

The NormSys registry for modeling standards in systems and synthetic biology

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The NormSys Registry for Modeling Standards

This registry aims at surveying standard formats for computational modeling in biology. It not only lists the standards, but also compares their major features, their possible fields of biological application and use cases (including model examples), as well as their relationships, commonalities and differences. This registry provides a common entry point for modelers and software developers who plan to apply the standards for their respective case of application, and serves them with detailed information and links to the standards, their specifications and APIs.

The information provided in this system does not claim to be complete or all-encompassing, nor can we guarantee any absence of defectiveness. However, we collect and assemble the information to the best of our knowledge and belief to assist in selecting the appropriate standard format for your specific requirements. Please note that the system is work in progress and is constantly revised and extended. Any feedback and suggestions for corrections or improvements, as well as for new fields of applications to be included (with example models) are highly welcome.

<http://normsys.h-its.org/>

Format Classes

Systems Biology Markup Language (SBML)

[Formats](#)

[Details](#)

CellML

[Formats](#)

[Details](#)

Systems Biology Graphical Notation (SBGN)

[Formats](#)

[Details](#)

Simulation Experiment Description Markup Language (SED-ML)

[Formats](#)

[Details](#)

Pharmacometrics Markup Language (pharmML)

[Formats](#)

[Details](#)

NeuroML

[Formats](#)

[Details](#)

FieldML

[Formats](#)

[Details](#)

Synthetic Biology Open Language (SBOL)

[Formats](#)

[Details](#)

Supported by:

Show results for:

Select

Format

or filter by

Format class

- ✓ CellML
- FieldML
- NeuroML
- Pharmacometrics Markup Language (pharmML)
- Simulation Experiment Description Markup Language (SED-ML)
- Synthetic Biology Open Language (SBOL)
- Systems Biology Graphical Notation (SBGN)
- Systems Biology Markup Language (SBML)

Software

Api language

Supported biological scale

- ☐ molecular
- ☐ cellular
- ☐ tissue

Standard Formats

Displaying: 1 Found: 1 Total: 16

CellML 1.1

CellML 1.1

Synopsis

CellML represents models as a network of components, representing abstract concepts, that are connected through well-defined Interfaces.

CellML is a XML-based exchange format developed by the University of Auckland in collaboration with Physiome Sciences, Inc. CellML 1.1 has a modular architecture allowing a modeller to build complex systems of models that expand and reuse previously published models. CellML 1.1 is a format for encoding contextual information for a model. CellML 1.1 can be used in conjunction with CellML Metadata to provide a complete description of the structure and underlying mathematics of biological models. A repository of over 200 electrophysiological, mechanical, signal and metabolic pathway models is available at www.cellml.org.*

*(Autumn A. Cuellar et al. SIMULATION December 2003 79: 740-747, doi:10.1177/0037549703040939)

Biological Applications		Class	Details	License	Links	Transformations	APIs	Validator								
Biological Application	Format	Multi-organism Process	Cell Cycle	Signaling	Pharmacokinetic	Pharmacodynamics	Metabolic Process	Immune Response	Circadian Rhythm	Regulation of Gene Expression	Electrophysiology	Neuronal Network	Multicellular Organismal Process	Regulation of Growth	Predatory Beh	Qv
		CellML 1.1	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

Supported by:

Show results for:

Select

Format

or filter by

Format class

Biological application

Modeling formalism

Software

Api language

Supported biological scale

- ☐ molecular
- ☐ cellular
- ☐ tissue
- ☐ organ
- ☐ organism
- ☐ ecosystem

Spatial representation

- ☐ Compartment
- ☐ Dimensions

Standard Formats

Displaying: 1 Found: 1 Total: 16

SBML L3V1 Core

Systems Biology Markup Language Level 3 Version 1 Core

Synopsis

Representation of biological processes as a set of processes, that are converting pools of entities into other pools entities.

Description

Systems Biology Markup Language (SBML), a free, open, XML-based format for representing biochemical reaction networks. SBML is a software-independent language for describing models common to research in many areas of computational biology, including cell signaling pathways, metabolic pathways, gene regulation, and others.*

*(M. Hucka et al. Bioinformatics (2003) 19 (4): 524-531)

Biological Applications

Class

Details

License

Links

Transformations

APIs

Validator

Publication Date

🕒 10/2010

Authors

👤 Hucka, Michael
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👤 C. Schaff, James

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👤 P. Smith, Lucian

👤 M. Keating, Sarah
👤 J. Wilkinson, Darren

Organizations

- combine

Biological Scales

Scale	molecular	cellular	tissue	organ	organism	ecosystem
Support	Intrinsic	potential	potential	unknown	unknown	potential

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Spatial Representation

- ☐ Compartment
- ☐ Dimensions
- ☐ Gradients
- ☐ SpatialStructures

Support for Units

Filter

Support

Intrinsic

potential

potential

unknown

unknown

potential

Spatial Representation

Spatial Representation Level

Compartment

Dimensions

Gradients

SpatialStructures

Support

Intrinsic

Intrinsic

unknown

unknown

Modeling Formalisms for this format

Software support for this format

Examples for this format

Advantage

- Multiscale Models

Modularity:

no

Components Relation Flat Network:

no

Supported Math

MathML Support:

yes

Full MathML Support:

no

Unit Support

Unit Required:

no

Support:

Intrinsic

Description

units are more like a form of annotation; every transformation of values implied by units must be encoded explicitly

Annotation Support

Miriam Support:

yes

identifiers.org Support:

yes

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and Energy



Spatial representation

- ☐ Compartment
- ☐ Dimensions
- ☐ Gradients
- ☐ SpatialStructures

Support for Units

Multiscale Models

Models that are capable to integrate multiple biological scales at once.

Advantage

Multiscale Models

Support

Intrinsic

potential

potential

unknown

unknown

potential

Spatial Representation

Spatial Representation Level	Compartment	Dimensions	Gradients	SpatialStructures
Support	Intrinsic	Intrinsic	unknown	unknown

[Modeling Formalisms](#) for this format

[Software support](#) for this format

[Examples](#) for this format

Modularity:

no

Components Relation Flat Network:

no

Supported Math

MathML Support:

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Full MathML Support:

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Unit Required:

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Miriam Support:

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Show results for:

Select

Format

or filter by

Format class

Biological application

Modeling formalism

Software

Api language

Supported biological scale

☐ molecular

Standard Formats

Displaying: 1 Found: 1 Total: 16

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*M. Hucka et al. Bioinformatics (2003) 19 (4): 524-531

[Biological Applications](#)

[Class](#)

[Details](#)

[License](#)

[Links](#)

[Transformations](#)

[APIs](#)

[Validator](#)

Webpage

- [SBML](#)

Specification

- [SBML](#)
- [The Systems Biology Markup Language \(SBML\): Language Specification for Level 3 Version 1 Core](#)

Publication

- [The systems biology markup language \(SBML\): a medium for representation and exchange of biochemical network models.](#)

Model repository

- [BioModels Database](#)

Software Repository

- [SBML Software Guide](#)

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or filter by

Format class

Biological application

Modeling formalism

Software

Api language

Supported biological scale

- ☐ molecular
- ☐ cellular
- ☐ tissue
- ☐ organ
- ☐ organism
- ☐ ecosystem

Spatial representation

- ☐ Compartment

Standard Formats

Displaying: 1

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*(M. Hucka et al. Bioinformatics (2003) 19 (4): 524-531)

	Biological Applications	Class	Details	License	Links	Transformations	APIs	Validator
Output								
Input	SBML L3V1 Core	CellML 1.1	SBGN PD L1 V1.3	NeuroML 2 beta 3	SBOL v2.0	SBGN-ML 0.2		
SBML L3V1 Core	—	libAntimony	CellDesigner Arcadia	jNeuroML	—	SBML2SBGNML		
CellML 1.1	libAntimony	—	—	—	—	—		
SBGN PD L1 V1.3	—	—	—	—	—	—		
NeuroML 2 beta 3	jNeuroML	—	—	—	—	—		
SBOL v2.0	iBioSim	—	—	—	—	—		
SBGN-ML 0.2	—	—	—	—	—	—		

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Show results for:

Select

Software

libAntimony ▼

or

Search by name

filter by

Formats

Biophysics v1.8.1
CellML 1.1
ChannelML v1.8.1
FieldML v0.5

(hold ctrl for multiple selection or to deselect)

Filter

Software

Displaying: 1 Found: 1 Total: 13

libAntimony

Formats

- [Systems Biology Markup Language Level 3 Version 1 Core](#)
- [CellML 1.1](#)

Links

Software

- [libAntimony](#)



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[Software](#)
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Biological Applications

Format Transformation

Input \ Output	SBML L3V1 Core	CellML 1.1	SBGN PD L1 V1.3	NeuroML 2 beta 3	SBOL v2.0	SBGN-ML 0.2
SBML L3V1 Core	—	libAntimony	CellDesigner Arcadia	jNeuroML	—	SBML2SBGNML
CellML 1.1	libAntimony	—	—	—	—	—
SBGN PD L1 V1.3	—	—	—	—	—	—
NeuroML 2 beta 3	jNeuroML	—	—	—	—	—
SBOL v2.0	iBioSim	—	—	—	—	—
SBGN-ML 0.2	—	—	—	—	—	—

Biological Application	Format	<div> <div>Biological Applications</div> <div>Format Transformation</div> </div>												
		SBML L3V1 Core	CellML 1.1	SBGN ER L1 V1.2	SBGN PD L1 V1.3	SBGN AF L1 V1.0	MorphML v1.8.1	NeuroML 2 beta 3	PharmML v0.6	SBOL v2.0	SBOL Visual v1.0.0	ChameiML v1.8.1	Biophysics v1.8.1	NetworkML v1.8.1
Multi-organism Process		✓	✓	—	—	—	—	—	—	—	—	—	—	—
Cell Cycle		✓	✓	✓	—	—	—	—	—	—	—	—	—	—
Signaling		✓	✓	✓	✓	—	—	—	—	—	—	—	—	—
Single Cell Morphology		—	—	—	—	✓	✓	—	—	—	—	—	—	—
Pharmacokinetic		✓	✓	—	—	—	—	✓	—	—	—	—	—	—
Pharmacodynamics		✓	✓	—	—	—	—	✓	—	—	—	—	—	—
Izhikevich-based Neuron Models		✓	—	—	—	—	✓	—	—	—	—	—	—	—
Synthetic Gene Regulatory Network		✓	—	✓	✓	✓	—	—	✓	✓	—	—	—	—
Metabolic Process		✓	✓	—	✓	—	—	✓	—	—	—	—	—	—
Immune Response		✓	✓	—	—	✓	—	—	—	—	—	—	—	—
Circadian Rhythm		✓	✓	✓	—	—	✓	—	—	—	—	—	—	—
Regulation of Gene Expression		✓	✓	✓	✓	✓	—	—	✓	✓	—	—	—	—
Electrophysiology		✓	✓	—	—	—	✓	—	—	—	✓	✓	—	—

The NormSys Registry: Biological Applications

NORMSYS Modeling Standards in Systems Biology

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Show results for:

Select

Biological Application

Cell Cycle ▾

or

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filter by

Formats

Biophysics v1.8.1
CellML 1.1
ChannelML v1.8.1
FieldML v0.5

(hold ctrl for multiple selection or to deselect)

Filter

Biological Application

Displaying: 1 Found: 1 Total: 34

Cell Cycle

Description

The progression of biochemical and morphological phases and events that occur in a cell during successive cell replication or nuclear replication events. Canonically, the cell cycle comprises the replication and segregation of genetic material followed by the division of the cell, but in endocycles or syncytial cells nuclear replication or nuclear division may not be followed by cell division.

Formats

- [Systems Biology Markup Language Level 3 Version 1 Core](#)
- [CellML 1.1](#)
- [SBGN Entity Relationship language Level 1 Version 1.2](#)
- [Systems Biology Markup Language Level 2 Version 5](#)

Details

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- [CellML 1.1](#)
- [SBGN Entity Relationship language Level 1 Version 1.2](#)
- [Systems Biology Markup Language Level 2 Version 5](#)

Details

Examples

- [Mathematical model of the cell division cycle of fission yeast](#)
- [Modeling the control of DNA replication in fission yeast.](#)
- [A comprehensive molecular interaction map of the budding yeast cell cycle](#)

Links

Ontology

- cell cycle

Links to Ontology Terms (GO)



AmiGO 2

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[AmiGO 1.8](#)



cell cycle

Term Information ⓘ

Accession GO:0007049

Name cell cycle

Ontology biological_process

Synonyms cell-division cycle

Alternate IDs None

Definition The progression of biochemical and morphological phases and events that occur in a cell during successive cell replication or nuclear replication events. Canonically, the cell cycle comprises the replication and segregation of genetic material followed by the division of the cell, but in endocycles or syncytial cells nuclear replication or nuclear division may not be followed by cell division. *Source:* GOC:go_curators, GOC:mtg_cell_cycle

Comment None

History See term [history](#) for GO:0007049 at QuickGO

Subset gosubset_prok
goslim_plant
goslim_generic
goslim_pir
goslim_candida
gocheck_do_not_manually_annotate
goslim_aspergillus
goslim_chembl

Related [Link](#) to all **genes and gene products** annotated to cell cycle.

[Link](#) to all direct and indirect **annotations** to cell cycle.

[Link](#) to all direct and indirect **annotations download** (limited to first 10,000) for cell cycle.

[Data health](#) ♥



Show results for:

Select

Biological Application

Cell Cycle ▾

or

Search by name

filter by

Formats

[Biophysics v1.8.1](#)
[CellML 1.1](#)
[ChannelML v1.8.1](#)
[FieldML v0.5](#)

(hold ctrl for multiple selection or to deselect)

Filter

Biological Application

Displaying: 1 Found: 1 Total: 34

Cell Cycle

Description

The progression of biochemical and morphological phases and events that occur in a cell during successive cell replication or nuclear replication events. Canonically, the cell cycle comprises the replication and segregation of genetic material followed by the division of the cell, but in endocycles or syncytial cells nuclear replication or nuclear division may not be followed by cell division.

Formats

- [Systems Biology Markup Language Level 3 Version 1 Core](#)
- [CellML 1.1](#)
- [SBGN Entity Relationship language Level 1 Version 1.2](#)
- [Systems Biology Markup Language Level 2 Version 5](#)

Details

Examples

- [Mathematical model of the cell division cycle of fission yeast](#)
- [Modeling the control of DNA replication in fission yeast.](#)
- [A comprehensive molecular interaction map of the budding yeast cell cycle](#)

Links

Ontology

- [cell cycle](#)

Show results for:

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Example

Mathematical model of the cell divisio ▾

or

Search by name

filter by

Formats

Biophysics v1.8.1
CellML 1.1
ChannelML v1.8.1
FieldML v0.5

(hold ctrl for multiple selection or to deselect)

Filter

Example

Displaying: 1 Found: 1 Total: 69

Mathematical model of the cell division cycle of fission yeast

Description

Mathematical model of the cell division cycle of fission yeast

Model Status

This CellML version of the model has been checked in COR and PCEnv and the model runs to replicate the results in the original published paper. The units have been checked and are consistent.

Model Structure

ABSTRACT: Much is known about the genes and proteins controlling the cell cycle of fission yeast. Can these molecular components be spun together into a consistent mechanism that accounts for the observed behavior of growth and division in fission yeast cells? To answer this question, we propose a mechanism for the control system, convert it into a set of 14 differential and algebraic equations, study these equations by numerical simulation and bifurcation theory, and compare our results to the physiology of wild-type and mutant cells. In wild-type cells, progress through the cell cycle ($G1 \rightarrow S \rightarrow G2 \rightarrow M$) is related to cyclic progression around a hysteresis loop, driven by cell growth and chromosome alignment on the metaphase plate. However, the control system operates much differently in double-mutant cells, *wee1(-) cdc25Delta*, which are defective in progress through the latter half of the cell cycle (G2 and M phases). These cells exhibit "quantized" cycles (interdivision times clustering around 90, 160, and 230 min). We show that these quantized cycles are associated with a supercritical Hopf bifurcation in the mechanism, when the *wee1* and *cdc25* genes are disabled. (c) 2001 American Institute of Physics.

The original paper reference is cited below:

Mathematical model of the cell division cycle of fission yeast, Bela Novak, and Zsuzsa Pataki, 2001, *CHAOS*, 11, 277-286. PubMed ID: 12779461

Formats

- [CellML 1.1](#)

Links

Example

- Mathematical model of the cell division cycle of fission yeast

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Novak, Pataki, Ciliberto, Tyson, 2001

Exposure Information

[Latest Exposure](#)

If you are a new user to the repository, you may wish to view the exposure for this workspace. An exposure will show the summarized information for the content contained here.

Workspace Summary








Owner

admin

URI for git clone/pull/push

https://models.physiomeproject.org/workspace/novak_pataki_ciliberto_tyson_2001

Files

Filename	Size	Date	Options
 .DS_Store	6148	2010-07-05	[browse]
 novak_2001.ai	248622	2010-07-05	[browse]
 novak_2001.png	52931	2010-07-05	[browse]
 novak_2001.svg	169462	2010-07-05	[browse]
 novak_pataki_ciliberto_tyson_2001.cellml	55389	2010-07-05	[browse]
 novak_pataki_ciliberto_tyson_2001.session.xml	21189	2010-07-05	[browse] [run]
 novak_pataki_ciliberto_tyson_2001.xul	217596	2010-07-05	[browse]

Show results for:

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Format

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Format class

Biological application

Modeling formalism

Software

Api language

Supported biological scale

- ☐ molecular
- ☐ cellular
- ☐ tissue

Standard Formats

Displaying: 1 Found: 1 Total: 18

FieldML v0.5

FieldML Version 0.5

Synopsis

Declarative language for representing hierarchical models using generalized mathematical fields.

Description

The FieldML project has made significant progress towards the goal of addressing the need to have open standards and open source software for representing finite element method (FEM) models and, more generally, multivariate field models, such as many of the models that are core to the euHeart project and the Physiome project. FieldML version 0.5 is the most recently released format from the FieldML project. It is an XML format that already has sufficient capability to represent the majority of euHeart's explicit models such as the anatomical FEM models and simulation solution fields. The details of FieldML version 0.5 are presented, as well as its limitations and some discussion of the progress being made to address these limitations.*

*(Britten RD et al. Medical & Biological Engineering & Computing. 2013;51(11):1191-1207.)

Biological Applications	Class	Details	License	Links	Transformations	APIs	Validator
<div> <div>Biological Application</div> <div> <div>Single Cell Morphology</div> <div>Organ Morphology</div> <div>Tissue Morphology</div> </div> </div>							
Format							
FieldML v0.5	✓	✓	✓				

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The NormSys Registry for Modeling Standards

NORMSYS Modeling Standards in Systems Biology

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Show results for:

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Biological Application

Single Cell Morphology ▾

or

Search by name

filter by

Formats

Biophysics v1.8.1
CellML 1.1
ChannelML v1.8.1
FieldML v0.5

(hold ctrl for multiple selection or to deselect)

Filter

Biological Application

Displaying: 1 Found: 1 Total: 34

Single Cell Morphology

Description

Model featuring the spatial structure of a Neuron.

Formats

- [NeuroML Version 1.8.1 Level 1 MorphML](#)
- [NeuroML 2 beta 3](#)
- [FieldML Version 0.5](#)

Details

Examples

- [CA1 Pyramidal Cell](#)

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The NormSys Registry for Modeling Standards

NORMSYS Modeling Standards in Systems Biology

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Example

CA1 Pyramidal Cell

or

Search by name

filter by

Formats

Biophysics v1.8.1
CellML 1.1
ChannelML v1.8.1
FieldML v0.5

(hold ctrl for multiple selection or to deselect)

Filter

Example

Displaying: 1 Found: 1 Total: 69

CA1 Pyramidal Cell

Description

Conversion of hippocampal CA1 pyramidal cell from Migliore et al 2005.

Formats

- [NeuroML Version 1.8.1 Level 1 MorphML](#)
- [NeuroML 2 beta 3](#)

Links

Example

- CA1 Pyramidal Cell

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The NormSys Registry: Links to Model Databases

CA1 Pyramidal Cell Migliore et al. 2005

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OSB endorsed project 

Curation against published models: Medium ★★

[Vertebrate](#) / [Mammalian](#) / [Rodent](#) / [Hippocampus](#) / [CA1 Pyramidal cell](#) / CA1 Pyramidal Cell - Migliore et al. 2005

Übersicht Wiki Other tools ▾

- Description >
- Status >
- Members >
- References >

Description



NormSys Registry for Modelling Standards

- **Information** resource for community standards
- **Comparison** of their main characteristics and features
- **Classification** by fields of application (with examples)
- **Transformation** options between the standards
- **Bundled links** to corresponding web resources: specifications, websites, publications, repositories, APIs...
- Direct links to **validation** tools for models
- **Faceted browsing** and search by different criteria
- Initial focus on commonly used community standards: COMBINE standards and related efforts

<http://normsys.h-its.org/>

Concept & project lead: Martin Golebiewski

Design: Jill Zander

Implementation: Nils Wötzel

Content: Martin Golebiewski, Alexander Nikolaew

Collaboration partners:

Susanne Hollmann & Bernd Müller-Röber (University of Potsdam, D)

Babette Regierer (formerly: LifeGlimmer GmbH, Berlin, D)