

Systems Biology Ontology: *Update*

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**COMBINE 2010
Edinburgh, 6th - 9th October**

- Brief introduction SBO
 - annotation layer issue
 - reiterate / clarify the problem
 - describe resolution process

- OBO Foundry Status
 - what it is, and how to get it

- Relationship between Systems Biology Graphical Notation (SBGN) with SBO
 - new glyphs

<http://www.ebi.ac.uk/sbo/>

- Provide a strictly defined relational vocabulary of terms for use in Systems Biology
- A navigable structure of terms that has 'parents', 'children'

6 orthogonal vocabularies:

- entity (macromolecule)
- interaction (transport, reactions)
- mathematical expression (mass action rate law)
- modelling framework (discrete)
- participant roles (S, P, M)
- quantitative parameters (Hill coefficient)

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  <species id="B" sboTerm="SBO:0000247" /
  <species id="C" sboTerm="SBO:0000014" />
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      <listOfParameters>
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        <parameter id="V" sboTerm="SBO:0000025"/>
      </listOfParameters>
    </kineticLaw>
  </reaction>
</listOfReactions>
```

Semantic layer:

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

SBO annotation layer
(as it was):

SBML component

<speciesReference>

::

<parameter>

::

<kineticLaw>

::

<Species>

::

SBO branch

participant role

quantitative parameter

rate law

entity

SBO annotation layer
(as it was):

SBML component	EXAMPLE	SBO branch
<speciesReference>	substrate inhibitor	participant role
.. <parameter>	kinetic constant time	quantitative parameter
.. <kineticLaw>	mass action rate law	rate law
.. <Species>	simple chemical enzyme	entity
..		

SBO annotation layer
(as it was):

SBML component

<speciesReference>

<kineticLaw>

SBO branch

participant role

rate law

SBO annotation layer
(as it was):

SBML component

<speciesReference>

<kineticLaw>

<bvar>

<ci definitionURL="http://biomodels.net/SBO/#SBO:0000015"> substrate <..
<ci definitionURL="http://biomodels.net/SBO/#SBO:0000011"> product <..

SBO branch

participant role

rate law

MathML



SBO annotation layer
(as it was):

SBML component

SBO branch

<speciesReference>

substrate
product

participant role

<kineticLaw>

rate law

MathML

<bvar>

SBO:0000015"> substrate <..

SBO:0000011"> product <..

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

SBML component

<speciesReference>

<kineticLaw>

SBO branch

participant role

rate law

MathML

<bvar>
SBO:0000015"> substrate <..
SBO:0000011"> product <..

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

SBML component

<speciesReference>

<parameter>

<kineticLaw>

SBO branch

participant role

quantitative parameter

rate law

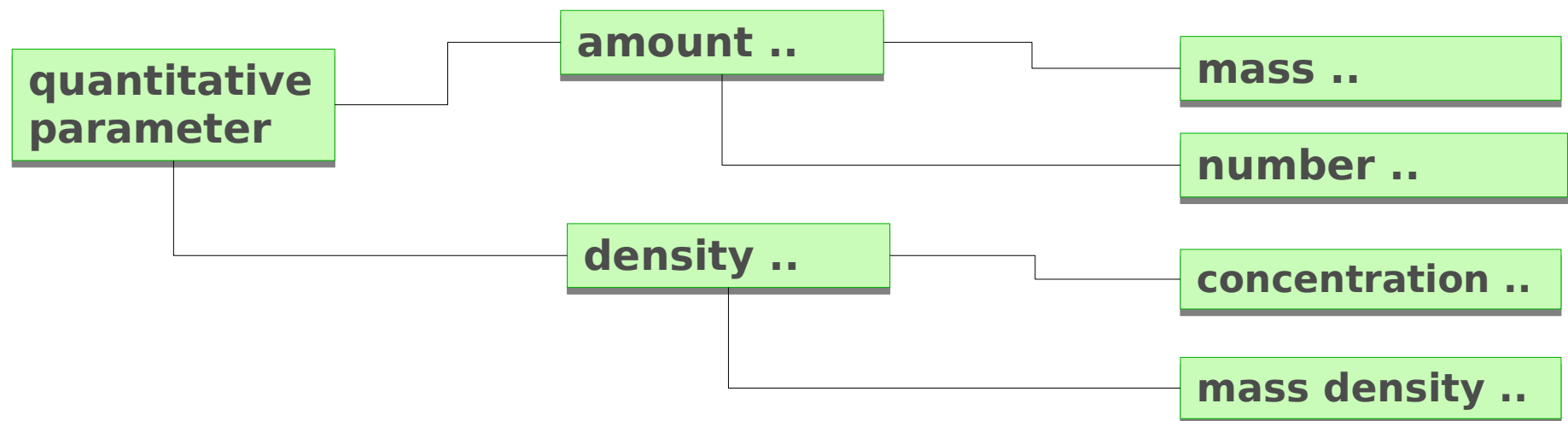
MathML

<bvar>

SBO:0000515"> substrate <..

SBO:0000511"> product <..

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



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

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- Open Biomedical ontologies – open community-level collaborative ontology development
- First Principles:
 - open - terms should be available for use without restriction
 - changeable – modified by community effort
 - orthogonal – additivity and modularity
 - machine friendly – interpretable and syntactically sound
 - identifiers – backward compatible
- >80 library members, 8 Foundry



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  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	2008/08/19
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	WBIs	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
Cell type	phenotype	CT	cell_type.obo 	2009/08/19
Concept Ontology for Rheumatology	health	COBARDM	cobardm.obo	
Systems Biology	biochemistry	SBO	SBO_OBO.obo 	
Tissue anatomy and development	anatomy	TAD	tissue_anatomy.obo 	2009/08/19

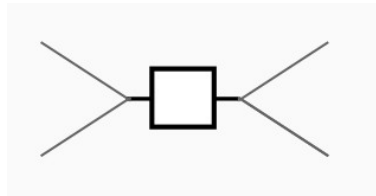
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- SBO is an OBO candidate ontology
 - Review 15th Feb 2010
 - Issues to address include:
 - Expose MathML terms (hidden relationships)
 - Versioning
 - Uniqueness/orthogonality
 - MIREOT (direct import)
 - Cross reference
 - Cross products
- Interface:
 - References for term (creation)
 - Cross references (relationships to other ontologies)

SBGN

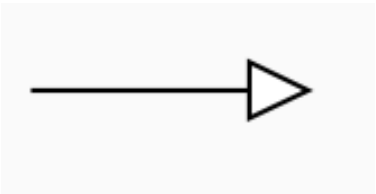


SBO



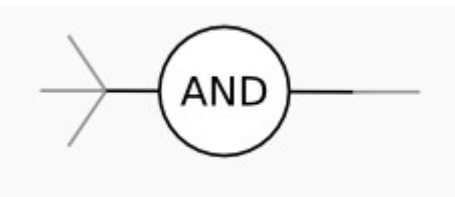
Process (PD)

SBO:0000375



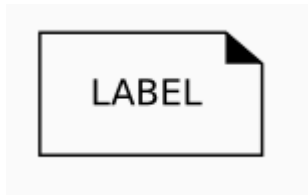
Stimulation (ER)

SBO:0000170



And (AF)

SBO:0000173

SBGN**SBO**Annotation
(ER)

?

- Do we need a 7th branch in SBO to accommodate:
 - Annotation,
 - cross-references,
 - metadata

EBI

Mélanie Courtot
Camille Laibe
Nicolas Le Novère
Lukas Endler
Karim Tazibt

SBML team

Michael Hucka
Sarah Keating

BioModels Database
developers and curators



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

<https://sourceforge.net/projects/sbo>



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