

# **Systems Biology Ontology: *Update***

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**COMBINE 2010  
Edinburgh, 6<sup>th</sup> - 9<sup>th</sup> 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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  <compartment id="C" sboTerm="SBO:0000289">
</listOfCompartments>
<listOfSpecies>
  <species id="A" sboTerm="SBO:0000247" />
  <species id="B" sboTerm="SBO:0000247" /
  <species id="C" sboTerm="SBO:0000014" />
</listOfSpecies>
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    <listOfReactants>
      <speciesReference species="A" sboTerm="SBO:0000015"/>
    </listOfReactants>
    <listOfProducts>
      <speciesReference species="B" sboTerm="SBO:0000011"/>
    </listOfProducts>
    <listOfModifiers>
      <speciesReference species="C" sboTerm="SBO:0000014"/>
    </listOfModifiers>
    <kineticLaw sboTerm="SBO:0000031">
      <listOfParameters>
        <parameter id="U" sboTerm="SBO:0000027"/>
        <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):

<b>SBML component</b>	<b>EXAMPLE</b>	<b>SBO branch</b>
<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

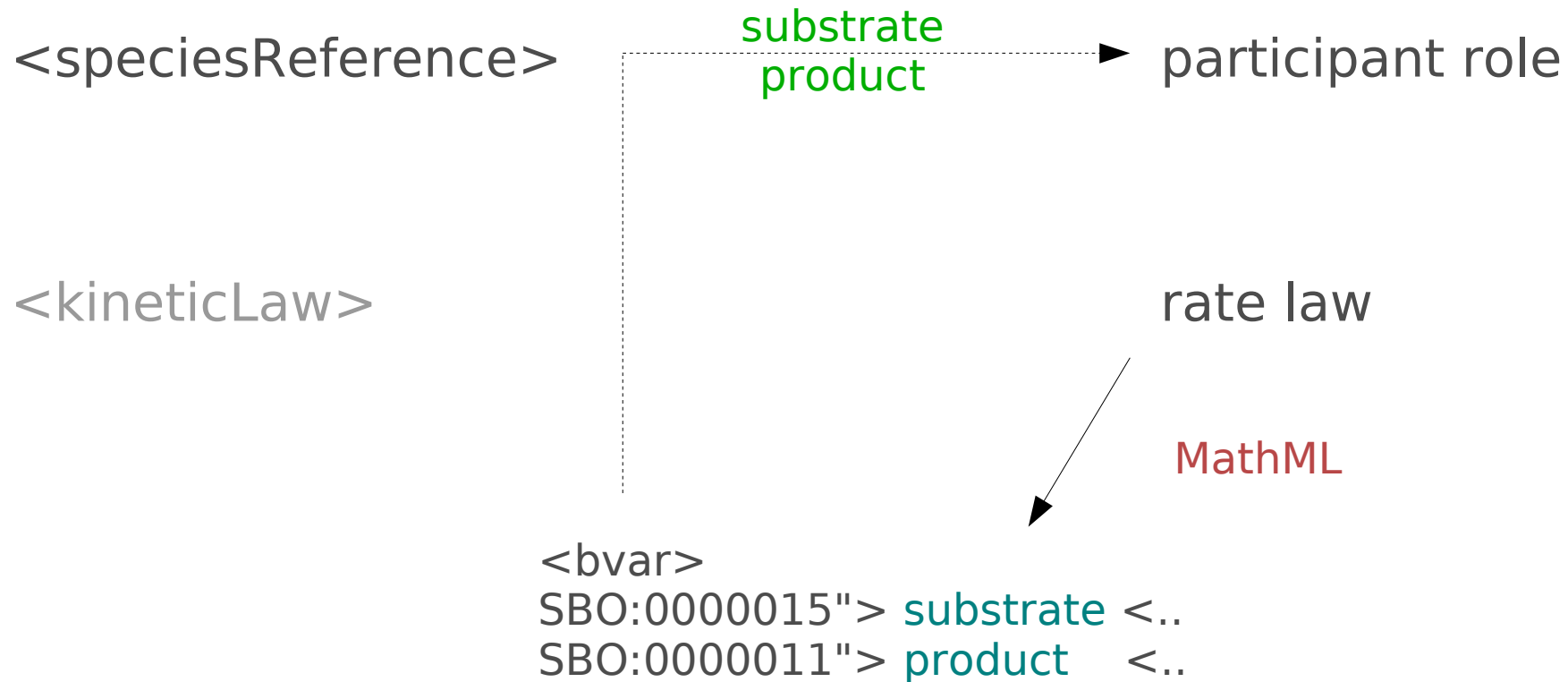
MathML



SBO annotation layer  
(as it was):

## SBML component

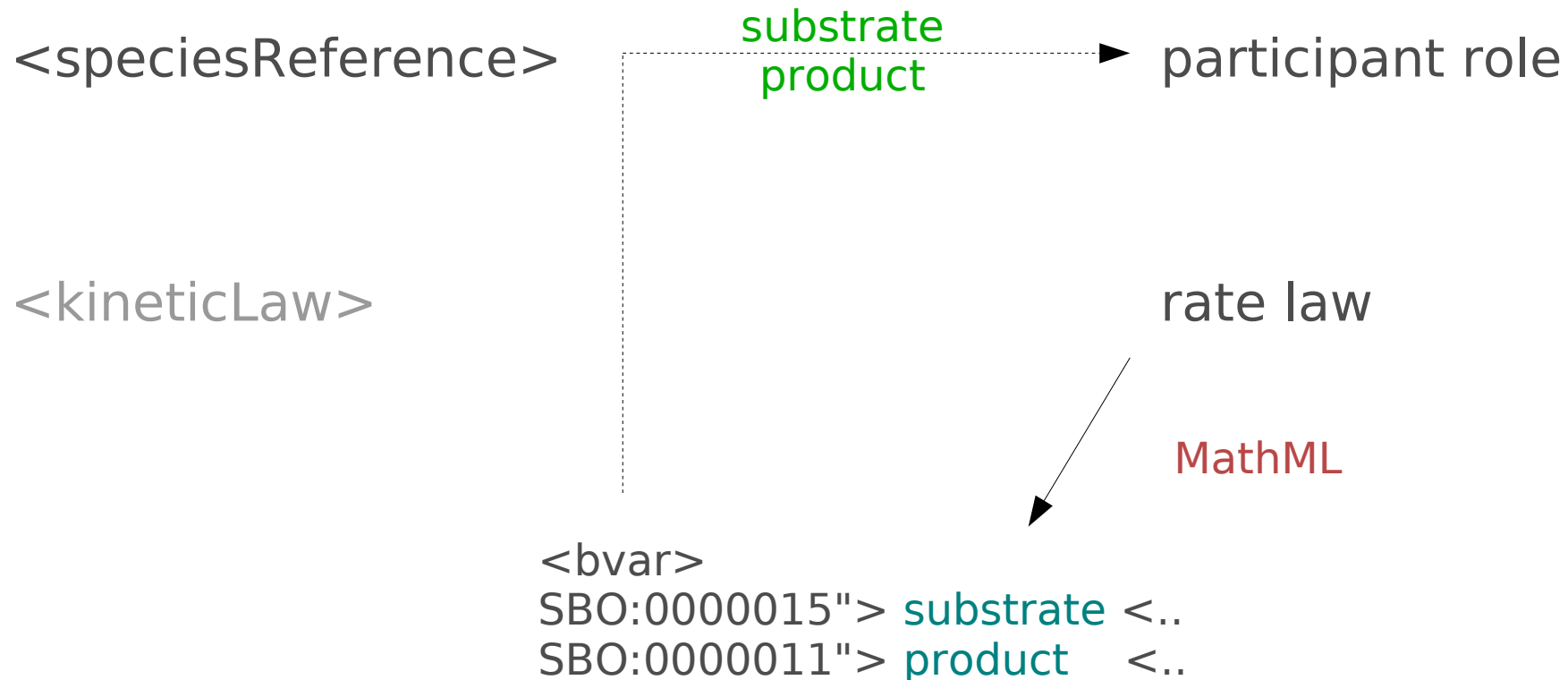
## SBO branch



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

### SBML component

### SBO branch



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

### SBML component

<speciesReference>

<parameter>

<kineticLaw>

### SBO branch

participant role

quantitative parameter

rate law

MathML

<bvar>

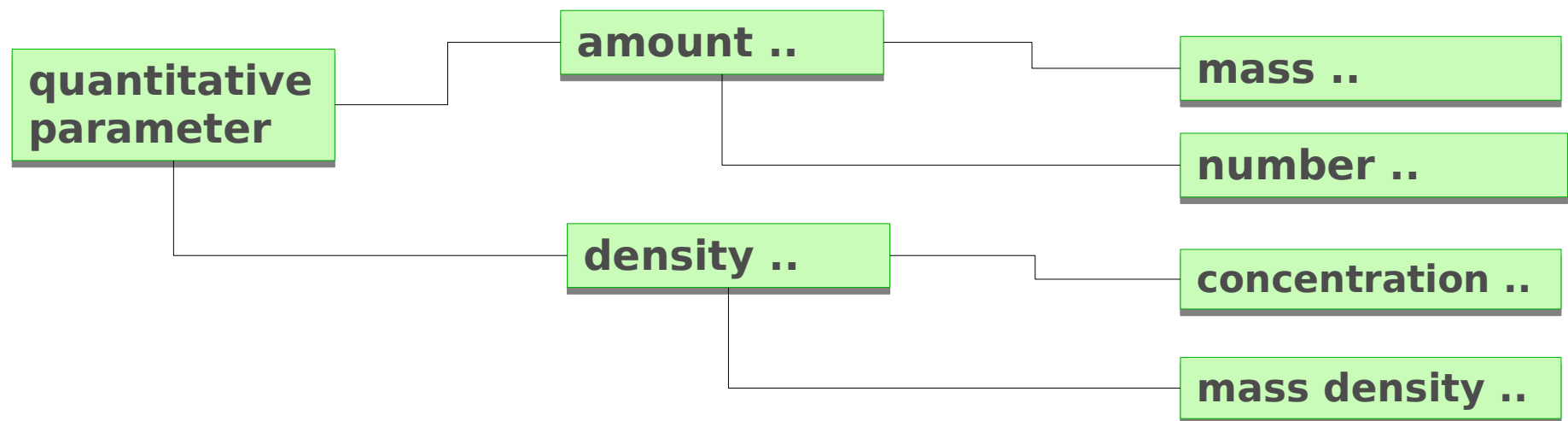
SBO:0000515"> substrate <..

SBO:0000511"> product <..

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- 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)

- 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.

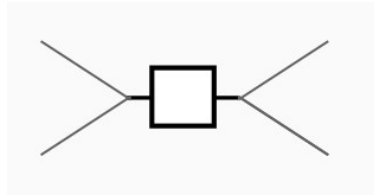
Click any column header to sort the table by that column. The  link to the term request trackers for the listed ontologies.

### OBO Foundry candidate ontologies

<u>Title</u>	<u>Domain</u>	<u>Prefix</u>	<u>File</u>	<u>Last changed</u>
<a href="#">Amphibian gross anatomy</a>	anatomy	AAO	<a href="#">amphibian_anatomy.obo</a>	2008/08/19
<a href="#">Amphibian taxonomy</a>	anatomy	ATO	<a href="#">amphibian_taxonomy.obo</a>	
<a href="#">Ascomycete phenotype ontology</a>	phenotype	APO	<a href="#">ascomycete_phenotype.obo</a>	2009/07/10
<a href="#">Biological process</a>	biological process	GO	<a href="#">gene_ontology_edit.obo</a> 	2009/08/21
<a href="#">C. elegans development</a>	anatomy	WBIs	<a href="#">worm_development.obo</a>	2008/01/31
<a href="#">C. elegans gross anatomy</a>	anatomy	WBbt	<a href="#">WBbt.obo</a> 	2009/08/19
<a href="#">C. elegans phenotype</a>	phenotype	WBPhenotype	<a href="#">worm_phenotype.obo</a>	2009/08/19
<a href="#">Cell type</a>	phenotype	CT	<a href="#">cell_type.obo</a> 	2009/08/19
<a href="#">Concept Ontology for Rheumatology</a>	health	COB-RHM	<a href="#">cob_rhm.obo</a>	
<a href="#">Systems Biology</a>	biochemistry	SBO	<a href="#">SBO_OBO.obo</a> 	
<a href="#">Tissue anatomy and development</a>	anatomy	TAD	<a href="#">tissue_anatomy.obo</a> 	2009/08/19

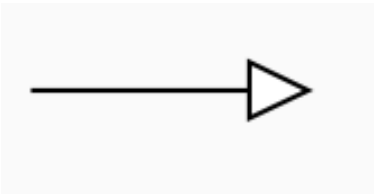
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- SBO is an OBO candidate ontology
  - Review 15<sup>th</sup> Feb 2010
  - Issues to address include:
    - Expose MathML terms (hidden relationships)
    - Versioning
    - Uniqueness/orthogonality
      - MIREOT (direct import)
      - Cross reference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

**SBGN****SBO**

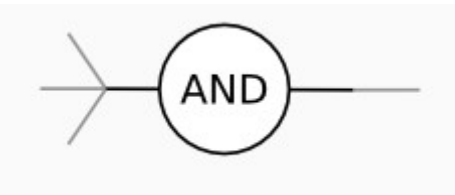
Process (PD)

SBO:0000375



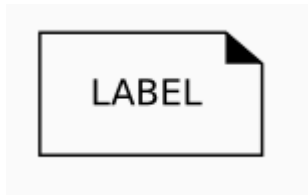
Stimulation (ER)

SBO:0000170



And (AF)

SBO:0000173

**SBGN****SBO**Annotation  
(ER)

?

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

## EBI

Mélanie Courtot  
Camille Laibe  
Nicolas Le Novère  
Lukas Endler  
Karim Tazibt

BioModels Database  
developers and curators

## SBML team

Michael Hucka  
Sarah Keating



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

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

