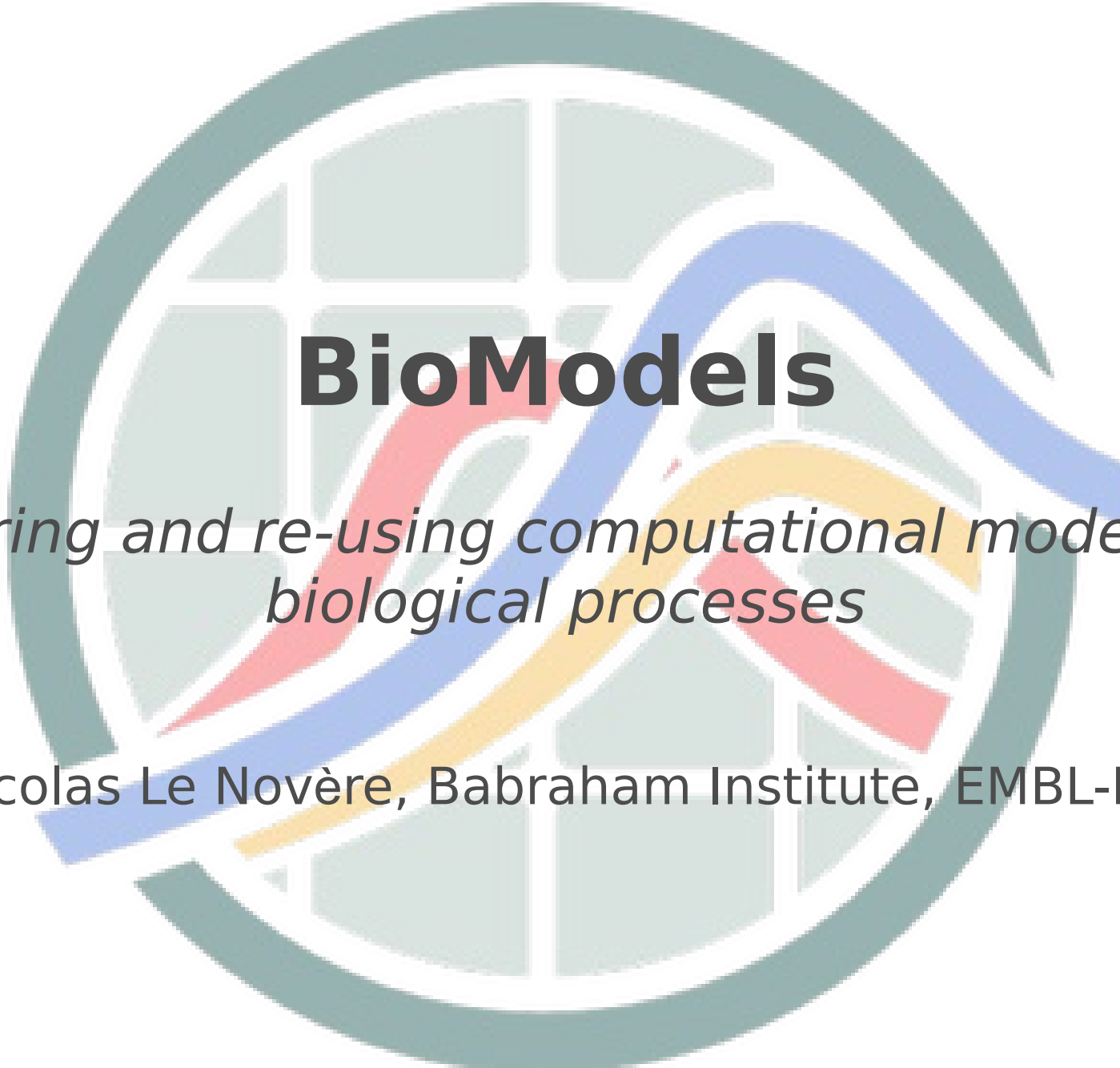




BioModels

*Sharing and re-using computational models of
biological processes*

Nicolas Le Novère, Babraham Institute, EMBL-EBI



The world before BioModels

- List of models on webpages. Generally a link to the model in some format
- Main repositories were ModelsDb (neuroscience), DOQCS (neuroscience), the CellML and the SBML repositories. Plus a handful of personal web pages
- 100% of the models in the SBML repository were wrong. Wrong structure, wrong parametrisation, or did not produce the correct result
- It was generally not possible to test the other repositories because of the lack of tools



What is BioModels?

- Store and serve quantitative models of **biological** 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** relevant quantitative or qualitative models
- **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**

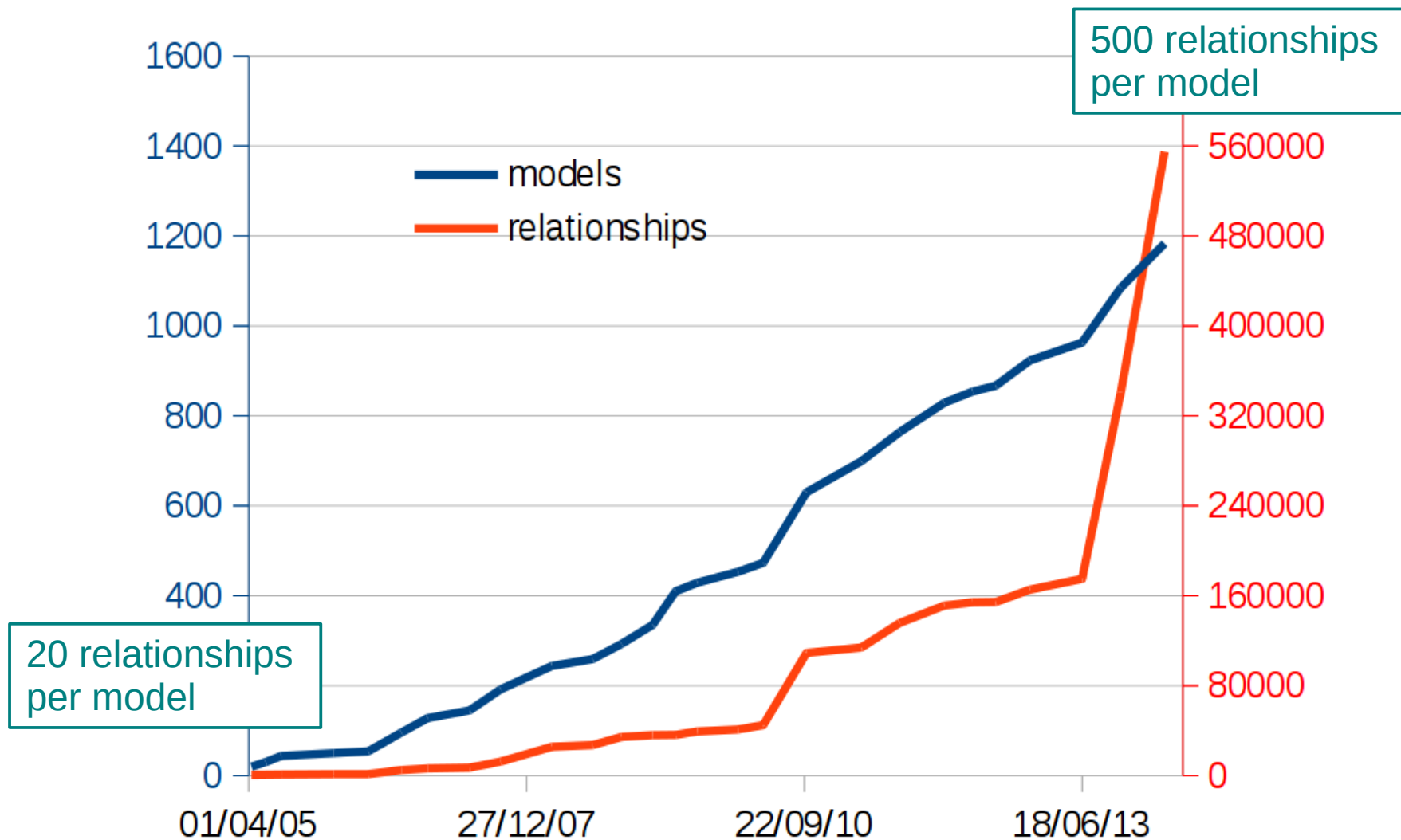


Where do models come from?

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



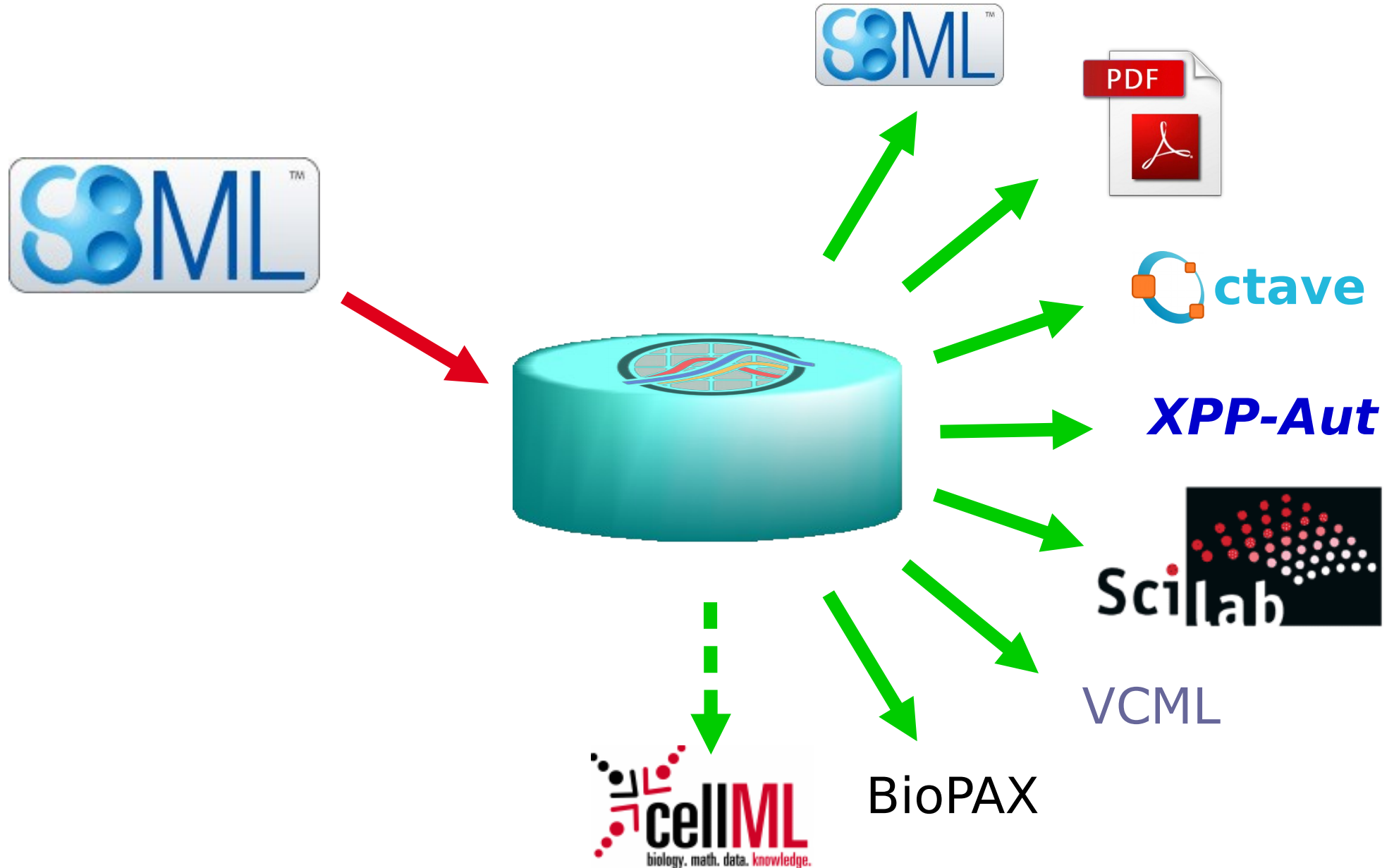
Computational models on the rise



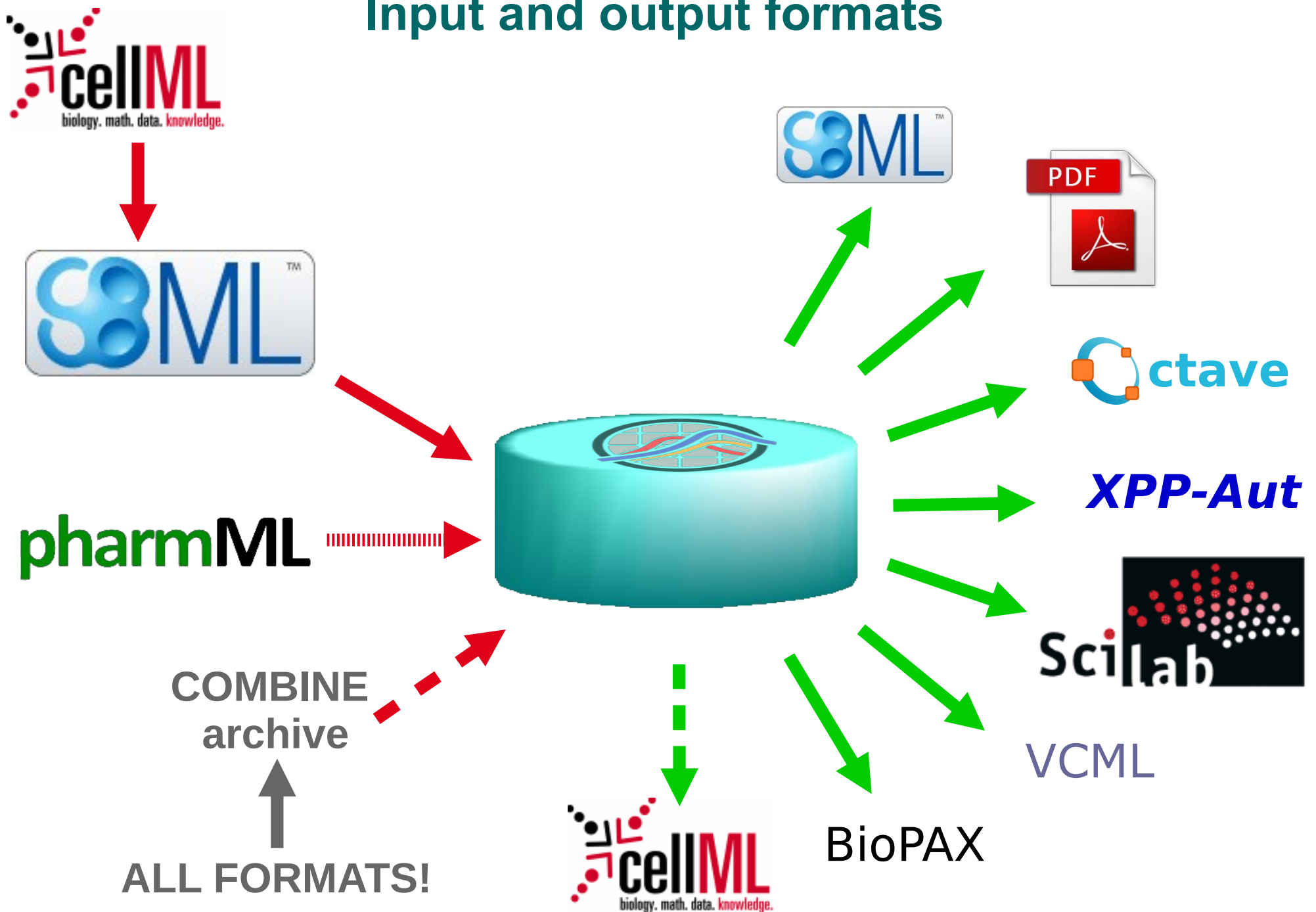
BioModels Database growth (published models branch) since its creation



Input and output formats



Input and output formats



Systems Biology Format Converter

Contents [\[hide\]](#)

- 1 The System Biology Format Converter
 - 1.1 Converters
 - 1.1.1 SBML to Octave
 - 1.1.2 SBML to XPP
 - 1.1.3 SBML to BioPax
 - 1.1.4 SBML to Dot
 - 1.2 Download
 - 1.3 Online converters service
 - 1.4 Development
 - 1.5 Getting Help and Support
- 2 Other Converters

The System Biology Format Converter

The System Biology Format Converter (SBFC) aims to provide a generic framework that potentially allows any conversion between two formats. Interoperability between formats is a recurring issue in Systems Biology. Although there are various tools available to convert models from one format to another, most of them have been independently developed and cannot easily be combined, specially to provide support for more formats. The framework is written in Java and can be used as a standalone executable. This is a collaborative project and we hope that developers will provide support for more formats by creating new modules. SBFC allows anyone to easily add new converters and to integrate existing converters with a minimum of changes. We will also allow to combine several existing converters.

The SBFC framework currently supports conversion from [SBML](#) to [BioPAX](#) Level 2 and Level3, [XPP](#), [Octave](#) and [Dot](#).

Several others converters are in development:

- [SBGN](#) related:
 - SBML to [SBGN-ML](#)
 - SBGN-ML to an SBGN enriched graphical representation designed for use in a web browser

The main Sourceforge page for the SBFC project is <http://sourceforge.net/projects/sbfc/>

Converters

Here is a small description of all the conversions currently supported. You can access to a more detailed page by clicking on a converter name.



Step 1 : Choose your input format

The Input format you choose should match the model(s) you will submit, otherwise you will get an error. We strongly advise you validate your model(s) before the conversion

At the moment only SBML files can be selected as Input.

Model format :



Step 2 : Choose your output format

The output format you choose will determine the converter to use, If the format you want doesn't appear here it means the converter is not implemented yet

Output format :

- Select the output format
- BioPax Level 2
- BioPax level 3
- Octave
- XPP
- SBML_L3V1
- SBML_L2V4
- SBML_L2V1
- SBML_L1V2

Step 3 : Enter Get a URL to your results (optional)

Step 4 : Choose the model(s) you want to convert



BioModels is not limited to biochemistry!

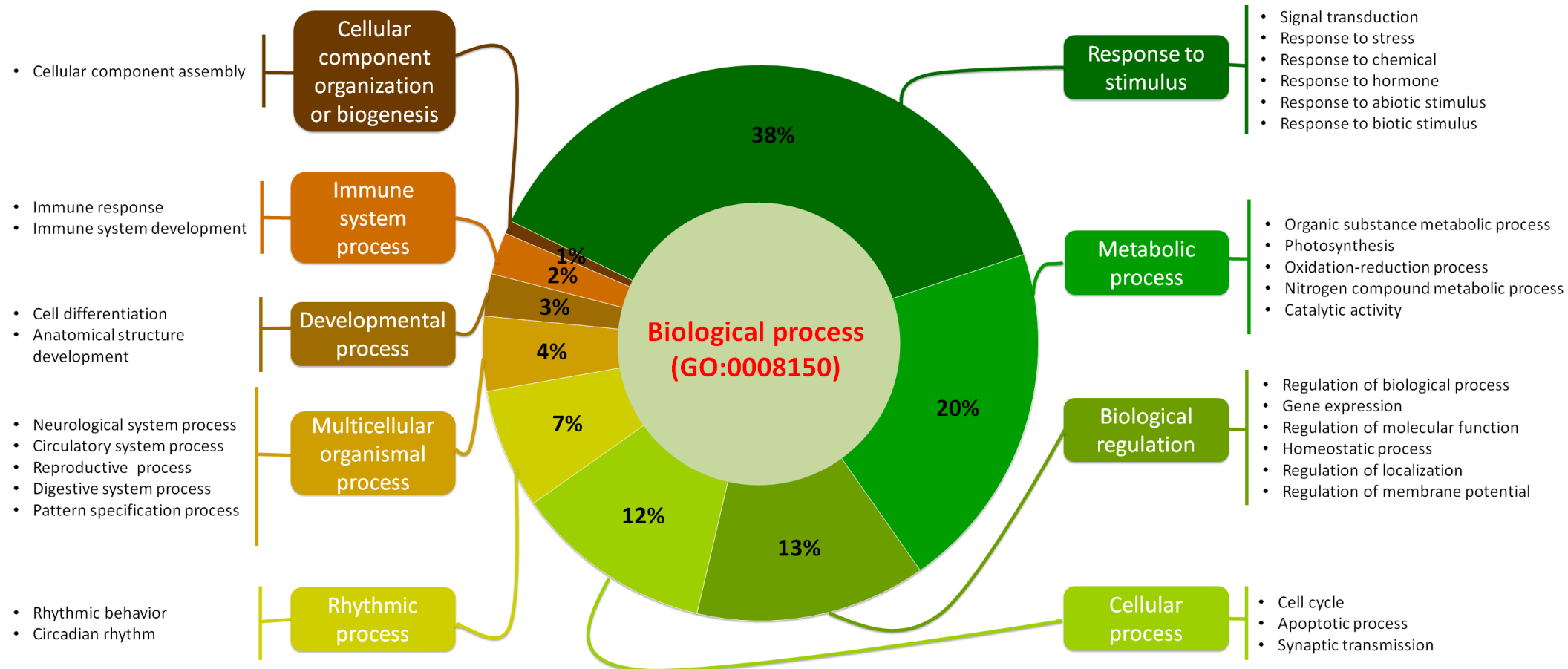
Is it about bio[logy|chemistry|medicine]?

Is it a computational model?

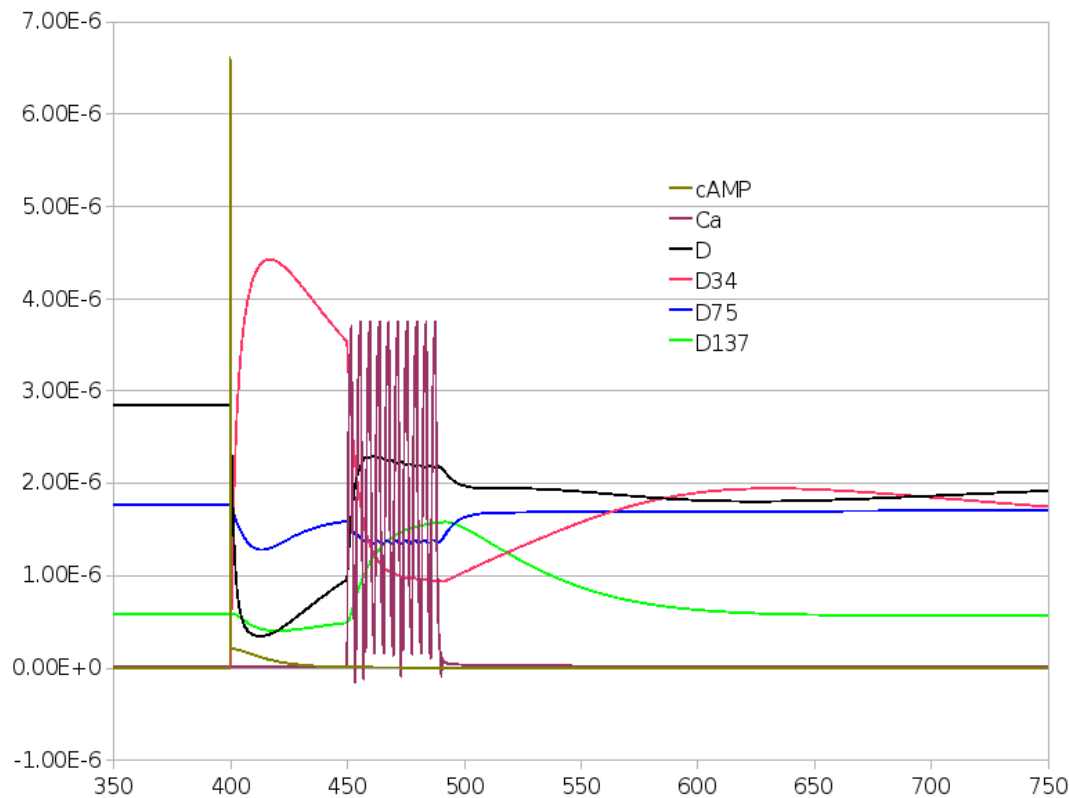
Is it published?

Then it should be in BioModels





Biochemical models



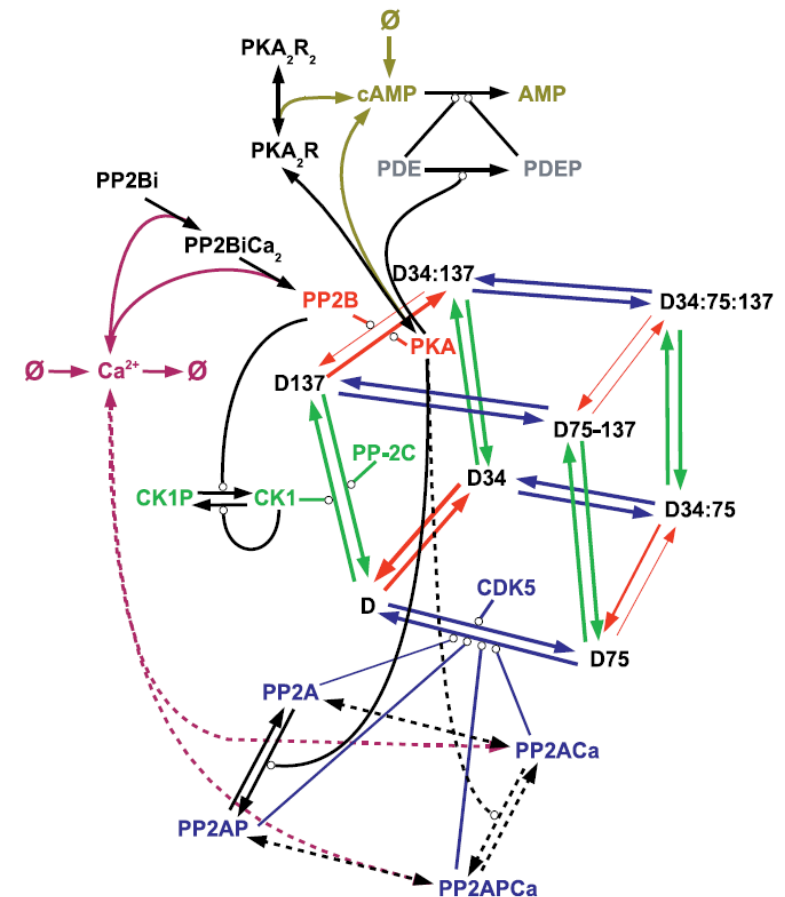
reaction:

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

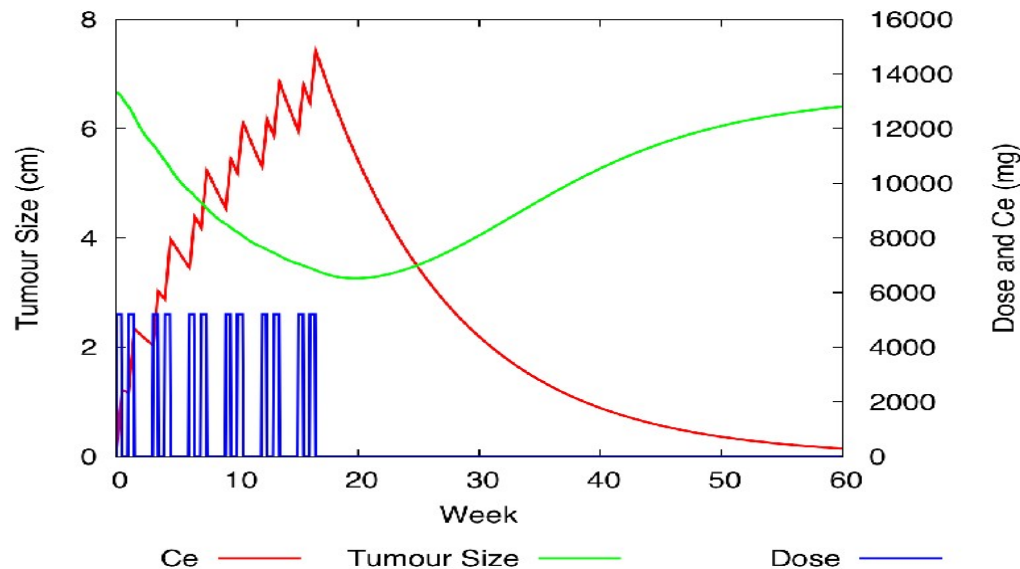
Fernandez et al. DARPP-32 is a robust integrator of dopamine and glutamate signals
PLoS Comput Biol (2006) 2: e176.



BIOMD0000000153



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

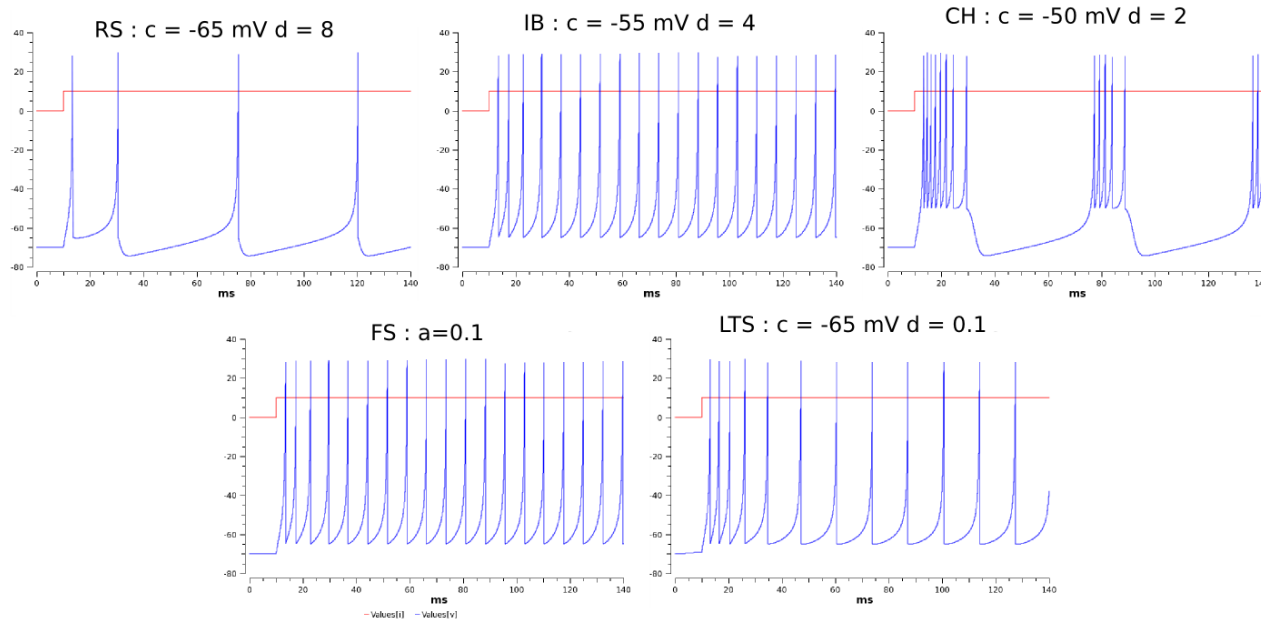
rate rule:

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

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

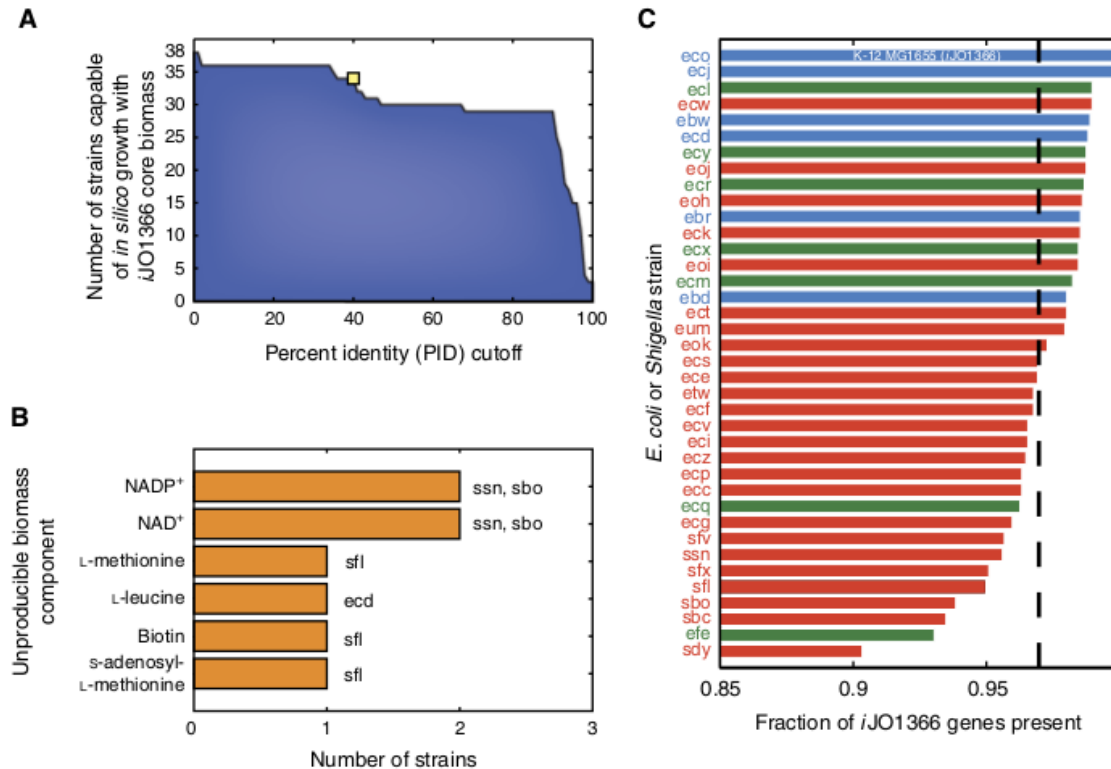
rate rule:

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

event:

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

Flux Balance Analysis models



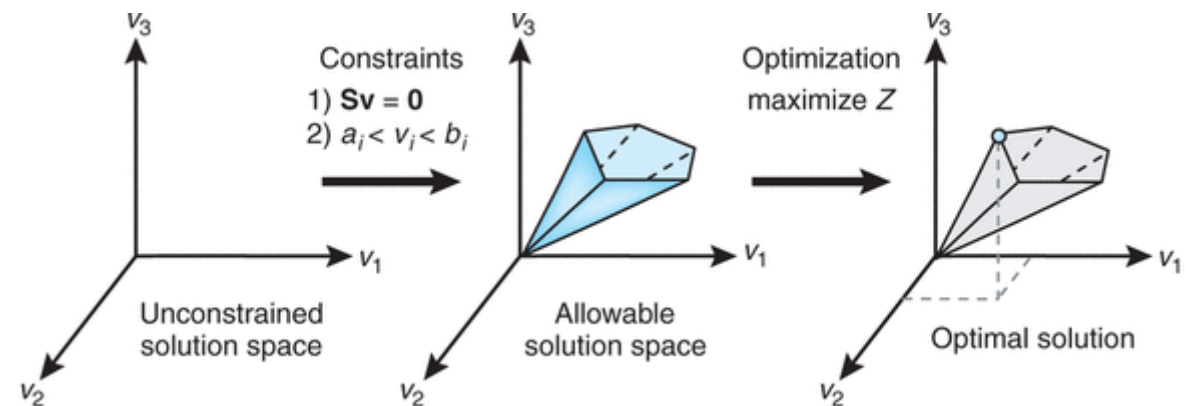
Orth et al. A comprehensive genome-scale reconstruction of *Escherichia coli* metabolism - 2011
Mol Syst Biol (2011);7:535



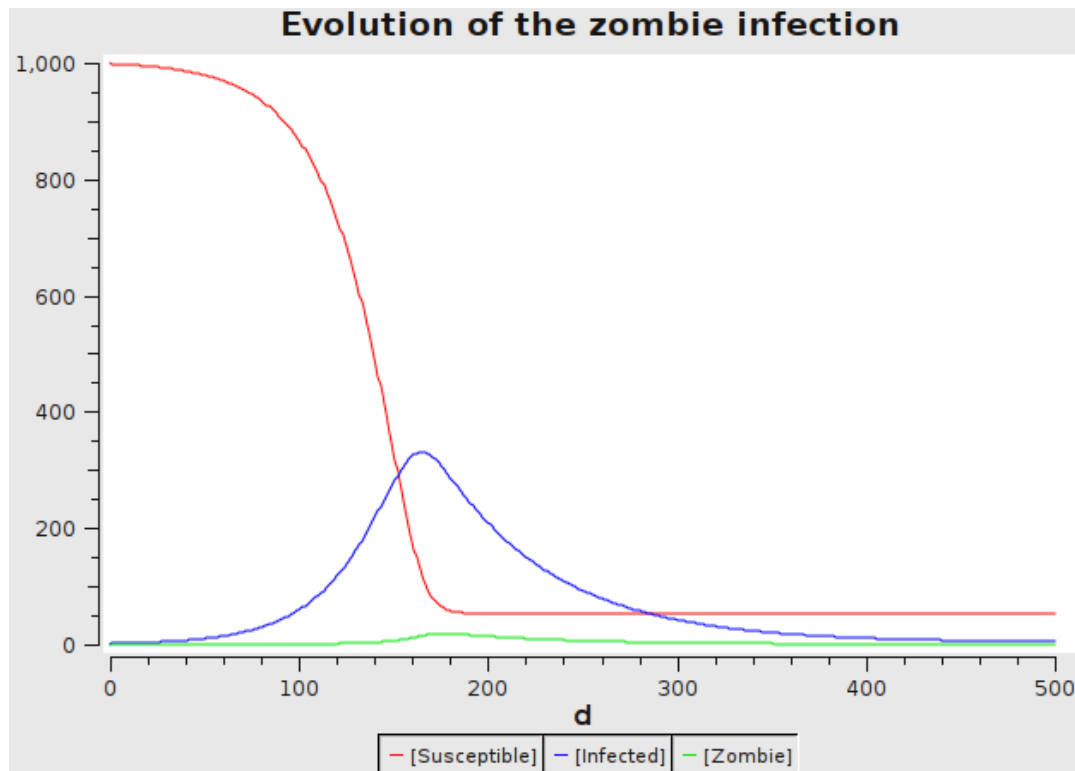
MODEL1108160000

reaction:

$$v_i = flux_i$$



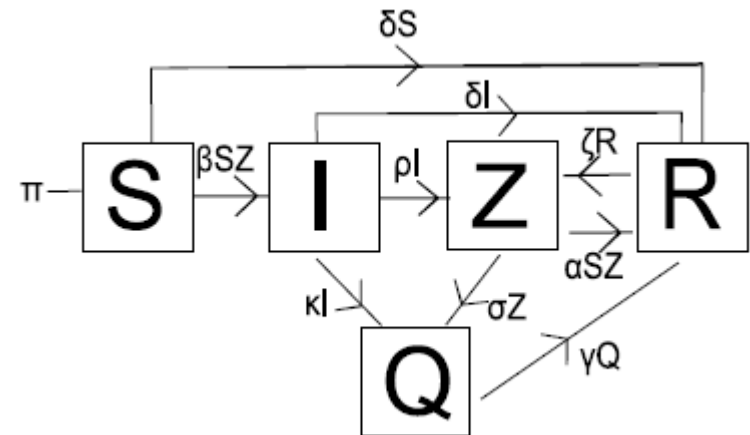
Epidemiology models



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



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](#)

No Copyright



The person who associated a work with this deed has **dedicated** the work to the public domain by waiving all of his or her rights to the work worldwide under copyright law, including all related and neighboring rights, to the extent allowed by law.

You can copy, modify, distribute and perform the work, even for commercial purposes, all without asking permission. See **Other Information** below.



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



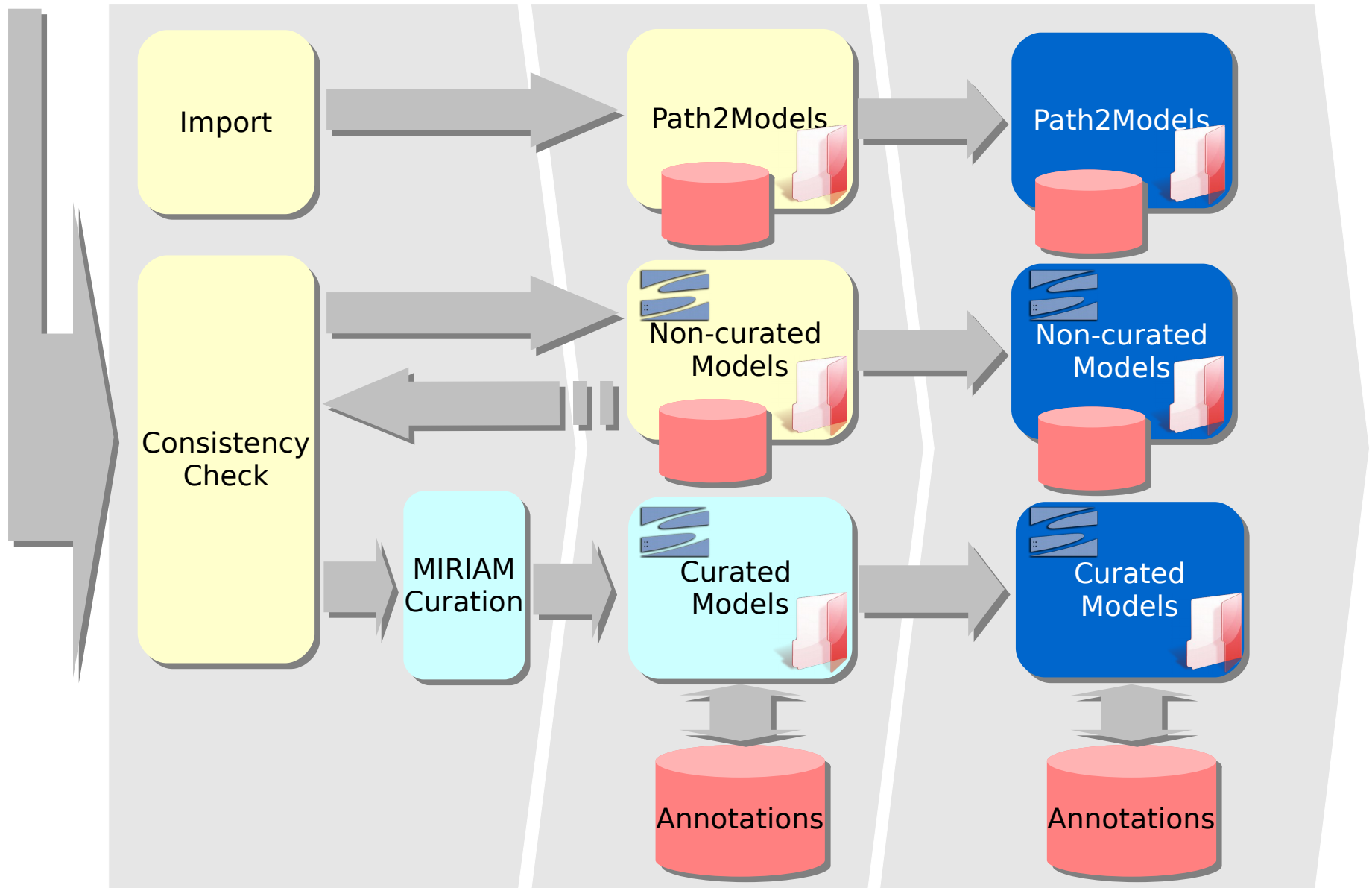
Current production pipeline

Submission

Curation

Annotation

distribution





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](#)
 (562 models)



[Non curated](#)
 (696 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](#)



[Dedicated search](#)

[Model of the month](#)

March, 2015

Alpha-synuclein related pathogenic mechanism play a significant role in the development of Parkinson's

disease. In this model, the effects of alpha-synuclein oligomerization on cells' homeostasis has been proposed.



[Access this model of the month.](#)

[News](#)


[26 February 2015](#) [New CPT:PSP publication](#)
[BioModels: Content, Features, Functionality, and Use](#) published in CPT: Pharmacometrics & Systems Pharmacology


[21 November 2014](#) [New NAR publication](#)
[BioModels: ten-year anniversary](#) published in Nucleic Acids Research, Database issue.


[11 November 2014](#) [ISBE Business Case](#)
[Infrastructure for Systems Biology Europe \(ISBE\)](#) releases its [Business Case](#), explaining the need for a pan-European infrastructure, what this infrastructure would entail, together with its plans for data stewardship, standardisation and services. BioModels is featured as a success story

BioModels Database

Advanced

BioModels Home Models Submit Support About BioModels Contact us

BioModels processes. Models are enriched with more information.

- Curated models
- Non-curated models
- Gene Ontology categories (*new*)
- Gene Ontology tree
- Taxonomy cloud

Path2Models

AgedBrainsYSBIC

Advanced search

Simulate in JWS (*ext*)

Models of the Month

Archives (*ext*)

Non curated
(696 models)

of computational models of biological structure are manually curated and models are provided in the Public Domain. base can be found in the FAQ.

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



Dedicated search

Model of the month

March, 2015

Alpha-synuclein related pathogenic mechanism play a significant role in the development of Parkinson's

disease. In this model, the effects of alpha-synuclein oligomerization on cells' homeostasis has been proposed.



Access this model of the month.

News

26 February 2015 New CPT:PSP publication
BioModels: Content, Features, Functionality, and Use published in CPT: Pharmacometrics & Systems Pharmacology

21 November 2014 New NAR publication
BioModels: ten-year anniversary published in Nucleic Acids Research, Database issue.

11 November 2014 ISBE Business Case Infrastructure for Systems Biology Europe (ISBE) releases its Business Case, explaining the need for a pan-European infrastructure, what this infrastructure would entail, together with its plans for data stewardship, standardisation and services. BioModels is featured as a success story in Systems Biology, and is presented as a



BioModels Database

Search

Advanced

[BioModels Home](#)
[Models](#)
[Submit](#)
[Support](#)
[About BioModels](#)
[Contact us](#)

BioModels Database
processes. Models
with cross-referenc
information about BioModels Database

- Submit a new model
- Annotation information
- Curation guidelines
- Annotation guidelines

of computational models of biological
ture are manually curated and enriched
provided in the Public Domain. More
information about BioModels Database can be found in the FAQ.

Models published in the literature

Browse



Manually curated
(562 models)



Non curated
(696 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



Dedicated search

Model of the month

March, 2015

Alpha-synuclein related pathogenic mechanism play a significant role in the development of Parkinson's



disease. In this model, the effects of alpha-synuclein oligomerization on cells' homeostasis has been proposed.

[Access this model of the month.](#)

News


26 February 2015
[New CPT:PSP publication](#)
[BioModels: Content, Features, Functionality, and Use](#) published in CPT: Pharmacometrics & Systems Pharmacology


21 November 2014
[New NAR publication](#)
[BioModels: ten-year anniversary](#) published in Nucleic Acids Research, Database issue.


11 November 2014
[ISBE Business Case](#)
[Infrastructure for Systems Biology Europe \(ISBE\)](#) releases its [Business Case](#), explaining the need for a pan-European infrastructure, what this infrastructure would entail, together with its plans for data stewardship, standardisation and services. BioModels is featured as a success story in



BioModels Database

Search

Advanced

[BioModels Home](#)
[Models](#)
[Submit](#)
[Support](#)
[About BioModels](#)
[Contact us](#)



BioModels Database is a

processes. Models describe

with cross-references. All

information about BioModels

[FAQ](#)
[Courses](#)
[Converters \(ext\)](#)
[Web Services](#)
[SPARQL Endpoint](#)
[Develop](#)
[SourceForge \(ext\)](#)

Computational models of biological

are manually curated and enriched

in the Public Domain. More

can be found in the [FAQ](#).

Models published in the literature

Browse



Manually curated
(562 models)



Non curated
(696 models)

Development with BioModels Database source code

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



Dedicated search



Model of the month

March, 2015

Alpha-synuclein related pathogenic mechanism play a significant role in the development of Parkinson's disease. In this model, the effects of alpha-synuclein oligomerization on cells' homeostasis has been proposed.



[Access this model of the month.](#)



News

26 February 2015 [New CPT:PSP publication](#)

[BioModels: Content, Features, Functionality, and Use](#) published in CPT: Pharmacometrics & Systems Pharmacology

21 November 2014 [New NAR publication](#)

[BioModels: ten-year anniversary](#) published in Nucleic Acids Research, Database issue.

11 November 2014 [ISBE Business Case](#)

[Infrastructure for Systems Biology Europe \(ISBE\)](#) releases its [Business Case](#), explaining the need for a pan-European infrastructure, what this infrastructure would entail, together with its plans for data stewardship, standardisation and services. BioModels is featured as a success story in Systems Biology, and is presented as a [Case Study](#).



BioModels Database

Search

Advanced

[BioModels Home](#)
[Models](#)
[Submit](#)
[Support](#)
[About BioModels](#)
[Contact us](#)



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

[Terms of Use](#)
[Citation](#)
[News](#)
[Acknowledgements](#)
[Jobs](#)
[Curator Sign in](#)

Models published in the literature

Browse



Manually curated
(562 models)



Non curated
(696 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



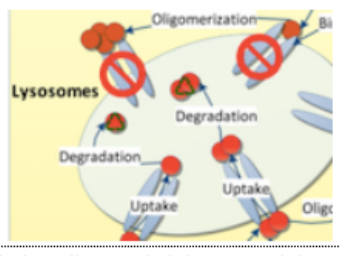
Dedicated search



Model of the month

March, 2015

Alpha-synuclein related pathogenic mechanism play a significant role in the development of Parkinson's disease. In this model, the effects of alpha-synuclein oligomerization on cells' homeostasis has been proposed.



[Access this model of the month.](#)



News



26 February 2015

New CPT:PSP publication

[BioModels: Content, Features, Functionality, and Use](#) published in CPT: Pharmacometrics & Systems Pharmacology



21 November 2014

New NAR publication

[BioModels: ten-year anniversary](#) published in Nucleic Acids Research, Database issue.



11 November 2014

ISBE Business Case Infrastructure for Systems Biology Europe (ISBE) releases its Business Case, explaining the need for a pan-European infrastructure, what this infrastructure would entail, together with its plans for data stewardship, standardisation and services. BioModels is featured as a success story in Systems Biology, and is presented as a Case Study.

Submit - Step 1

You can submit here models to be included in BioModels Database.

The following formats are currently accepted:

- [SBML Level 3: Version 1](#) (including [any packages](#))
- [CellML: 1.0](#) and [1.1](#)
- [SBML Level 2: Version 1](#), [Version 2](#), [Version 3](#) and [Version 4](#)
- [SBML Level 1: Version 1](#) and [Version 2](#)

If you wish to submit a model under a different format, please [contact us](#).

If you wish to provide additional files with your submission, please [contact us](#).

The submitted model will not be publicly available from BioModels Database straightaway. If you wish to know more about the [submission](#), [curation](#) and [annotation](#) processes, please refer to the relevant sections of the [Frequently Asked Questions](#).

To ensure a prompt processing of your model, please follow those simple guidelines:

- Check that your model is valid according to the format you chose. If your model is encoded in SBML, you can use the official [online validator](#).
- Enter all relevant information which could help the work of our curators (relation between the model and publication, modifications or clarifications of the model, etc.) either directly into the model file (for example using the *notes* elements if your model is encoded in *SBML*), or in the *Comment* field provided in step 2 of this form.
- If you created the model (or collaborated to its creation) but are not an author of the associated publication, please add your personal information (first and last name, organisation and email address) in the model, so that your contribution can be acknowledged. If you used *SBML*, this can be done by adding to the *model* element a *dc:creator* annotation, as in this [example](#) which you can re-use (skip the blue part if already present).
- Choose a meaningful name for your model. You can follow the pattern *AuthorNameYear - Topic, Method*, for example: *Levchenko2000 - MAPK, noScaffold* or *Edelstein1996 - EPSP AChEvent*.

All models in BioModels Database are available under the terms of the [Creative Commons CC0 1.0 \(Public Domain Dedication\)](#). Therefore you need to agree to release the encoded model in the **Public Domain** before submitting it to BioModels Database.

Thank you for contributing to BioModels Database!

Please enter the identifier of the scientific publication associated with the model, and then click *Continue*. If the model has not been published, please select the 'Unpublished' option.

Publication Identifier:

Type of identifier: ☒ PubMed ID ([Search Medline](#)) ☐ DOI ([Resolve a DOI](#)) ☐ URL ☐ Unpublished

The submitted models will not be incorporated into the BioModels Database straightaway, since they have to undergo a curation phase before. During this curation phase, the models will be first converted to the *SBML Level 2 Version 4* format in case they were submitted under a different format, and then tested to verify that they both are [consistent](#) and reproduce the results published in the respective reference publication. To actually facilitate this curation phase, prior to submitting a model, please do the following:

- Enter all the relevant information you believe is necessary for the curation (reference publication, modifications or clarifications of the model, etc.) either directly into the model file if allowed (for example using the *notes* elements if your model is under one of the *SBML* formats), or into the *Curation comment* text field provided by the form below.
- If you created the model, or collaborated to its creation, and you are not an author of the reference publication, add to the *model* element a *dc:creator* annotation containing your data (first and last name, organisation, email), so that your contribution can be acknowledged. Click [here](#) to view an example of a *dc:creator* annotation which you can re-use (skip blue part if already present).
- Choose a meaningful value for the attribute *name* of the *model* element. Examples of good model names are *NameAuthorYear_Topic_Method*, *Levchenko2000_MAPK_noScaffold* or *Edelstein1996_EPSP_AChEvent*.
- Check the validity of the model (for example by using this [online validator](#) if your model is encoded in the *SBML* format). All the models undergo a primary XML validity check upon submission anyway, and, as mentioned before, a more thorough testing during the curation phase, but an already valid model is of great help nevertheless!
- If the model was not created directly in SBML, or if it requires a specific software to be simulated adequately, please enter in the *Original Model* form a URL pointing to the model in the original repository. Refrain from entering a generic URL to the repository itself.

Please enter your personal details and any comment useful for the curation step (underlined fields are required), and then click *Submit*.

First name:

Last name:

Organisation:

Email:

Comment:

Original model:

Model file:

Browse...

No file selected.

Submit

Reset



Browse - Curated models

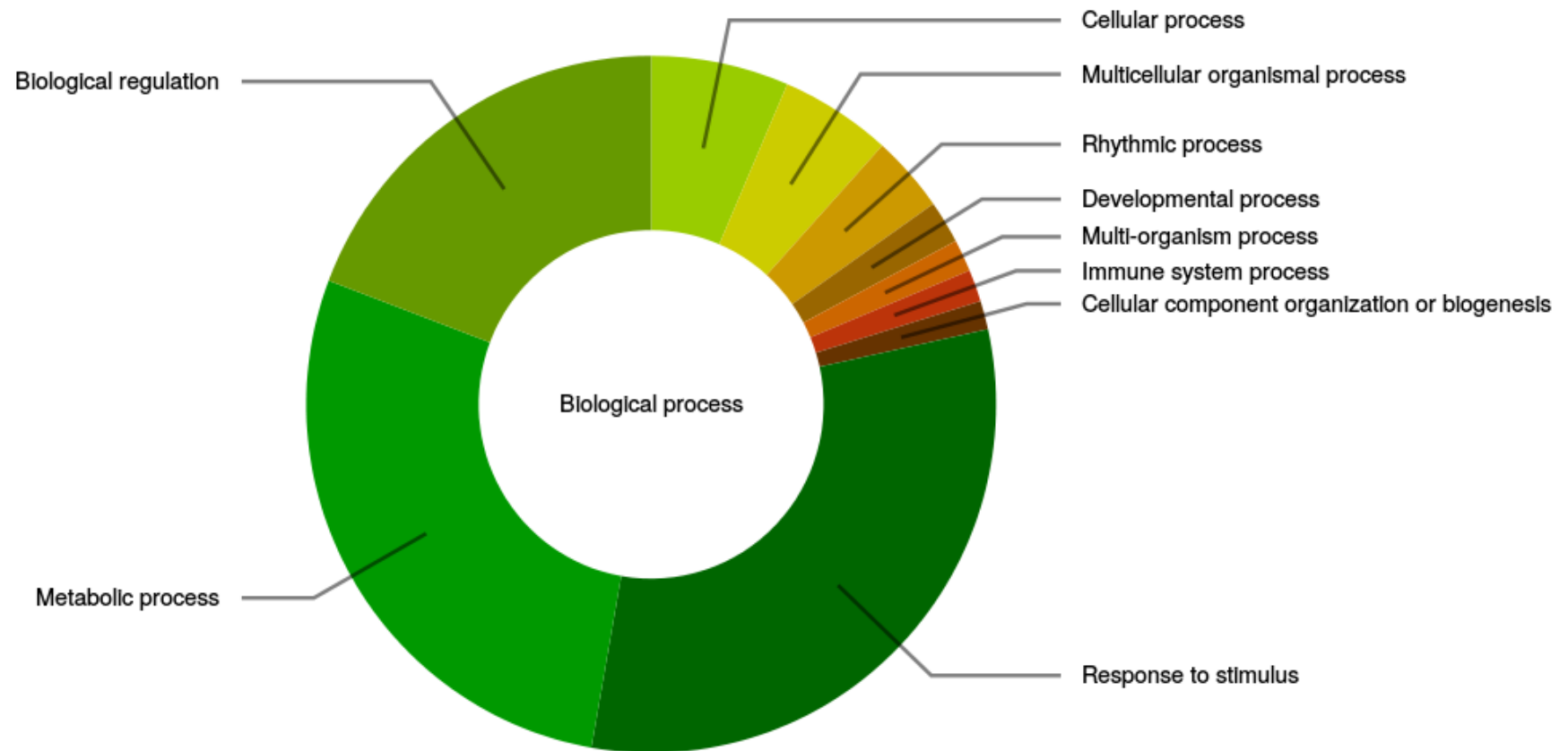
⊞ The following fields are used to describe a model: ...

⏪ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 ⏩ 10 | 50 | 100 | All

BioModels ID	Name ▼	Publication ID	Last Modified
BIOMD0000000355	Abell2011_CalciumSignaling_WithAdaptation	21844332	2011-09-08T12:03:57+00:00
BIOMD0000000354	Abell2011_CalciumSignaling_WithoutAdaptation	21844332	2011-09-08T12:16:51+00:00
BIOMD0000000428	Achcar2012 - Glycolysis in bloodstream form T. brucei	22379410	2013-06-10T13:41:07+00:00
BIOMD0000000476	Adams2012 - Locke2006 Circadian Rhythm model refined with Input Signal Light Function	22855577	2013-09-11T15:39:47+00:00
BIOMD0000000169	Aguda1999_CellCycle	10619492	2012-07-05T14:42:01+00:00
BIOMD0000000295	Akman2008_Circadian_Clock_Model1	18277380	2014-05-28T01:56:26+00:00
BIOMD0000000214	Akman2008_Circadian_Clock_Model2	18277380	2014-05-28T01:57:42+00:00
BIOMD0000000220	Albeck2008_extrinsic_apoptosis	18406323	2012-07-05T14:42:40+00:00
BIOMD0000000211	Albert2005_Glycolysis	15955817	2014-05-27T23:52:38+00:00
BIOMD0000000289	Alexander2010_Tcell_Regulation_Sys1	20195912	2014-03-11T13:38:50+00:00



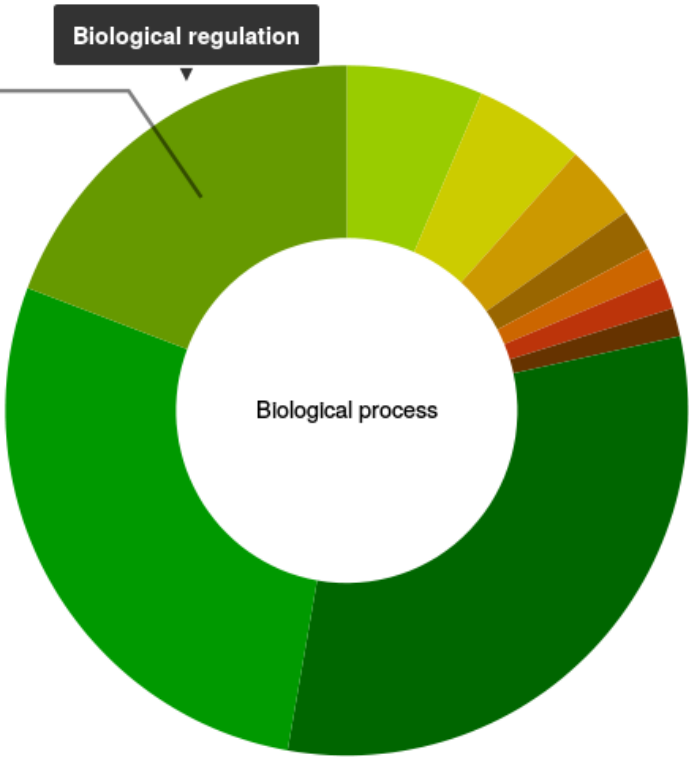
Classification of models published in the literature, based on GO



Classify models by biological literature, based on GO

Biological regulation (232)

- [Regulation of biological process](#) (109)
- [Regulation of membrane potential](#) (65)
- [Homeostatic process](#) (27)
- [Regulation of localization](#) (21)
- [Regulation of molecular function](#) (10)



Selected GO term: [Regulation of biological process](#)

Curated Models

BioModels ID	Name	Publication ID	Last Modified
BIOMD0000000012	Elowitz2000 - Represslator	10659856	2013-07-10
BIOMD0000000065	Yildirim2003_Lac_Operon	12719218	2014-02-12
BIOMD0000000067	Fung2005_Metabolic_Oscillator	15875027	2012-05-16
BIOMD0000000079	Goldbeter2006_weightCycling	16595882	2012-07-05
BIOMD0000000080	Thompson1989_AdenylateCyclase	2574092	2014-02-12

BioModels Database: GO tree

This is a tree view of the curated models based on their [Gene Ontology](#)  annotation.

To browse the models, please click the ► icon on the left of the term to expand the related branch and similarly click on the ▼ icon to collapse an already opened branch. By clicking on a term's name, the list of models annotated with this term (or one of its descendant) will be displayed on the right panel.

- ▼ [GO:0008150 - biological_process](#) (529)
 - [GO:0022610 - biological adhesion](#) (1)
 - ▼ [GO:0065007 - biological regulation](#) (373)
 - ▼ [GO:0050789 - regulation of biological process](#) (316)
 - ▼ [GO:0048519 - negative regulation of biological process](#) (77)
 - ▼ [GO:0051129 - negative regulation of cellular component organization](#) (5)
 - ▼ [GO:0010639 - negative regulation of organelle organization](#) (5)
 - ▼ [GO:0051784 - negative regulation of nuclear division](#) (5)
 - ▼ [GO:0045839 - negative regulation of mitosis](#) (5)
 - ▼ [GO:0045841 - negative regulation of mitotic metaphase/anaphase transition](#) (5)
 - [GO:0007094 - mitotic spindle assembly checkpoint](#) (5)
 - [GO:0048523 - negative regulation of cellular process](#) (71)
 - [GO:0051093 - negative regulation of developmental process](#) (1)
 - [GO:0045926 - negative regulation of growth](#) (1)
 - [GO:0002683 - negative regulation of immune system process](#) (1)
 - [GO:0009892 - negative regulation of metabolic process](#) (54)
 - [GO:0043901 - negative regulation of multi-organism process](#) (5)
 - [GO:0051241 - negative regulation of multicellular organismal process](#) (1)
 - [GO:0048585 - negative regulation of response to stimulus](#) (32)
 - [GO:0051283 - negative regulation of sequestering of calcium ion](#) (7)
 - [GO:0023057 - negative regulation of signaling](#) (33)
 - [GO:0051051 - negative regulation of transport](#) (8)
 - [GO:0048518 - positive regulation of biological process](#) (91)
 - [GO:0044087 - regulation of cellular component biogenesis](#) (2)
 - [GO:0051128 - regulation of cellular component organization](#) (12)
 - [GO:0050794 - regulation of cellular process](#) (274)

Model(s) annotated with the GO term [GO:0007094](#)  or one of its descendant(s):

- [Chen2004 - Cell Cycle Regulation](#) ([BIOMD0000000056](#))
- [Ibrahim2008 - Mitotic Spindle Assembly Checkpoint - Convey variant](#) ([BIOMD0000000187](#))
- [Ibrahim2008 - Mitotic Spindle Assembly Checkpoint - Dissociation variant](#) ([BIOMD0000000186](#))
- [Ibrahim2008_Cdc20_Sequestering_Template_Model](#) ([BIOMD0000000194](#))
- [Ibrahim2008_MCC_assembly_model_KDM](#) ([BIOMD0000000193](#))



- *Person* → Search BioModels Database for model submitter and/or creator(s) names, or model reference publication author(s) names (for example *Nicolas L. 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 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 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 *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. *Person* for *Shapl* or *shapl* will return the same results as searching for *Shapiro* or *shapiro*. In addition, since search strings are treated as words, do not use 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, models satisfying at least one of the criteria will be returned.

BioModels identifier:

Person:

SBML elements:

☐ match the exact phrase

Annotation (full text):

UniProt Knowledgebase ▾



Annotation (full text):

Publication ▾

cell cycle



Annotation (full text):

Gene Ontology ▾



Annotation (identifier):

PubChem-compound ▾



Annotation (identifier):

KEGG Reaction ▾



Annotation (identifier):

Enzyme Nomenclature ▾



Compose by: ☒ and ☐ or

Search

Reset

Search - Models

Query: *Publication* **cell cycle** [resources]

The search returned **44** models.

 [New Search](#)

 **33** Curated models returned:

| BioModels ID  | Name | Publication ID | Last Modified |
|---|---|--------------------------|---------------------------|
| BIOMD0000000003  | Goldbeter1991 - Min Mit Oscil | 1833774 | 2013-05-16T14:38:01+00:00 |
| BIOMD0000000004  | Goldbeter1991 - Min Mit Oscil, Expl Inact | 1833774 | 2012-12-11T15:30:15+00:00 |
| BIOMD0000000005  | Tyson1991 - Cell Cycle 6 var | 1831270 | 2013-05-16T14:40:43+00:00 |
| BIOMD0000000006  | Tyson1991 - Cell Cycle 2 var | 1831270 | 2013-05-16T14:38:56+00:00 |
| BIOMD0000000007  | Novak1997 - Cell Cycle | 9256450 | 2014-03-26T14:20:21+00:00 |
| BIOMD0000000008  | Gardner1998 - Cell Cycle Goldbeter | 9826676 | 2014-07-24T10:59:34+00:00 |
| BIOMD0000000018  | Morrison1989_FolateCycle | 2732237 | 2012-07-05T14:40:37+00:00 |
| BIOMD0000000056  | Chen2004 - Cell Cycle Regulation | 15169868 | 2013-06-07T10:59:38+00:00 |
| BIOMD0000000109  | Haberichter2007_cellcycle | 17299420 | 2012-07-05T14:49:20+00:00 |
| BIOMD0000000110  | Qu2003_CellCycle | 14645053 | 2012-05-16T10:13:14+00:00 |
| BIOMD0000000111  | Novak2001_FissionYeast_CellCycle | 12779461 | 2012-07-05T16:47:55+00:00 |
| BIOMD0000000150  | Morris2002_CellCycle_CDK2Cyclin | 11959850 | 2010-12-01T22:10:11+00:00 |

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): 7328-7332
Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg 24061. [more] |
|---|---|

Model

| | | | |
|---|--------|--------------------|---|
| Original Model: BIOMD0000000005.xml.origIn | set #1 | bqbiol:hasVersion | Reactome REACT_152 |
| Submitter: Nicolas Le Novère | set #2 | bqbiol:isVersionOf | KEGG Pathway sce04111
Gene Ontology mitotic cell cycle |
| Submission ID: MODEL6614644188 | | bqbiol:occursIn | Taxonomy Opisthokonta |
| Submission Date: 13 Sep 2005 12:31:08 UTC | | | |
| Last Modification Date: 16 May 2013 14:40:43 UTC | | | |
| Creation Date: 08 Feb 2005 18:28:27 UTC | | | |
| Encoders: Bruce Shapiro
Vijayalakshmi Chelliah | | | |

Notes

Tyson1991 - Cell Cycle 6 var

Mathematical model of the interactions of cdc2 and cyclin.

This model is described in 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

[Download SBML](#) | [Other formats \(auto-generated\)](#) | [Actions](#) | [Send feedback](#)

- Model
- Overview
- Math
- Physical entities
- Parameters
- Curation

| | |
|---|--|
| + Spatial dimensions: 3.0 Compartment size: 1.0 | |
| EmptySet | Initial amount: 0.0 |
| Compartment: cell | |
| + cdc2k | Initial amount: 0.0 |
| Compartment: cell | |
| + cdc2k-P | Initial amount: 0.75 |
| Compartment: cell | |
| - p-cyclin_cdc2 | Initial amount: 0.0 |
| Compartment: cell | |
| Annotations: | set #1 bqbiol:hasPart UniProt Knowledgebase CDK1_SCHPO
InterPro IPR006670 |
| + p-cyclin_cdc2-p | Initial amount: 0.25 |
| Compartment: cell | |
| + cyclin | Initial amount: 0.0 |
| Compartment: cell | |
| + p-cyclin | Initial amount: 0.0 |
| Compartment: cell | |



Reactions (9)

| | | |
|--|--|---|
| <div>+ cyclin_cdc2k dissociation</div> | $[p\text{-cyclin_cdc2}] \rightarrow [cdc2k] + [p\text{-cyclin}];$ | |
| <div>+ cdc2k phosphorylation</div> | $[cdc2k] \rightarrow [cdc2k\text{-P}];$ | |
| <div>+ cdc2k dephosphorylation</div> | $[cdc2k\text{-P}] \rightarrow [cdc2k];$ | |
| <div>+ cyclin cdc2k-p association</div> | $[cdc2k\text{-P}] + [cyclin] \rightarrow [p\text{-cyclin_cdc2-p}];$ | |
| <div>- deactivation of cdc2 kinase</div> | $[p\text{-cyclin_cdc2}] \rightarrow [p\text{-cyclin_cdc2-p}];$ | |
| <div>Math:</div> | $cell \times k5notP \times M$ (Details: ⓘ) | |
| <div>Annotations:</div> | bqbiol:hasVersion | Reactome REACT_6327
Reactome REACT_3178 |
| | set #1 | Enzyme Nomenclature 2.7.10.2 |
| | bqbiol:isVersionOf | Gene Ontology negative regulation of cyclin-dependent protein serine/threonine kinase activity
Gene Ontology protein phosphorylation |
| <div>+ cyclin biosynthesis</div> | $[EmptySet] \rightarrow [cyclin];$ | |
| <div>+ default degradation of cyclin</div> | $[cyclin] \rightarrow [EmptySet];$ | |
| <div>+ cdc2 kinase triggered degradation of cyclin</div> | $[p\text{-cyclin}] \rightarrow [EmptySet];$ | |
| <div>+ activation of cdc2 kinase</div> | $[p\text{-cyclin_cdc2-p}] \rightarrow [p\text{-cyclin_cdc2}];$ $\{total_cdc2\}$ | |

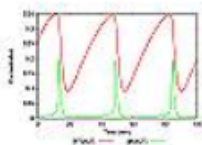
Rules (2)

| | |
|---|-----------------------------------|
| <div>+ Assignment Rule (name: YT)</div> | $total_cyclin = Y + YP + M + pM$ |
| <div>+ Assignment Rule (name: CT)</div> | $total_cdc2 = C2 + CP + M + pM$ |

BIOMD0000000005 - Tyson1991 - Cell Cycle 6 var

[Download SBML](#)[Other formats \(auto-generated\)](#)[Actions](#)[Send feedback](#)[Model](#)[Overview](#)[Math](#)[Physical entities](#)[Parameters](#)[Curation](#)

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/).

[\[BIOMD0000000005_SED-ML.xml\]](#)



Download SBML

Other formats (auto-generated)

Actions

Send feedback

Model

Overview

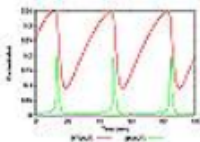
Math

Physical entities

Parameters

Curation

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 file]

Reproduction with COPASI

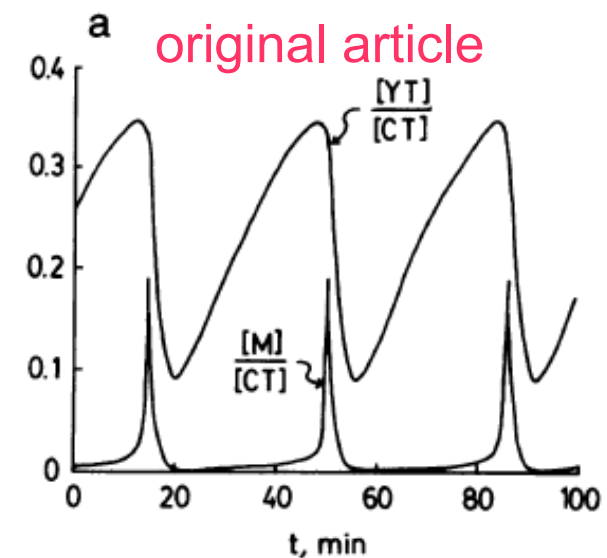
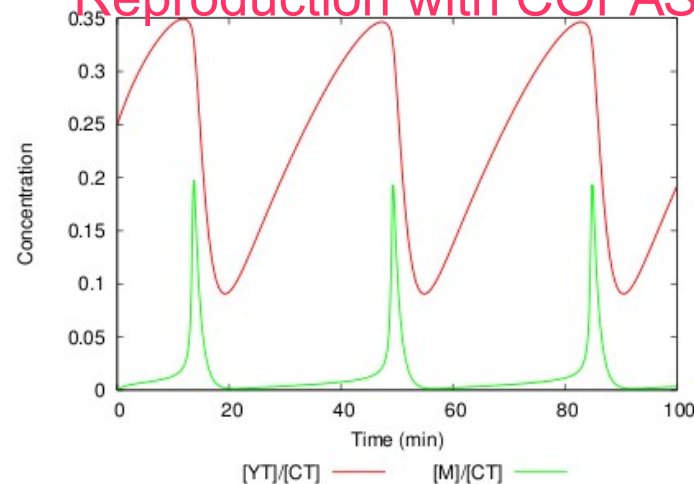


FIG. 3. Dynamical behavior of the cdc2-cyclin relative to total cdc2 ($[CT] = [C2] + [CP] + [nM]$)

[Download SBML](#) | [Other formats \(auto-generated\)](#) | [Actions](#) | [Send feedback](#)

- 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: 16 May 2013 14:40:43 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 degradation of cyclin |
| ☐ activation of cdc2 kinase | | | |

| | | | |
|--|--|--|--|
| Rules | | | |
| Assignment Rule (variable: total_cyclin) | | Assignment Rule (variable: total_cdc2) | |

Physical entities

| | | | |
|---------------------------------------|--|--|---|
| ☐ Compartments | ☐ Species | | |
| ☐ cell | ☐ EmptySet | ☐ cdc2k | ☐ cdc2k-P |
| | ☐ p-cyclin_cdc2 | ☐ p-cyclin_cdc2-p | ☐ cyclin |
| | ☐ p-cyclin | ☐ total_cyclin | ☐ total_cdc2 |

Download SBML

Other formats (auto-generated)

Actions

[Send feedback](#)

Model

Overview

Math

Physical entities

Parameters

Curation

Submodel1

Create a submodel with selected elements

Deselect All

Model

Publication ID: [1831270](#)

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

Last Modification Date: 16 May 2013 14:40:43 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 degradation of cyclin](#)

☐ [activation of cdc2 kinase](#)

Rules

[Assignment Rule \(variable: total_cyclin\)](#)

[Assignment Rule \(variable: total_cdc2\)](#)

Physical entities

☐ Compartments

☐ Species

☐ cell

☐ [EmptySet](#)

☐ [cdc2k](#)

☐ [cdc2k-P](#)

☐ [p-cyclin_cdc2](#)

☐ [p-cyclin_cdc2-p](#)

☐ [cyclin](#)

☐ [p-cyclin](#)

☐ [total_cyclin](#)

☐ [total_cdc2](#)



BIOMD0000000005 - Tyson1991 - Cell Cycle 6 var

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

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

 View the submodel in SBML

Reactions (1)

+ cdc2k dephosphorylation [\[cdc2k-P\]](#) → [\[cdc2k\]](#);

Compartments (1)

| | | | |
|----------------------|--------|-----------|------------------------------------|
| cell | set #1 | bqbiol:ls | Gene Ontology cell |
| Referred to as: cell | | | |

Species (2)

| | |
|-------------------|----------------------|
| + cdc2k | Initial amount: 0.0 |
| Compartment: cell | |
| + cdc2k-P | Initial amount: 0.75 |
| Compartment: cell | |

Fully valid SBML model containing only the dephosphorylation of cdc2k

- Download SBML
- SBML L2 V1 (auto-generated)
- SBML L2 V3 (auto-generated)
- SBML L2 V4 (curated)**
- SBML L3 V1 (auto-generated)
- SBML L2 V4 (curated with URNs)

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

Reference Publication

Publication ID: [1831270](#)

Curated version of the model

ate 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: 16 May 2013 14:40:43 UTC

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

Encoders: [Bruce Shapiro](#)
[Vijayalakshmi Chelliah](#)

| | | |
|--------|--------------------|--|
| set #1 | bqbiol:hasVersion | Reactome REACT_152 |
| set #2 | bqbiol:isVersionOf | KEGG Pathway sce04111 |
| | | Gene Ontology mitotic cell cycle |
| | bqbiol:occursIn | Taxonomy Opisthokonta |

Notes

Tyson1991 - Cell Cycle 6 var

Mathematical model of the interactions of cdc2 and cyclin.

This model is described in 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

BIOMD0000000005 - Tyson1991_CellCycle_6var

Download SBML

Other formats (auto-generated)

Actions

Submit Model Comment/Bug

Model

Publication ID: [1831270](#)

Original Model

Submitter

Submission

Submission

Last Modified

Creation

Encoders

SBML Model Report

Model name: "Tyson1991_CellCycle_6var"



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 Shapiro¹ and Vijayalakshmi Chelliah² 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.

| 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 |
|-------------|
| |

¹NASA Jet Propulsion Laboratory, bshapiro@jpl.nasa.gov

²EMBL-EBL, vij@ebi.ac.uk

Produced by SBML2LaTeX

Math

Physical

Reference Publications

1831270

promoting factor) th

I show that the co

We associate the

growth-controlled

of Annotated Pub

triquez N. Dharur,

ated resource for published quantitative kinetic models. BMC Syst Biol., 4:92.

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>
```


BIOMD0000000005 - Tyson1991_CellCycle_6var

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

Model | Overview | Math

Publication ID: [1831270](#)

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

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

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

Biomodels Home | Index | JWS Online

Model

Original Model: [BIOMD0000000005.xml.origin](#)

Submitter: [Nicolas Le Novère](#)

Submission ID: MODEL6614644188

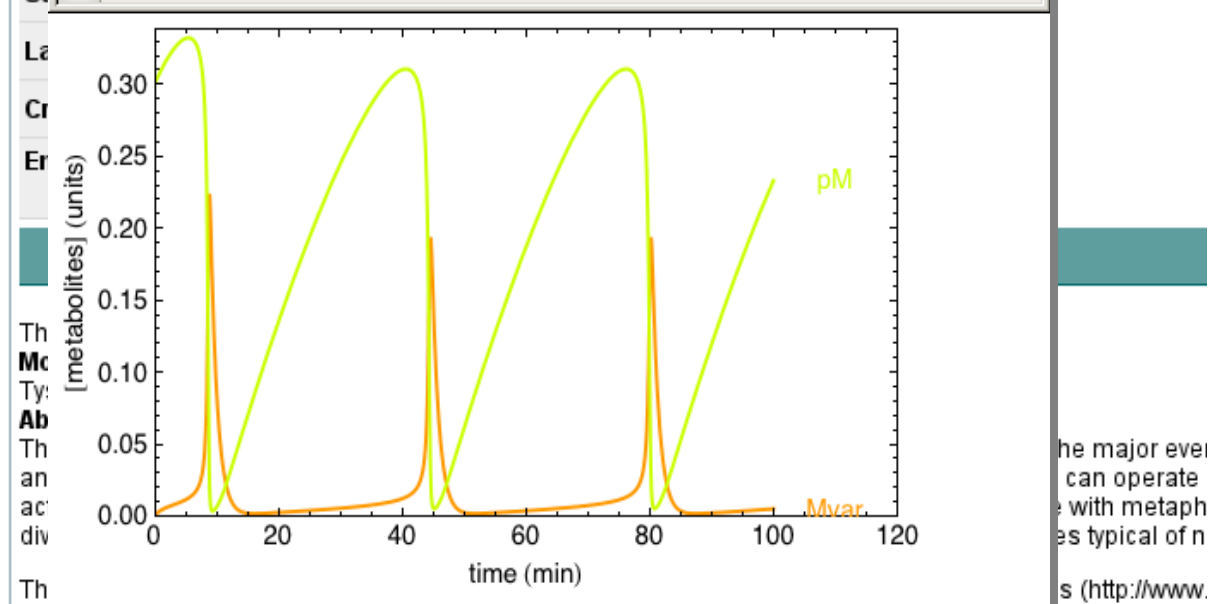
St [http://jjj.mib.ac.uk/webMathematica/Examples/PlotScript11.jsp?fun="JWS`Tyson199](#)

bqbiol:hasVersion [Reactome REACT_152](#)

set#1 bqbiol:isVersionOf [KEGG Pathway sce0411](#)

bqbiol:occursIn [Taxonomy Fungi/Metazo](#)

[Gene Ontology mitotic ce](#)



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

Chelliah V. L. [et al. \(2006\) Quantitative kinetic models. BMC Syst Biol., 4:92.](#)

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 | vRea... | ☐ |
| F2 | vRea... | ☐ |
| F3 | vRea... | ☐ |
| F4 | vRea... | ☐ |
| F5 | vRea... | ☐ |
| F6 | vRea... | ☐ |
| F7 | vRea... | ☐ |
| F8 | vRea... | ☐ |

Reset

POWERED BY webMATHEMATICA2

Applet jjjApplet started

zotero

From pathways to models ... Path2Models



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



Path2Models is a branch of BioModels Database dedicated to hosting models automatically generated from pathway resources, such as [KEGG](#), [BioCarta](#), [MetaCyc](#), [PID](#) and [SABIO-RK](#).

Browse models

Models from this branch 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:

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)

Additional information

Those automatically generated models are only partially parameterized. In the case of KEGG signaling pathways for which no mechanistic details are provided, the models (with qual constructs) contain only topological relationships together with interaction signs. No logical rules specify the effects of (combined) interactions, and these models should be seen as scaffolds to be further parameterized before use in simulation. This can be done either by considering default, yet biologically meaningful, logical functions

Here are all the whole genome metabolism models available:

- [\[Eubacterium\] cylindroides T2-87](#)
- [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 \(strain ATCC 23270 / DSM 14882 / NCIB 8455\)](#)
- [Acidithiobacillus ferrooxidans \(strain ATCC 53993\)](#)
- [Acidobacterium capsulatum \(strain ATCC 51196 / DSM 11244 / JCM 7670\)](#)
- [Acidothermus cellulolyticus \(strain ATCC 43068 / 11B\)](#)
- [Acidovorax avenae \(strain ATCC 19860 / DSM 7227 / JCM 20985 / NCPPB 1011\)](#)
- [Acidovorax citrulli \(strain AAC00-1\)](#)
- [Acidovorax ebreus \(strain TPSY\)](#)
- [Acidovorax sp. \(strain JS42\)](#)

Whole Genome Metabolism - Homo sapiens

[Download SBML](#)[SBML L2 V4](#)[SBML L2 V4 \(with Identifiers.org URLs\)](#)[Send feedback](#)

Model information

Identifier: [BMID000000140905](#)**Project:** [path2models](#)**Submission:** 19 May 2012 15:48:00 UTC**Format:** SBML L2 V4**Categories:** [genome-scale](#)**Last modified:** 04 Oct 2013 04:05:27 UTC**Published:** 19 May 2012 23:49:21 UTC

Annotations

| | | |
|-------------------------------|--|--------------------|
| occursIn | Homo sapiens | <i>Taxonomy</i> |
| IsDerivedFrom | Homo sapiens (human) | <i>KEGG Genome</i> |
| IsDescribedBy | Initial sequencing and analysis of the human genome. | <i>PubMed</i> |
| IsDescribedBy | The sequence of the human genome. | <i>PubMed</i> |
| IsDescribedBy | Finishing the euchromatic sequence of the human genome. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence and biological annotation of human chromosome 1. | <i>PubMed</i> |
| IsDescribedBy | Generation and annotation of the DNA sequences of human chromosomes 2 and 4. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence, annotation and analysis of human chromosome 3. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence and comparative analysis of human chromosome 5. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence and analysis of human chromosome 6. | <i>PubMed</i> |
| IsDescribedBy | Human chromosome 7: DNA sequence and biology. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence of human chromosome 7. | <i>PubMed</i> |
| IsDescribedBy | DNA sequence and analysis of human chromosome 8. | <i>PubMed</i> |
| IsDescribedBy | DNA sequence and analysis of human chromosome 9. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence and comparative analysis of human chromosome 10. | <i>PubMed</i> |
| IsDescribedBy | Human chromosome 11 DNA sequence and analysis including novel gene identification. | <i>PubMed</i> |
| IsDescribedBy | The finished DNA sequence of human chromosome 12. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence and analysis of human chromosome 13. | <i>PubMed</i> |
| IsDescribedBy | The DNA sequence and analysis of human chromosome 14. | <i>PubMed</i> |
| IsDescribedBy | Analysis of the DNA sequence and duplication history of human chromosome 15. | <i>PubMed</i> |
| IsDescribedBy | The sequence and analysis of duplication-rich human chromosome 16. | <i>PubMed</i> |

BioModels Web Services

With BioModels Web Services, users can programmatically access up-to-date information from BioModels Database without installing a local copy of the database. They provide a wide range of features for searching and retrieving models. Furthermore, some features can help users to extract interesting parts from a large model and assemble them into a fully valid submodel. For any comments or new feature enquiries, please feel free to [contact us](#).

Available features

- [Available features](#)
- [WSDL](#)

The list of available features's page describes all the available services in a nice human readable way, included a detailed description of all methods. The WSDL (Web Services Description Language) defines the provided services in an XML format file. This enables third-party software to automatically generate clients for accessing the services.

Java library

The Java library provides a very convenient way to use the web services. It gives access to improved methods (for example giving access to 'SimpleModel' objects rather than raw XML) in order to make the use of the web services easier.

Documentation

The library documentation gives information for developers wishing to use the API:

- [Java library documentation \(Javadoc\)](#)

Get the library via Maven

The library is available from the EBI Maven repository.

You just need to add the following to your pom.xml to get it and all its dependencies:

```
<dependencies>
  <dependency>
    <groupId>uk.ac.ebi.biomodels</groupId>
    <artifactId>biomodels-wslib</artifactId>
    <version>1.21</version>
  </dependency>
</dependencies>

<repositories>
<repository>
  <id>ebi-repo</id>
  <name>The EBI internal repository</name>
  <url>http://www.ebi.ac.uk/~maven/m2repo</url>
  <releases>
    <enabled>true</enabled>
  </releases>
</repository>
</repositories>
```

Index of ftp://ftp.ebi.ac.uk/pub/databases/biomodels/weekly_archives/2012/

[Up to higher level directory](#)

| Name | Size | Last Modified |
|---|----------|-------------------|
|  BioModels-Database-weekly-2012-01-02-sbmls.tar.gz | 11734 KB | 22/03/12 00:00:00 |
|  BioModels-Database-weekly-2012-01-09-sbmls.tar.gz | 11735 KB | 22/03/12 00:00:00 |
|  BioModels-Database-weekly-2012-01-16-sbmls.tar.gz | 11734 KB | 22/03/12 00:00:00 |

Index of ftp://ftp.ebi.ac.uk/pub/databases/biomodels/releases/

[Up to higher level directory](#)

| Name | Size | Last Modified |
|--|------|-------------------|
|  2005-04-11 | | 08/02/12 00:00:00 |
|  2005-06-01 | | 08/02/12 00:00:00 |
|  2005-07-28 | | 08/02/12 00:00:00 |
|  2006-01-31 | | 08/02/12 00:00:00 |

Index of ftp://ftp.ebi.ac.uk/pub/databases/biomodels/releases/latest/

[Up to higher level directory](#)

| Name | Size | Last Modified |
|--|------------|-------------------|
|  BioModels_Database-r23_p2m-metabolic.tar.bz2 | 1966032 KB | 10/08/12 15:19:00 |
|  BioModels_Database-r23_p2m-non_metabolic.tar.bz2 | 78726 KB | 10/08/12 15:19:00 |
|  BioModels_Database-r23_p2m-whole_genome_metabolism.tar.bz2 | 509109 KB | 10/08/12 15:20:00 |
|  BioModels_Database-r23_pub-all_files.tar.bz2 | 601968 KB | 10/08/12 21:03:00 |
|  BioModels_Database-r23_pub-sbml_files.tar.bz2 | 10992 KB | 11/08/12 13:10:00 |

[Services](#) >
[BioModels](#) >
 BioModels SPARQL Endpoint

BioModels SPARQL Endpoint

Enter SPARQL Query

```

PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX owl: <http://www.w3.org/2002/07/owl#>
PREFIX xsd: <http://www.w3.org/2001/XMLSchema#>
PREFIX dc: <http://purl.org/dc/elements/1.1/>
PREFIX dcterms: <http://purl.org/dc/terms/>
PREFIX foaf: <http://xmlns.com/foaf/0.1/>
PREFIX skos: <http://www.w3.org/2004/02/skos/core#>
PREFIX sbmlrdf: <http://identifiers.org/biomodels.vocabulary#>

SELECT ?speciesid ?name WHERE {
  <http://identifiers.org/biomodels.db/BIOMD0000000001> sbmlrdf
    ?speciesid sbmlrdf:name ?name}
  
```

<

>

Results per page: 25

Output: HTML

Submit Query

Reset

Example Queries

Query 1

List all species identifiers and their names in model <http://identifiers.org/biomodels.db/BIOMD0000000001>

Query 2

Get element annotations of the model <http://identifiers.org/biomodels.db/BIOMD0000000001>

Query 3

All model elements with annotations to acetylcholine-gated channel complex (<http://identifiers.org/go/GO:0005892>)

Additional example queries can be found in the [documentation](#) page.

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](#), Vincent Knight-Schrijver, Audald Lloret, 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



EMBL-EBI



Innovative Medicines Initiative

