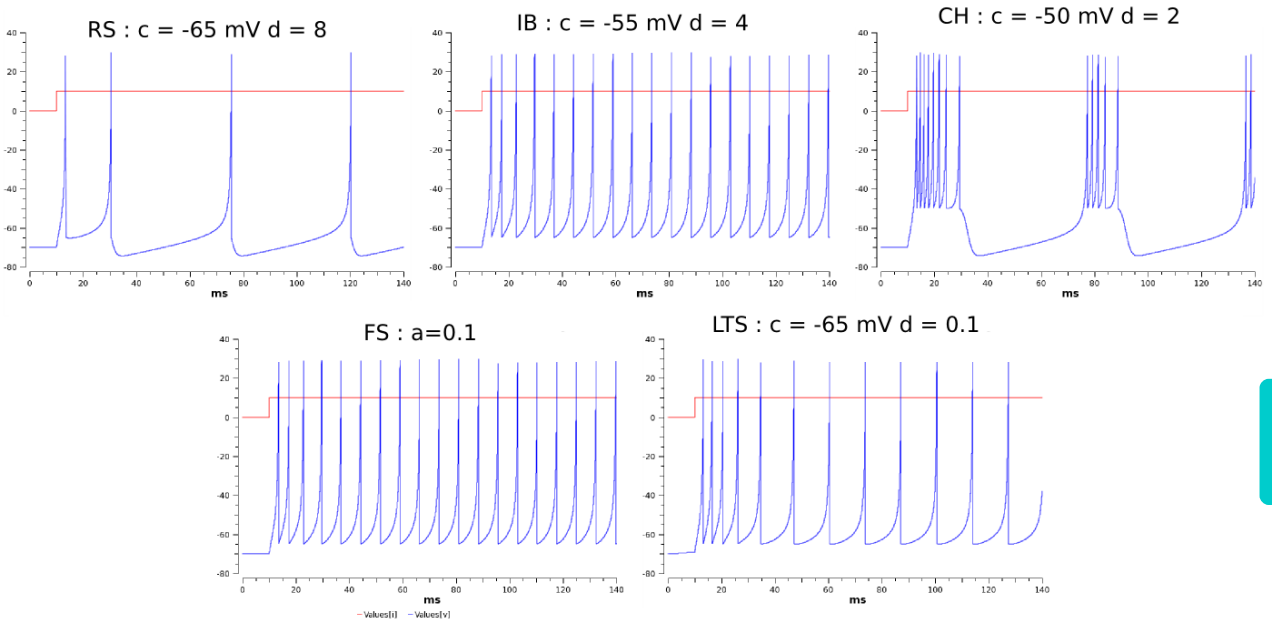
rate rule:

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

assignment rule:

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

Single-compartment neurons



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

BIOMD0000000127

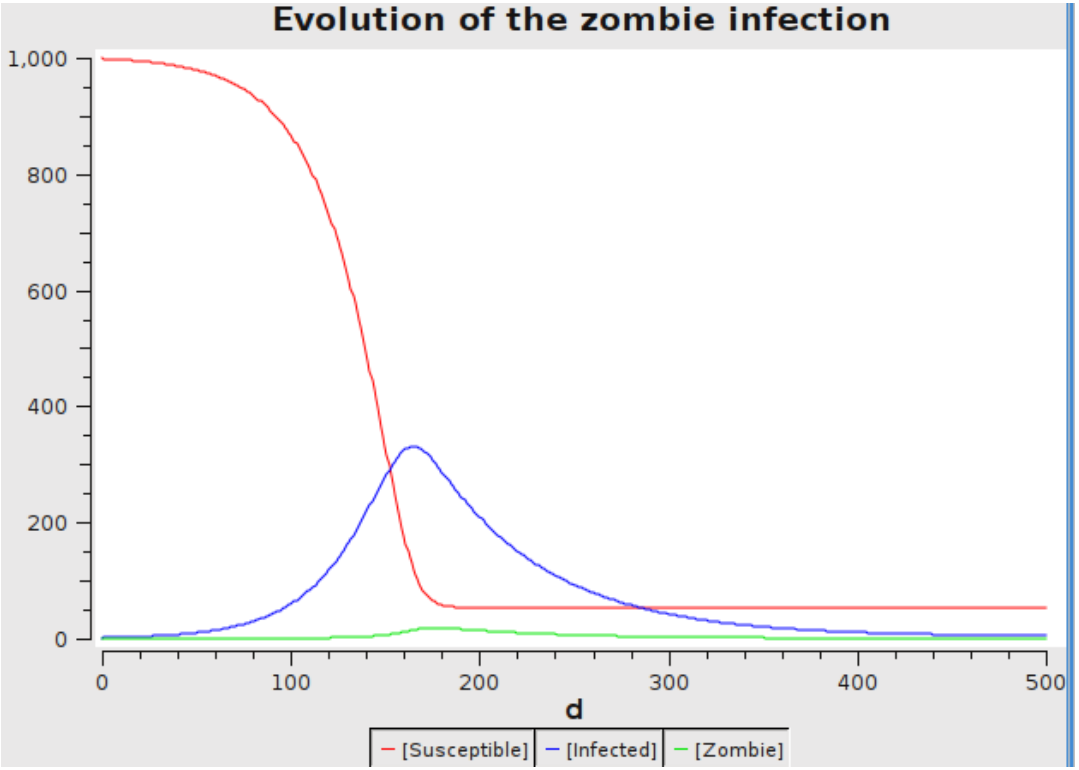
rate rule:

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

event:

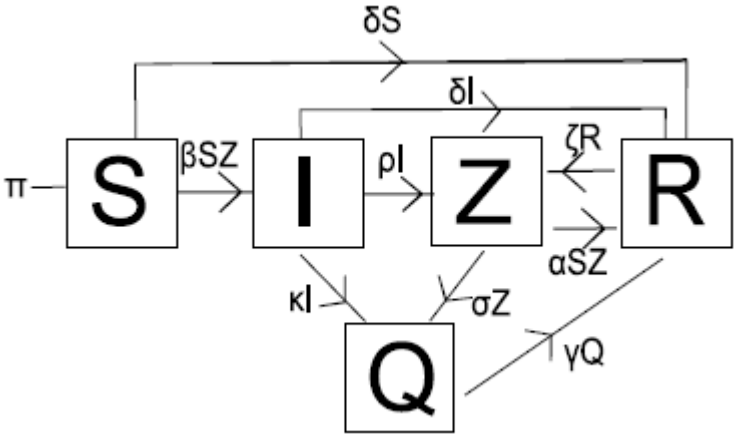
$$\text{when } v > V_{thresh} \begin{cases} v = c \\ U = U + d \end{cases}$$

Spread of infection diseases ...

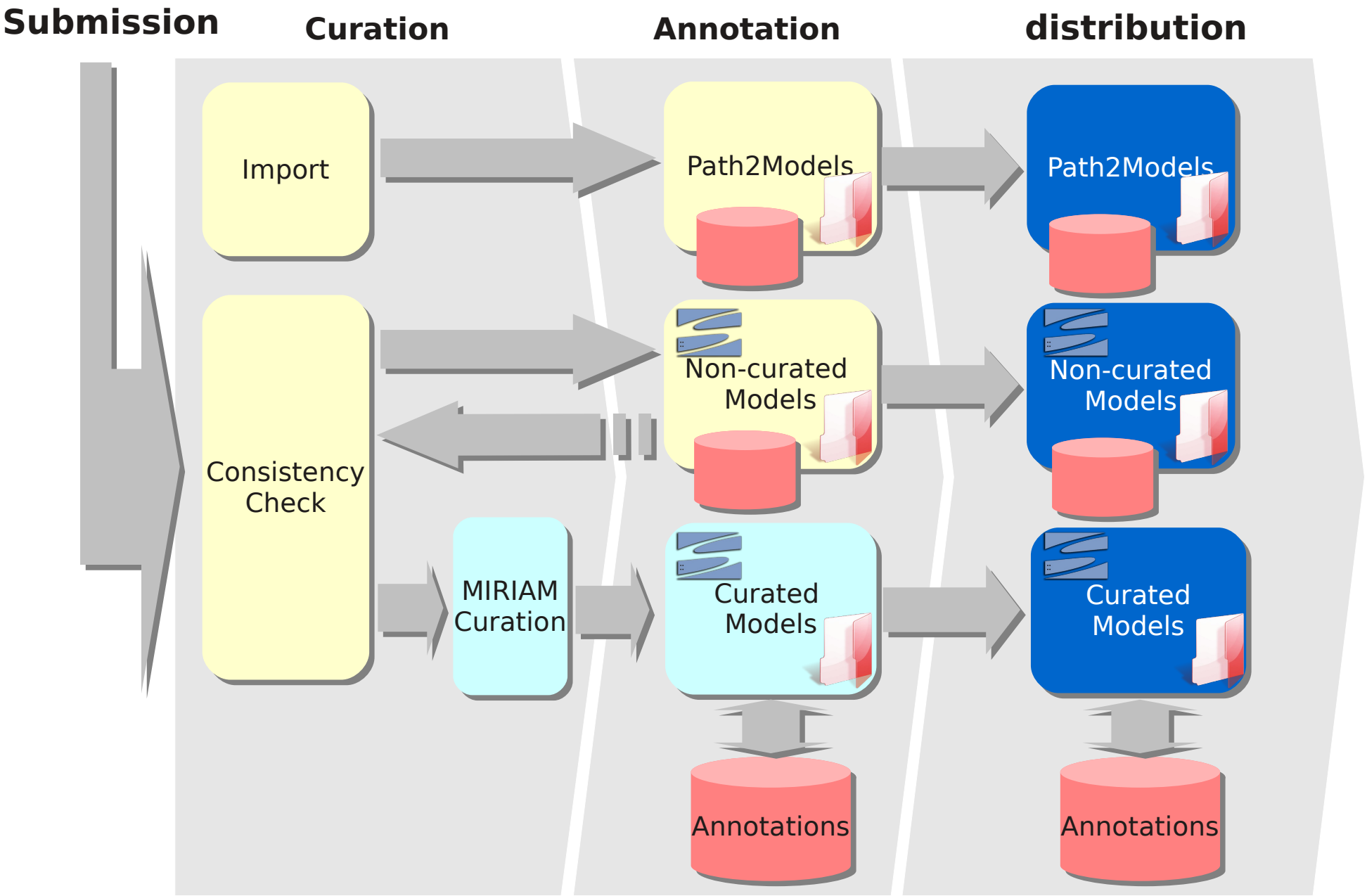


Munz P et al. When zombies attack!: Mathematical modelling of an outbreak of zombie infection. in "Infectious Disease Modelling Research Progress", (2009)133-150

MODEL1008060001



Current production pipeline



BioModels Db does not belong to anyone!

CC0 1.0 Universal (CC0 1.0)
Public Domain Dedication

This is a human-readable summary of the **Legal Code (read the full text)**.

Disclaimer

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Minimum Information Required in the Annotation of Models (simplified)

Models must :

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

Curated and Non-curated Models

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

    cannot reproduce results published in the paper.

    differ in model structure

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

    models contain kinetics that we cannot curate at present (e.g. reaction-diffusion models)

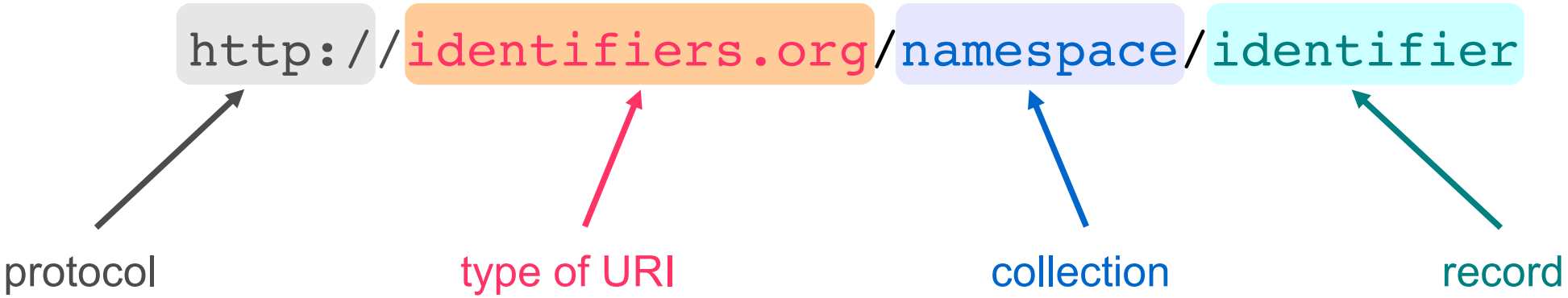
    models are yet to be curated

Why are annotations important?

Annotation of model components are essential to:

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

Enter identifiers.org (aka new MIRIAM URIs)



http://identifiers.org/uniprot/P62158

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

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

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MIRIAM Registry

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The **MIRIAM Registry** provides a set of online services for the generation of unique and perennial identifiers, in the form of URIs.

The *Registry* was initially created to support MIRIAM, a set of guidelines for the annotation and curation of computational models.

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

The *Registry* is developed and maintained under the BioModels.net initiative. All provided services and data is free for use by all.

Quick links

Browse
by data collection name
by tags

Web Services
services available
usage of the services
online demonstration

Search
generic search

Exports
XML

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

Registry

The *MIRIAM Registry* is composed of four components: a database, some Web Services, a Java library and this web application.

Database

The core of the system is a MySQL database. It allows us to store the data collections (which can be controlled vocabularies or databases), their URIs and the corresponding physical URLs, and other details such as documentation and resource identifier patterns.

Each entry contains a diverse set of details about the data collection: official name and synonyms, root URI, pattern of identifiers, documentation, etc. Moreover, each data collection can be associated with several resources (or physical locations).

Web Services

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

4 physical locations (or resources) are available for accessing *1.1.1.1* (from Enzyme Nomenclature):

Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)
Swiss Institute of Bioinformatics

Switzerland

(Uptime: 99%)

ExploreEnz at Trinity College
Trinity College, Dublin

Ireland

(Uptime: 100%)

KEGG Ligand Database for Enzyme Nomenclature
Kyoto University Bioinformatics Center

Japan

(Uptime: 100%)

IntEnZ (Integrated relational Enzyme database)
European Bioinformatics Institute

United Kingdom

(Uptime: 100%)

Powered by MIRIAM Registry

Information also available in: RDF

Search - Models

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

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

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

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

BioModels identifier:

Person:

SBML elements: match the **exact phrase**

Annotation (full text): UniProt

Annotation (full text): Publication — cell cycle

Annotation (full text):

Publication
ChEBI
Gene Ontology
Taxonomy
UniProt

Annotation (identifier):

Annotation (identifier): KEGG Reaction

Annotation (identifier): Enzyme Nomenclature

Compose by: and or

Search Reset

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Search - Models

Query: *Gene Ontology* **cell cycle** [resources]

The search returned **50** models.

New Search

50 Curated models returned:

BioModels ID	Name	Publication ID	Last Modified
BIOMD0000000003	Goldbeter1991_MinMitOscil	1833774	2012-05-15T15:45:17+00:00
BIOMD0000000004	Goldbeter1991_MinMitOscil_ExplInact	1833774	2012-05-15T15:45:30+00:00
BIOMD0000000005	Tyson1991_CellCycle_6var	1831270	2012-06-18T13:11:11+00:00
BIOMD0000000006	Tyson1991_CellCycle_2var	1831270	2012-05-15T15:45:49+00:00
BIOMD0000000007	Novak1997_CellCycle	9256450	2012-05-15T15:46:12+00:00
BIOMD0000000008	Gardner1998_CellCycle_Goldbeter	9826676	2012-07-11T17:07:14+00:00
BIOMD0000000056	Chen2004_CellCycle	15169868	2012-05-15T21:53:24+00:00
BIOMD0000000069	Fuss2006_MitoticActivation	16873466	2012-05-16T10:20:18+00:00
BIOMD0000000087	Proctor2006_telomere	17015293	2012-07-05T14:40:05+00:00

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BIOMD0000000005 - Tyson1991_CellCycle_6var

Download SBML | Other formats (auto-generated) | Actions | Send feedback

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

Reference Publication

Publication ID: 1831270

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

Model

Original Model: *BIOMD0000000005.xml.origin*

Submitter: Nicolas Le Novère

Submission ID: MODEL6614644188

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

Last Modification Date: 18 Jun 2012 13:11:11 UTC

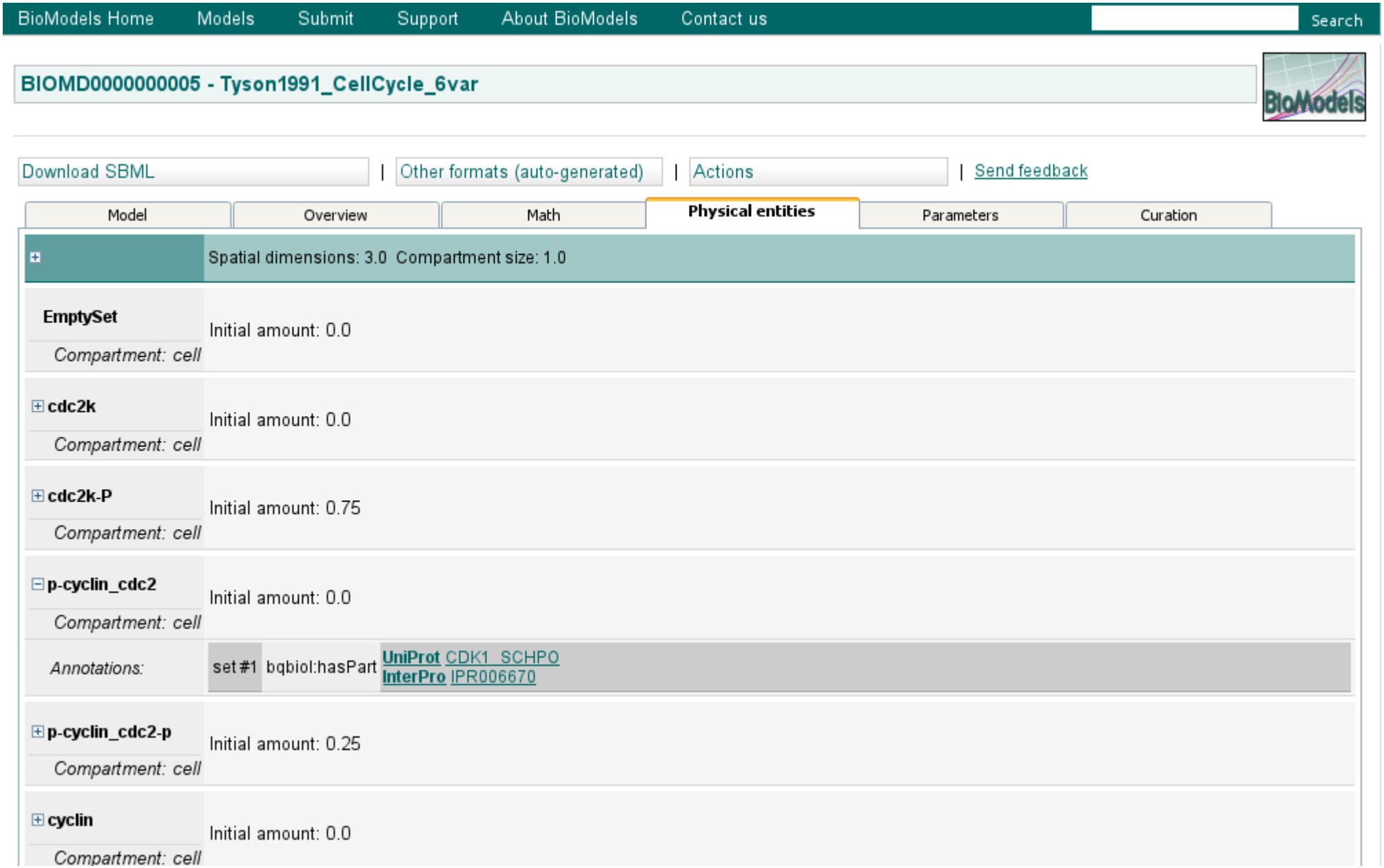
Creation Date: 08 Feb 2005 18:28:27 UTC

Encoders: Bruce Shapiro
Vijayalakshmi Chelliah

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

Notes

This a model from the article: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Spatial dimensions: 3.0 Compartment size: 1.0
EmptySet
Compartment: cell
Initial amount: 0.0
cdc2k
Compartment: cell
Initial amount: 0.0
cdc2k-P
Compartment: cell
Initial amount: 0.75
p-cyclin_cdc2
Compartment: cell
Initial amount: 0.0
Annotations:
set #1
bqbiol:hasPart
UniProt CDK1_SCHPO
InterPro IPR006670
p-cyclin_cdc2-p
Compartment: cell
Initial amount: 0.25
cyclin
Compartment: cell
Initial amount: 0.0

BIOMD0000000005 - Tyson1991_CellCycle_6var

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

Reactions (9)

⊞ **cyclin_cdc2k dissociation**	[p-cyclin_cdc2] → [cdc2k] + [p-cyclin];
⊞ **cdc2k phosphorylation**	[cdc2k] → [cdc2k-P];
⊞ **cdc2k dephosphorylation**	[cdc2k-P] → [cdc2k];
⊞ **cyclin cdc2k-p association**	[cdc2k-P] + [cyclin] → [p-cyclin_cdc2-p];
⊟ **deactivation of cdc2 kinase**	[p-cyclin_cdc2] → [p-cyclin_cdc2-p];
Math:	$cell \times k5notP \times M$ *(Details:*)
Annotations:	set #1 bqbiol:isVersionOf **Enzyme Nomenclature** 2.7.10.2 **Gene Ontology** protein phosphorylation **Gene Ontology** negative regulation of cyclin-dependent protein kinase activity
	set #2 bqbiol:hasVersion **Reactome** REACT_3178 **Reactome** REACT_6327
⊞ **cyclin biosynthesis**	[EmptySet] → [cyclin];
⊞ **default degradation of cyclin**	[cyclin] → [EmptySet];
⊞ **cdc2 kinase triggered degration of cyclin**	[p-cyclin] → [EmptySet];

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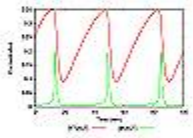
BIOMD0000000005 - Tyson1991_CellCycle_6var

Download SBML | Other formats (auto-generated) | Actions | Send feedback

Overview | Math | Physical entities | Parameters | **Curation** | Submodel1

Representative curation result(s)



Curator's comment: (*updated:* 08 Feb 2010 10:29:04 GMT)

The model reproduces figure 3A of the reference publication. The model was integrated and simulated using Copasi v4.5 (Build 30).

Additional file(s)

- **Simulation experiment description:**
  This SED-ML file allows you to reproduce the curation result (Fig 3a), for example, by loading it into SED-ML Web Tools (http://sysbioapps.dyndns.org/SED-ML_Web_Tools/).
  [BIOMD0000000005_SED-ML.xml]

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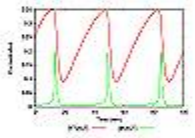
BIOMD0000000005 - Tyson1991_CellCycle_6var

Download SBML | Other formats (auto-generated) | Actions | Send feedback

Overview | Math | Physical entities | Parameters | **Curation** | Submodel1

Representative curation result(s)



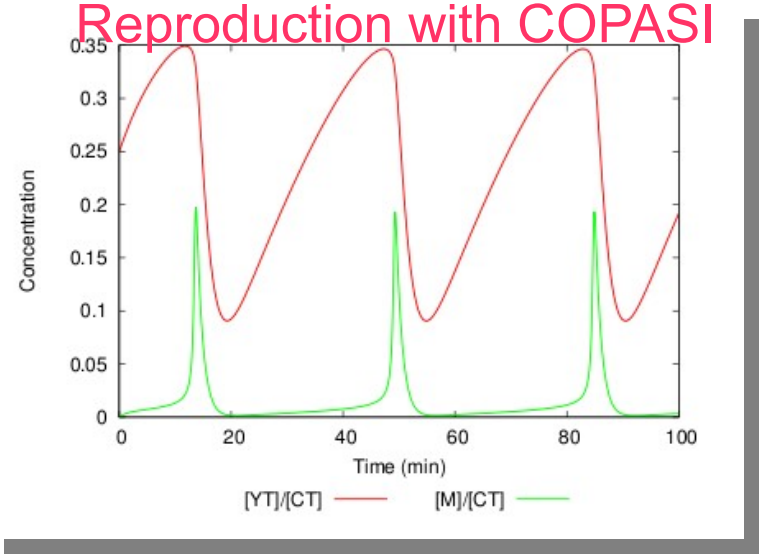
Curator's comment: (*updated:* 08 Feb 2010 10:29:04 GMT)

The model reproduces figure 3A of the reference publication. The model was integrated and simulated using Copasi v4.5 (Build 30).

Additional file(s)

- **Simulation experiment description:**
  This SED-ML file allows you to reproduce the curation result (Fig 3a), for example by loading it into SED-ML Web Tools (http://sysbioapps.dyndns.org/SED-M
  [BIOMD0000000005_SED-ML.xml]

Reproduction with COPASI



original article

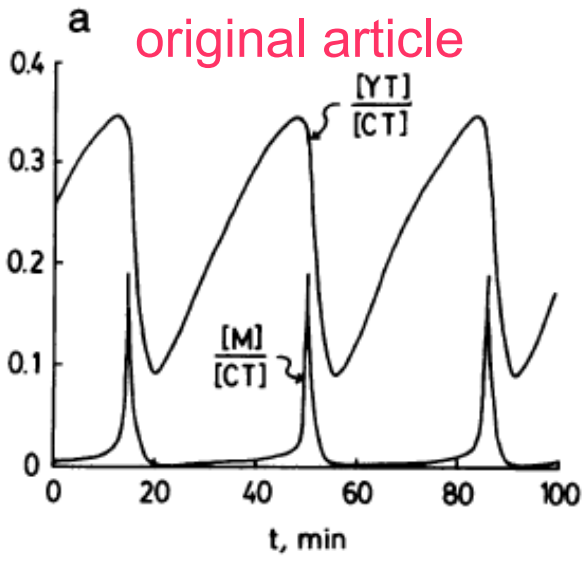


FIG. 3. Dynamical behavior of the cdc2–cycli
relative to total cdc2 ([CT] = [C2] + [CP] + [pM]

BIOMD0000000005 - Tyson1991_CellCycle_6var

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

Create a submodel with selected elements | Deselect All

Model

Publication ID: 1831270 **Submission Date:** 13 Sep 2005 12:31:08 UTC **Last Modification Date:** 18 Jun 2012 13:11:11 UTC **Creation Date:** 08 Feb 2005 18:28:27 UTC

Mathematical expressions

Reactions

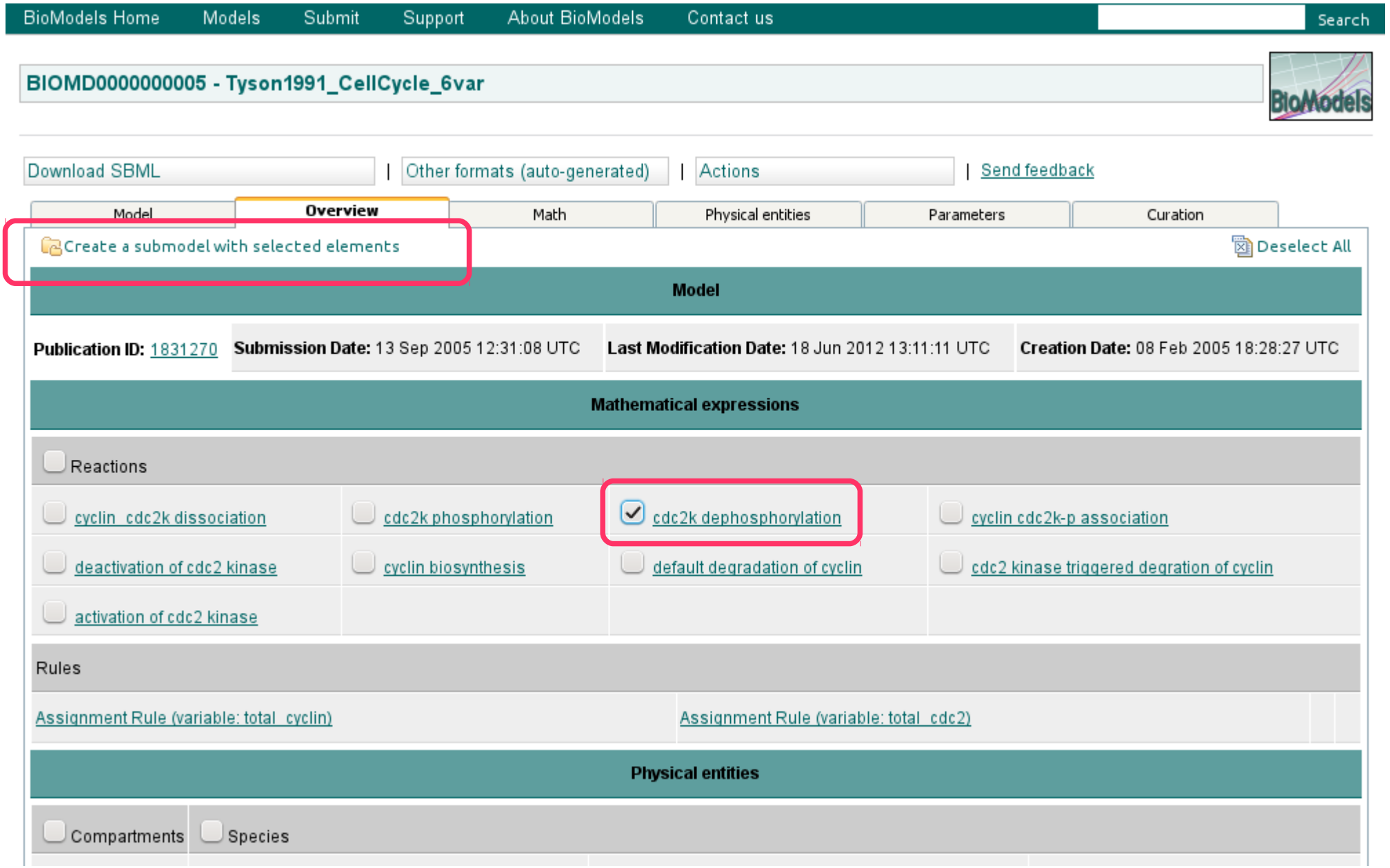
cyclin_cdc2k dissociation	cdc2k phosphorylation	cdc2k dephosphorylation	cyclin cdc2k-p association
deactivation of cdc2 kinase	cyclin biosynthesis	default degradation of cyclin	cdc2 kinase triggered degration of cyclin
activation of cdc2 kinase			

Rules

Assignment Rule (variable: total_cyclin)	Assignment Rule (variable: total_cdc2)

Physical entities

Compartments | Species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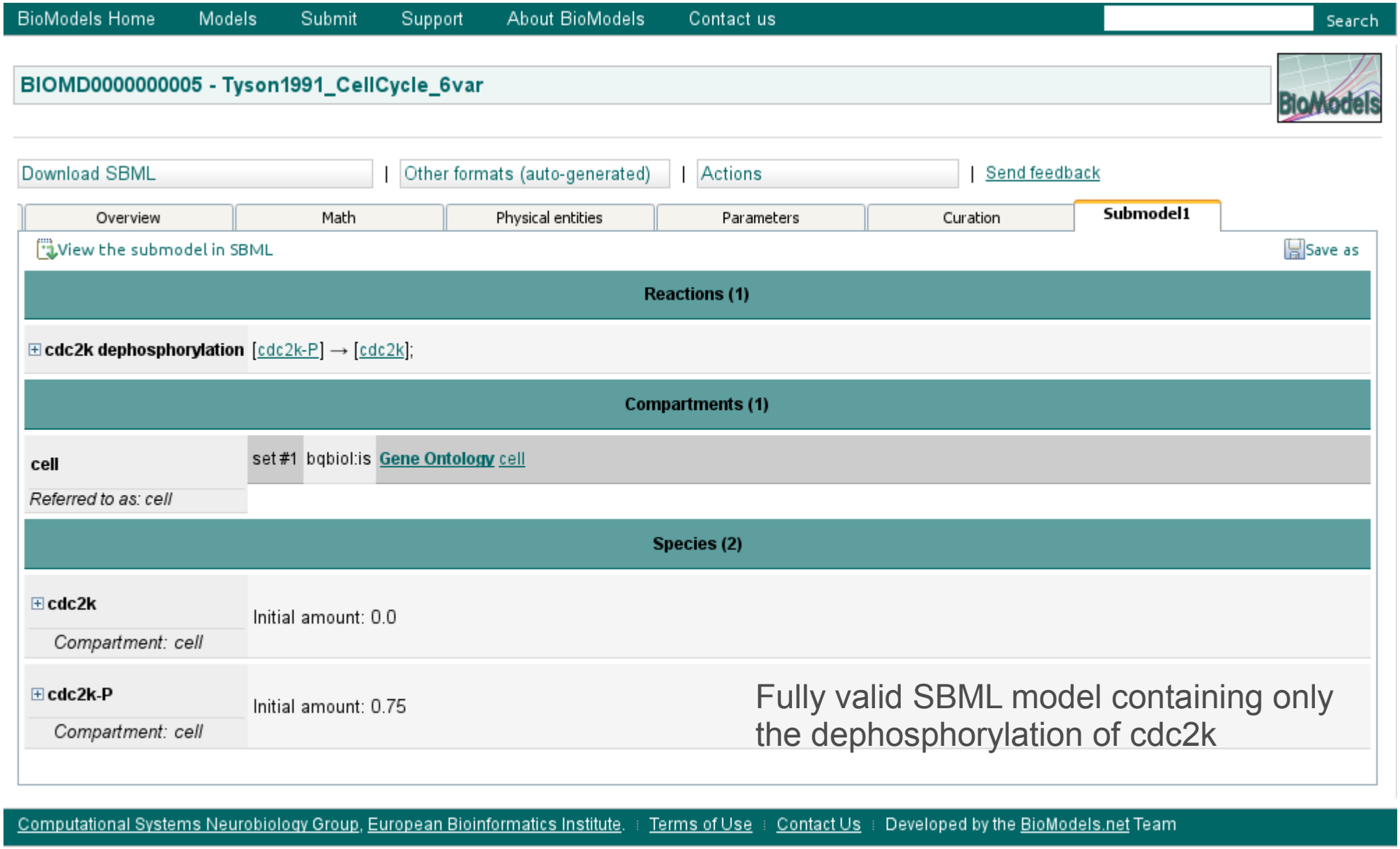
Deselect All
Model
Publication ID: 1831270
Submission Date: 13 Sep 2005 12:31:08 UTC
Last Modification Date: 18 Jun 2012 13:11:11 UTC
Creation Date: 08 Feb 2005 18:28:27 UTC
Mathematical expressions
Reactions
cyclin_cdc2k dissociation
cdc2k phosphorylation
cdc2k dephosphorylation
cyclin cdc2k-p association
deactivation of cdc2 kinase
cyclin biosynthesis
default degradation of cyclin
cdc2 kinase triggered degration of cyclin
activation of cdc2 kinase
Rules
Assignment Rule (variable: total_cyclin)
Assignment Rule (variable: total_cdc2)
Physical entities
Compartments
Species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View the submodel in SBML
Save as
Reactions (1)
cdc2k dephosphorylation [cdc2k-P] → [cdc2k];
Compartments (1)
cell
set #1 bqbiol:is Gene Ontology cell
Referred to as: cell
Species (2)
cdc2k
Compartment: cell
Initial amount: 0.0
cdc2k-P
Compartment: cell
Initial amount: 0.75
Fully valid SBML model containing only the dephosphorylation of cdc2k
Computational Systems Neurobiology Group, European Bioinformatics Institute.
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Developed by the BioModels.net Team

BIOMD0000000005 - Tyson1991_CellCycle_6var

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SBML L2 V1 (auto-generated)
SBML L2 V2 (auto-generated)
SBML L2 V3 (auto-generated)
SBML L2 V4 (curated)

Automatically generated using libsbml (http://sbml.org/Software/libSBML)

Curated version of the model

ameters | Curation

Reference Publication

Publication ID: 1831270

Proc Natl Acad Sci U S A 1991 Aug;88(16):7328-32.
Modeling the cell division cycle: cdc2 and cyclin interactions.
tate University, Blacksburg 24061. [more]

Original Model: *BIOMD0000000005.xml.origin*

Submitter: Nicolas Le Novère

Submission ID: MODEL6614644188

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

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

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

Encoders: Bruce Shapiro
Vijayalakshmi Chelliah

	bqbiol:hasVersion	Reactome REACT_102
set #1	bqbiol:isVersionOf	KEGG Pathway sce04111 Gene Ontology mitotic cell cycle
	bqbiol:occursIn	Taxonomy Fungi/Metazoa group

Notes

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

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BIOMD0000000005 - Tyson1991_CellCycle_6var

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- BioPAX (Level 3)
- Octave
- PDF
- SciLab
- VCML (VCell)
- XPP

Model | ath | Physica

Reference Publica

Publication ID: 1831270

Sci U S A 1991 Aug;88(16):7
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ted resource for published quantitative kinetic models. BMC Syst Biol., 4:92.

e C

net

SBML Model Report

Model name: "Tyson1991_CellCycle_6var"

SBML2LaTeX

9th February 2009

1 General Overview

This is a document in SBML Level 2 Version 3 format. This model was created by the following two authors: Bruce Shapiro[1] and Vijayalakshmi Chelliah[2] at February eighth 2005 at 6:28 p.m. and last modified at August 21st 2008 at 11:31 a.m. Table 1 gives an overview of the quantities of all components of this model.

Table 1: The SBML components in this model.
All components are described in more detail in the following sections.

Element	Quantity	Element	Quantity
compartment types	0	compartments	1
species types	0	species	9
events	0	constraints	0
reactions	9	function definitions	0
global parameters	0	unit definitions	5
rules	2	initial assignments	0

Model Notes

Cell Cycle Model; Tyson (1991, 6 variables)

Description

[1]NASA Jet Propulsion Laboratory, bshapiro@jpl.nasa.gov
[2]EMBL-EBI, vijik@ebi.ac.uk

Produced by SBML2LaTeX 1

BioPAX versions of the model generated from SBML+MIRIAM

```
<?xml version="1.0" encoding="UTF-8"?>
<rdf:RDF xmlns:bp="http://www.biopax.org/release/biopax-level2.owl#"
xmlns:xsd="http://www.w3.org/2001/XMLSchema#"
xmlns:owl="http://www.w3.org/2002/07/owl#"
xmlns:base="http://www.ebi.ac.uk/biomodels/biopax.owl#"
xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#">
<owl:Ontology rdf:about="">
 <owl:imports rdf:resource="http://www.biopax.org/release/biopax-
level2.owl#"/>
</owl:Ontology>

<bp:physicalEntity rdf:about="EmptySet">
 <bp:NAME rdf:datatype="xsd:string">EmptySet</bp:NAME>
</bp:physicalEntity>

<bp:physicalEntityParticipant rdf:about="RIGHT_conversion_Reaction1_C2">
 <bp:PHYSICAL-ENTITY rdf:resource="C2"/>
 <bp:CELLULAR-LOCATION rdf:resource="cell"/>
 <bp:STOICHIOMETRIC-COEFFICIENT
rdf:datatype="xsd:double">1.0</bp:STOICHIOMETRIC-COEFFICIENT>
</bp:physicalEntityParticipant>

<bp:physicalEntityParticipant rdf:about="LEFT_conversion_Reaction4_CP">
 <bp:PHYSICAL-ENTITY rdf:resource="CP"/>
 <bp:CELLULAR-LOCATION rdf:resource="cell"/>
 <bp:STOICHIOMETRIC-COEFFICIENT
rdf:datatype="xsd:double">1.0</bp:STOICHIOMETRIC-COEFFICIENT>
</bp:physicalEntityParticipant>

<bp:physicalEntityParticipant rdf:about="LEFT_conversion_Reaction1_M">
 <bp:PHYSICAL-ENTITY rdf:resource="M"/>
 <bp:CELLULAR-LOCATION rdf:resource="cell"/>
 <bp:STOICHIOMETRIC-COEFFICIENT
rdf:datatype="xsd:double">1.0</bp:STOICHIOMETRIC-COEFFICIENT>
</bp:physicalEntityParticipant>
```

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BIOMD0000000005 - Tyson1991_CellCycle_6var

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- View Bitmap Reaction Graph
- View SVG Reaction Graph
- View Dynamic Reaction Graph
- View Model of Month
- JWS Online Simulation
- BioModels Online Simulation

Model | Overview | Math | Parameters | Curation

Publication ID: 1831270

Proc Natl Acad Sci
Modeling the cell di
Tyson JJ.
Department of Biology, Virginia Polytechnic Institute and St

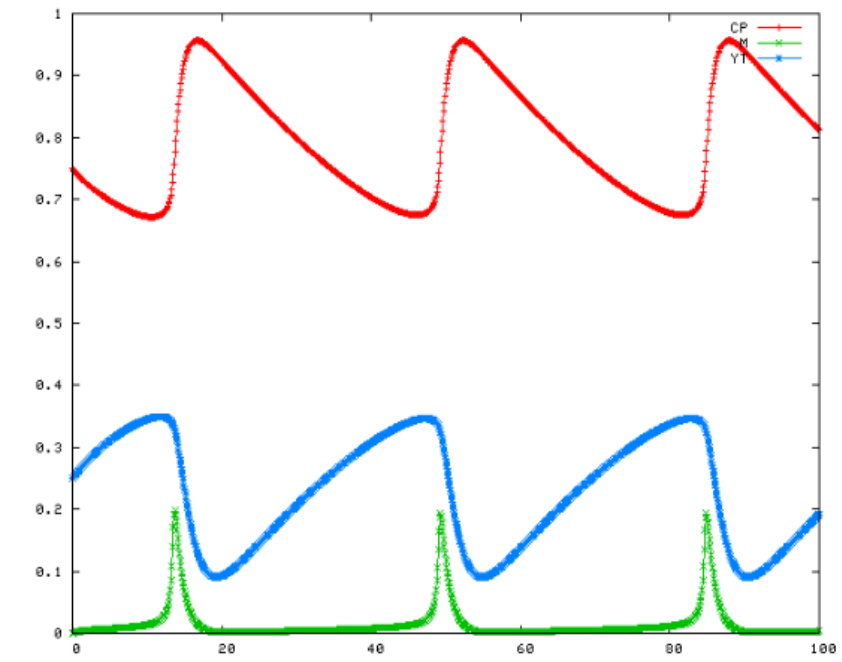
http://www.ebi.ac.uk/biomodels-main/publ-model-tab.do?cmd=MODEL:SIMU:RESULT

The simulation request has been submitted to the queue of our server cluster.

You could save following links and retrieve your simulation result later.

Link of simulation result:

http://www.ebi.ac.uk/biomodels-main/publ-model.do?cmd=SIMU:RETRIEVE&simuid=SIMU1234453623040



Close

http://www.ebi.ac.uk/biomodels/models-main/ode_simu/SIMU1234453623... zotero

Model

Reactome REACT_152

KEGG Pathway sce04111
Gene Ontology mitotic cell cycl

Taxonomy Fungi/Metazoa grou

Notes

at controls the major events of
ntrol system can operate in thre
steady state with metaphase a
division cycles typical of nonem

ished Models (http://www.ebi.ac

H, Endler L, Chelliah V, Li L, He
ublished quantitative kinetic m

http://www.ebi.ac.uk/biomodels-main/publ-model-tab.do?cmd=MODEL:SIMU

Model - Simulation

For doing an online simulation, please select the species below. After specifying the *simulation time* and *print step*, and then click *Submit* to submit simulation job to our research cluster.

Click *Cancel* to close the window.

Cancel

Species

☐ EmptySet	☐ cdc2k	☑ cdc2k-P	☑ p-cyclin_cdc2
☐ p-cyclin_cdc2-p	☐ cyclin	☐ p-cyclin	☑ total_cyclin
☐ total_cdc2			

Simulation Time (use scientific notation e.g. 1e7 for 10000000): 100

Print step: 1000

Submit

Done zotero

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- View SVG Reaction Graph
- View Dynamic Reaction Graph
- View Model of Month
- JWS Online Simulation
- BioModels Online Simulation

Model | Overview | Math

Publication ID: 1831270

Proc Natl Acad Sci
Modeling the cell di
Tyson JJ.
Department of Biology, Virginia Polytechnic Institute

Model

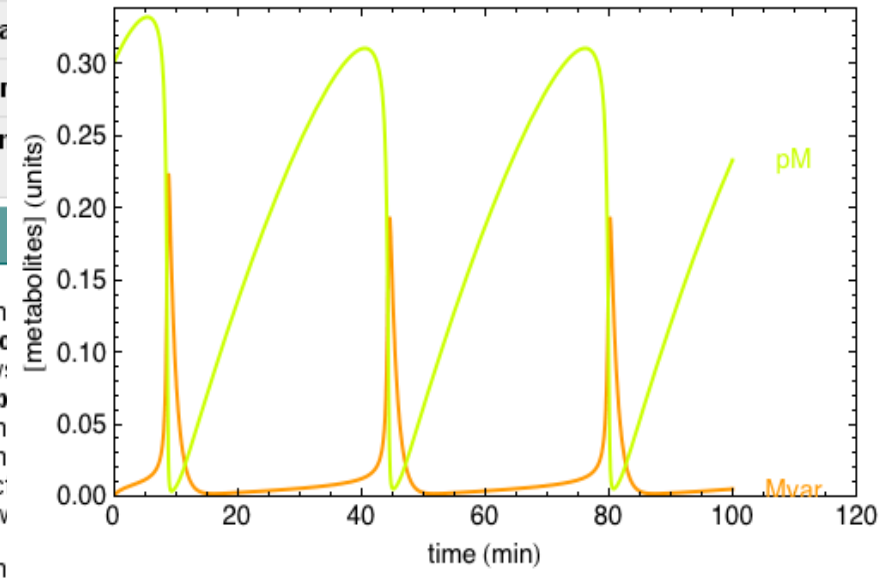
Original Model: *BIOMD0000000005.xml.origin*

Submitter: Nicolas Le Novère

Submission ID: MODEL6614644188

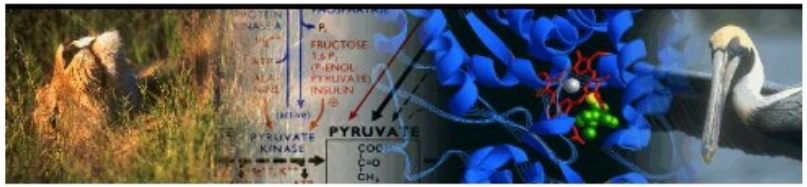
set #1	bqbiol:hasVersion	Reactome REACT_152
	bqbiol:isVersionOf	KEGG Pathway sce0411
		Gene Ontology mitotic ce
	bqbiol:occursIn	Taxonomy Fungi/Metazo

http://jjj.mib.ac.uk/webMathematica/Examples/PlotScript11.jsp?fun="JWS`Tyson199



Download the results in text or comma separated value format (e.g. for Excel import):

http://jjj.mib.ac.uk/biomodels/Tyson1991/index.html



Biomodels Home | Index | JWS Online

Biomodels: BIOMD0000000005

Tyson1991

Powered by JWS Online

JWSApplet – ver 5.0.3 Tyson1991

	Parameter	Value
P1_v1	cell	1
P2_v1	k6	1
P3_v1	k8notP	1.0e6
P4_v1	k9	1000
P5_v1	k3	200
P6_v1	k5notP	0.
P7_v1	k1aa	0.015
P8_v1	k2	0.
P9_v1	k7	0.6
P10_v1	k4	180
P11_v1	k4prime	0.018
E1	EmptySet	0.
I1	C2[0]	0.
I2	CP[0]	1
I3	Mvar[0]	0.
I4	Y[0]	0.
I5	YP[0]	0.
I6	pM[0]	0.3

Evaluate Model

Sim | State

StartTime 0 EndTime 100

Rates Metabolites

Type	Output	Plot
M1	C2	
M2	CP	
M3	Mvar	✔
M4	Y	
M5	YP	
M6	pM	✔
F1	v[Rea...	
F2	v[Rea...	
F3	v[Rea...	
F4	v[Rea...	
F5	v[Rea...	
F6	v[Rea...	
F7	v[Rea...	

POWERED BY webMATHEMATICA2

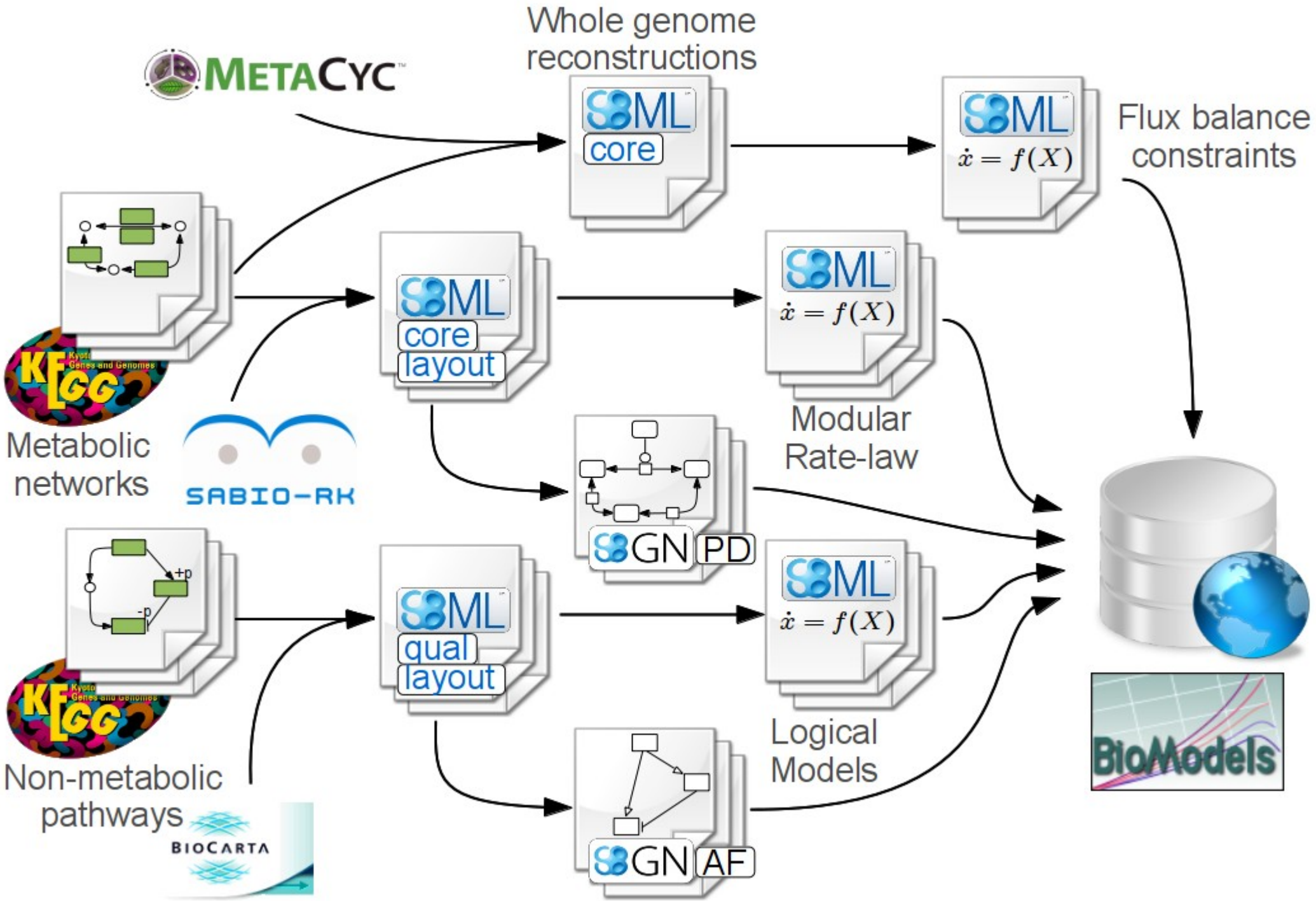
Reset

Applet jjjApplet started

zotero

Chelliah V, L
antitative kinetic models. BMC Syst Biol., 4:92.

Büchel *et al* Large-scale generation of computational models from biochemical pathway maps. Submitted



Path2Models

The path2models project aims at the large scale generation of quantitative models form pathways.

Browse models

Models from this project are classified in 3 distinct categories:

- metabolic models
- non-metabolic models
- whole genome metabolism models

One can also browse those models by organism:

- list of all organisms

Search models

The following search will only look for models coming from the path2models project:

Search

Help about the search

- The keywords *AND* or *OR* (in upper cases) are available to refine the search. By default, if more than one word is present in a query, *OR* will be used to combine them.
- Double quotes (") can be used to force the search engine to match a whole expression containing several words.
- The colon character (:) must be escaped in the queries; one can use a backslash for this purpose (\:).

Download all models

- Archives of all models (from the latest release)

Path2Models:

Here are all the whole genome metabolism models available:

- Acaryochloris marina (strain MBIC 11017)
- Accumulibacter phosphatis (strain UW-1)
- Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)
- Acetobacter pasteurianus IFO 3283-01-42C
- Acetobacter pasteurianus IFO 3283-03
- Acetobacter pasteurianus IFO 3283-07
- Acetobacter pasteurianus IFO 3283-12
- Acetobacter pasteurianus IFO 3283-22
- Acetobacter pasteurianus IFO 3283-26
- Acetobacter pasteurianus IFO 3283-32
- Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)
- Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)
- Acholeplasma laidlawii (strain PG-8A)
- Achromobacter xylosoxidans (strain A8)
- Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4)
- Acidaminococcus intestini (strain RyC-MR95)
- Acidianus hospitalis (strain W1)
- Acidilobus saccharovorans (strain DSM 16705 / VKM B-2471 / 345-15)
- Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)
- Acidiphilium cryptum (strain JF-5)
- Acidiphilium multivorum (strain DSM 11245 / JCM 8867 / AIU301)
- Acidithiobacillus caldus (strain SM-1)
- Acidithiobacillus ferrivorans SS3
- Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / NCIB 8455)

Whole Genome Metabolism - Homo sapiens

Download SBML | Send feedback

Model information

Identifier: BMID000000140905
Format: SBML L2 V4
Project: path2models
Categories: genome-scale
Submission: 19 May 2012 15:48:00 UTC
Last modified: 08 Aug 2012 21:02:14 UTC
Published: 19 May 2012 23:49:21 UTC

Annotations

occursIn	Homo sapiens	*Taxonomy*

Notes

Whole Genome Metabolism of "Homo sapiens"

This is a whole genome metabolism model of Homo sapiens.

This model has been automatically generated by the SuBliMinaL Toolbox using information coming from KEGG and MetaCyc.

This model has been produced by the path2models project and is currently hosted on BioModels Database and identified by: BMID000000140905.

BioModels Web Services

Available features

With BioModels Web Services, users can access the up-to-date resources in BioModels Database without installing a local copy of the database. There are a range of available features for searching and retrieving models. Furthermore, some features can help users to extract interesting parts from a large model and construct them into a submodel. For any comments or new feature enquiries, please feel free to contact us.

- Available features
- javadoc
- WSDL

The WSDL (Web Services Description Language) defines and describes the available features in an XML format file. This enables third-party sofware to automate parsing all available features of BioModels Web Services. Comparing with WSDL, Javadoc is API documentation which provides more information to the developers.

Download

We provide two versions of the library for querying BioModels Database Web Services. These are available for download from the SourceForge project download page (latest release: 1.12):

- light version (you need a couple of external jars to use it)
- standalone version (all the dependencies are already included in the jar)

These are the dependencies only needed by light-weight library.

- axis.jar (version 1.4)
- commons-discovery.jar (version 0.4)
- commons-logging.jar (version 1.1.1)
- jaxrpc.jar
- mail.jar (version 1.4.3)
- saaj.jar
- wsdl4j.jar (version 1.6.2)

Note: you can find the latest version of each of these packages on their official web site.

Java 1.5 (or newer) is required in order to use the library.

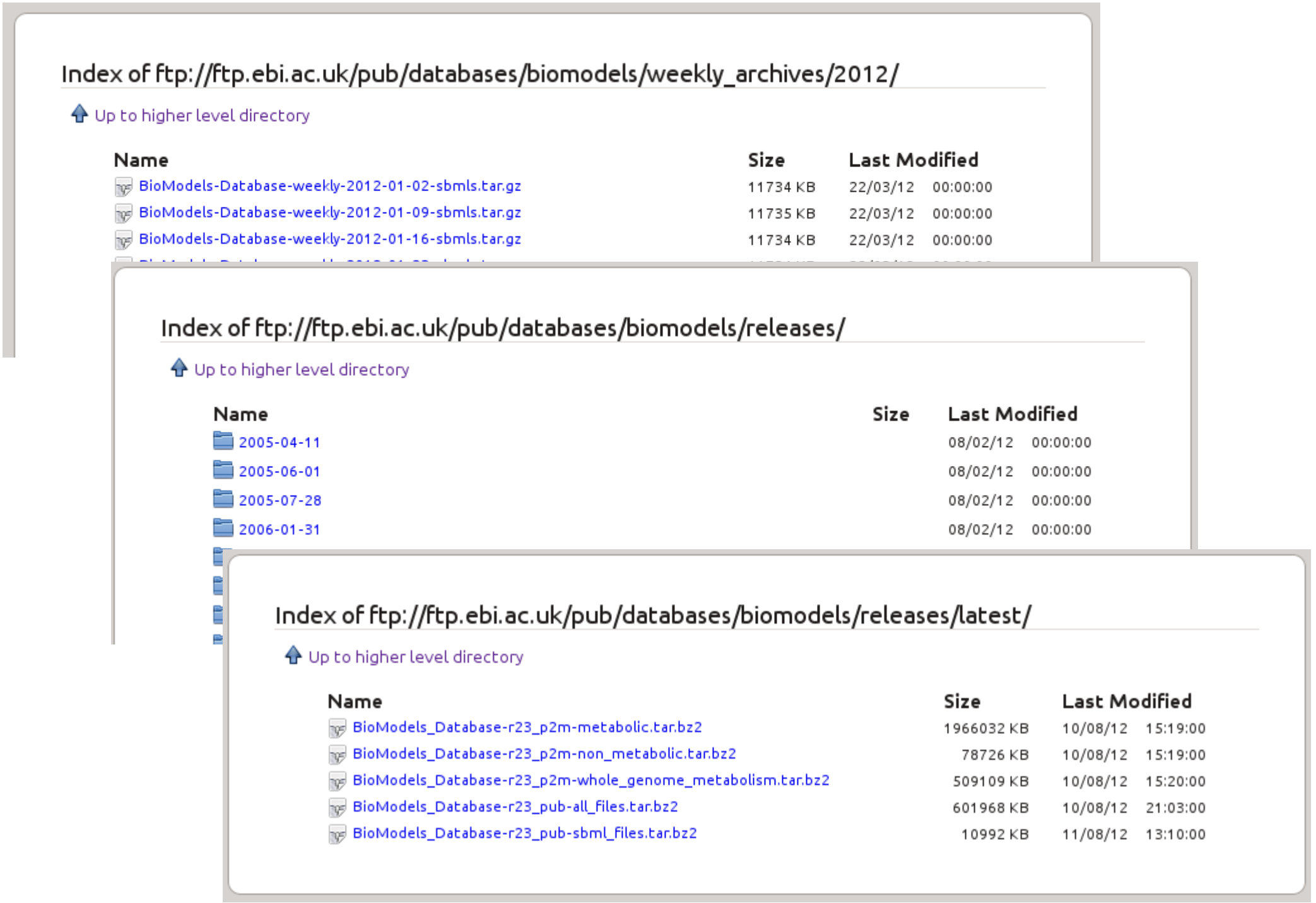
Basics - Getting Started

First, download the library we provide.

Assuming that you downloaded the biomodels-wslib_standalone.jar, let's write a simple HelloBioModels.java to test if it works on your environment.

```
import uk.ac.ebi.biomodels.*;

public class HelloBioModels
{
```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Size
Last Modified
BioModels-Database-weekly-2012-01-02-sbmls.tar.gz
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78726 KB
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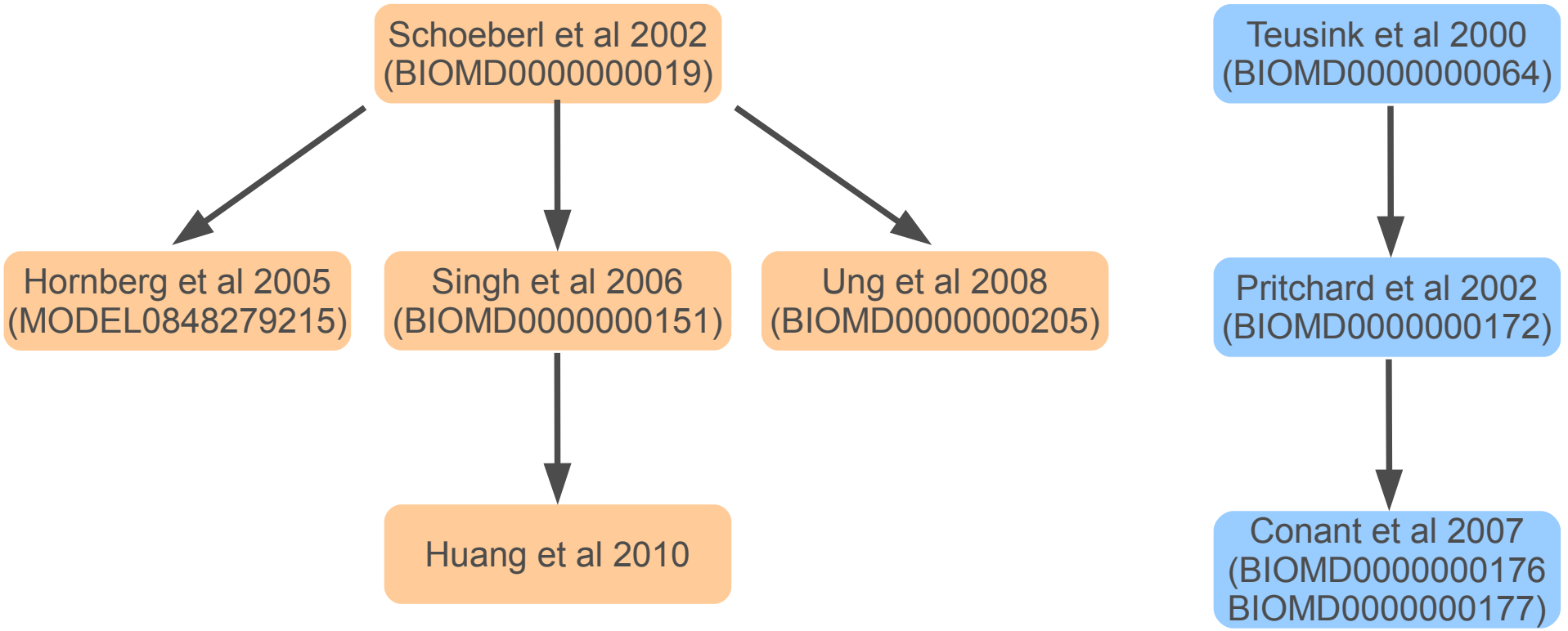
601968 KB
10/08/12 21:03:00
BioModels_Database-r23_pub-sbml_files.tar.bz2
10992 KB
11/08/12 13:10:00

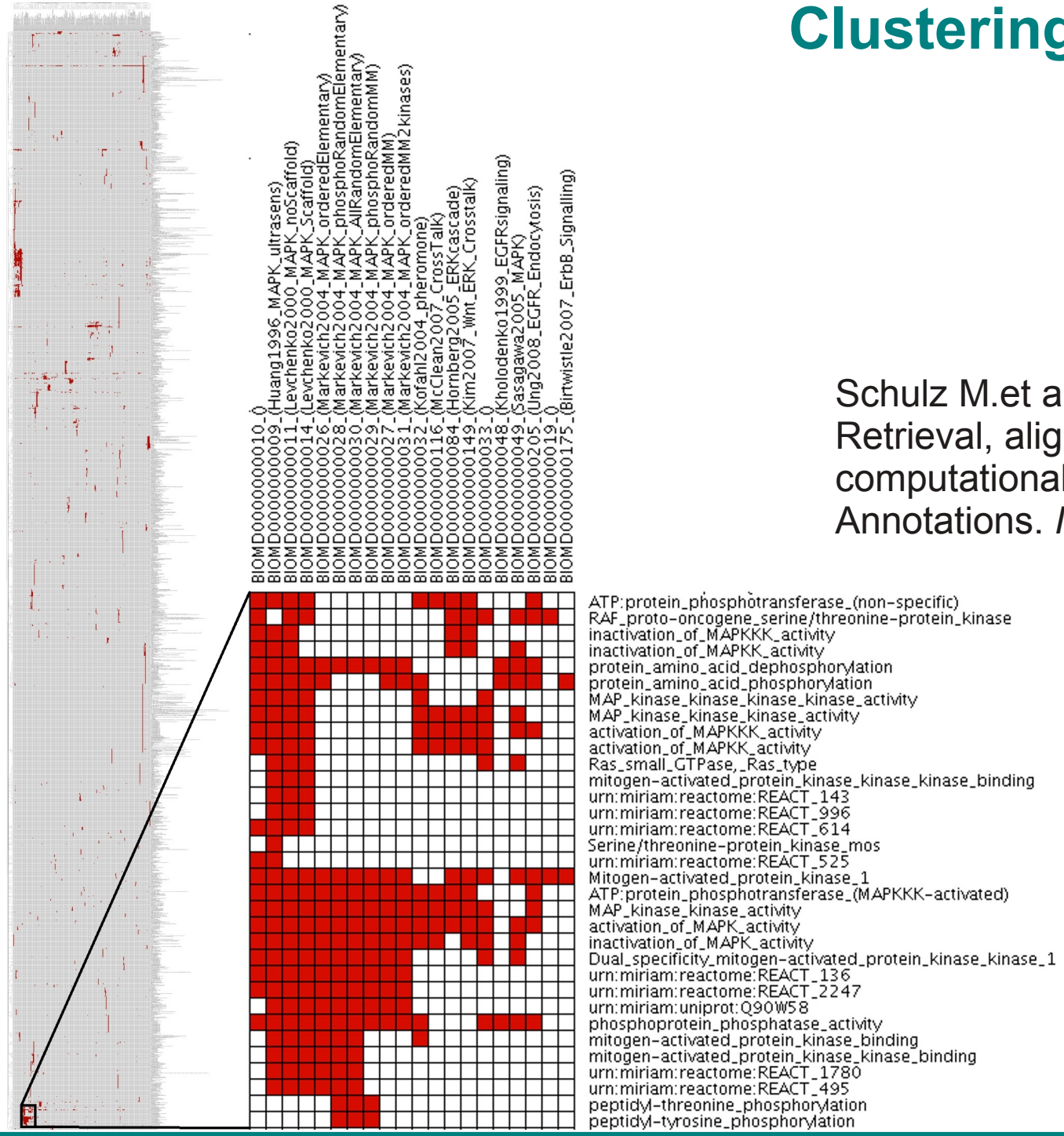
Direct model re-use: e.g. EGFR signalling and glycolysis



Standard formats generate new research

- Herrgård et al (2008) A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnol*, 26: 1155-1160
  - MODEL0072364382: 2152 species, 1857 reactions
    - stoichiometric map, no concentrations, no kinetics
- Smallbone et al (2010) Towards a genome-scale kinetic model of cellular metabolism. *BMC Syst Biol*, 4:6
  - MODEL1001200000: 1748 species, 1059 reactions
    - Concentrations and flux from BioModels Database
    - Constraint-based model and simplified linlog kinetics
- Dobson et al (2010) Further developments towards a genome-scale metabolic model of yeast. *BMC Syst Biol,* 4:145
  - MODEL1012110000: 2657 species, 1865 reactions
- Li et al (2010) Systematic integration of experimental data and models in systems biology. *BMC Bioinfo,* 11: 582
  - MODEL1012110001
    - Workflows using experimental kinetic information database (SABIO-RK) plus metabolomics and proteomics database
    - Full quantitative chemical kinetics descriptions

Clustering models (and data) based on metadata



Schulz M.et al (2010)
Retrieval, alignment, and clustering of computational models based on semantic Annotations. *Mol Syst Bio*, 7: 512

Ranking and retrieval of models

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

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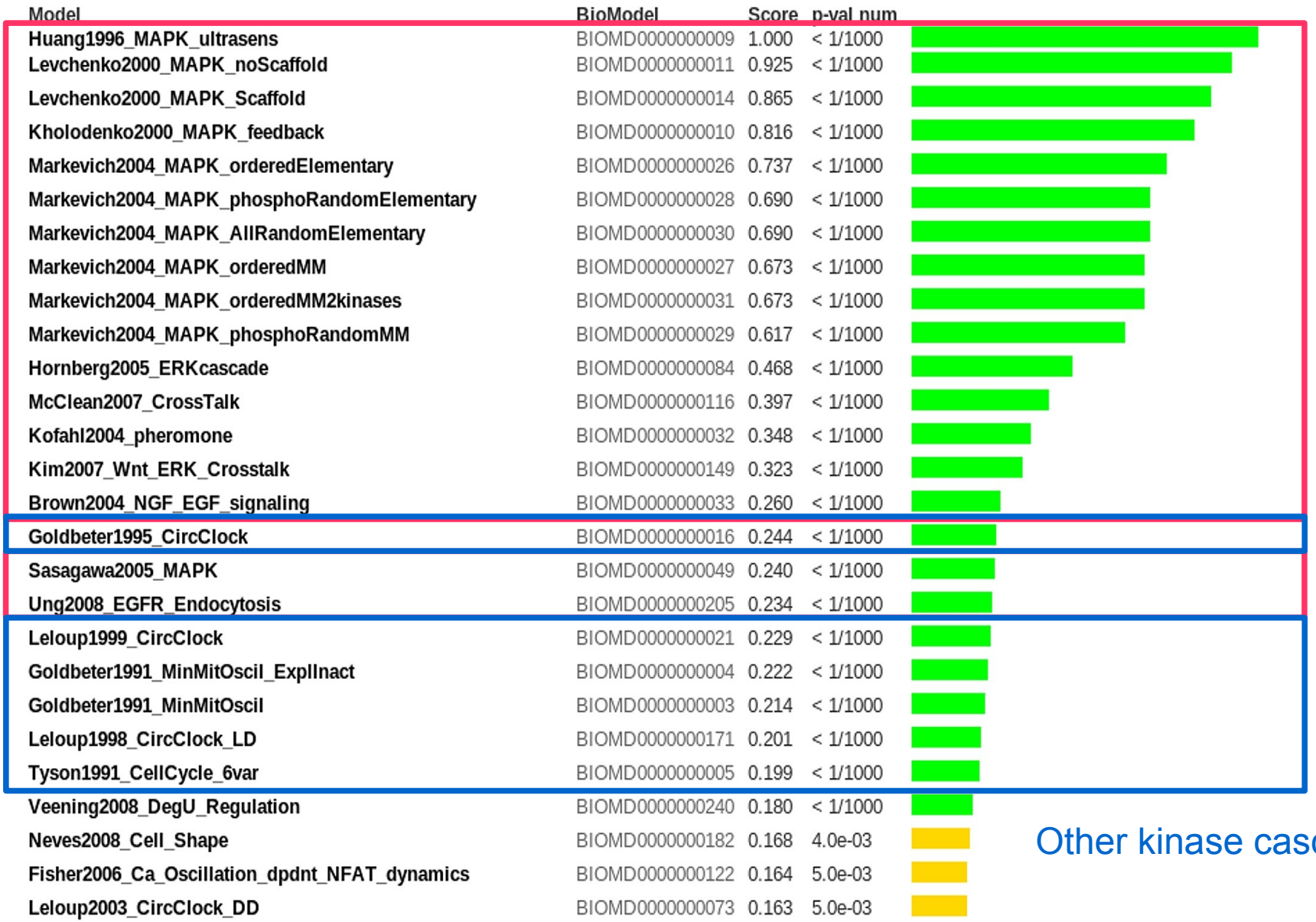
MAPK

Ranking and retrieval of models



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MAPK

Other kinase cascades

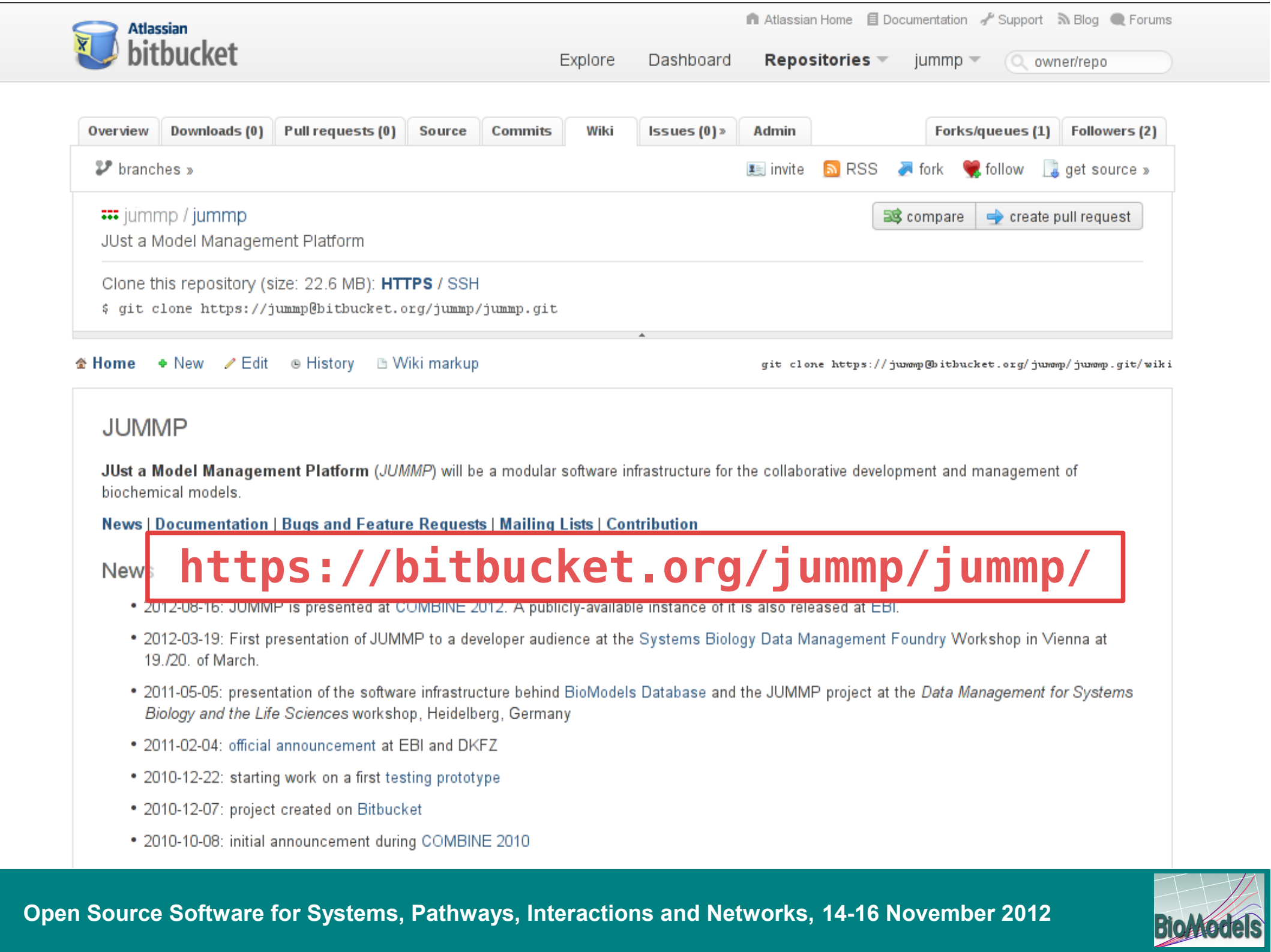
FOSS house made of FOSS bricks

- **BioModels Db** [GPLv2] → http://sourceforge.net/projects/biomodels/
- **LibSBML** [LGPLv2] → http://sourceforge.net/projects/sbml/
- **JSBML** [LGPLv2] → http://sourceforge.net/projects/jsbml/
- **Systems Biology Format Converter** [GPLv2] → http://sourceforge.net/projects/sbfc/
- **Tomcat** [Apache v2] → http://tomcat.apache.org/
- **MySQL** [Oracle FOSS] → http://dev.mysql.com/
- **Subversion** [Apache v2] → http://subversion.apache.org/
- **Lucene** [Apache v2] → http://lucene.apache.org/
- **Axis** [Apache v2] → http://axis.apache.org/
- **SOSlib** [GPLv2] → http://www.tbi.univie.ac.at/~raim/odeSolver/
- **Gnuplot** [own opensource license] → http://www.gnuplot.info/
- + 33 FOSS libraries

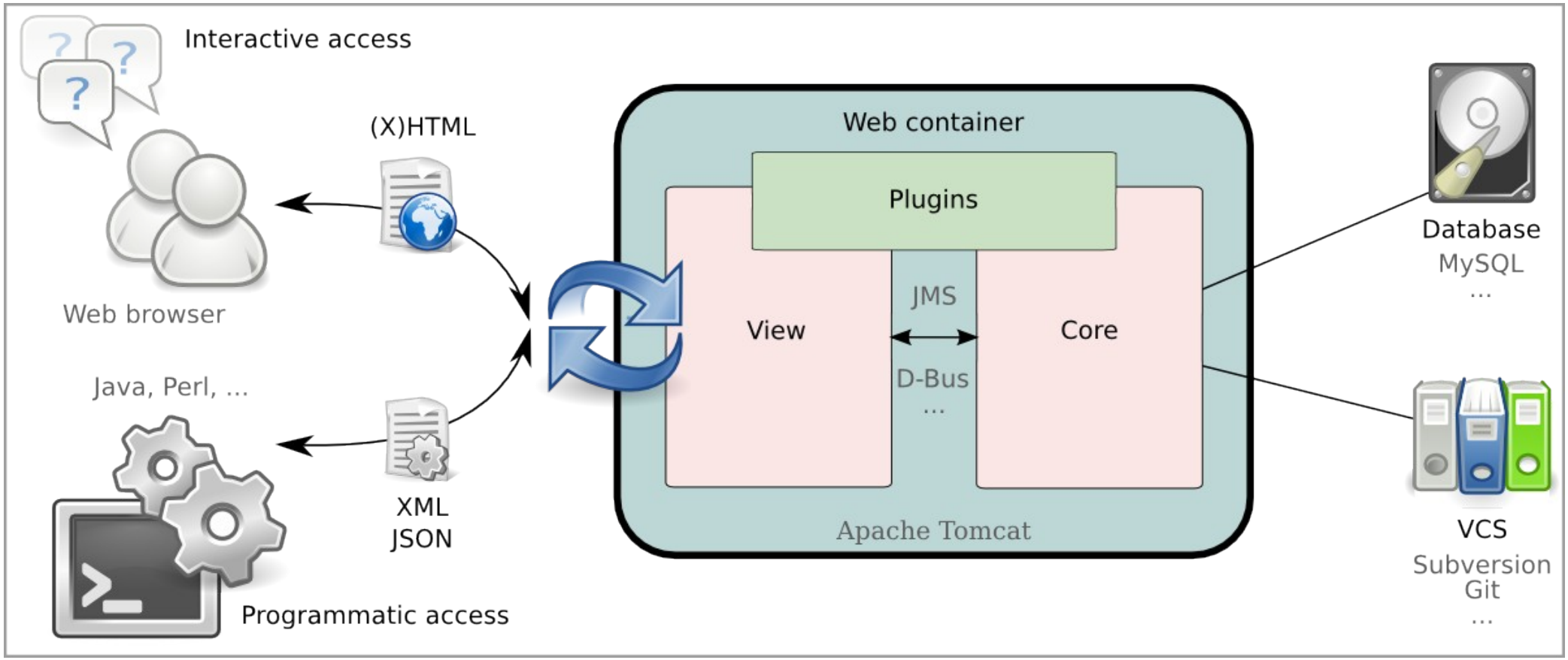
Future directions for BioModels Database

- Improvement of the software infrastructure
  - More portable (mirrors, re-use in other projects)
  - Better authentication, logging and security
  - More flexible: groups of models, or users, more converters, views, services ...
  - Community development model
- Extension of the coverage
  - Different types of models: Neuroscience, PK/PD, physiology ...
  - Parametrisation procedures, simulation descriptions ...
  - Large scale project (e.g. Path2Models)

Just a Model Management Platform (JUMMP)

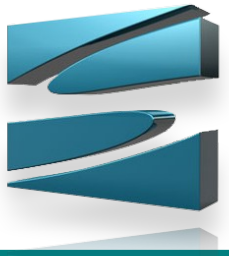

Atlassian Home
Documentation
Support
Blog
Forums
Atlassian bitbucket
Explore
Dashboard
Repositories
jummp
owner/repo
Overview
Downloads (0)
Pull requests (0)
Source
Commits
Wiki
Issues (0) »
Admin
Forks/queues (1)
Followers (2)
branches »
invite
RSS
fork
follow
get source »
jummp / jummp
JUst a Model Management Platform
compare
create pull request
Clone this repository (size: 22.6 MB): HTTPS / SSH
$ git clone https://jummp@bitbucket.org/jummp/jummp.git
Home
New
Edit
History
Wiki markup
git clone https://jummp@bitbucket.org/jummp/jummp.git/wiki
JUMMP
JUst a Model Management Platform (JUMMP) will be a modular software infrastructure for the collaborative development and management of biochemical models.
News | Documentation | Bugs and Feature Requests | Mailing Lists | Contribution
News
https://bitbucket.org/jummp/jummp/
2012-08-16: JUMMP is presented at COMBINE 2012. A publicly-available instance of it is also released at EBI.
2012-03-19: First presentation of JUMMP to a developer audience at the Systems Biology Data Management Foundry Workshop in Vienna at 19./20. of March.
2011-05-05: presentation of the software infrastructure behind BioModels Database and the JUMMP project at the Data Management for Systems Biology and the Life Sciences workshop, Heidelberg, Germany
2011-02-04: official announcement at EBI and DKFZ
2010-12-22: starting work on a first testing prototype
2010-12-07: project created on Bitbucket
2010-10-08: initial announcement during COMBINE 2010

JUMMP architecture



FOSS again

- Groovy
- Grails (Spring, Hibernate, …)
- Spring Security
- Hibernate Search
- Apache ActiveMQ / D-Bus
- jQuery, jQuery UI
- JSBML
- Subversion / Git



Many many thanks

EMBL-EBI

- **Developers**
  Mélanie Courtot, Alexander Broicher, Finja Büchel, Marco Donizelli, Marine Dumousseau, Gael Jalowicki, Mihai Glont, Ron Henkel, Arnaud Henri, Sarah Keating, Christian Knuepfer, Camille Laibe, Chen Li, Lu Li, Florian Mittag, Kedar Nath Natarajan, Jean-Baptiste Pettit, Nicolas Rodriguez, Karim Tazibt, Martijn van Iersel, Dagmar Waltemath, Sarala Wimalaratne, Yangyang Zhao, Anna Zhukova
- **Curators**
  Ishan Ajmera, Vijayalakshmi Chelliah, Harish Dharuri, Lukas Endler, Enuo He, Nick Juty, Michael Schubert, Melanie Stefan
- Henning Hermjakob, Janet Thornton

External contributions

- **Collaborators**
  Upi Bhalla, Andreas Dräger, Jürgen Eils, Mike Hucka, Hiroaki Kitano, Ion Moraru, Julio Saez-Rodriguez, Herbert Sauro, Maria Schilstra, Falk Schreiber, Jacky Snoep, Neil Swainston
- **Scientific Advisory Board**
  Upi Bhalla, Carole Goble, Thomas Lemberger, Pedro Mendes, Ion Moraru, Wolfgang Müller, Philippe Sanseau, Herbert Sauro, Jacky Snoep
- All the computational systems Biology community, in particular: Rainer Machne, Bruce Shapiro, Kieran Smallbone

Current member
coordinator

Generous funders