EMBL-EBI

Update: MIRIAM Registry and SBO

Nick Juty, EMBL-EBI

3rd Sept, 2011

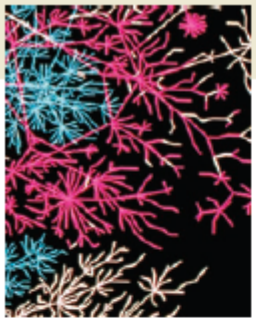
Overview

MIRIAM Registry

- MIRIAM Guidelines ..
- MIRIAM Registry
  - content
  - URIs (URN form), example
  - Summary/current developments

SBO

- Purpose and origins
- Term information stored
- Summary of changes since Edinburgh



_computational BIOLOGY

PERSPECTIVE

http://biomodels.net/miriam

Minimum information requested in the annotation of biochemical models (MIRIAM)

Nicolas Le Novère[1,15], Andrew Finney[2,15], Michael Hucka[3], Upinder S Bhalla[4], Fabien Campagne[5], Julio Collado-Vides[6], Edmund J Crampin[7], Matt Halstead[7], Edda Klipp[8], Pedro Mendes[9], Poul Nielsen[7], Herbert Sauro[10], Bruce Shapiro[11], Jacky L Snoep[12], Hugh D Spence[13] & Barry L Wanner[14]

Publishing Group http://www.nature.com/naturebiotechnology

Most of the published quantitative models in biology are lost for the community because they are either not made available or they are insufficiently characterized to allow them to be reused. The lack of a standard description format, lack of stringent reviewing and authors' carelessness are the main causes for incomplete model descriptions. With today's increased interest in detailed biochemical models, it is necessary to define a minimum quality standard for the encoding of those models. We propose a set of rules for curating quantitative models of biological systems. These rules define procedures for encoding and annotating models represented in machine-readable form. We believe their

During the genomic era we have witnessed a vast increase in availability of large amounts of quantitative data. This is motivating a shift in the focus of molecular and cellular research from qualitative descriptions of biochemical interactions towards the quantification of such interactions and their dynamics. One of the tenets of systems biology is the use of quantitative models (see **Box 1** for definitions) as a mechanism for capturing precise hypotheses and making predictions[1,2]. Many specialized models exist that attempt to explain aspects of the cellular machinery. However, as has happened with other types of biological information, such as sequences, macromolecular structures or

MIRIAM guidelines for models and attribution

Models must :

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

MIRIAM guidelines for annotations

Annotation specification:

- unambiguously relate component to external resource
- be encoded in a defined triplet format
  - as a URI
  - identifier unique for the data type
  - optional use of qualifiers to refine relationship
  - use a defined set of data types – community agreed
    - approved data types stored in MIRIAM Registry

Datatype definition

- A data type is a set of data within which all data points refer to comparable entities, in terms of the 'properties' they can/do possess
- Individual data points (entities/records) share a common identifier scheme which can be used to distinguish them
- Data of the same 'kind'
  - UniProt – protein data
  - Chebi – small molecules
  - PubMed – publication records

MIRIAM-compliant datatype

- **Open access**

Anybody can access any public data without restriction (no commercial licence; no login page etc.)

- **Atomicity**

The granularity of the data distributed has to be appropriately selected (A database of “reactions” distributes reactions and not pathways) and consistent (e.g. classes or instances but not classes AND instances)

- **Identifier**

An atomic data is associated to a unique and perennial identifier

- **Community recognition**

The resource has to be “recognised” by the corresponding experimental community, be reasonably supported etc

EMBL-EBI

MIRIAM Registry

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- Search
- Tags
- Query services
- Submit new
- Export
- Curator Sign in

- Web Services
- Documents
  - MIRIAM Guidelines
  - FAQ
  - Documentation
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  - Identification systems
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  - BioModels.net Qualifiers

- MIRIAM on SourceForge

EBI > Groups > Computational Neurobiology > Research > MIRIAM Registry

MIRIAM Registry

MIRIAM Registry are a set of online services created in support of MIRIAM, a set of guidelines for the annotation and curation of computational models.

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

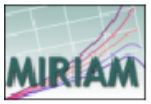
MIRIAM Registry is developed and maintained under the BioModels.net initiative, and are free for use by all.

Quick links

Browse	Web Services
by data type name by tags	services available usage of the services online demonstration
Search	**Exports**
generic search	XML

Registry

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



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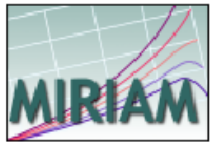
MIRIAM Registry



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

Registry

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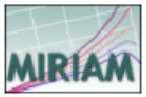
MIRIAM Registry data types



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- MIRIAM on SourceForge

- Support
- Contact

EBI > Groups > Computational Neurobiology > Research > MIRIAM Registry

Browse data types: *recently updated*

Recently updated | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V | W | X | Y | Z

Name	Namespace	Definition
UniProt	uniprot	UniProt (Universal Protein Resource) is the world's most comprehensive catalog of information on proteins. It is a central repository of protein sequence and function created by joining the information contained in Swiss-Prot, TrEMBL, and PIR.
PubChem-substance	pubchem.substance	PubChem provides information on the biological activities of small molecules. It is a component of NIH's Molecular Libraries Roadmap Initiative. PubChem Substance archives chemical substance records.
EDAM Ontology	edam	EDAM is an ontology of general bioinformatics concepts, including topics, data types, formats, identifiers and operations. EDAM provides a controlled vocabulary for the description, in semantic terms, of things such as: web services (e.g. WSDL files), applications, tool collections and packages, work-benches and workflow software, databases and ontologies, XSD data schema and data objects, data syntax and file formats, web portals and pages, resource catalogues and documents (such as scientific publications).
Ontology for Biomedical Investigations	obo.obi	The Ontology for Biomedical Investigations (OBI) project is developing an integrated ontology for the description of biological and clinical investigations. The ontology will represent the design of an investigation, the protocols and instrumentation used, the material used, the data generated and the type analysis performed on it. Currently OBI is being built under the Basic Formal Ontology (BFO).
MACiE	macie	MACiE (Mechanism, Annotation and Classification in Enzymes) is a database of enzyme reaction mechanisms. Each entry in MACiE consists of an overall reaction describing the chemical compounds involved, as well as the species name in which the reaction occurs. The individual reaction stages for each overall reaction are listed with mechanisms, alternative mechanisms, and amino acids involved.
FMA	obo.fma	The Foundational Model of Anatomy Ontology (FMA) is a biomedical informatics ontology. It is concerned with the representation of classes or types and relationships necessary for the symbolic representation of the phenotypic structure of the human body. Specifically, the FMA is a domain ontology that represents a coherent body of explicit declarative knowledge about human anatomy.
OMIA	omia	Online Mendelian Inheritance in Animals is a a database of genes, inherited disorders and traits in animal species (other than human and mouse).
MIRIAM Registry data type	miriam.datatype	MIRIAM Registry is an online resource created to catalogue data types (Gene Ontology, Taxonomy or PubMed are some examples), their URIs and the corresponding resources (physical locations), whether these are controlled vocabularies or databases.
MIRIAM Registry resource	miriam.resource	MIRIAM Registry is an online resource created to catalogue data types (Gene Ontology, Taxonomy or PubMed are some examples), their URIs and the corresponding resources (or physical locations), whether these are controlled vocabularies or databases.
Anatomical Therapeutic Chemical	atc	The Anatomical Therapeutic Chemical (ATC) classification system, divides active substances into different groups according to the organ or system on which they act and their therapeutic, pharmacological and chemical properties. Drugs are classified in groups at five different levels; Drugs are divided into fourteen main groups (1st level), with pharmacological/therapeutic subgroups (2nd level). The 3rd and 4th levels are chemical/pharmacological/therapeutic subgroups and the 5th level is the chemical substance. The Anatomical Therapeutic Chemical (ATC) classification system and the Defined Daily Dose (DDD) is a tool for exchanging and comparing data on drug use at international,

MIRIAM data type

Data type: ***Enzyme Nomenclature***

General | Tags | Example Usage | Web Services

General information about the data type

Name		
Identifier		MIR:00000004
Name		Enzyme Nomenclature
Synonyms		EC code
		Enzyme Classification
		EC
URIs		
MIRIAM URN		urn:miriam:ec-code
Deprecated		http://www.ec-code.org/
		urn:lsid:ec-code.org
		http://www.ebi.ac.uk/IntEnz/
Information		
Definition		The Enzyme Classification contains the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology on the nomenclature and classification of enzyme-catalysed reactions.
Identifier Pattern		^\d+\.-\.-\.-|\d+\.\d+\.-\.-|\d+\.\d+\.\d+\.-|\d+\.\d+\.\d+\.\d+$
Physical Locations		
Resource MIR:00100002	**Access URL**	http://www.genome.jp/dbget-bin/www_bget?ec:**$id** [Example: 1.1.1.1]
	Website	http://www.genome.jp/dbget-bin/www_bfind?enzyme
	Description	KEGG Ligand Database for Enzyme Nomenclature
	Institution	Kyoto University Bioinformatics Center, Japan
Resource MIR:00100003	**Access URL**	http://us.expasy.org/cgi-bin/nicezyme.pl?**$id** [Example: 1.1.1.1]
	Website	http://us.expasy.org/enzyme/
	Description	Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)
	Institution	Swiss Institute of Bioinformatics, Switzerland
Resource MIR:00100001	**Access URL**	http://www.ebi.ac.uk/intenz/query?cmd=SearchEC&ec=**$id** [Example: 1.1.1.1]
	Website	http://www.ebi.ac.uk/intenz/
	Description	IntEnZ (Integrated relational Enzyme database)
	Institution	European Bioinformatics Institute, United Kingdom
References		
URL(s)		http://www.chem.qmul.ac.uk/iubmb/enzyme/
		⊞ http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:10812475]
Miscellaneous		
Date of creation		2006-08-14 19:38:06 GMT
Date of last modification		2010-12-09 08:45:47 GMT

MIRIAM data type

General | Tags | Example Usage | Web Services

General information about the data type

Name		
Identifier		MIR:00000004
Name		Enzyme Nomenclature
Synonyms		EC code
		Enzyme Classification
		EC
URIs		
MIRIAM URN		urn:miriam:ec-code
Deprecated		http://www.ec-code.org/
		urn:lsid:ec-code.org
		http://www.ebi.ac.uk/IntEnz/
Information		
Definition		The Enzyme Classification contains the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology on the nomenclature and classification of enzyme-catalysed reactions.
Identifier Pattern		^\d+\.-\.-\.-|\d+\.\d+\.-\.-|\d+\.\d+\.\d+\.-|\d+\.\d+\.\d+\.\d+$
Physical Locations		
Resource MIR:00100002	**Access URL**	http://www.genome.jp/dbget-bin/www_bget?ec:**$id** [Example: 1.1.1.1]
	Website	http://www.genome.jp/dbget-bin/www_bfind?enzyme
	Description	KEGG Ligand Database for Enzyme Nomenclature
	Institution	Kyoto University Bioinformatics Center, Japan
Resource MIR:00100003	**Access URL**	http://us.expasy.org/cgi-bin/nicezyme.pl?**$id** [Example: 1.1.1.1]
	Website	http://us.expasy.org/enzyme/
	Description	Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)
	Institution	Swiss Institute of Bioinformatics, Switzerland
Resource MIR:00100001	**Access URL**	http://www.ebi.ac.uk/intenz/query?cmd=SearchEC&ec=**$id** [Example: 1.1.1.1]
	Website	http://www.ebi.ac.uk/intenz/
	Description	IntEnz (Integrated relational Enzyme database)
	Institution	European Bioinformatics Institute, United Kingdom
References		
URL(s)		http://www.chem.qmul.ac.uk/iubmb/enzyme/
		⊞ http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:10812475]
Miscellaneous		
Date of creation		2006-08-14 19:38:06 GMT
Date of last modification		2010-12-09 08:45:47 GMT

Resources

EMBL-EBI

Resource monitoring

Resource: MIR:00100050

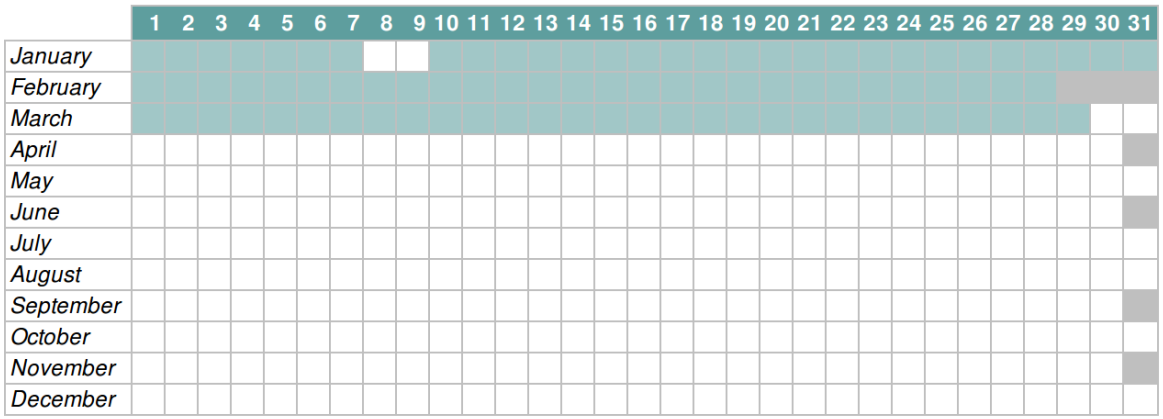
General information about the resource: ***The FlyBase Database*** (associated with the data type: FlyBase).

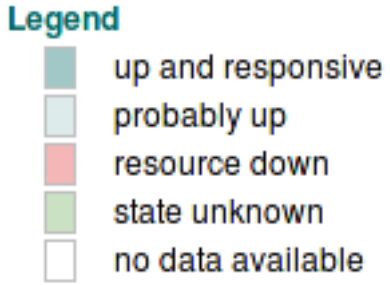
Health statistics	
Last known state	up
Last check	2011-03-29 06:37:48
Uptime ratio	100% (763 checks)
Downtime ratio	0% (0 checks)
Unknown ratio	0% (0 checks)
URL used	http://www.flybase.org/reports/FBgn0011293.html

Health history

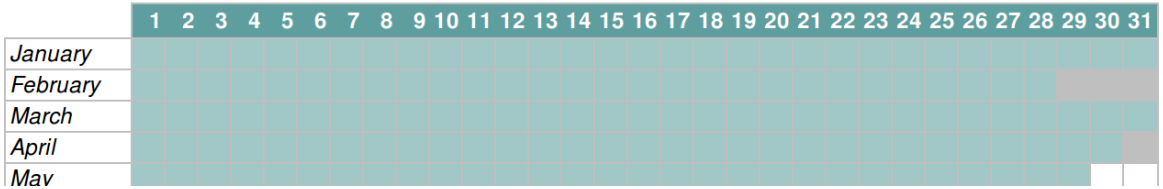
Full record of the health checks performed on this resource.

2011





2010



Resource: MIR:00100042

WARNING! This resource has been deprecated!
Please use the other resources providing the same dataset.

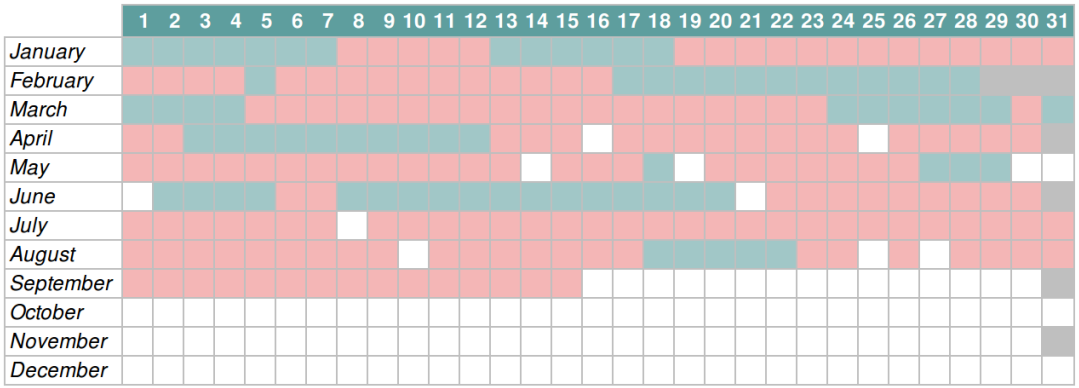
General information about the resource: ***WormBase Mirror at Marseille-Nice Genopole*** (associated with the data type: WormBase).

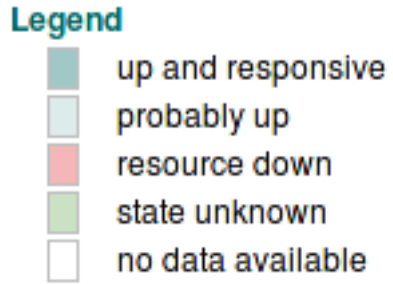
Health statistics	
Last known state	down
Last check	2010-09-15 09:11:48
Uptime ratio	43% (245 checks)
Downtime ratio	56% (318 checks)
Unknown ratio	0% (0 checks)
URL used	http://crfb-3.univ-mrs.fr/db/gene/gene?name=WBGene00000001;class=Gene

Health history

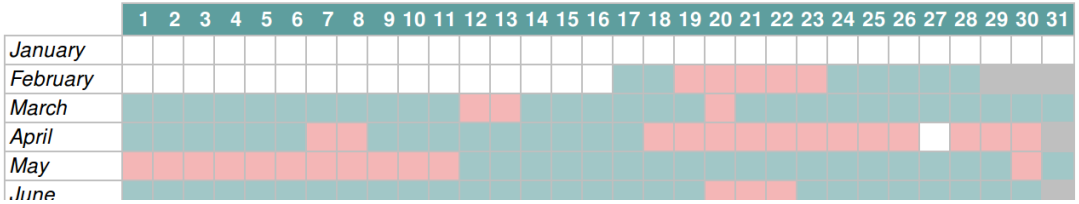
Full record of the health checks performed on this resource.

2010





2009



Add a data type

Please fill this form in order to submit a new data type to MIRIAM Resources. Alternatively, you can contact us with your query.

The new data type will not be directly publicly available after you pressed the **Submit** button. A curator will first check if it complies with the terms and conditions of MIRIAM Resources before publishing it.

Help

You can display all help bubbles by clicking on: Displays all the help messages, or hide them: Hides all the help messages.

Moreover, you can display the individual help by clicking on the button: located in the title of each section.

Add a new data type

First you need to enter the name of the data type you want to add to the database. After you can add as much synonyms as you want.

Name and synonyms

Primary name:

[Add a synonym]

Here is some information about the data type: definition and regular expression (*i.e.* pattern for identifiers of elements, following the PERL style).

Definition and pattern

Definition: Enter definition here...

Identifier pattern: Enter Identifier pattern here...

MIRIAM Registry

- **MIRIAM Database**

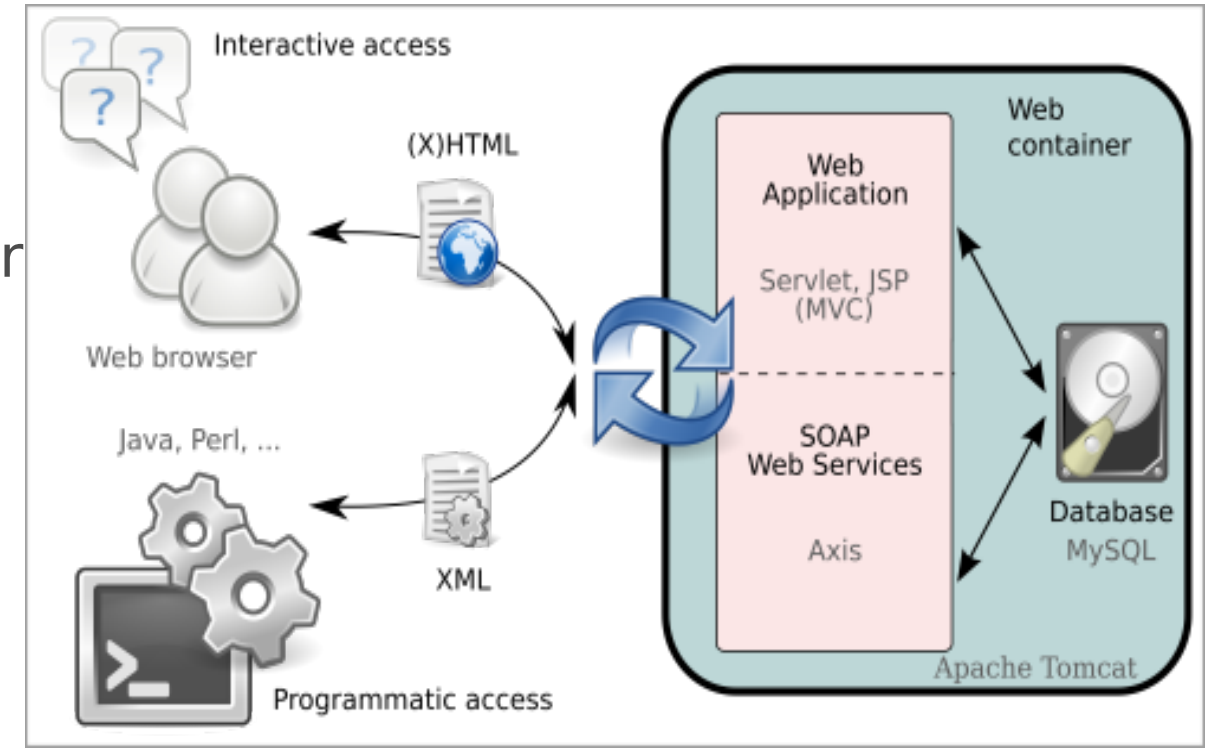
  data type catalogue

- **MIRIAM Web Services**

  programming interface for querying database

- **MIRIAM Library**

  ready to use Java code



- **MIRIAM Web Site**
  - web page for browsing and querying
  - allows new submission (curated)

Laibe and Le Novère.
MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology.
BMC Systems Biology, 2007

Web Services: generate URI

Web Services Demonstration

Here is a Web interface which allows you to perform some queries on MIRIAM Database.

These queries are an example of what MIRIAM Web Services can provide you.

For more information, please refer to the complete list of available queries.

Query

Choose one action from the list: get the MIRIAM URI of an element Go!

Get the MIRIAM URI of an element or entity:

getURI

data type name: pubmed

element id: 18078503

Search

Answer

urn:miriam:pubmed:18078503

Web Services: resolve URI

Web Services Demonstration

Here is a Web interface which allows you to perform some queries on MIRIAM Database.

These queries are an example of what MIRIAM Web Services can provide you.

For more information, please refer to the complete list of available queries.

Query

Choose one action from the list: get links to access an element Go!

Get links to access an element:

getLocations

MIRIAM URI um:miriam:pubmed:18078503

Search

Answer

- http://www.ncbi.nlm.nih.gov/pubmed/18078503
- http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:18078503]
- http://www.ebi.ac.uk/citexplore/citationDetails.do?dataSource=MED&externalId=18078503
- http://www.hubmed.org/display.cgi?uids=18078503

MIRIAM URN identifier - Example

Data type identifier	Data-set Identifier	Annotation qualifier
↑	↑	↑
scheme identifier	text string	optional text string

urn:miriam:pubmed:16333295 (MIRIAM publication)

urn:miriam:chembl.compound:chembl113 (Caffeine)

- Qualifiers are a Controlled vocabulary (CV)
- CV established by the community
- http://biomodels.net/qualifiers/

MIRIAM URIs in SBML

```
<species id="Ca_calmodulin" metaid="cacam">
  <annotation>
    <rdf:RDF
        xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
        xmlns:bqbiol="http://biomodels.net/biology-qualifiers/">
      <rdf:Description rdf:about="#cacam">
        <bqbiol:hasPart>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P62158"/>
            <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A29108"/>
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```

cacam hasPart P62158 and CHEBI:29108

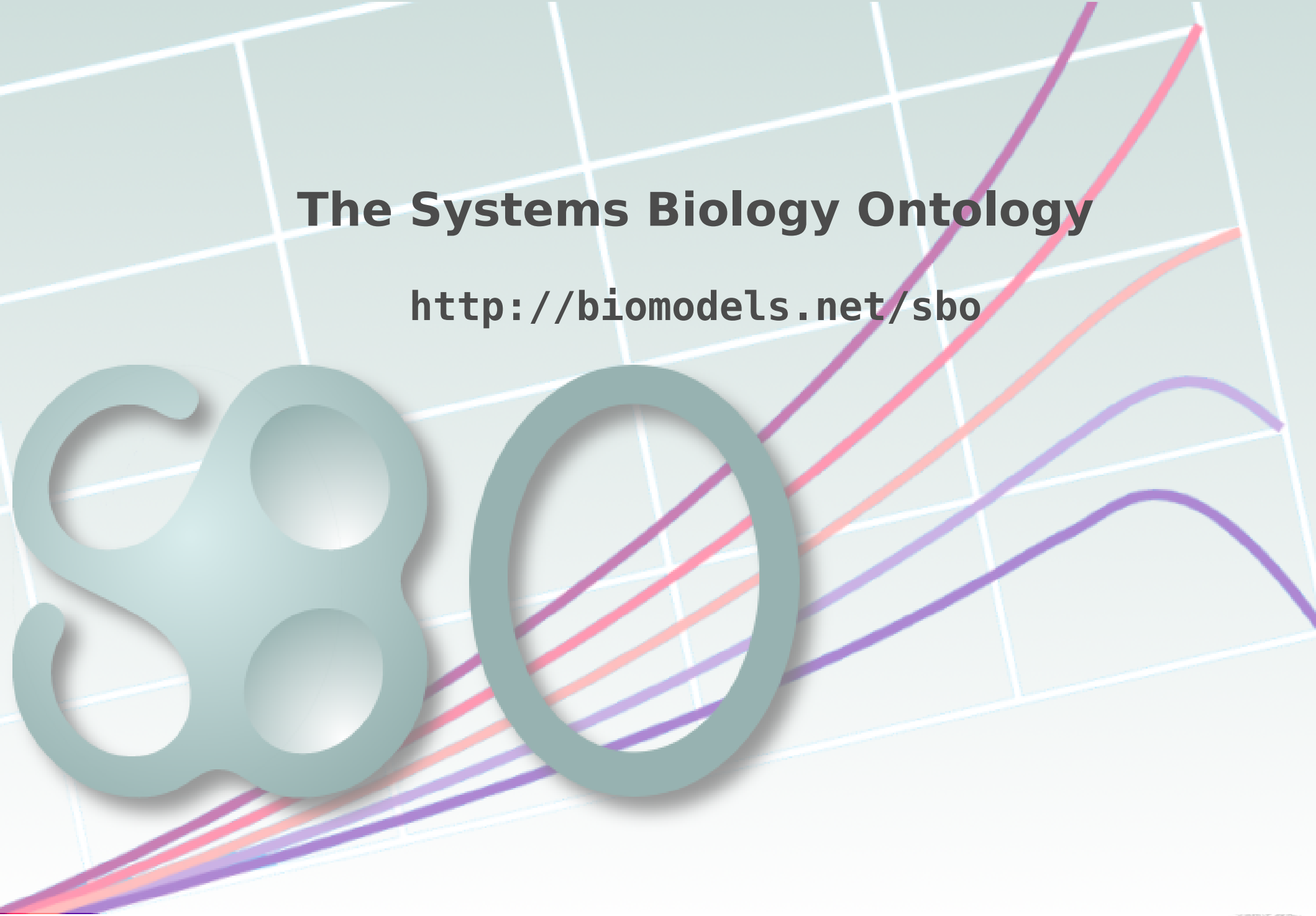
model component relationship external resource(s)

Current developments

- Introduction of a **URL scheme**, in addition to the URN namespace
- In discussions with *Bio2RDF*
- Collaboration with *BioDbCore*
- More structured tags
- Growth in content/coverage
- Limited support 'branch'
- ...

The Systems Biology Ontology

http://biomodels.net/sbo



The Open Biomedical Ontologies

Ontologies | Resources | Participate | About

The OBO Foundry is a collaborative experiment involving developers of science-based ontologies who are establishing a set of principles for ontology development with the goal of creating a suite of orthogonal interoperable reference ontologies in the biomedical domain. The groups developing ontologies who have expressed an interest in this goal are listed below, followed by other relevant efforts in this domain.

In addition to a listing of OBO ontologies, this site also provides a statement of the OBO Foundry principles, discussion fora, technical infrastructure, and other services to facilitate ontology development. We welcome feedback and encourage participation.

Click any column header to sort the table by that column. The s link to the term request trackers for the listed ontologies.

OBO Foundry candidate ontologies

Title	Domain	Prefix	File	Last changed
Amphibian gross anatomy	anatomy	AAO	amphibian_anatomy.obo	2008/06/19
Amphibian taxonomy	anatomy	ATO	amphibian_taxonomy.obo	
Ascomycete phenotype ontology	phenotype	APO	ascomycete_phenotype.obo	2009/07/10
Biological process	biological process	GO	gene_ontology_edit.obo	2009/08/21
C. elegans development	anatomy	WBls	worm_development.obo	2008/01/31
C. elegans gross anatomy	anatomy	WBbt	WBbt.obo	2009/08/19
C. elegans phenotype	phenotype	WBPhenotype	worm_phenotype.obo	2009/08/19
Systems Biology	biochemistry	SBO	SBO_OBO.obo	

The Systems Biology Ontology
http://biomodels.net/sbo

- A navigable taxonomic structure of terms that has 'parents', 'children'
- Provide a strictly defined relational vocabulary of terms for use in Computational Biology
- Describe model components and how they are intended to be used

- 7 orthogonal vocabularies containing domain knowledge:
  - type of entity (compartment / macromolecule)
  - roles of entities (modifier / product)
  - how they interact (reaction / transport)
  - ...

SBO tree and term ...

EBI › SBO › Browsing

SBO Tree

- SBO:0000000 - systems biology representation
  - SBO:0000064 - mathematical expression
    - SBO:0000355 - conservation law
    - SBO:0000474 - convenience function
    - SBO:0000001 - rate law
      - SBO:0000268 - enzymatic rate law
        - SBO:0000150 - enzymatic rate law for irreve
          - SBO:0000151 - enzymatic rate law for
          - SBO:0000152 - enzymatic rate law for
          - SBO:0000028 - enzymatic rate law for
            - **SBO:0000031 - Briggs-Halda**
            - SBO:0000029 - Henri-Michaelis
            - SBO:0000199 - normalised enzy
            - SBO:0000030 - Van Slyke-Culle
        - SBO:0000429 - enzymatic rate law for multir
        - SBO:0000269 - enzymatic rate law for unirea
        - SBO:0000425 - reversible Hill-type enzymat
      - SBO:0000192 - Hill-type rate law, generalised form
      - SBO:0000012 - mass action rate law
      - SBO:0000527 - modular rate law
    - SBO:0000391 - steady state expression
  - SBO:0000544 - metadata representation
  - SBO:0000004 - modelling framework
  - SBO:0000231 - occurring entity representation
  - SBO:0000003 - participant role
  - SBO:0000236 - physical entity representation
  - SBO:0000545 - systems description parameter

Systems Biology Ontology - Mozilla Firefox

http://www.ebi.ac.uk/sbo/main/browse.jsp?nodeId=32

Term: SBO:0000031

Name
Briggs-Haldane rate law

Definition
The Briggs-Haldane rate law is a general rate equation that does not require the restriction of equilibrium of Henri-Michaelis-Menten or irreversible reactions of Van Slyke, but instead make the hypothesis that the complex enzyme-substrate is in quasi-steady-state. Although of the same form than the Henri-Michaelis-Menten equation, it is semantically different since Km now represents a pseudo-equilibrium constant, and is equal to the ratio between the rate of consumption of the complex (sum of dissociation of substrate and generation of product) and the association rate of the enzyme and the substrate.

MathML

```
<math xmlns="http://www.w3.org/1998/Math/MathML">
<semantics definitionURL="http://biomodels.net/SBO/#SBO:0000062">
   <lambda>
     <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000025">kcat</ci></bvar>
     <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000505">Et</ci></bvar>
     <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000515">S</ci></bvar>
     <bvar><ci definitionURL="http://biomodels.net/SBO/#SBO:0000371">Km</ci></bvar>
     <apply>
```

Rendered equation

$$\lambda(kcat, Et, S, Km) = \frac{kcat \times Et \times S}{Km + S}$$

Comment
Rate-law presented by G.E. Briggs and J.B.S. Haldane (1925): "A note on the kinetics of enzyme action, Biochem. J., 19: 338-339".

Miscellaneous
Date of creation:
23 February 2006, 14:00
Date of last modification:
05 February 2010, 10:48

Parent(s)
SBO:0000028 *enzymatic rate law for irreversible non-modulated non-interacting unireactant enzymes* (is a)

Children
This term has no child.

History [+]

Continuous framework

Entity

Quantitative parameter

Semantics

Semantic layer:

- conversion to semantically enriched computing formats (such as BioPAX)
- link between models encoded in SBML and graphical notations (such as SBGN)
- translation of models between *continuous deterministic frameworks* and *discrete stochastic framework*
- merging and integration of models

Systems Biology Ontology

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Summary Files Reviews Support Develop Tracker Forums Code

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Tracker: Term request

List of suggested SBO term creations or modifications.

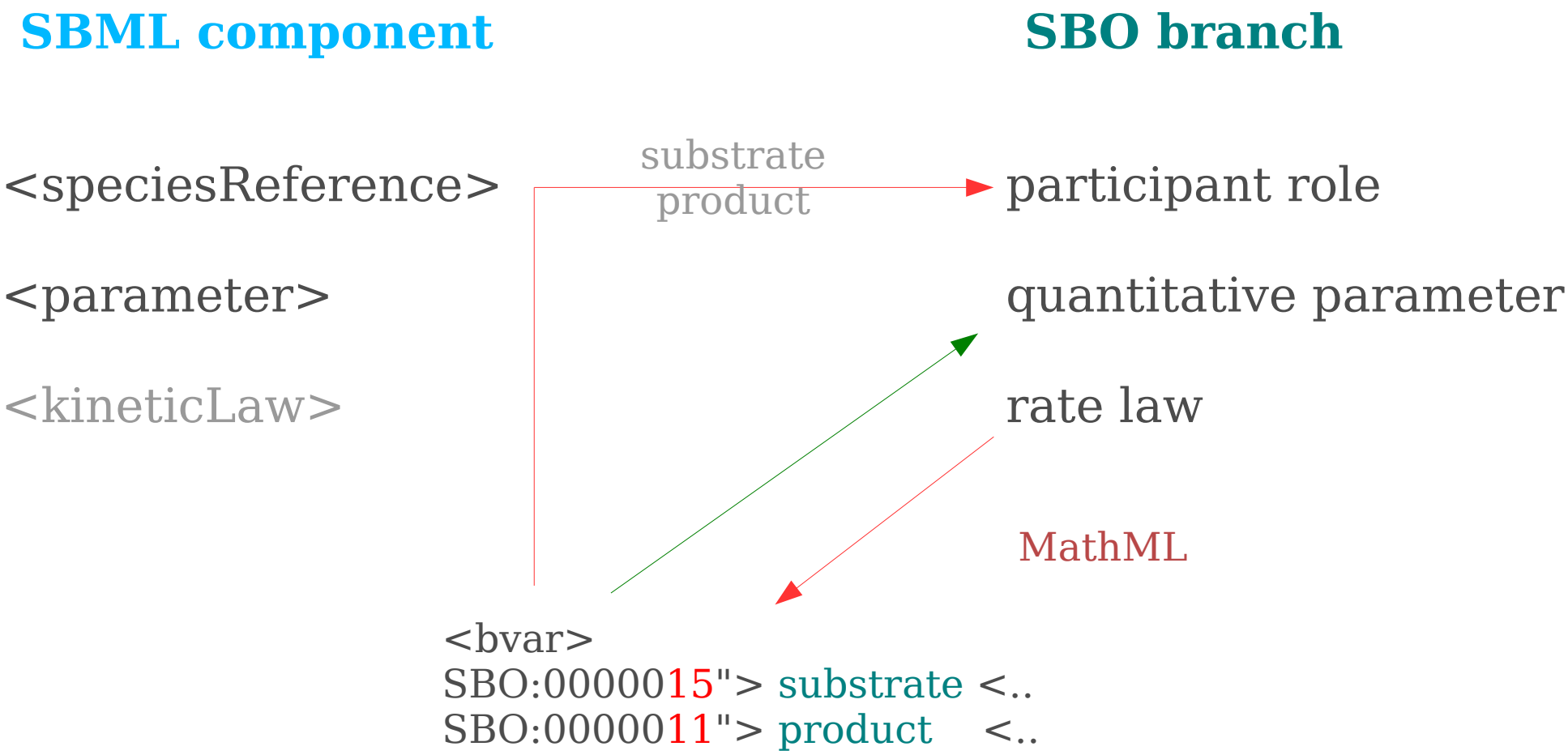
Search: Search Advanced Options RSS

Page: Page 1 Next → 1 - 25 of 81 Results - Display 25

ID	Summary	Status	Opened	Assignee	Submitter	Priority
Assignee: Any Status: Any Category: Any Group: Any Submitter: Keyword: Artifact ID: Filter Reset Permalink						
3356372	Ion channel terms (SBPAX/SGMP)	Open	2011-07-06	njuty	njuty	6
3325167	mass action rate laws for essential stimulators	Closed	2011-06-23	njuty	njuty	5
3314182	sbo terms for reaction rates	Open	2011-06-09	nobody	nobody	5
3308330	SBO:0000061 has wrong rate constant	Closed	2011-05-27	njuty	njuty	5
3301506	specific activity	Closed	2011-05-13	njuty	njuty	4
3293425	Goldman & Nernst Equations	Open	2011-04-27	njuty	luen	5
3286595	Gibbs free energy of reaction	Closed	2011-04-14	njuty	nobody	6

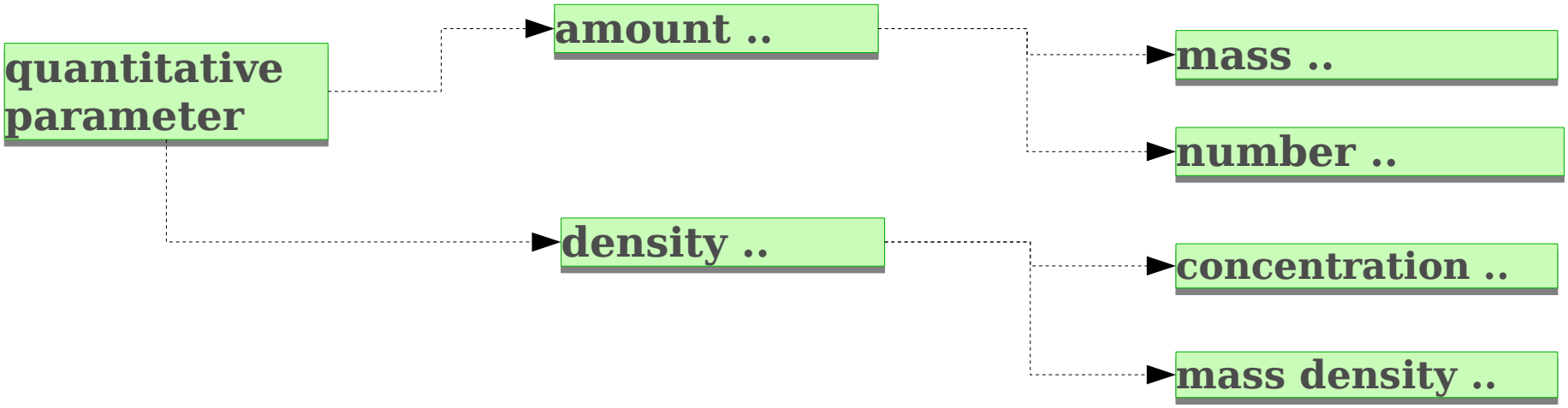
SBO term - MathML error rectified

Problem: 'substrate' (participant role) = amount? concentration?



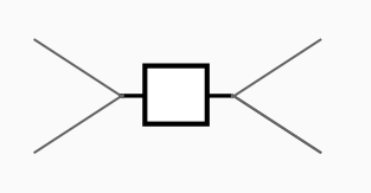
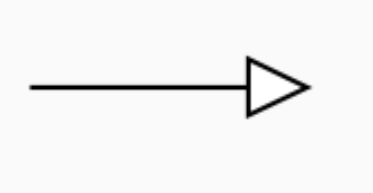
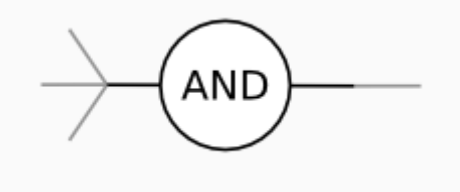
SBO term - MathML error rectified II

- Initial changes made on SBO 'demo'
- Introduce 'quantitative parameter's for 'participant role' terms



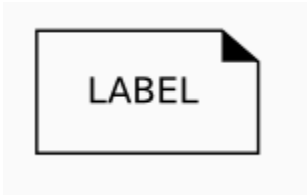
- Modify <bvar> links in all MathML - redirect to quantitiative parameter branches
- Request feedback for selected users (validate)
- Move changes to SBO 'main' (implement → live version)

SBO / SBGN relationship

SBGN	<---------->	SBO
	Process (PD)	SBO:0000375
	Stimulation (ER)	SBO:0000170
	And (AF)	SBO:0000173

SBO / SBGN metadata

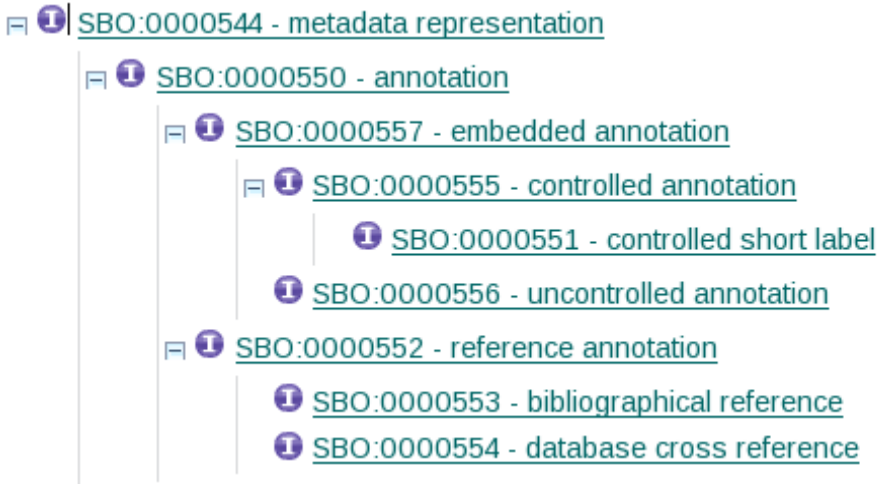
SBGN <----------> **SBO**



Annotation
(ER)

?

- 7th branch: Annotation, cross-references, metadata



Acknowledgements

SBO + MIRIAM

- Mélanie Courtot
- Camille Laibe
- Nicolas Le Novère
- Lukas Endler

SBML team

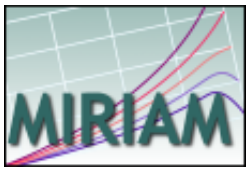
- Michael Hucka
- Sarah Keating

BioModels Database
developers and curators

The Systems Biology community for their contributions, software support and their comments.

Models

Minimal requirements

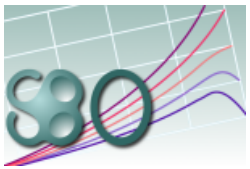


implemented by

Example Data-model

adds meaning to

Ontology



SBML and MIRIAM URIs

```
<species id="Ca_calmodulin" metaid="cacam">
  <annotation>
    <rdf:RDF
        xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
        xmlns:bqbiol="http://biomodels.net/biology-qualifiers/">
      <rdf:Description rdf:about="#cacam">
        <bqbiol:hasPart>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P62158"/>
            <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A29108"/>
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```

SBML and MIRIAM URIs

```
<species id="Ca_calmodulin" metaid="cacam">
  <annotation>
    <rdf:RDF
        xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
        xmlns:bqbiol="http://biomodels.net/biology-qualifiers/">
      <rdf:Description rdf:about="#cacam">
        <bqbiol:hasPart>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P62158"/>
            <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A29108"/>
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
```

cacam hasPart P62158 and CHEBI:29108