

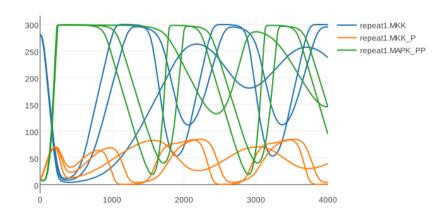
07: Systems Biology Markup Language (SBML)

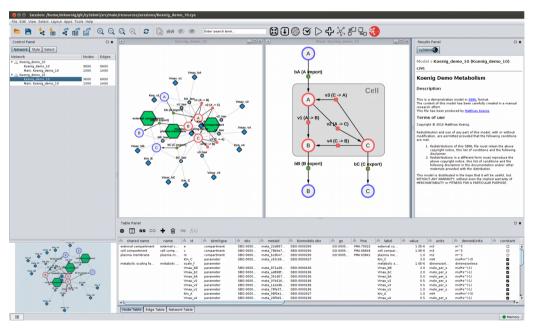
https://github.com/matthiaskoenig/itbtechtalks

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Standard Formats

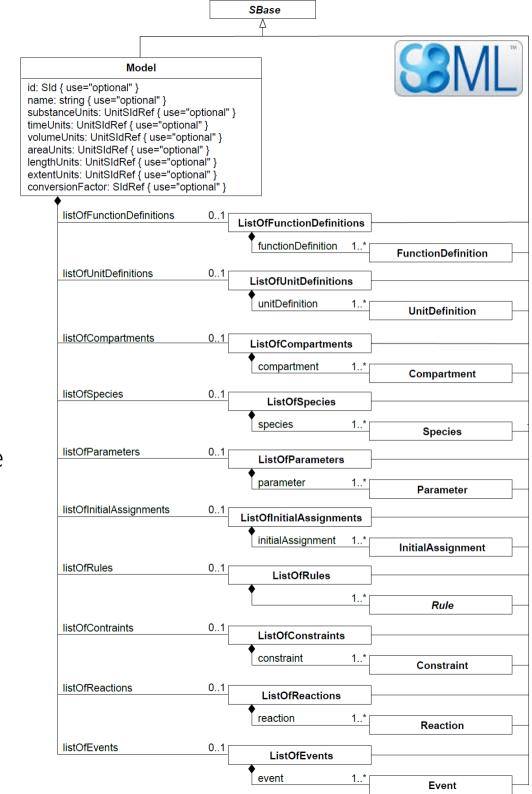
- Encoding of information in computer readable format
 - Minimal Information for models and simulation (MIRIAM, MIASE)
- Exchangeability & Reusability
- Reproducibility
 - Identical results with multiple simulators (roadrunner, COPASI, JWS)
- Annotations (to ontologies)
 - Knowledge integration (biological, computational)
 - Documentation (what is my model component)
- Quality
 - Automatic validation, e.g., model quality (unit checking, model consistency)
- Software & Tools
 - Simulation, Visualization, Analysis, Model Repositories, Parameter fitting



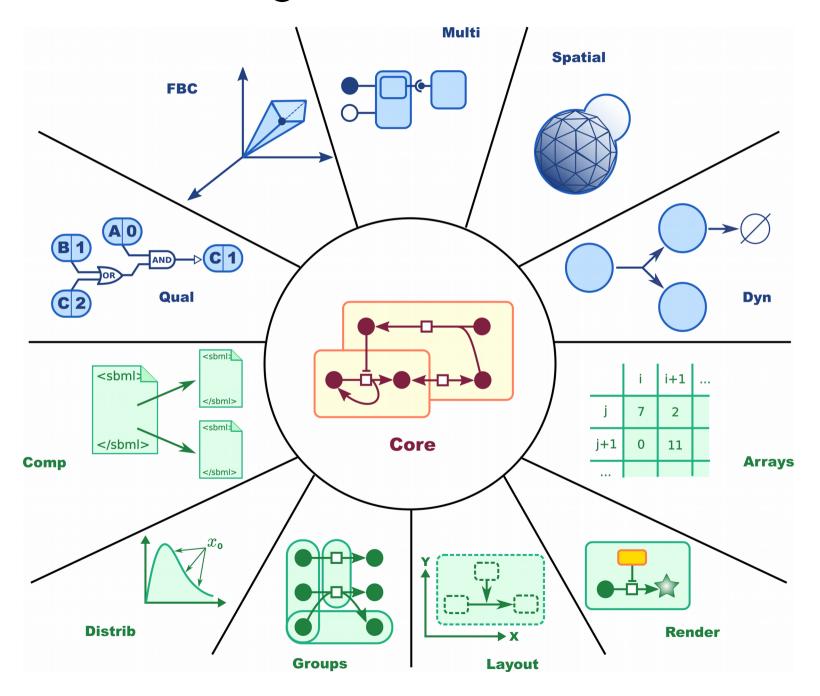


Systems Biology Markup Language

- De facto standard for encoding computational models (ODE)
- >280 software tools (simulation, visualization, parameter fitting, ...)
- Model data bases Biomodels, JWS
- libsbml: LibSBML is a free, open-source programming library to read, write, manipulate, translate, and validate SBML files (C++, python, R, JavaScript, Matlab, Java, ...)



SBML Packages



A

```
<?xml version="1.0" encoding="UTF-8"?>
                            <sbml xmlns="http://www.sbml.org/sbml/level3/version1/core" level="3" version="1"</pre>
                                            xmlns:layout="http://www.sbml.org/sbml/level3/version1/layout/version1"
                                           layout:required="false">
                                                                                                                                                  declaration of packages
                                 <model name="Tiny model example" >
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                                      <listOfSpecies> ... </listOfSpecies>
                                                                                                                                                                              variables
                                     <listOfParameters> ... </listOfParameters>
                                      <listOfInitialAssignments> ... </listOfInitialAssignments>
                                      <listOfRules> ... </listOfRules>
                                      <listOfConstraints> ... </listOfConstraints>
                                       <listOfReactions> ... </listOfReactions>
                                                                                                                                                              relationships
                                                                                                                                                                                                                                Core
                                      <listOfEvents> ... </listOfEvents>
                                      <layout:listOfLayouts xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" >
                                           <layout:layout layout:id="layout_1" layout:name="Layout">
                                                <layout:dimensions layout:width="620" layout:height="400"/>
                                                <layout:listOfCompartmentGlyphs> ... </layout:listOfCompartmentGlyphs>
                                               <layout:listOfSpeciesGlyphs> ... </layout:listOfSpeciesGlyphs>
                                               <layout:listOfReactionGlyphs> ... </layout:listOfReactionGlyphs>
References <a href="References">References</a> <a href="References
                                           </layout:layout>
                                                                                                                                                                                                                 Package
                                      </layout:listOfLayouts>
                                 </model>
                            </sbml>
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        hasonlySubstanceUnits="false" boundaryCondition="false" constant="false"/>
hasOnlySubstanceUnits="false" | oundaryCondition="false" | constant="false" |
  <annotation>
   <bgbiol:isVersionOf>
           <rdf:li rdf:resource="http://identifiers.org/chebi/CHEBI:58247"/>
<parameter id="Vm" value="10" constant="krue" sboTerm="SBO:0000186"/>
<parameter id="Km" value="10" constant=</pre>
                                      true" sboTerm="SBO:0000371"/>
<reaction id="R1" name="glucokinase"</pre>
                                   reversible="false">
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    speciesReference species="Gop" stoichiometry="1" constant="true" boTerm="SBO:0000011"/>
<kineticLaw sboTerm="SBO:0000031">
    math xmlns="http://www.w3.prg/1998/Math/MathML">
      <apply>
       <divide />
        apply>
         <times/>
         <ci>Vm </ci>
         <ci>Glu </ci>
       </apply>
```