



Context-based generation of kinetic equations with SBMLsqueezer 1.3

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$$v_j(\mathbf{S}, \mathbf{p}) = F_j(\mathbf{S}, \mathbf{p}) \left(k_{+j} \prod_i S_i^{n_{ij}^-} - k_{-j} \prod_i S_i^{n_{ij}^+} \right)$$

Generalized mass-action equation

Reversible Michaelis-Menten equation with inhibition

$$v_j = \frac{\frac{v_+^m}{K_S^M} [S] - \frac{v_-^m}{K_P^M} [P]}{1 + \frac{[I]}{K^{Ia}} + \left(\frac{[S]}{K_S^M} + \frac{[P]}{K_P^M} \right) \left(1 + \frac{[I]}{K^{Ib}} \right)}$$

$$v_j = \frac{k_{+j}^{\text{cat}} \prod_i \left(\frac{S_i}{K_{ji}^M} \right)^{n_{ij}^-} - k_{-l}^{\text{cat}} \prod_i \left(\frac{S_i}{K_{ji}^M} \right)^{n_{ij}^+}}{\prod_i \sum_{m=0}^{n_{ij}^-} \left(\frac{S_i}{K_{ji}^M} \right)^m + \prod_i \sum_{m=0}^{n_{ij}^+} \left(\frac{S_i}{K_{ji}^M} \right)^m - 1} \\ \cdot [E_j] \cdot \prod_m h_A(S_m, K_{jm}^A)^{w_{jm}^+} h_I(S_m, K_{jm}^I)^{w_{jm}^-}$$

Convenience rate law

Langevin equation

$$dx_i(t) = \sum_{j=1}^M n_{ij} a_j(\mathbf{x}(t)) + \sum_{j=1}^M n_{ij} \sqrt{a_j(\mathbf{x}(t))} dW_j, \quad i = 1, \dots, N$$



Reaction context in annotated systems

What we learn from a topology:

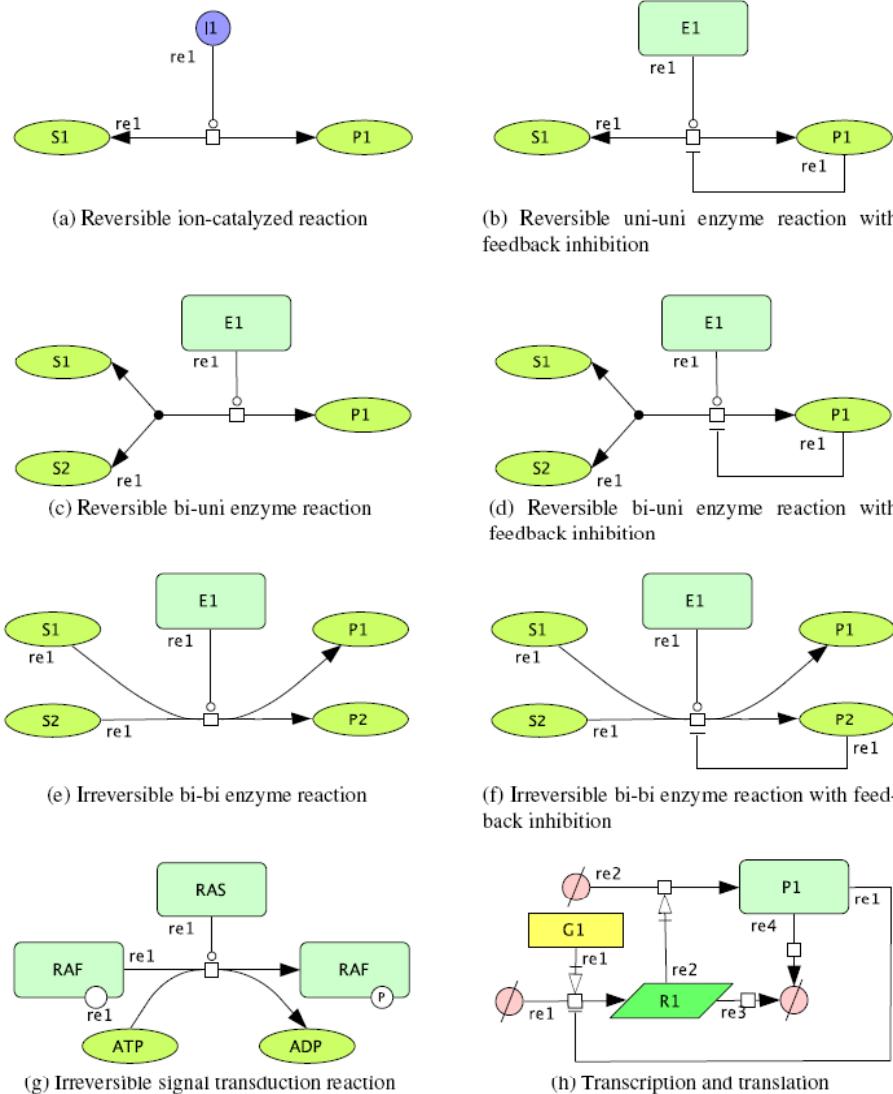
- Balance equations
- Species concentration dependencies
- Stoichiometric relationships

$$\frac{d\mathbf{S}}{dt} = \mathbf{N}\nu(\mathbf{S}(t), \mathbf{p})$$

And what we cannot learn:

- Regulatory relationships
- Reaction velocity

$$\nu(\mathbf{S}(t), \mathbf{p})$$



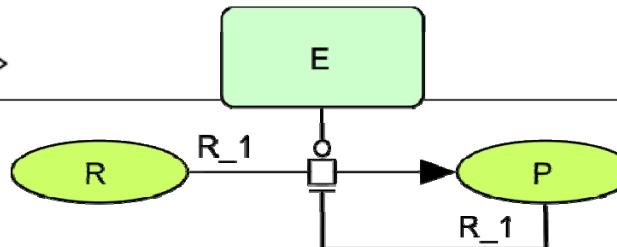


An example for a Reaction object in SBML

```

1 <listOfReactions>
2   <reaction id="R_1" reversible="false" sboTerm="SBO:0000393">
3     <!-- production -->
4     <listOfReactants>
5       <speciesReference sboTerm="SBO:0000015" species="R"/>
6         <!-- substrate -->
7     </listOfReactants>
8     <listOfProducts>
9       <speciesReference sboTerm="SBO:0000011" species="P"/>
10      <!-- product -->
11    </listOfProducts>
12    <listOfModifiers>
13      <modifierSpeciesReference sboTerm="SBO:0000460" species="E"/>
14        <!-- enzymatic catalyst -->
15      <modifierSpeciesReference sboTerm="SBO:0000020" species="P"/>
        <!-- inhibitor -->
16    </listOfModifiers>
17    <!-- A KineticLaw object can be placed here. -->
18  </reaction>
19 </listOfReactions>

```





Example: Definition of parameters and units

Definition of parameters in SBML using SBO annotations

```
1   <!-- ... -->
2   <listOfParameters> <!-- Defined globally or locally -->
3     <parameter id="V" units="mol_per_s" sboTerm="SBO:0000025"/>
4     <parameter id="Ks" units="substance" sboTerm="SBO:0000027"/>
5     <parameter id="Kp" units="substance" sboTerm="SBO:0000027"/>
6   </listOfParameters>
7   <!-- ... -->
```

catalytic rate constant

Michaelis constant

Definition of a unit in SBML

```
1   <!-- ... -->
2   <listOfUnitDefinitions>
3     <unitDefinition id="mol_per_s">
4       <listOfUnits>
5         <unit kind="mole"/>
6         <unit kind="second" exponent="-1"/>
7       </listOfUnits>
8     </unitDefinition>
9   </listOfUnitDefinitions>
10  <!-- ... -->
```

Predefined units in SBML:

- substance (in mole)
- volume (in litre)
- area (in square metres)
- length (in metre)
- time (in seconds)



Assignment of rate laws step by step

The reaction network diagram shows the following components:

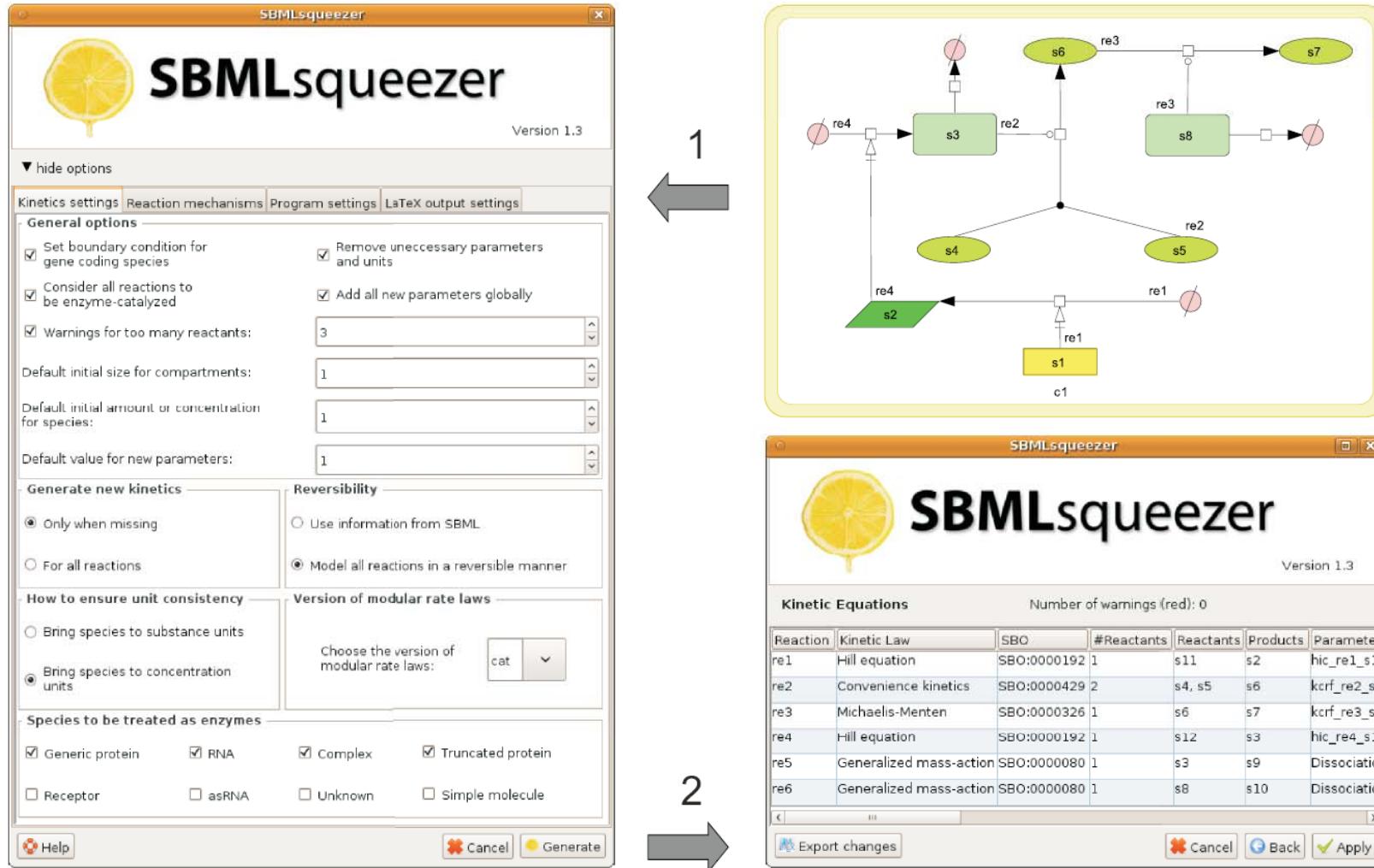
- Species: s_1 (yellow), s_3 (green), s_4 (green), s_5 (green), s_6 (green), s_8 (green).
- Reactions:
 - r_{e1} : $s_1 \rightarrow$ (enzymatic)
 - r_{e2} : $s_3 + s_4 \rightarrow s_5$ (modular)
 - r_{e3} : $s_6 \rightarrow s_8$ (modular)
 - r_{e3} : $s_8 \rightarrow$ (modular)

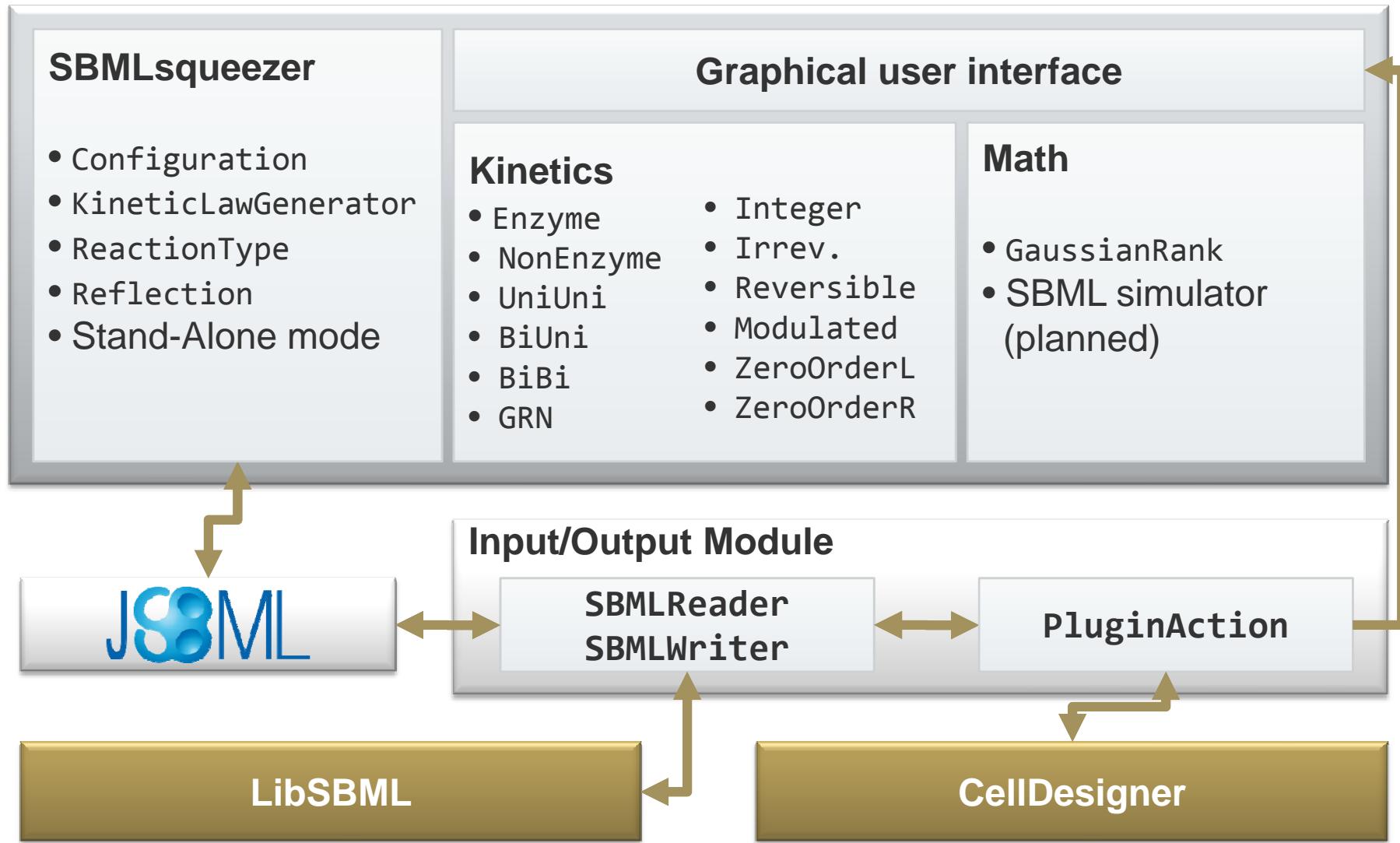
The SBMLsqueezer dialog box contains the following settings:

- Please choose one kinetic law**
 - Common modular rate law (CM)
 - Convenience kinetics
 - Direct binding modular rate law (DM)
 - Force-dependent modular rate law (FM)
 - Ordered mechanism
 - Power-law modular rate law (PM)
 - Random order mechanism
 - Simultaneous binding modular rate law (SM)
- Equation Preview**
$$\nu_{r_{e2}} = [s_3] \cdot \text{vol}(c_1) \cdot \frac{k_{\text{crf}} r_{e2} s_3 \cdot \frac{[s_5] \cdot \text{vol}}{k_{m\text{cre2}} s_4 s_3 \cdot k_{m\text{cre2}} s}}{\left(1 + \frac{[s_4] \cdot \text{vol}(c_1)}{k_{m\text{cre2}} s_4 s_3}\right) \cdot \left(1 + \frac{[s_5] \cdot \text{vol}}{k_{m\text{cre2}} s_4 s_3}\right)}$$
- Reaction options**
 - Consider this reaction to be enzyme-catalyzed
 - Reversible
 - Irreversible
 - Global parameters
 - Local parameters
- Buttons**
 - Cancel
 - OK



Rate law generation in one single step







Species Aliases

CellDesigner term	SBO term
ANTISENSE_RNA	small interfering RNA
COMPLEX	non-covalent complex
DEGRADED	empty set
DRUG	synthetic chemical compound
GENE	gene
GENERIC	polypeptide chain
ION	non-macromolecular ion
PHENOTYPE	phenotype
PROTEIN	protein complex
RECEPTOR	receptor
RNA	ribonucleic acid
ION_CHANNEL	channel
SIMPLE_MOLECULE	simple chemical
TRUNCATED	chemical macromolecule
UNKNOWN	material entity of unspecified nature

- Unique translation important
- Sometimes no exactly matching term available

Reaction Aliases

CellDesigner term	SBO term
KNOWN_TRANSITION OMITTED	omitted process
STATE_TRANSITION	biochemical reaction
TRANSCRIPTION	transcription
TRANSLATION	translation
TRANSPORT	transport reaction
UNKNOWN_TRANSITION	uncertain process
reactant	reactant
product	product

Modifier Aliases

CellDesigner term	SBO term
CATALYSIS	catalyst
INHIBITION	inhibitor
MODULATION	modifier
PHYSICAL_STIMULATION	potentiator
TRANSCRIPTIONAL_ACTIVATION	stimulator
TRANSCRIPTIONAL_INHIBITION	inhibitor
TRANSLATIONAL_ACTIVATION	stimulator
TRANSLATIONAL_INHIBITION	inhibitor
TRIGGER	essential activator
UNKNOWN_CATALYSIS	catalyst
UNKNOWN_INHIBITION	inhibitor



Nature Precedings : doi:10.1038/npre.2010.4983.1 : Posted 9 Oct 2010

urn:miriam:kegg.compound:C00092, SBO term: simple chemical, Compartment: default, Charge: 0, Initial amount: 0, Substance unit: mmol. Checkboxes for Constant, Boundary condition, and Has only substance units are present but unchecked."/>

Species

Identifier: g6p

Name: glucose-6-phosphate

Meta identifier: meta_g6p

MIRIAM annotation: biological entity is <urn:miriam:kegg.compound:C00092>.

SBO term: simple chemical

Compartment: default

Charge: 0

Initial amount: 0

Substance unit: mmol

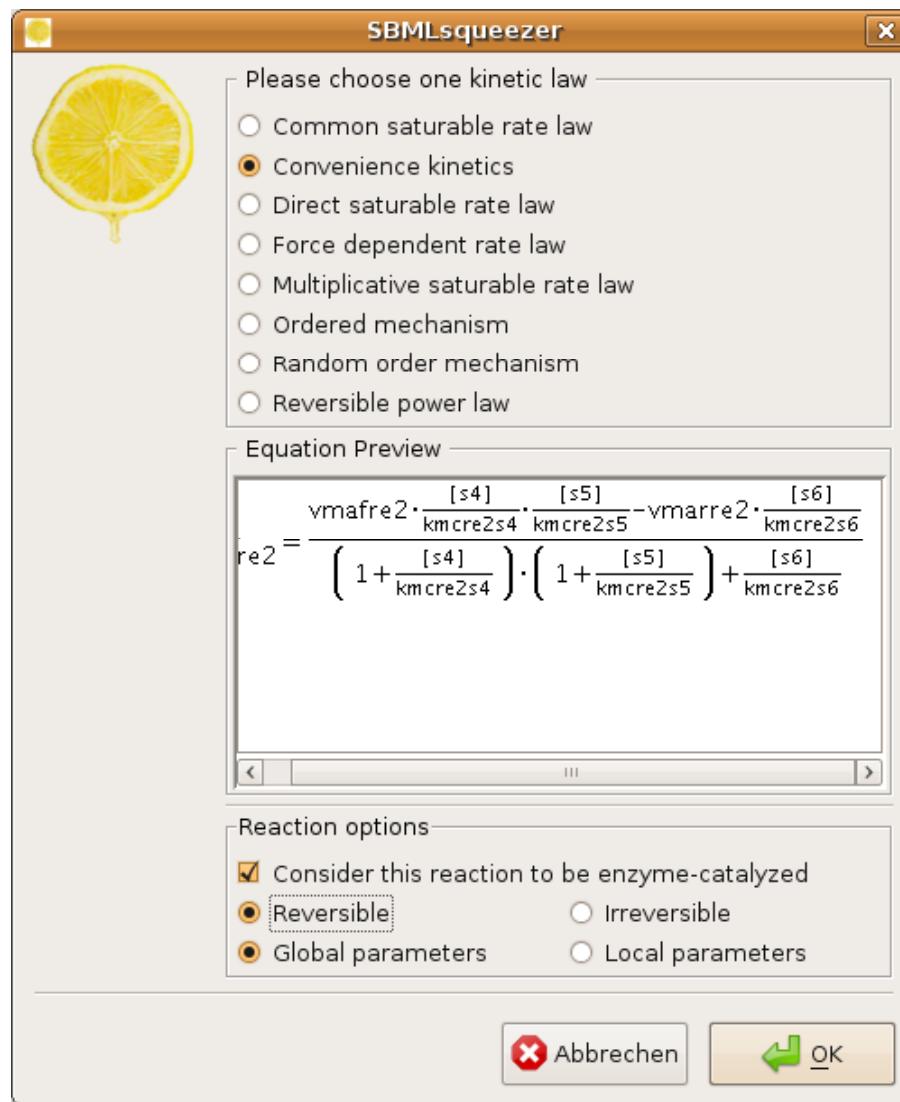
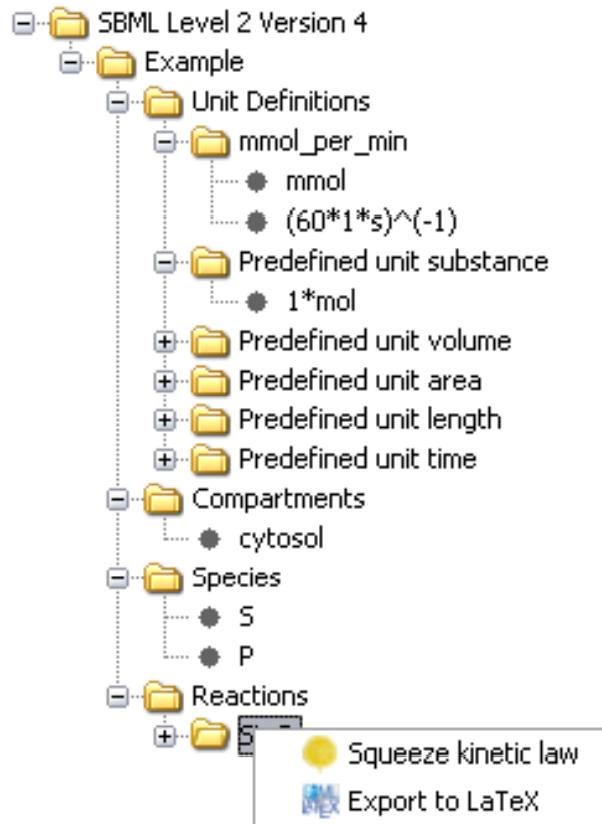
Constant

Boundary condition

Has only substance units

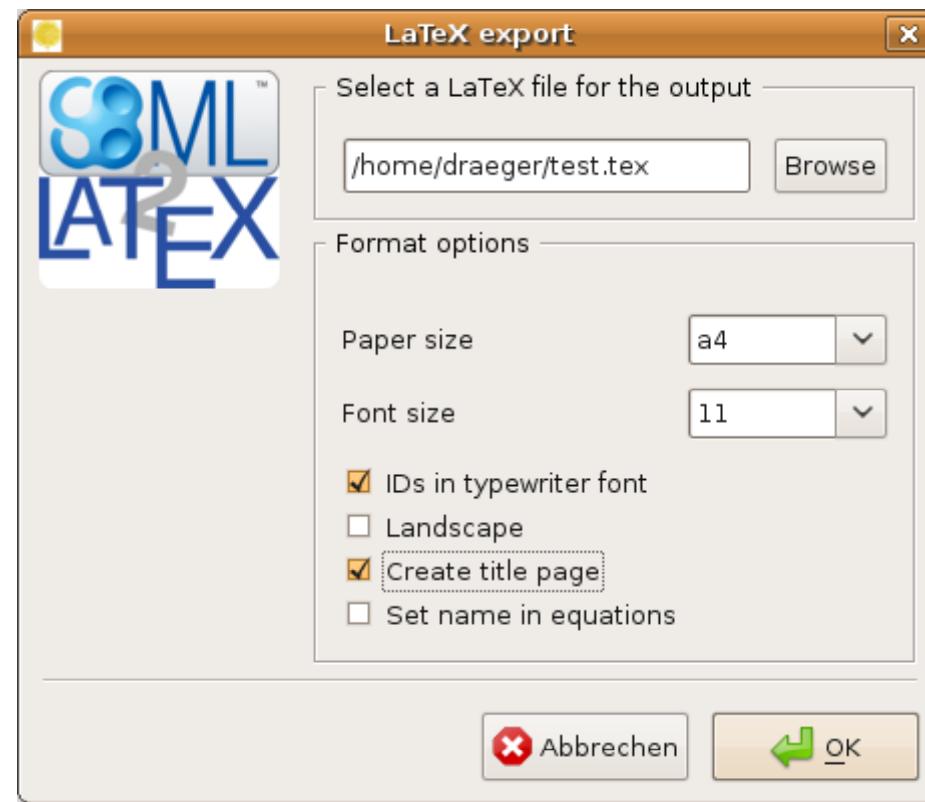
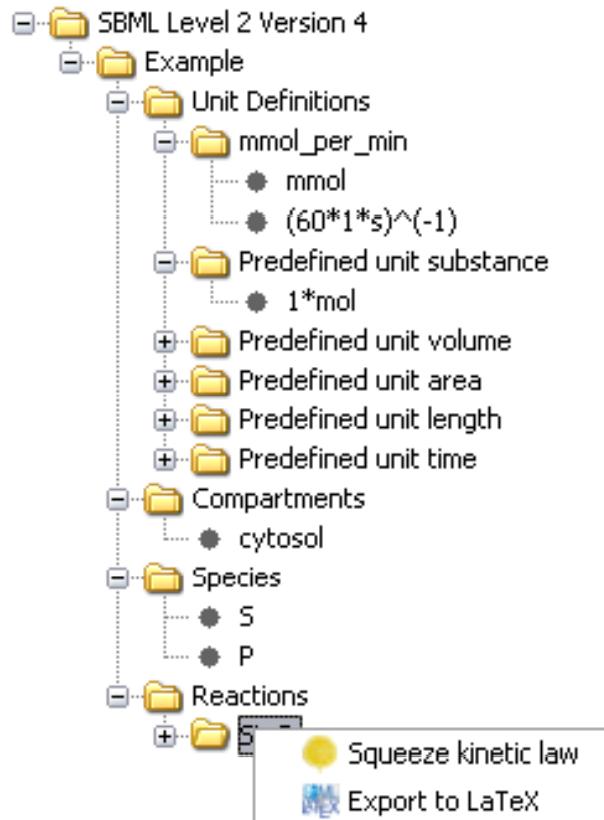


Equation generation for single reactions





Equation generation for single reactions





```
1 public static void main(String[] args) {
2     // Initialize SBMLsqueezer with appropriate SBML readers/writers
3     SBMLsqueezer sq = new SBMLsqueezer(new LibSBMLReader(), new
4         LibSBMLWriter());
5     // Configure SBMLsqueezer
6     sq.set(CfgKeys.OPT_ALL_REACTIONS_ARE_ENZYME_CATALYZED, true);
7     sq.set(CfgKeys.OPT_DEFAULT_COMPARTMENT_INITIAL_SIZE, 1d);
8     sq.set(CfgKeys.POSSIBLE_ENZYME_RNA, true);
9     sq.set(CfgKeys.KINETICS_UNI_UNI_TYPE, "MichaelisMenten");
10    sq.set(CfgKeys.KINETICS_OTHER_ENZYME_REACTIONS,
11        "ConvenienceKinetics");
12    try {
13        // Create kinetic equations, parameters, units etc. and save
14        // the result; args contains infile and outfile path
15        sq.squeeze(args[0], args[1]);
16    } catch (Throwable e) {
17        e.printStackTrace();
18    }
19 }
```

- Command-line mode: shell or batch scripts possible
- Just one central method: squeeze
- Easy adjustment of all settings through dedicated methods

Online version of SBMLsqueezer 1.3

University of Tübingen: Galaxy Webservice - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://webservices.cs.uni-tuebingen.de/

Most Visited ▾ Erste Schritte ▾ Aktuelle Nachrichten ▾

University of Tübingen: Galaxy W...

EBERHARD KARLS
UNIVERSITÄT
TÜBINGEN

Galaxy Webservices

Analyze Data Workflow Data Libraries Help User

Wilhelm-Schickard-Institute for Computer Science (WSI)
Centre for Bioinformatics Tübingen Prof. Dr. Andreas Zell Computer Architecture

Tools

- [SABINE](#)
- [SBML 2 LaTeX](#)
- [SBMLsqueezer](#)
- Upload SBML file from your computer
- Generate kinetic rate equations for a biochemical network
- [EDISA](#)
- [ModuleMaster](#)

SBML file:
4: exampleWithSBO.xml

Select uploaded SBML file.

Reversible reactions:
For all reactions ▾
Choose 'For all reactions' to model reactions reversibly. This option increases the number of applicable kinetics.

Kinetics for none-enzyme reactions:
Generalized Mass Action ▾
Select the type of kinetic equation to be applied if a reaction is catalyzed by a species that is not an enzyme or if no catalyst is assigned to the reaction and 'All reactions are enzyme catalyzed' is not selected.

Kinetics for uni-uni-type reactions:
Common Saturable ▾
Select the rate law to be applied for enzyme reactions with exactly one reactant and one product.

Kinetics for bi-uni-type reactions:
Common Saturable ▾
Select the kinetic equation for enzyme reactions with two substrate molecules (or one molecule a with stoichiometry of two) and one product.

Kinetics for bi-bi-type reactions:
Common Saturable ▾
Select the rate law for enzyme reactions with two reactants and two products. Here, two means either two distinct species or a stoichiometry of two.

Kinetics for other reactions:
Common Saturable ▾
Select the rate law for enzyme reactions that do not fit into any one of the reaction schemes above.

Kinetics for gene regulation:
Hill Equation ▾
Select a kinetic equation to be applied for gene-regulatory

History Options ▾

refresh | collapse all

Unnamed history

4: exampleWithSBO.xml
3: test.xml
2: Generate kinetics for oneReaction.xml
1: oneReaction.xml

Done



Thank you!

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