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.

**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.

**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.

**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.

**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.

**Shorthand SBML**

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

**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.