

Heidelberg Institute for Theoretical Studies



The NormSys registry for modeling standards in systems and synthetic biology

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The NormSys Registry for Modeling Standards

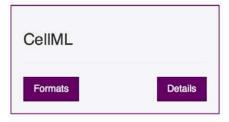
This registry aims at surveying standard formats for computational modeling in biology. It not only lists the standards, but also compares their major features, their possible fields of biological application and use cases (including model examples), as well as their relationships, commonalities and 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.

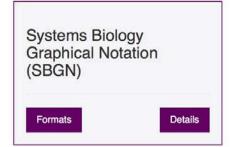
The information provided in this system does not claim to be complete or all-encompassing, nor can we guarantee any absence of defectiveness. However, we collect and assemble the information to the best of our knowledge and belief to to assist in selecting the appropriate standard format for your specific 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.

Format Classes

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

Systems Biology Markup Language (SBML)



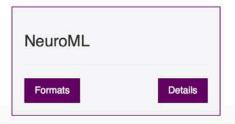




Pharmacometrics Markup Language (pharmML)

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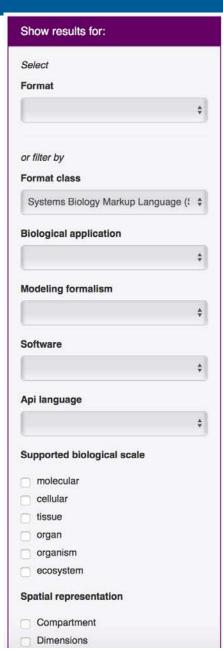


Home Standard Formats Biological Application Modeling Formalism Software Example Matrices -Show results for: Standard Formats Displaying: 1 Found: 1 Total: 16 Select **Format** CellML 1.1 CellML 1.1 or filter by Synopsis Format class es models as a network of components, representing abstract concepts, that are connected through well-defined Interfaces. √ CellML FieldML NeuroML VIL-based exchange format developed by the University of Auckland in collaboration with Physiome Sciences, Inc. CellML 1.1 has a Pharmacometrics Markup Language (pharmML) ied architecture allowing a modeller to build complex systems of models that expand and reuse previously published models. CellML Simulation Experiment Description Markup Language (SED-ML) prmat for encoding contextual information for a model. CellML 1.1 can be used in conjunction with CellML Metadata to provide a complete Synthetic Biology Open Language (SBOL) he structure and underlying mathematics of biological models. A repository of over 200 electrophysiological, mechanical, signal Systems Biology Graphical Notation (SBGN) nd metabolic pathway models is available at www.cellml.org.* Systems Biology Markup Language (SBML) *(Autumn A. Cuellar et al. SIMULATION December 2003 79: 740-747, doi:10.1177/0037549703040939) Software **Biological Applications** Class Details License Links Transformations **APIs** Validator Multicallulat Ardogas Regulation of Gene Biological Infining hesponse Meladolic Frocess Citizadian Bilginin Multi-dragatism Electrophysiology Hendra Hendry Application Api language Eddlession Format Supported biological scale CellML 1.1 molecular cellular tissue

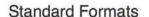








NORM5Y5



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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 softwareindependent 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

O 10/2010

Authors

A Hucka, Michael

- 1. Bergmann, Frank
- A Hoops, Stefan

M. Keating, Sarah

Sahle, Sven

L C. Schaff, James

P. Smith, Lucian

1. Wilkinson, Darren

Organizations

combine

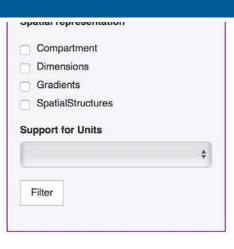
Biological Scales

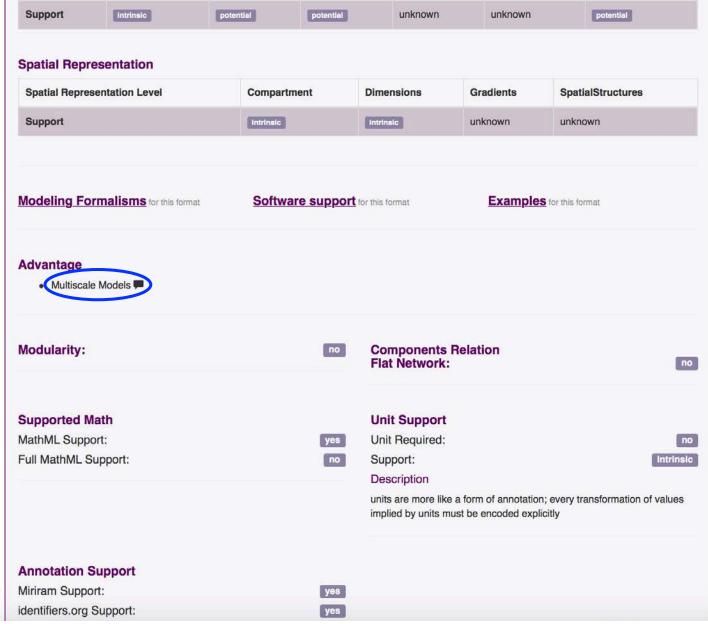
Scale	molecular	cellular	tissue	organ	organism	ecosystem	
Support	Intrinsic	potential	potential	unknown	unknown	potential	







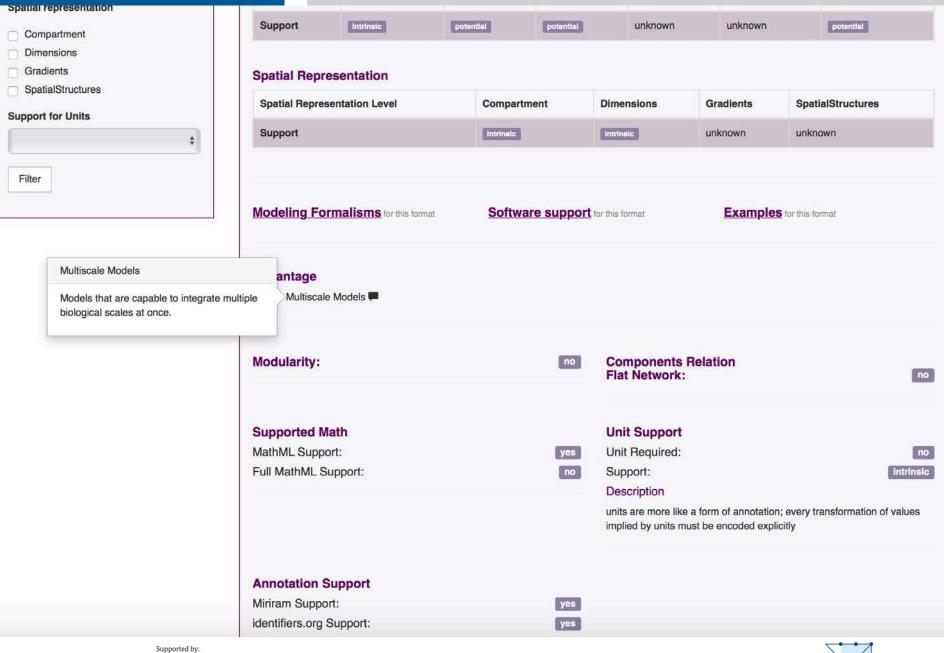


















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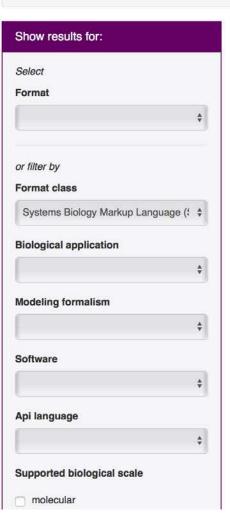
Biological Application

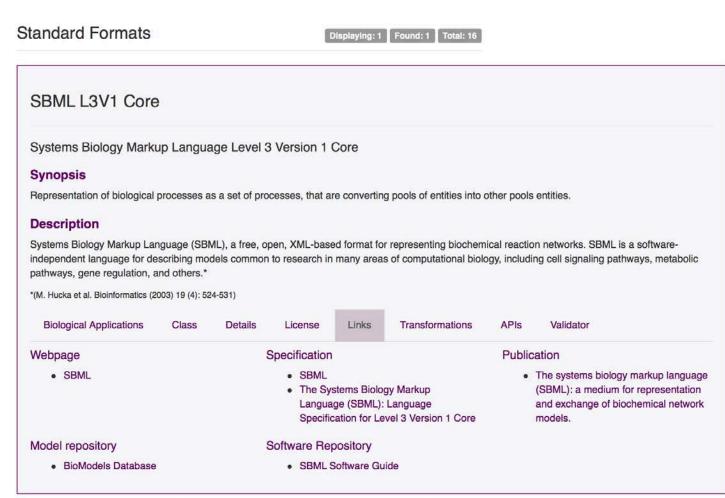
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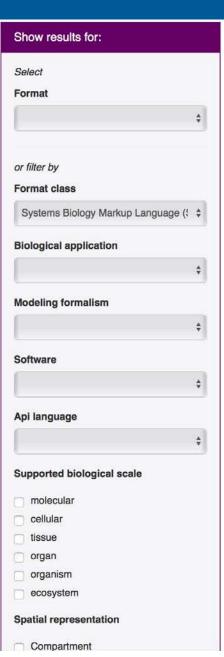














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SBML L3V1 Core

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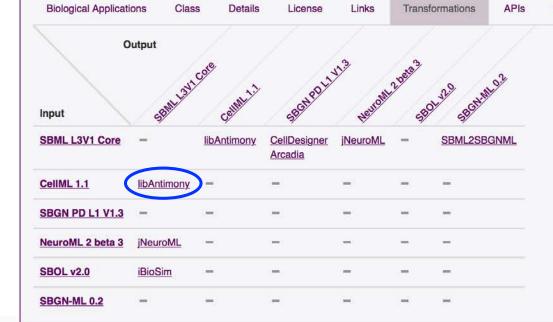
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Validator

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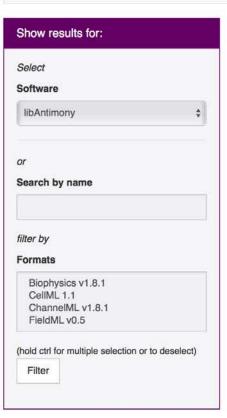
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Output Input SBML L3V1 Core libAntimony CellDesigner **iNeuroML** SBML2SBGNML Arcadia CellML 1.1 **libAntimony** SBGN PD L1 V1.3 NeuroML 2 beta 3 **NeuroML** SBOL v2.0 **iBioSim** SBGN-ML 0.2

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Multi-organism Process	~	1	-	-	-	-	-	-	-	-	-	-	-	
Cell Cycle	4	~	1		-		-		-		-		-	
Signaling	*	~	*	-	~	-	-	-	-	-	-	-	-	
Single Cell Morphology	-		-	— 6	_	1	~	— 6	-		-		-	
Pharmacokinetic Pharmacokinetic	4	~	_	-	_	-	-	4	-	-	-		-	
Pharmacodynamics	1	~	-		_		-	1	-		-		-	
zhikevich-based Neuron Models	4	-	_	-	_	-	*	-	-	-	-	-	-	
Synthetic Gene Regulatory Netwo	rk 🗸		~	~	~	-0	-		~	~	-		-	
Metabolic Process	4	~	-	1	-	-	-	4	-	-	-	-	-	
mmune Response	4	~	-	— 8	1	-	-	— 8	-		-		-	
Circadian Rhythm	*	~	*	-	-	-	*	-	-	-	-	-	-	
Regulation of Gene Expression	•	~	~	*	*	-0	-	-8	~	~	-		-	
<u>Electrophysiology</u>	*	*	-	-	-	-	*	-	-	-	*	*	-	

The NormSys Registry: Biological Applications

NORMSYS Modeling Standards in Systems Biology Standard Formats Biological Application Modeling Formalism Matrices -Home Software Example Show results for: **Biological Application** Displaying: 1 Found: 1 Total: 34 Select **Biological Application** Cell Cycle 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. Search by name 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** filter by Systems Biology Markup Language Level 3 Version 1 Core **Formats** CellML 1.1 SBGN Entity Relationship language Level 1 Version 1.2 Biophysics v1.8.1 Systems Biology Markup Language Level 2 Version 5 CellML 1.1 ChannelML v1.8.1 FieldML v0.5 (hold ctrl for multiple selection or to deselect) Filter







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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
- 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







Links to Ontology Terms (GO)



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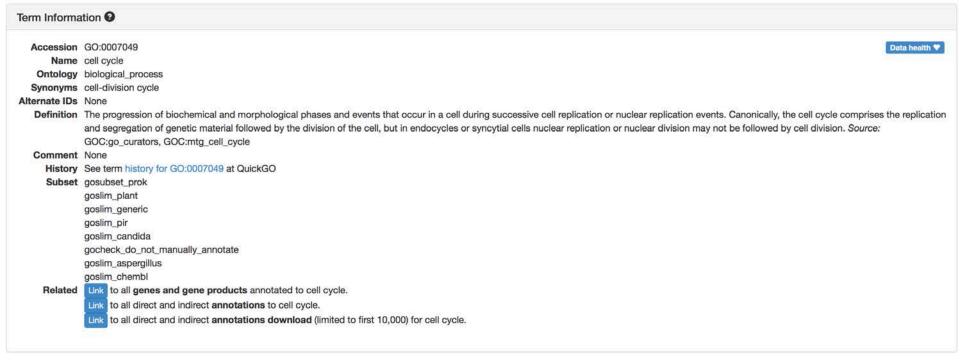
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cell cycle









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Biological Application

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Cell Cycle

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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.

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Links

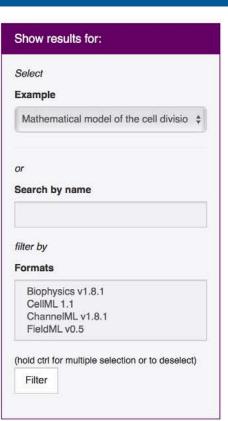
Ontology

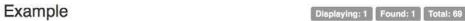
· cell cycle











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-->S-->G2-->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

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 Mathematical model of the cell division cycle of fission yeast











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Novak, Pataki, Ciliberto, Tyson, 2001

Exposure Information

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 Latest Exposure 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]
P.	55389	2010-07-05	[browse]
novak_pataki_ciliberto_tyson_2	2001.cellml		
Ľ	21189	2010-07-05	[browse] [run]
novak_pataki_ciliberto_tyson_2	2001.session.xml		
L	217596	2010-07-05	[browse]
novak pataki ciliberto tyson 2	2001.xul		

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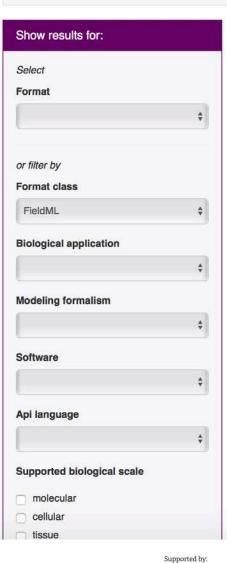
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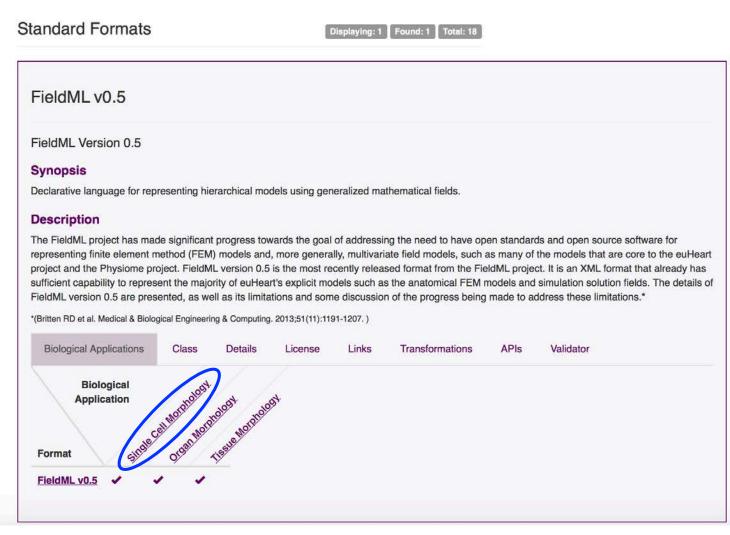
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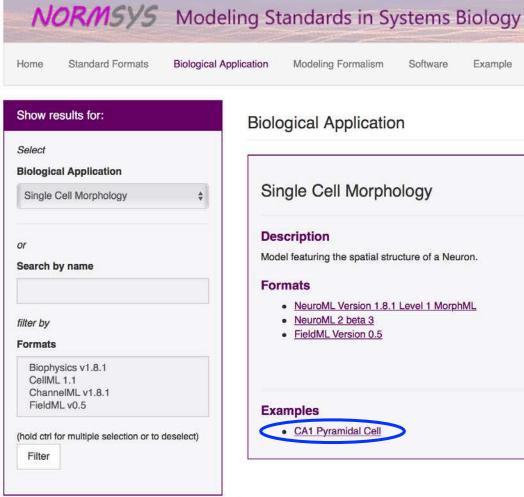
The NormSys Registry for Modeling Standards

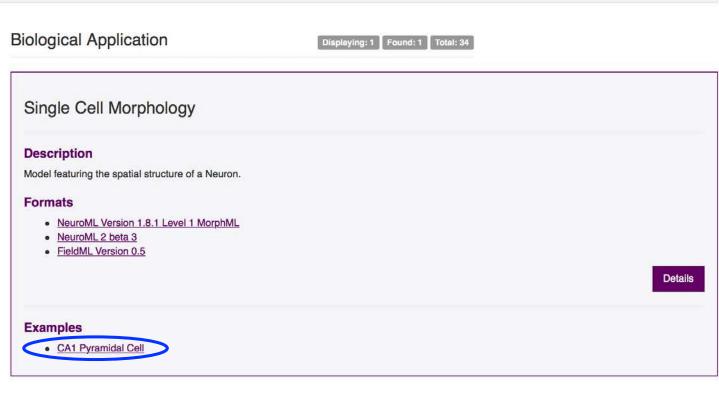
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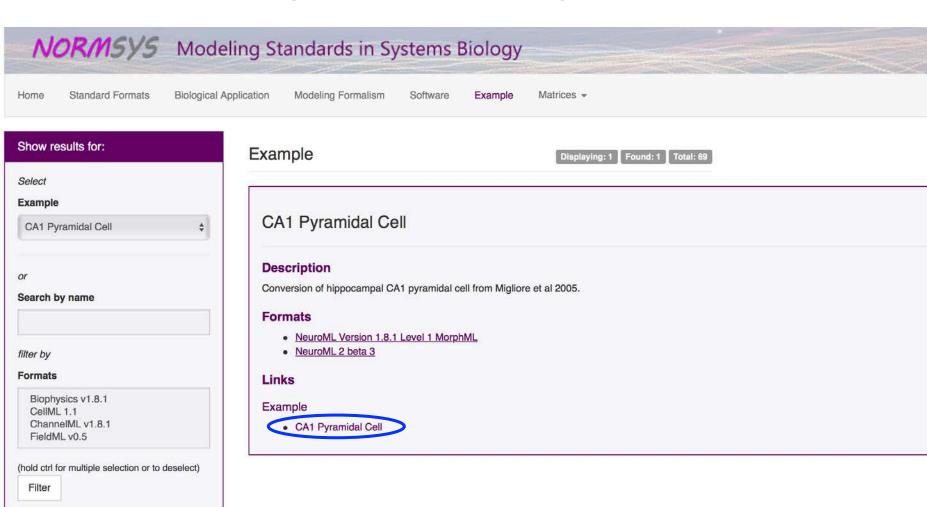








The NormSys Registry for Modeling Standards

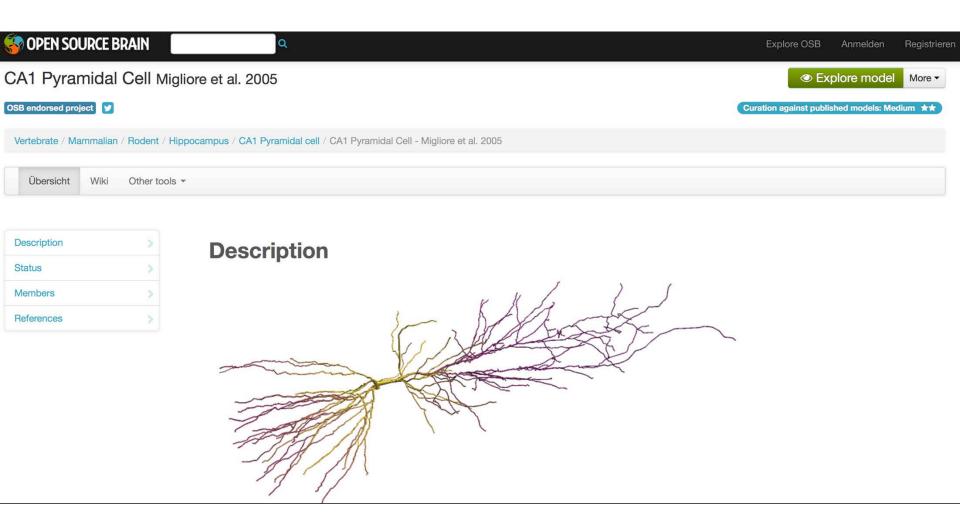








The NormSys Registry: Links to Model Databases









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









Heidelberg Institute for Theoretical Studies



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)



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