

semanticSBML 2.0

A Collection of Online Services for SBML Models

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semanticSBML 2.0 is a collection of online services for the processing of biochemical networks in the SBML (Systems Biology Markup Language) document format. It allows users to edit SBO (Systems Biology Ontology) and RDF based MIRIAM (Minimum Information Required in the Annotation of Models) annotations, check for

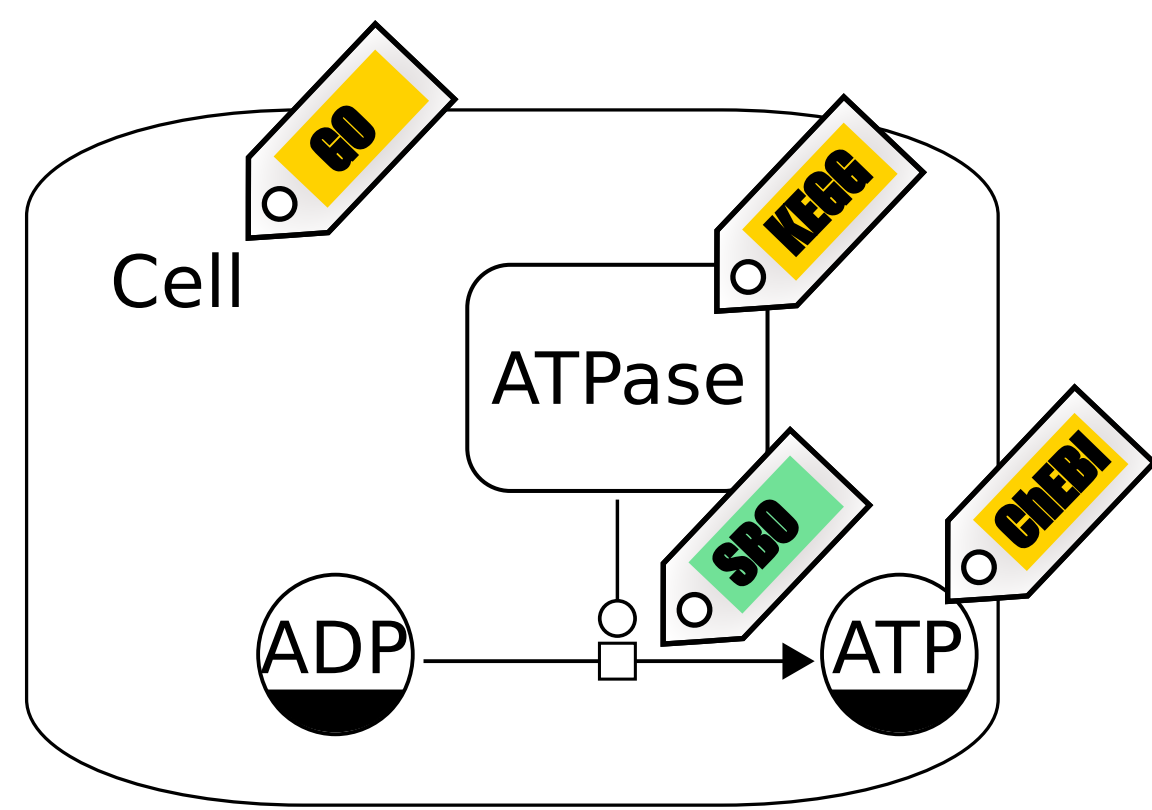
semantic validity, compare and merge SBML documents, and to create submodels. Given an annotated SBML document similar SBML documents can be retrieved from the BioModels Database via a ranked similarity search. Further features of semanticSBML 2.0 include graph visualization of SBML documents, parameter

balancing, creation of SBML documents using shorthand SBML, and an interface to the BioModels Database that allows the comparison of document version. Many of semanticSBML 2.0s features are available through a RESTful interface that is documented in a custom REST documentation interface.



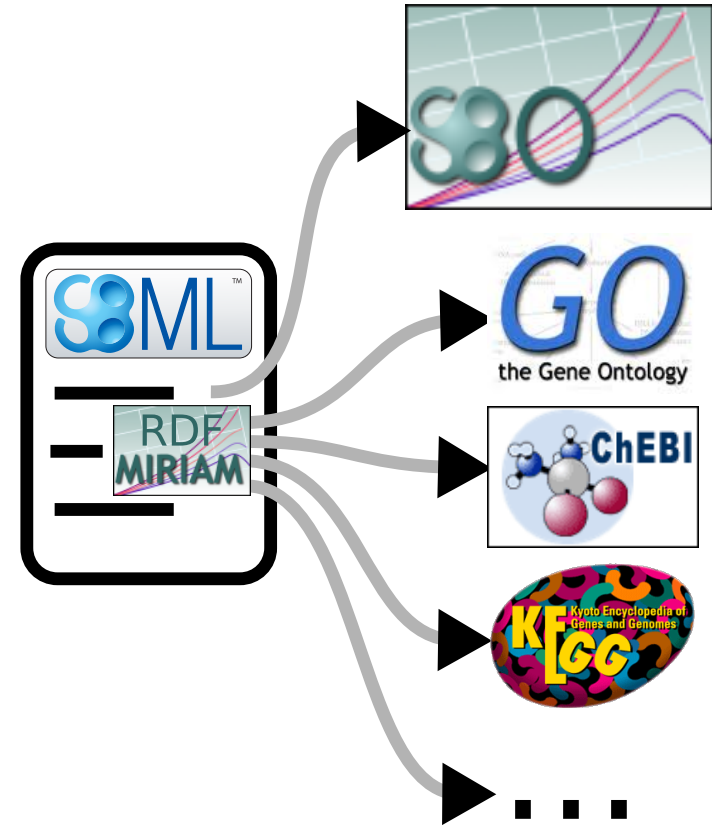
& semantic annotations

The SBML document format allows the storage of kinetic bio-chemical models that can be used for dynamical modeling. Currently there are more than 500 SBML models which can be used in over 200 software tools. To specify the how and what of its elements it uses two kinds of annotations. To specify how elements are used in a model each element can be annotated with an SBO term. To

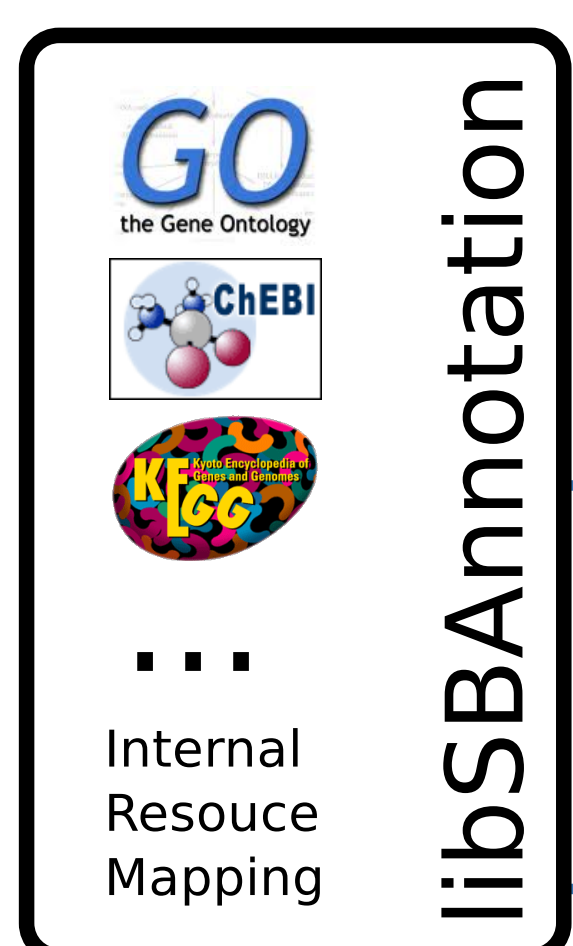


specify what the biological meaning of an element is RDF based MIRIAM annotations can be attached to an

element. semanticSBML includes an internal resource mapping called libSBAnnotation. It stores the SBO and maps several web resources like Gene Ontology, ChEBI,

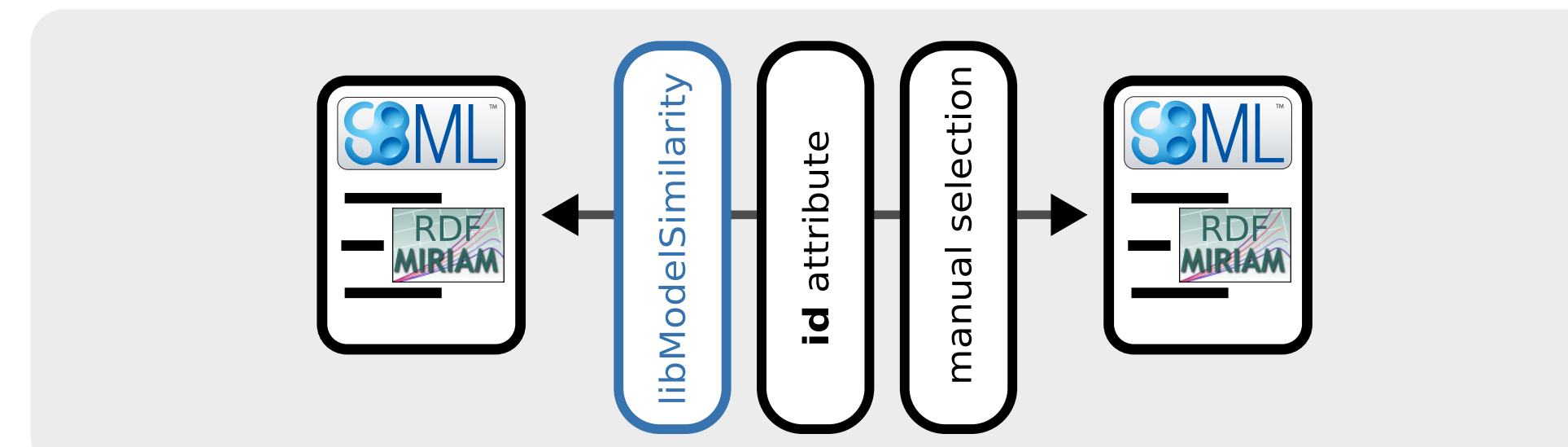


and KEGG onto each other using their crosslink information. This enables semanticSBML to search, add, edit, and remove semantic annotations for SBML models. The libSBAnnotation is furthermore used in the libModelSimilarity to compare SBML elements using their MIRIAM annotations and to compare and cluster complete SBML models.



libModelSimilarity

Comparing SBML Models



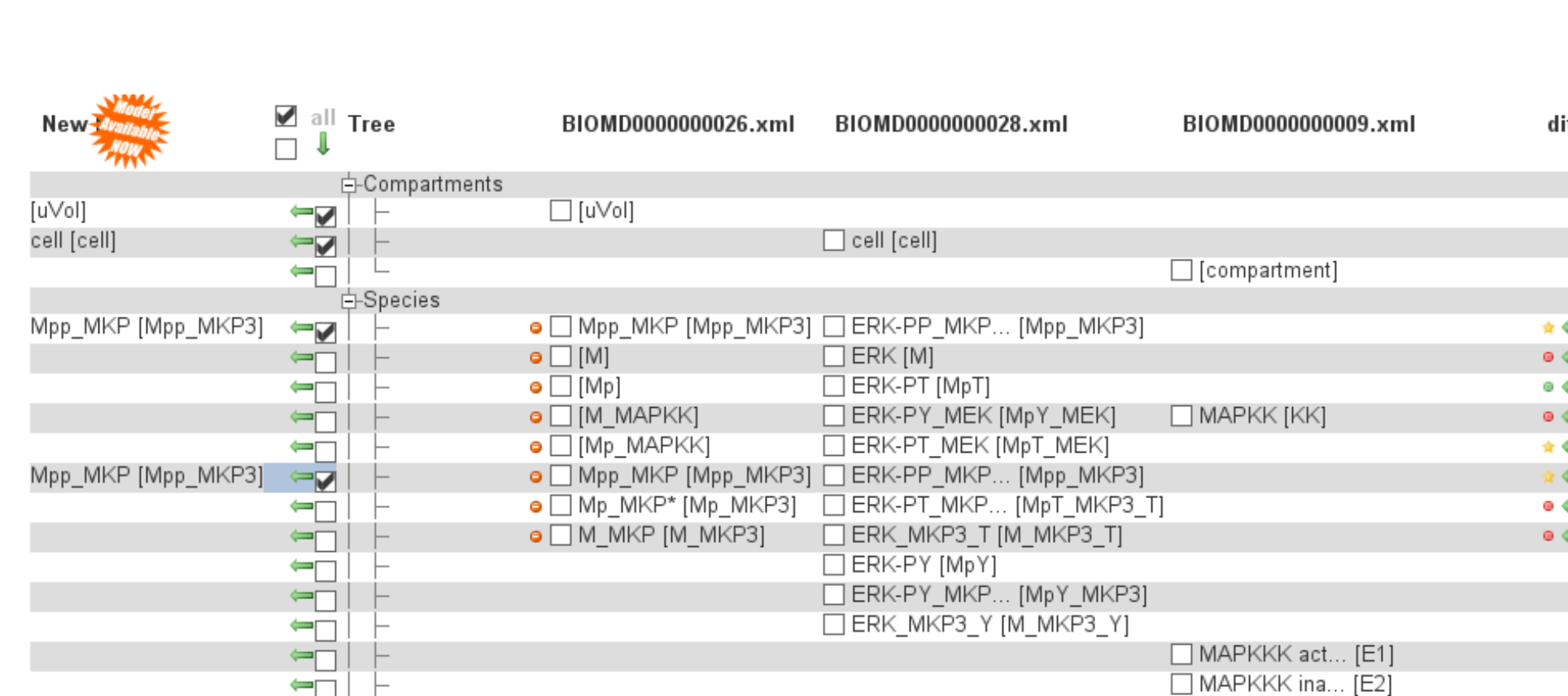
To compare two or more SBML models with each other users can: manually select models and model elements, use the elements id attribute or use the libModelSimilarity (see left box). For a comparison of two or more elements the elements attributes are listed and mismatches are highlighted. In a model merging (see below) this comparison can be used to create resolutions for attribute conflicts.

Attribute	Value of [vPDC]	Value of [vPDC]	Score
ElementName	reaction	reaction	1.0
Modifiers			
name	Pyruvate decarboxylase	Pyruvate decarboxylase	1.0
kinetic_law	$\text{cysitol} * (V1m * \text{Pyr} / (K11 + \text{Pyr}))$	$\text{cysitol} * \text{VnPDC} * (\text{pow}(\text{PYR}, \text{nPDC}) / (\text{pow}(\text{nPDCPYR}, \text{nPDC}) + 1 + \text{pow}(\text{PYR}, \text{nPDC}) / \text{pow}(\text{nPDCPYR}, \text{nPDC})))$	0.0
MIRIAM	bio:is pyruvic acid <-> acetaldehyde + carbon dioxide [pyruvate decarboxylase activity]	bio:is pyruvic acid <-> acetaldehyde + carbon dioxide	0.78
fast	False	False	1.0
internal_parameters	[V1m], [K11]	[VnPDC], [nPDC], [nPDCPYR]	0.0
reversible	True	False	0.0
Products	Acetaldehyde [ACA]	Acetaldehyde [ACE]	0.0
units	species quantity/time	species quantity/time	1.0

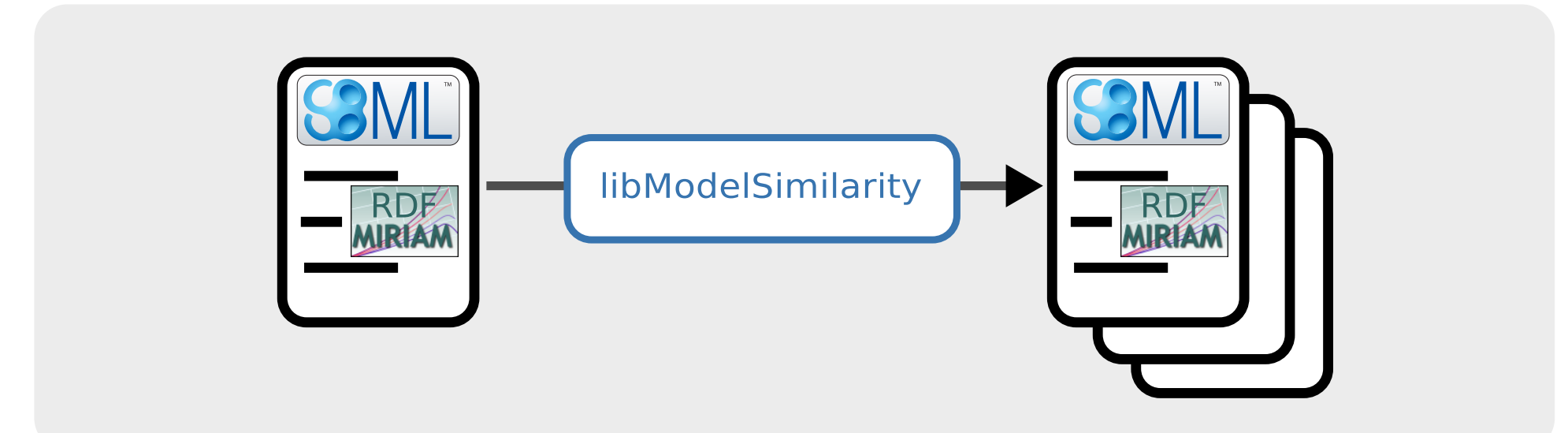
Merging Models and creating Submodels



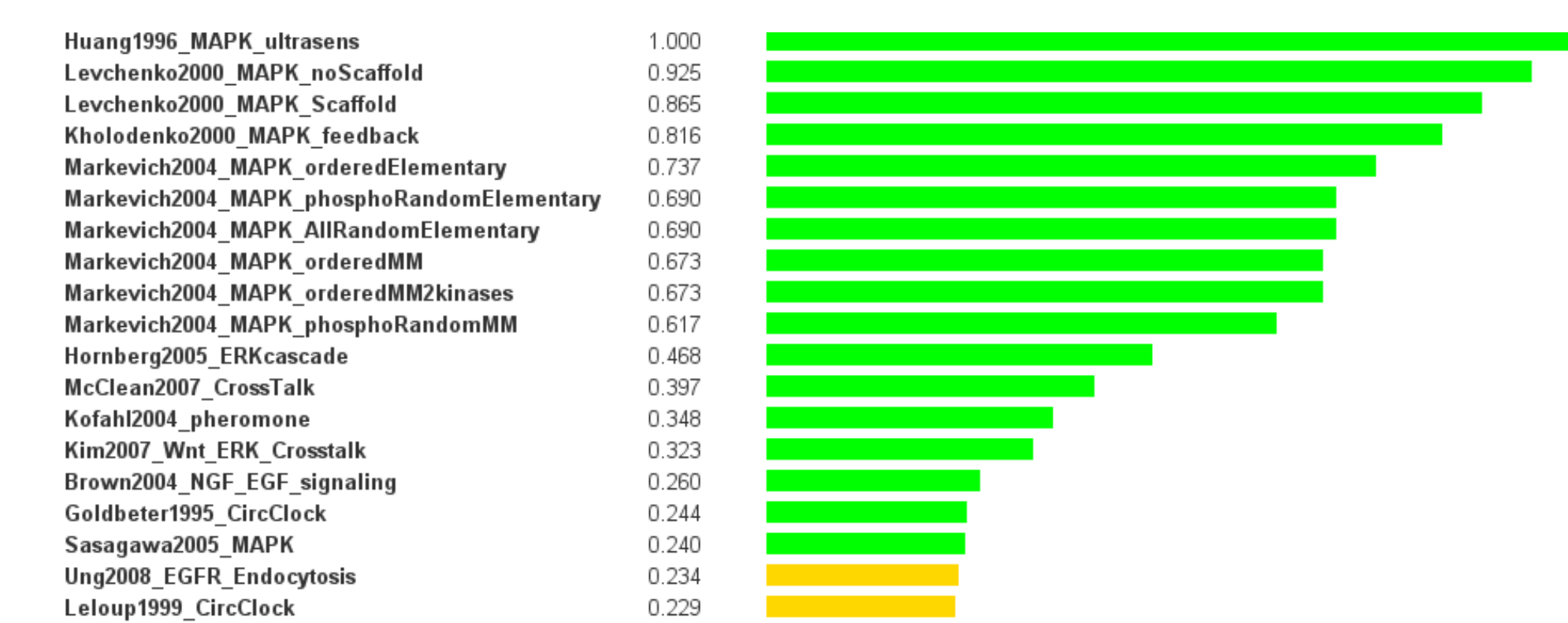
Based on a matching of model elements (see above) several models can be merged into one combined model. It is also possible to select several model elements to create a submodel. This requires the resolution of element attribute conflicts and the consideration of element dependencies.



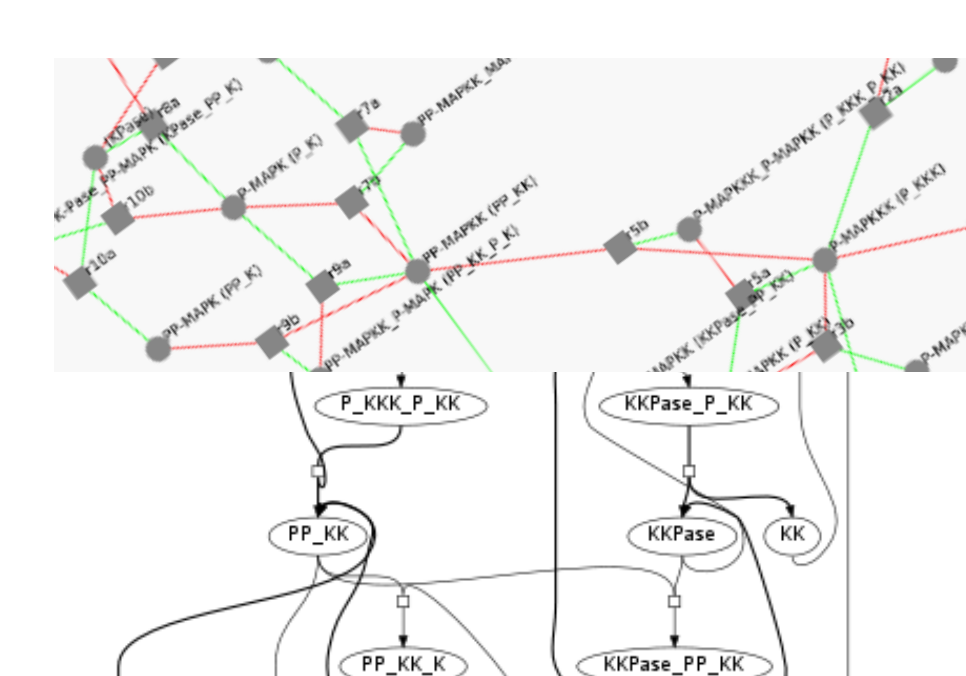
Finding Similar Models



Given an annotated model a ranked list of similar models, including a p-value indicating the significance of the similarity, can be returned. We have implemented and compared several clustering/ranking algorithms. In addition to that a local alignment of model elements can be returned and visualized. Via a RESTful interface this feature can be used for e.g experimental data or source-code.



Other Features of semanticSBML 2.0



Visualization

The network structure of models can be visualized using GraphViz or a JavaScript based force directed layout.

Parameter Balancing Kinetic parameters can be estimated based on prior distributions and input data sets within a Bayesian framework.

Parameter	Value
Strain constant	VGK 230
ard maximal velocity	VGK
story constant	VGK ADP 1.3
story constant	VGK AMP 1.3
story constant	VGK ATP 1.3
story constant	VGK PEP 7.9844
cells constant	VGK GLCI
cells constant	VGK P

fault values / prior distributions

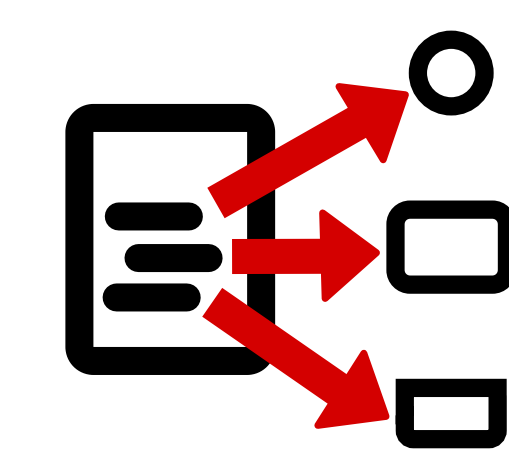
Shorthand SBML

Using the easy Shorthand SBML notation, SBML models can be build fast and efficiently.

```
@model:2.3.1=MichaelisMentenKinetics "Mi
@compartments
cell:1
@species
cell:Substrate=1000
cell:Enzyme=100
cell:Complex=0
cell:Product=0
@parameters
k1=1
k1r=2
@reactions
@rx=SubstrateEnzymeBinding "Substrate-en
```

RESTful API

Since semanticSBML 2.0 is based on the web framework web2py it inherits its ability to expose a RESTful interface to its functions. To solve the problem of a proper documentation semanticSBML 2.0 includes a generic REST documentation module. In its current state it can display information about available services, in the future we plan to extend it to also export WADL/WSDL2.0.



Annotate Your Model (AYM)

is a web service that was created to allow the MIRIAM annotation of non SBML source-code models (and now also data files e.g. in Excel format). Given a set of annotations AYM can be used to call the semanticSBML REST interface to retrieve similar SBML models.

