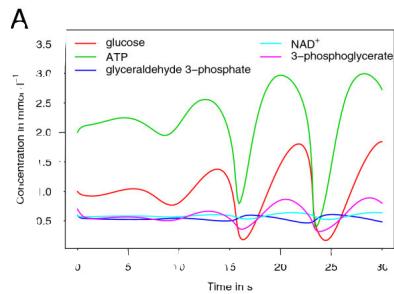




The ZBIT Systems Biology Software and Web-Service Collection

Andreas Dräger

Frequent tasks in systems biology



Steady-State
Analysis



Dynamic
Simulation

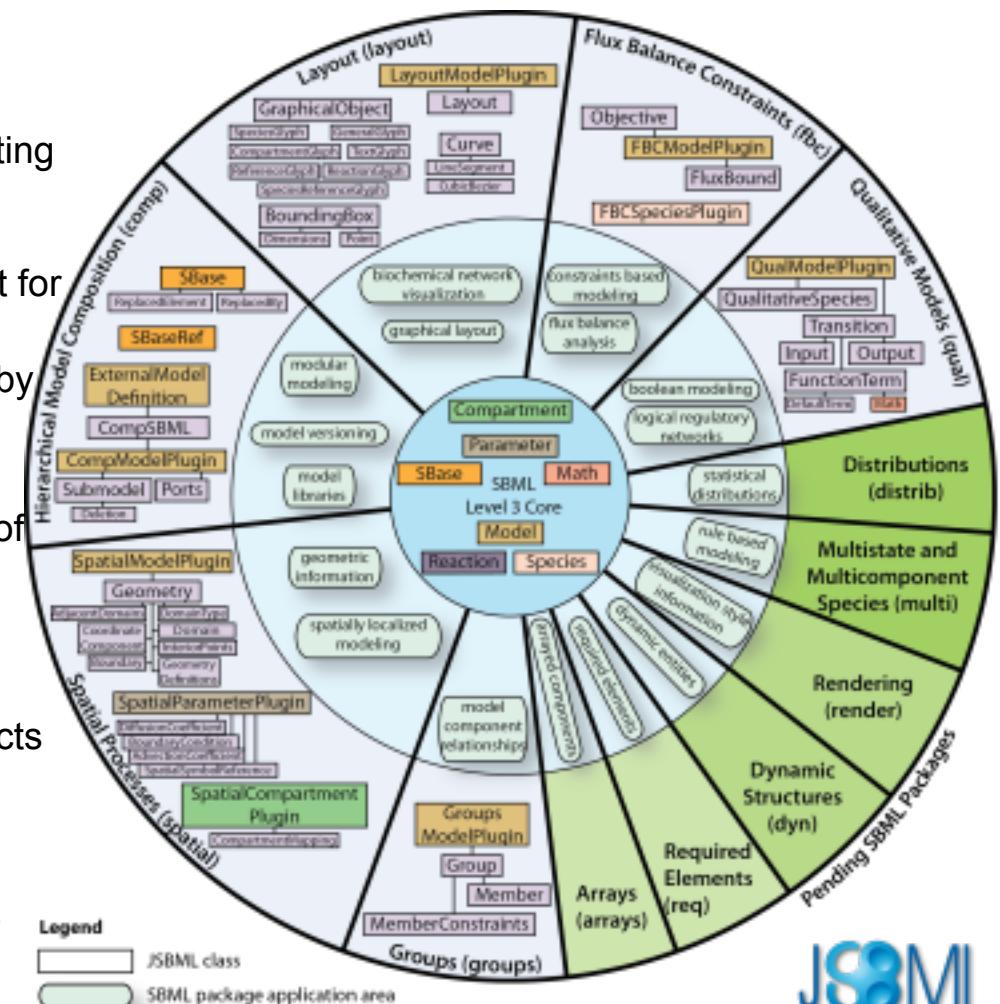
Model
JSBML



JSBML: a pure Java API for SBML

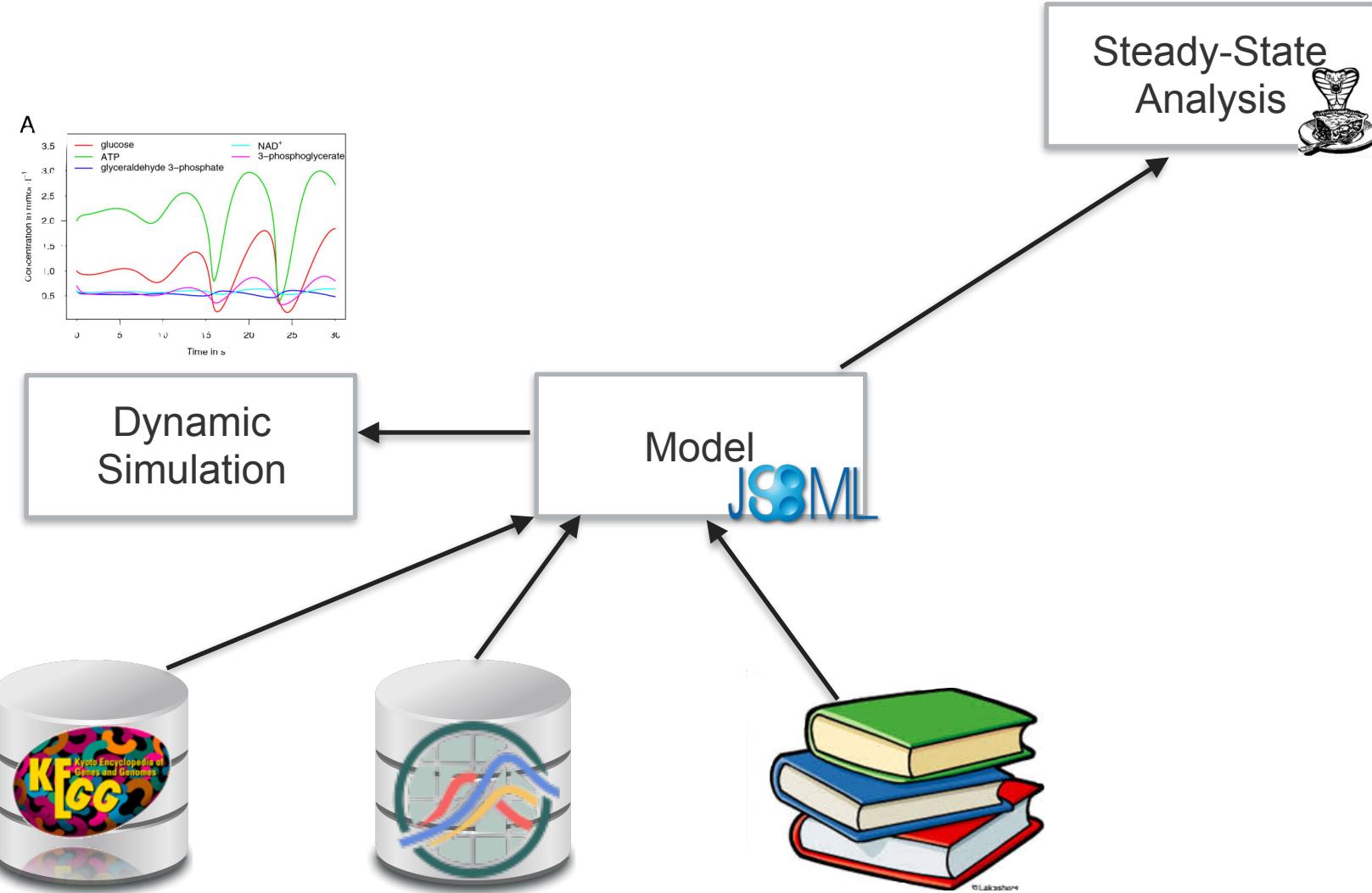
What is JSBML?

- The official, pure Java™ application programming library for reading, manipulating and writing SBML files and data objects
- Systems biology information in Java data structures patterned after the SBML format for fast access
- Open source project under LGPL, funded by NIH, EU, and Germany
- Features:
 - Full support for all Levels and Versions of SBML up to L3V2 and L2V5
 - All current SBML extension packages
 - Sophisticated type hierarchy
- SBML backend in several third-party projects
- More information:
 - <http://sbml.org/Software/JSBML>
 - jsbml-development@googlegroups.com
 - jsbml-team@caltech.edu



Rodriguez N, Thomas A, Watanabe L, Vazirabad IY, Kofia V, Gómez HF, Mittag F, Matthes J, Rudolph JD, Wrzodek F, Netz E, Diamantikos A, Eichner J, Keller R, Wrzodek C, Fröhlich S, Lewis NE, Myers CJ, Le Novère N, Palsson BØ, Hucka M, and Dräger A. JSBML 1.0: providing a smorgasbord of options to encode systems biology models. *Bioinformatics*, June 2015.

Frequent tasks in systems biology



From KEGG to draft models - common workflow

www.kegg.jp/kegg-bin/show_pathway?org_nar

Glycolysis / Gluconeogenesis - Homo sapiens (human)

Pathway menu | Organism menu | Pathway entry | Download KGM | Show description | User data mapping | Help

Homo sapiens (human) Go 100%

GLYCOLYSIS / GLUCONEOGENESIS

Starch and sucrose metabolism

ControlPanel Galaxy21-[Generate_kinetics_for_Glycolysis.xml].xml

File Edit Data Simulation

Time span

End Time: 100, Exp.: -6, Solver: SOSlib, COPASI, SimulationCore

Species Parameters Change amount Parameter Scan Interactive Simulation

ID	Name	Compartment	Quantity Type	Initial Quantity	Substance Type	Boundary Condition	Constant
s5	GAP	default	Amount	4.61	substance	false	false
s4	F16bP	default	Amount	10.00	substance	false	false
s3	F6P	default	Amount	0.00	substance	false	false
s2	Gluc6P	default	Amount	10.00	substance	false	false
s1	Gluc1P	default	Amount	3.15	substance	false	false
s6	GA13bP	default	Amount	2.74	substance	false	false
s7	Glycerate3P	default	Amount	4.02	substance	false	false
s8	5.4.2.2	default	Amount	0.00	substance	false	false
s9	5.3.1.9	default	Amount	0.00	substance	false	false
s10	3.1.3.11	default	Amount	0.00	substance	false	false
s11	2.7.1.11	default	Amount	0.00	substance	false	false
s12	4.1.2.13	default	Amount	0.00	substance	false	false
s13	1.2.1.12	default	Amount	0.00	substance	false	false
s14	5.4.2.4	default	Amount	0.00	substance	false	false
s15	Glucose	default	Amount	0.00	substance	false	false
s16	3.1.3.9	default	Amount	0.00	substance	false	false
s17	2.7.1.1	default	Amount	0.00	substance	false	false
s18	2.7.1.2	default	Amount	0.00	substance	false	false

Initialize Save As Execute Close show scatter plot

00010 6/16/16
(c) Kanehisa Laboratories

<http://identifiers.org/kegg.pathway/hsa00010>

CellDesigner

Glycolysis.xml

Gluc1P

5.4.2.2

5.3.1.9

2.7.1.11

4.1.2.13

1.2.1.12

5.4.2.4

3.1.3.9

2.7.1.1

2.7.1.2

2.7.1.147

Chloroform

Unselect all species search search

Concentration raw Species Fluxes Parameters Compartments

Graph Table

Visible Species Color

5.4.2.2

5.3.1.9

2.7.1.11

4.1.2.13

1.2.1.12

5.4.2.4

3.1.3.9

2.7.1.1

2.7.1.2

2.7.1.147

Chloroform

document saved.

Species Proteins Genes RNAs asRNAs Reactions

Edit Export

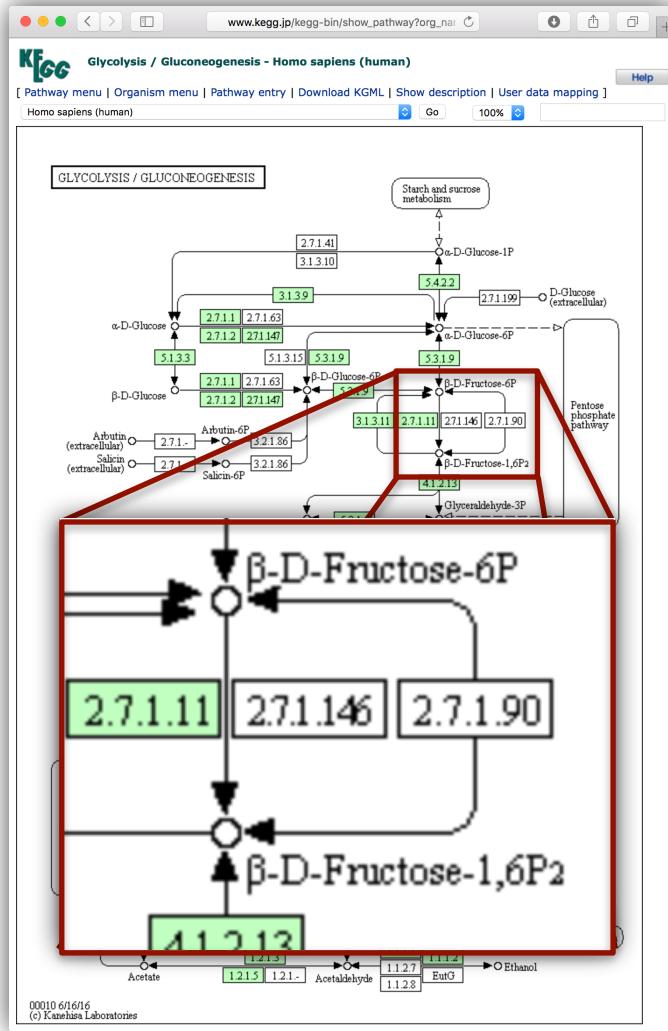
class	id	name	speciesType	compartment	position...	include...
SIMPLE_MOLECULE	s5	GAP	default	inside		
SIMPLE_MOLECULE	s4	F16bP	default	inside		
SIMPLE_MOLECULE	s3	F6P	default	inside		
SIMPLE_MOLECULE	s2	Gluc6P	default	inside		
SIMPLE_MOLECULE	s1	Gluc1P	default	inside		
SIMPLE_MOLECULE	s6	GA13bP	default	inside		
SIMPLE_MOLECULE	s7	Glycerate3P	default	inside		

NOTE MIRIAM

Edit Notes

<http://www.celldesigner.org>

Taking a closer look at KEGG pathway maps: missing reaction participants



<http://identifiers.org/kegg.pathway/hsa00010>

REACTION: R00756

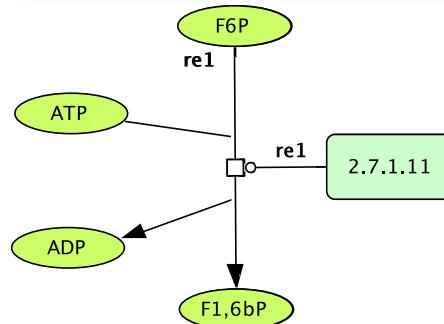
Entry	R00756	Reaction
Name	ATP:D-fructose-6-phosphate 1-phosphotransferase	
Definition	ATP + D-Fructose 6-phosphate <=> ADP + D-Fructose 1,6-bisphosphate	
Equation	C00002 + C00085 <=> C00008 + C00354	
Reactant pair	RP00003 C00002_C00008 main [RC:RC00002] RP00052 C00085_C00354 main [RC:RC00017]	
Enzyme	2.7.1.11	
Pathway	rn00680 Methane metabolism rn01120 Microbial metabolism in diverse environments rn01200 Carbon metabolism	
Module	M00345 Formaldehyde assimilation, ribulose monophosphate pathway	
LinkDB	All DBs	

Chemical structures for the reactants (C00002 and C00085) and products (C00008 and C00354) are shown, along with their SMILES representations:

Reactants: C00002: NC(=O)c1c[nH]c2c1n2COP(=O)([O-])[O-], C00085: NC(=O)c1c[nH]c2c1n2COP(=O)([O-])[O-]

Products: C00008: NC(=O)c1c[nH]c2c1n2COP(=O)([O-])[O-], C00354: NC(=O)c1c[nH]c2c1n2COP(=O)([O-])[O-]

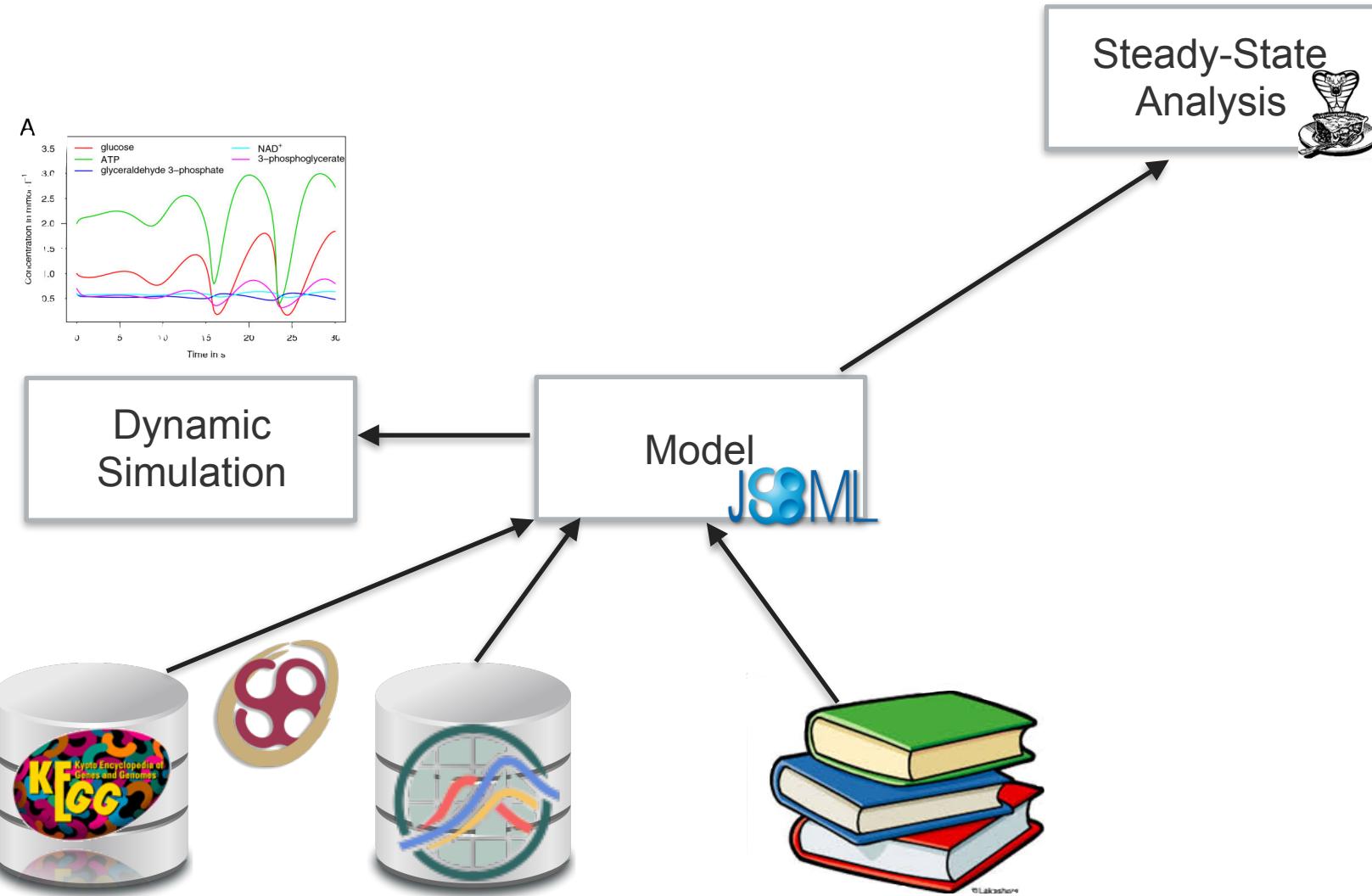
DBGET integrated database retrieval system



Conclusion:

- Additional reaction participants needed
- KEGG maps simplify processes
- Laborious check for each reaction

Frequent tasks in systems biology





Translating KEGG pathways to various file formats

- SBML (L2V4, L2V5, L3V1 with qual and layout extension)
- SBGN-ML
- BioPAX L2 or L3
- Cytoscape SIF
- Graph formats (GraphML, GML, TGF, YGF)
- Images (JPEG, GIF)
- Import of local files or download of pathways directly from KEGG PATHWAY database

Improve KEGG

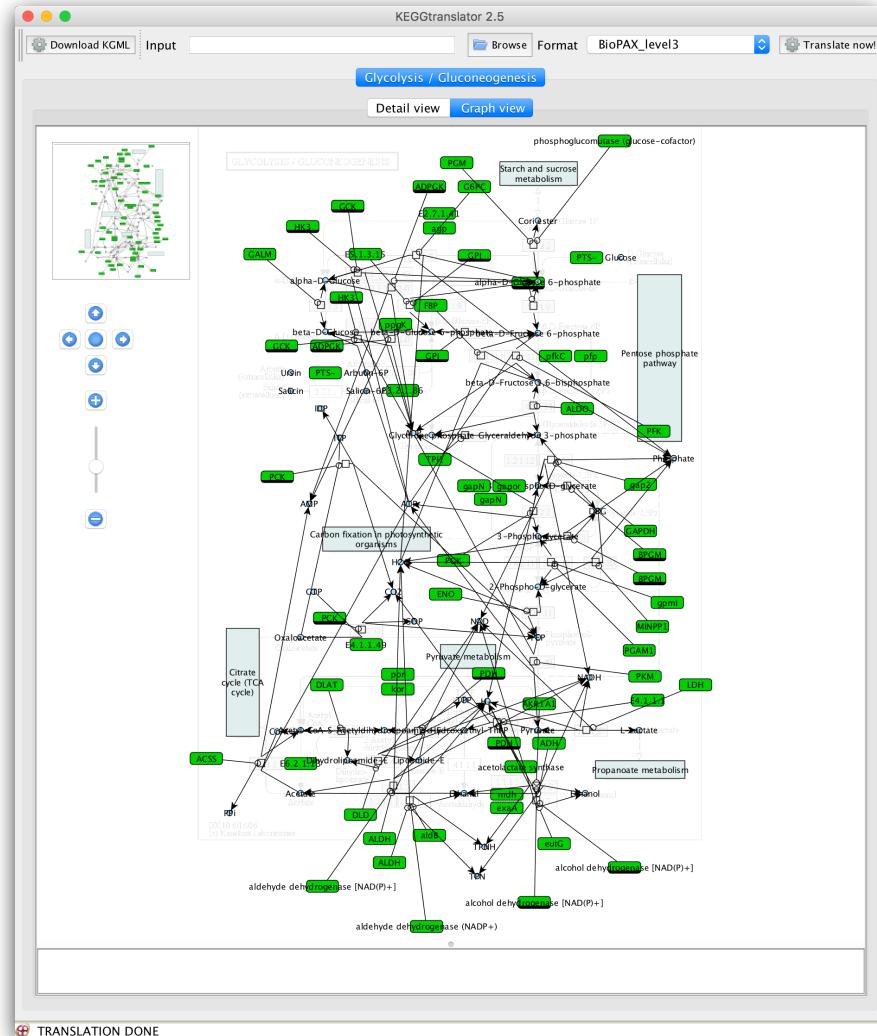
- Atom balance check
- Unbundling of reactions
- Addition of missing participants
- Removal of orphan nodes

Download link:

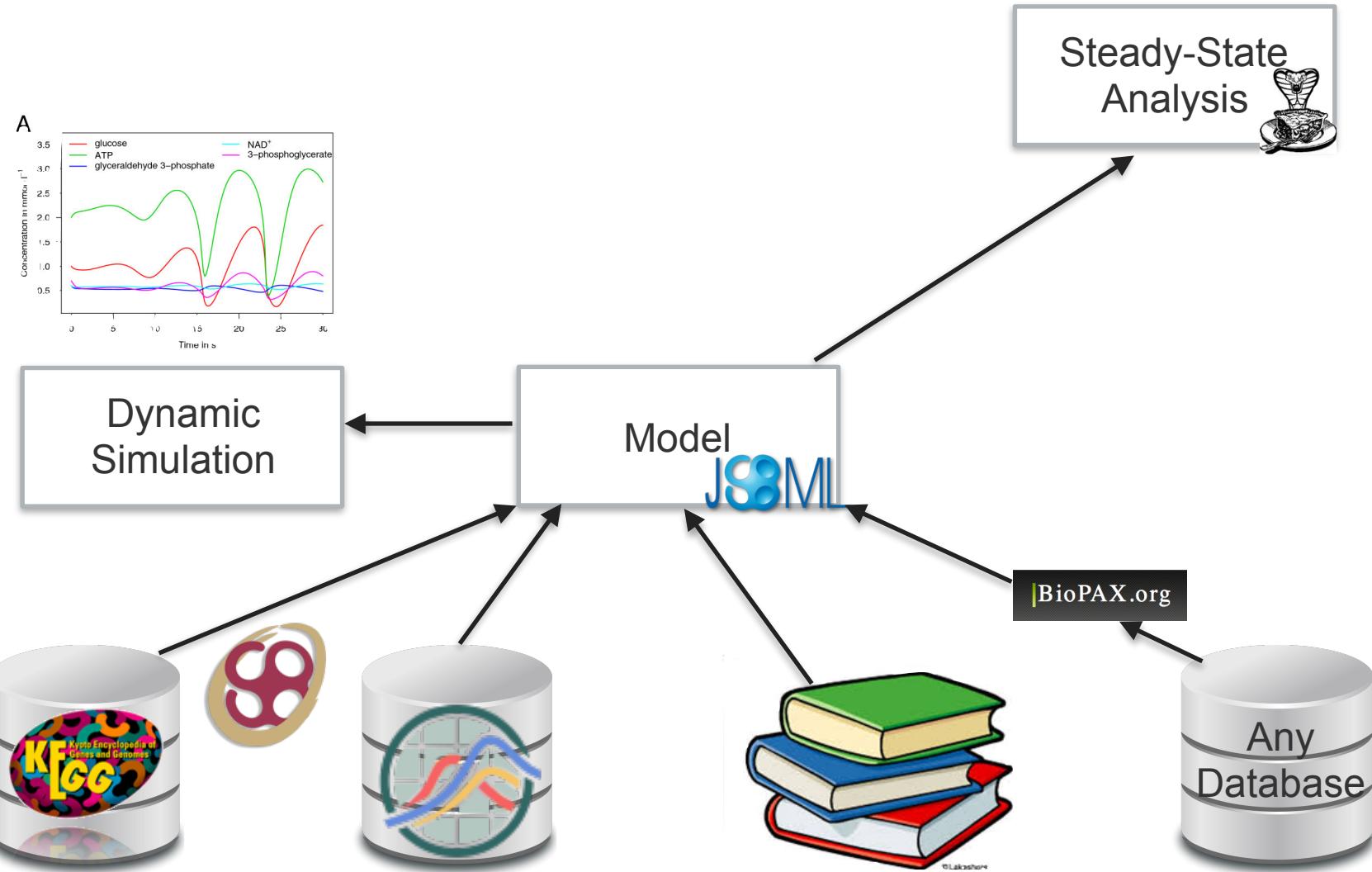
- <https://github.com/cogsys-tuebingen/KEGGtranslator/>

Wrzodek C, Büchel F, Ruff M, **Dräger A**, and Zell A. Precise generation of systems biology models from KEGG pathways. *BMC Systems Biology*, 7(1):15, January 2013.

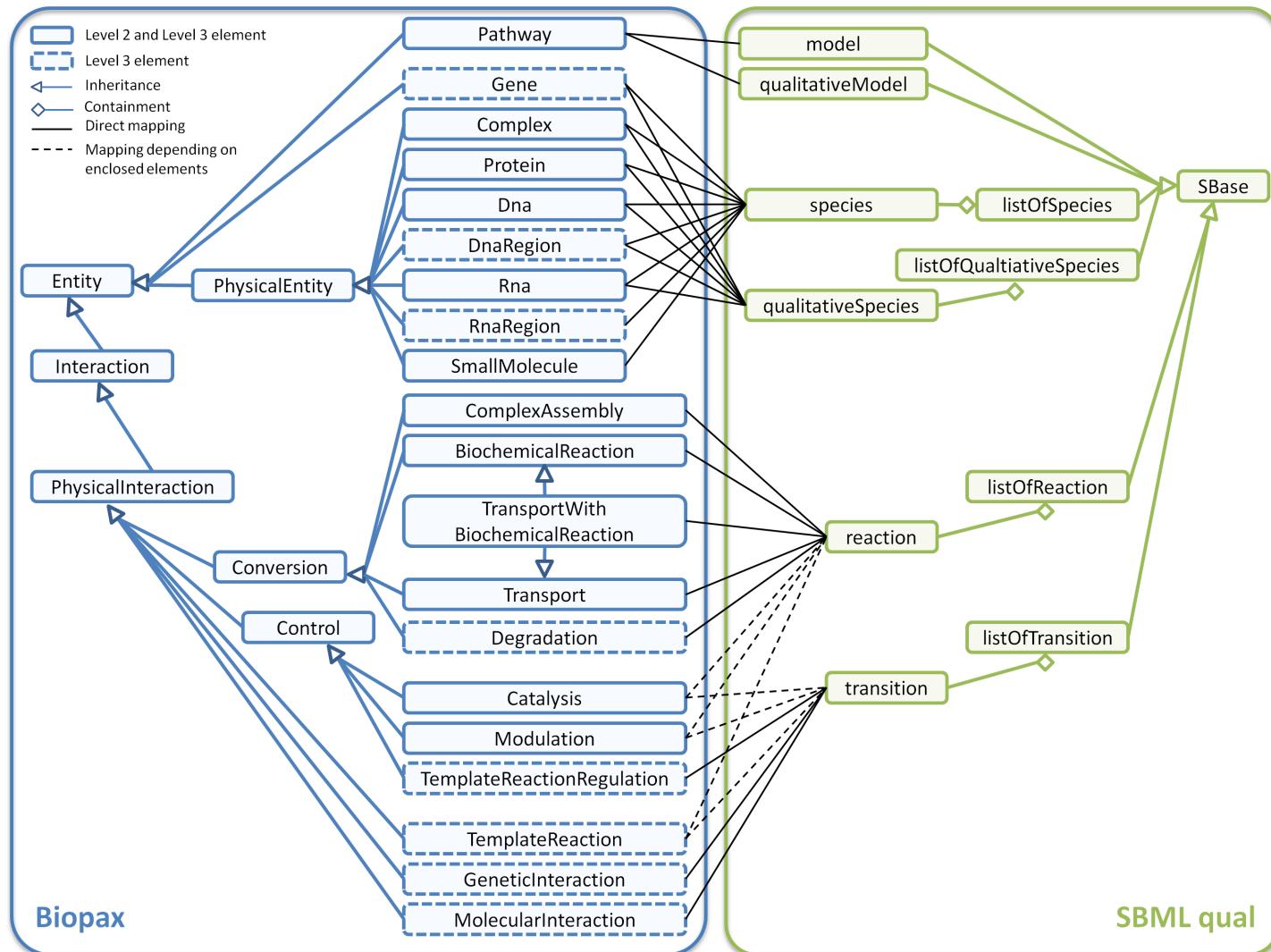
Wrzodek C, **Dräger A**, and Zell A. KEGGtranslator: visualizing and converting the KEGG PATHWAY database to various formats. *Bioinformatics*, 27(16):2314-2315, June 2011.



Frequent tasks in systems biology



BioPAX2SBML

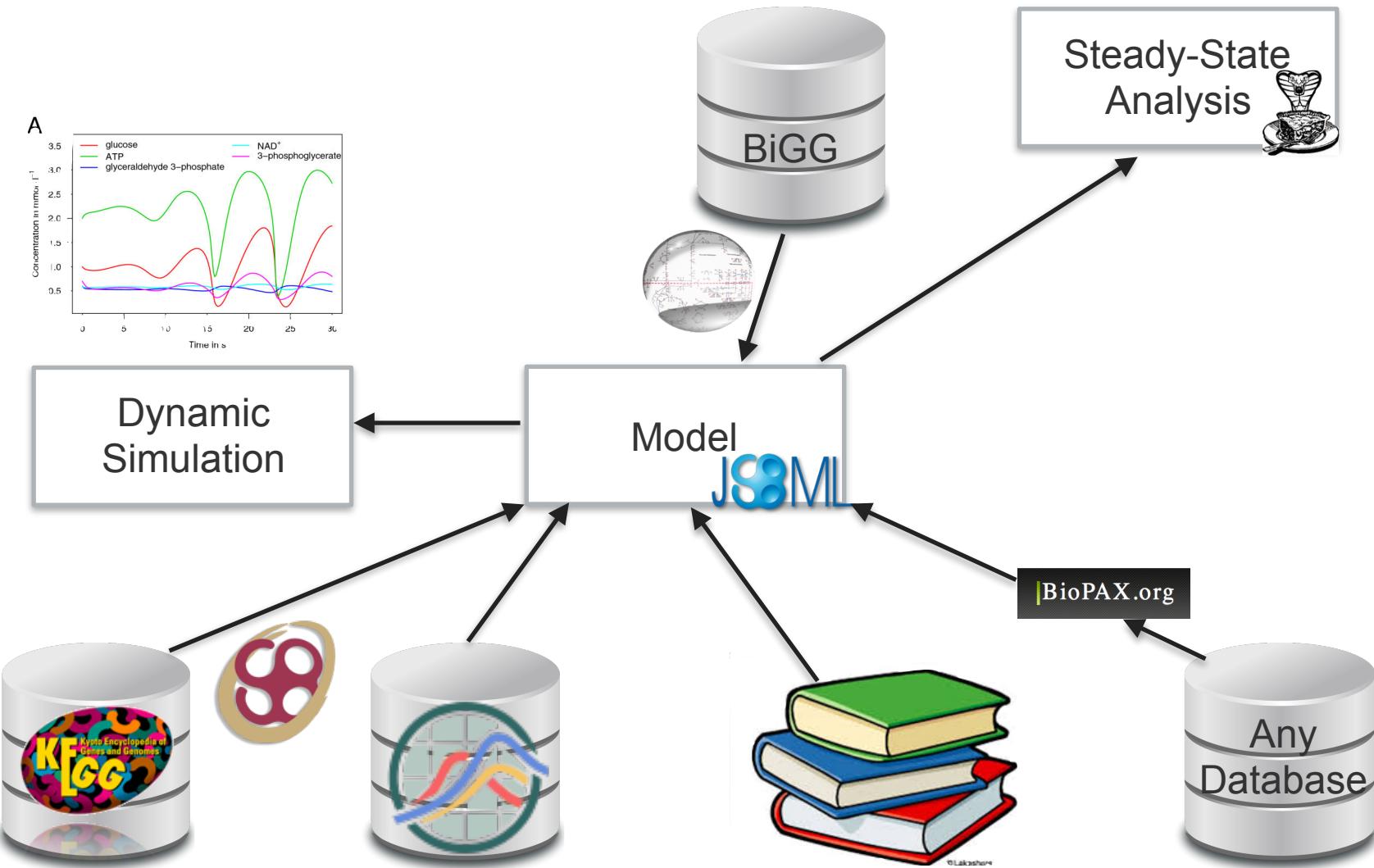


Büchel F, Wrzodek C, Mittag F, **Dräger A**, Eichner J, Rodriguez N, Le Novère N, and Zell A. Qualitative translation of relations from BioPAX to SBML qual. *Bioinformatics*, 28(20):2648-2653, August 2012.



Google
Summer of Code

Frequent tasks in systems biology



ModelPolisher: Model Annotation Tool



Input	SBML model(s) generated with COBRApy or COBRA Toolbox MAT format
Output	highly curated, well annotated SBML model(s) with all information from BiGG

```
draeger — screen — 112x19
screen
bash-3.2$ ./Documents/workspace/BioNetView/runModelPolisher.sh
-----
ModelPolisher version 0.2
Copyright © 2014-2015 University of California, San Diego
Systems Biology Research Group.
This program comes with ABSOLUTELY NO WARRANTY.
This is free software, and you are welcome
to redistribute it under certain conditions.
See http://creativecommons.org/licenses/by-nc-sa/4.0..
-----
INFO: Connected to SQL server localhost:5432 using database bigg.
INFO: Reading input file /Users/draeger/Documents/workspace/BioNetView/resources/edu/ucsd/sbrc/bigg/iJ01366.xml.
INFO: Processing model iJ01366.
          100% | 

INFO: Writing output file /Users/draeger/test.xml
INFO: Packing archive file /Users/draeger/test.xml.zip
INFO: Done (24.024 s).
bash-3.2$
```

Römer M, Eichner J, Dräger A, Wrzodek C, Wrzodek F, and Zell A. ZBIT Bioinformatics Toolbox: a Web-Platform for Systems Biology and Expression Data Analysis. *PLoS ONE*, 11(2):e0149263, February 2016.

Display of Models in Web Browser



```
file:///Users/draeger/test/ecoli.xml

GENE_ASSOCIATION: (b0351 or b1241)
SUBSYSTEM:
GENE_ASSOCIATION: s0001
SUBSYSTEM:
GENE_ASSOCIATION: (b3115 or b2296 or b1849)
SUBSYSTEM:
GENE_ASSOCIATION: (b0118 or b1276)
SUBSYSTEM:
GENE_ASSOCIATION: (b0118 or b1276)
SUBSYSTEM:
GENE_ASSOCIATION: 
SUBSYSTEM:
GENE_ASSOCIATION: b0474
SUBSYSTEM:
GENE_ASSOCIATION: (b0116 and b0726 and b0727)
SUBSYSTEM:
GENE_ASSOCIATION: b2587
SUBSYSTEM:
GENE_ASSOCIATION: (b0356 or b1478 or b1241)
SUBSYSTEM:
GENE_ASSOCIATION:
SUBSYSTEM:
GENE_ASSOCIATION: (((b3736 and b3737 and b3738) and (b3731 and b3732 and b3733 and b3734 and b3735)) or ((b3736 and b3737 and b3738) and (b3731 and b3732 and b3733 and b3734 and b3735) and b3739))
```

iSB619 - *Staphylococcus aureus* subsp. *aureus* N315

Terms of use

Copyright © 2015 The Regents of the University of California.

Permission to use, copy, modify and distribute any part of this model from BiGG Database for educational, research, and non-profit purposes, without fee, and without a written agreement is hereby granted, provided that the above copyright notice, this paragraph, and the following three paragraphs appear in all copies.

Those desiring to incorporate this BiGG database or parts of its content into commercial products or use for commercial purposes should contact the Technology Transfer & Intellectual Property Services
University of California, San Diego
9500 Gilman Drive # 0910
La Jolla, CA 92093-0910
United States of America
Phone: +1-858-534-5815
Fax: +1-858-534-7345
E-mail: invent@ucsd.edu

IN NO EVENT SHALL THE UNIVERSITY OF CALIFORNIA BE LIABLE TO ANY PARTY FOR DIRECT, INDIRECT, SPECIAL, INCIDENTAL, OR CONSEQUENTIAL DAMAGES, INCLUDING LOST PROFITS, ARISING OUT OF THE USE OF THIS BiGG DATABASE, EVEN IF THE UNIVERSITY OF CALIFORNIA HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGE.

THE BiGG DATABASE PROVIDED HEREIN IS ON AN "AS IS" BASIS, AND THE UNIVERSITY OF CALIFORNIA HAS NO OBLIGATION TO PROVIDE MAINTENANCE, SUPPORT, UPDATES, ENHANCEMENTS, OR MODIFICATIONS. THE UNIVERSITY OF CALIFORNIA MAKES NO REPRESENTATIONS AND EXTENDS NO WARRANTIES OF ANY KIND, EITHER IMPLIED OR EXPRESS, INCLUDING, BUT NOT LIMITED TO, THE IMPLIED WARRANTIES OF MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE, OR THAT THE USE OF THE BiGG DATABASE WILL NOT INFRINGE ANY PATENT, TRADEMARK OR OTHER RIGHTS.

Description

This is a metabolism model of *Staphylococcus aureus* subsp. *aureus* N315 in [SBML](#) format.

iSB619

The content of this model has been carefully created in a manual research effort. This file has been exported from the software [COBRApy](#) and further processed with a [SBML](#)-based application.
This file has been produced by the [Systems Biology Research Group](#) and is currently hosted on [BiGG knowledgebase](#) and identified by: [iSB619](#).

References

When using content from BiGG database in your research works, please cite
Schellenberger, J., Park, J. O., Conrad, T. C., and Palsson, B. Ø. (2010).
[BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions](#), *BMC Bioinformatics*, 11:213.

A COBRA model

B Polished BiGG model

ModelPolisher as Online Tool



The screenshot shows a web browser window for webservices.cs.uni-tuebingen.de. The title bar says "ZBIT Bioinformatics Toolbox". The main content area displays two tools: "EscherConverter" and "ModelPolisher".

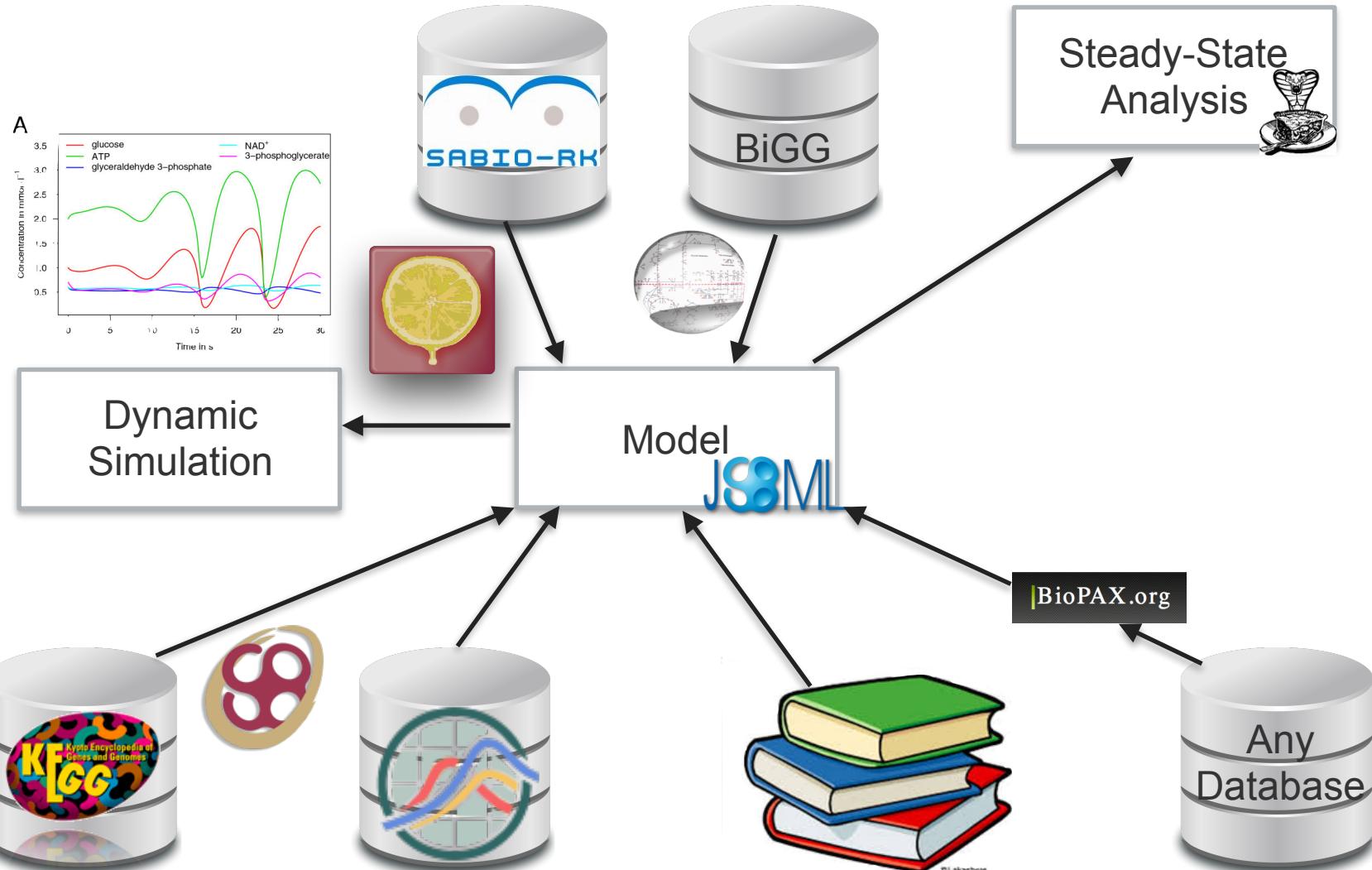
EscherConverter:
Conversion of graphical modeling formats
Devesh Khandelwal¹, Zachary A. King², Andreas Dräger^{2,3}
¹Department of Bioengineering, University of California, San Diego, La Jolla, CA, United States
³Center for Bioinformatics Tübingen (ZBIT), University of Tuebingen, Tübingen, Germany.

ModelPolisher:
Annotation of models using BiGG Models knowledgebase
Zachary A. King¹, Justin S. Lu¹, Andreas Dräger^{1,2}, Philip C. Miller¹, Steven Federowicz², Joshua A. Lerman¹, Ali Ebrahim¹, Bernhard O. Palsson^{1,3,4}, and Nathan E. Lewis^{3,4}
¹Department of Bioengineering, University of California, San Diego, La Jolla, CA, United States
²Center for Bioinformatics Tübingen (ZBIT), University of Tuebingen, Tübingen, Germany,
³Department of Pediatrics, University of California, San Diego, La Jolla, CA, United States

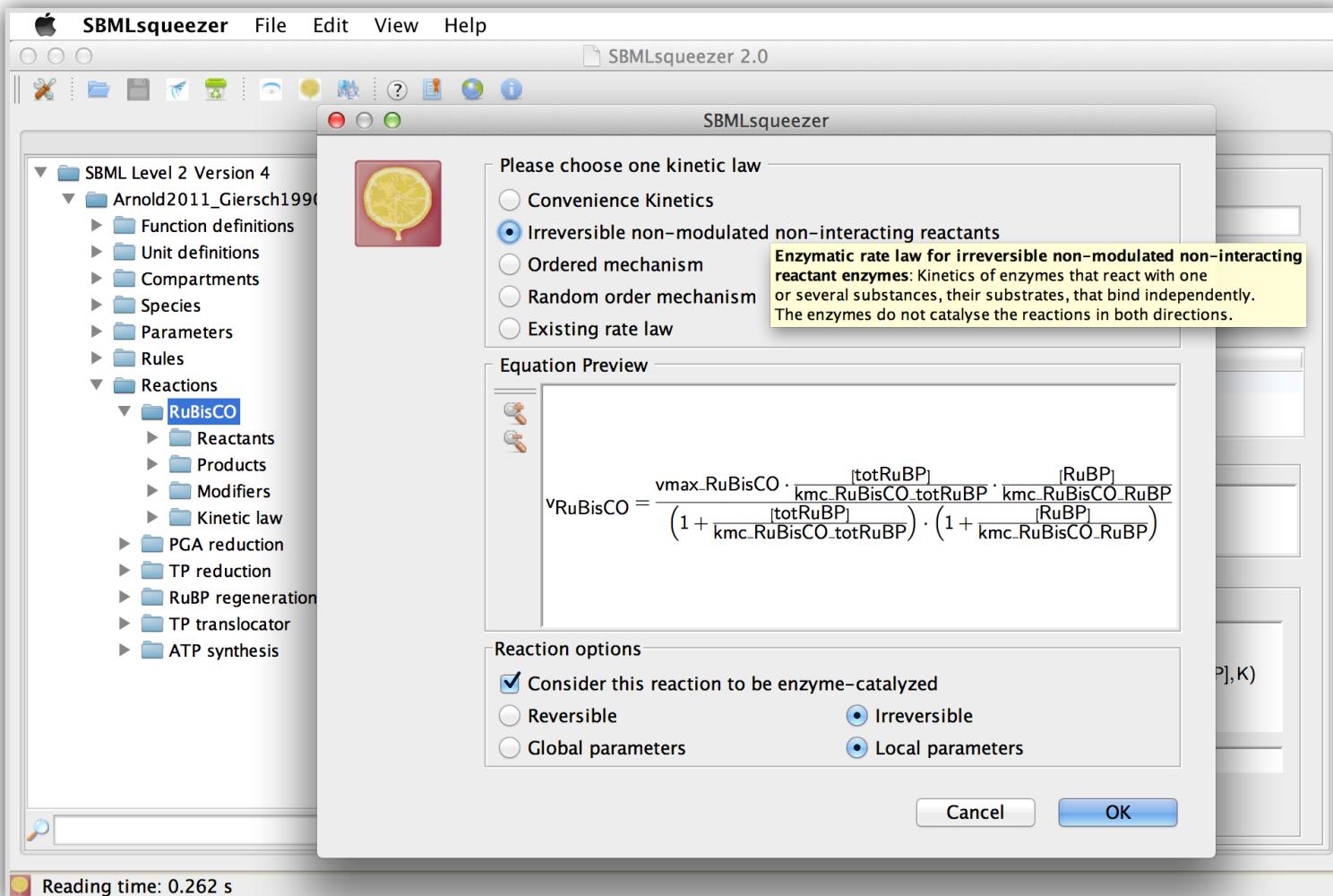
The right sidebar shows a "History" panel with an empty history and a message: "This history is empty. You can load your own data or get data from an external source".

Römer M, Eichner J, Dräger A, Wrzodek C, Wrzodek F, and Zell A. ZBIT Bioinformatics Toolbox: a Web-Platform for Systems Biology and Expression Data Analysis. *PLoS ONE*, 11(2):e0149263, February 2016.

Frequent tasks in systems biology

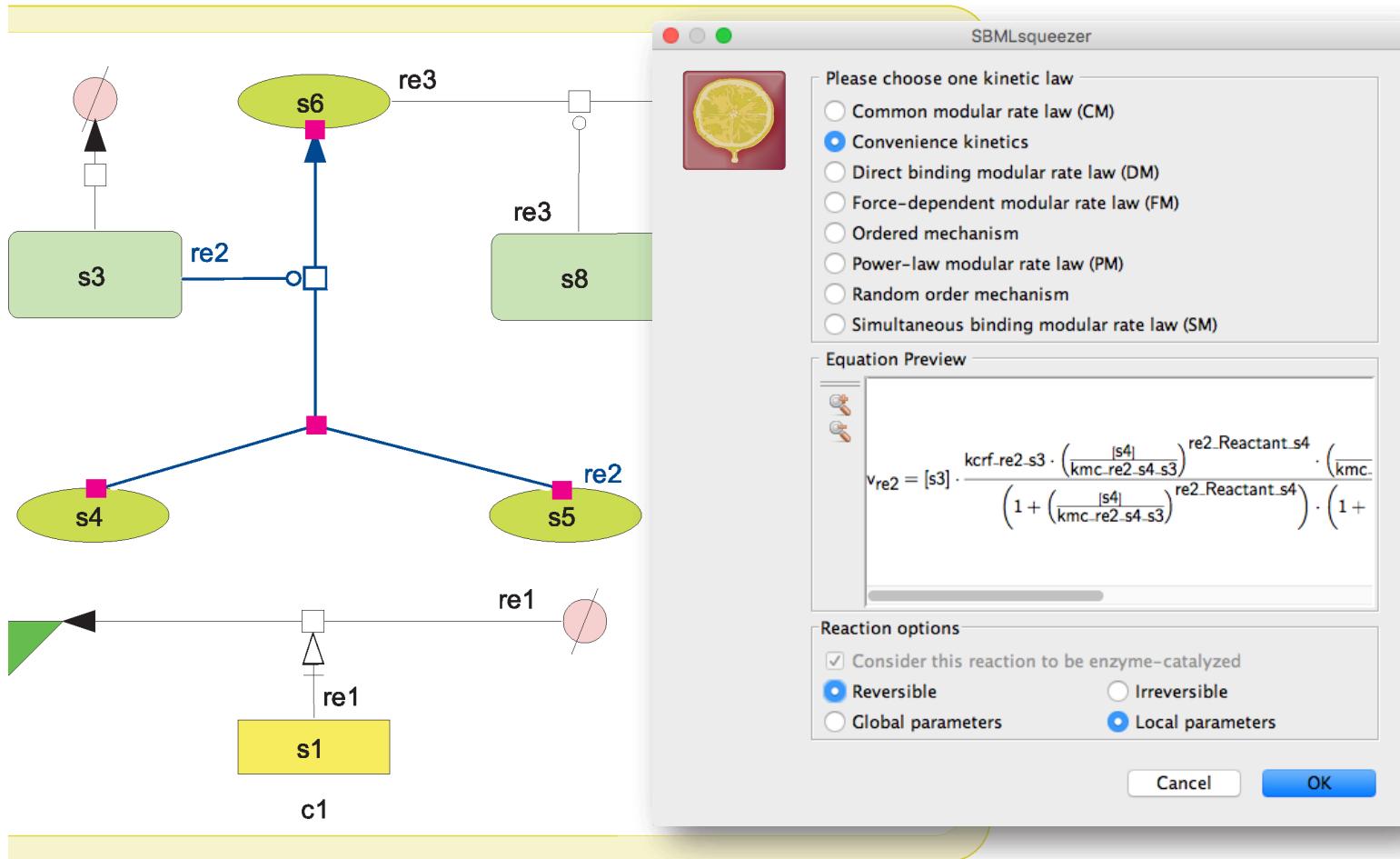


SBMLsqueezer: a Semantic Rate Law Generator



Dräger A, Zielinski DZ, Keller R, Rall M, Eichner J, BØ Palsson, Zell A. Context-sensitive creation of kinetic equations in biochemical networks, *BMC Systems Biology* 2015.

SBMLsqueezer Context Menu

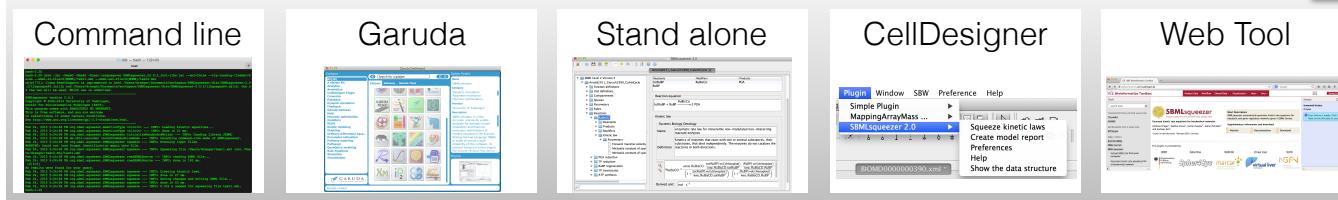


Dräger A, Zielinski DZ, Keller R, Rall M, Eichner J, BØ Palsson, Zell A. Context-sensitive creation of kinetic equations in biochemical networks, *BMC Systems Biology* 2015.

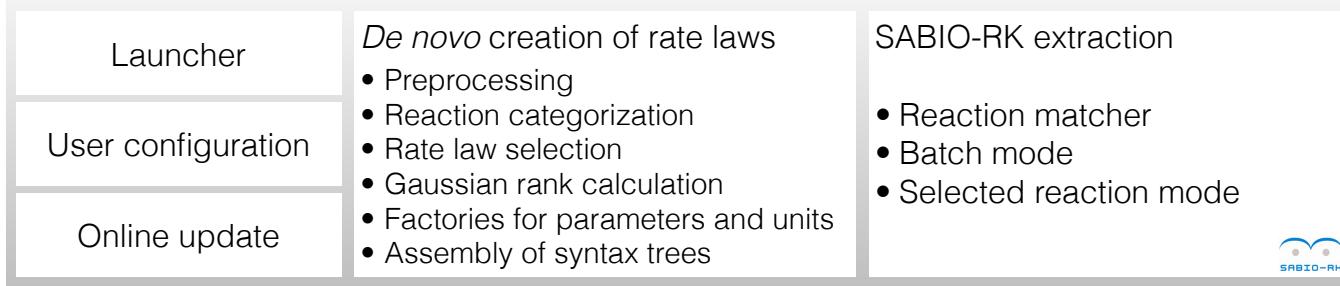
SBMLsqueezer: architecture



User Interface



Algorithms and program infrastructure

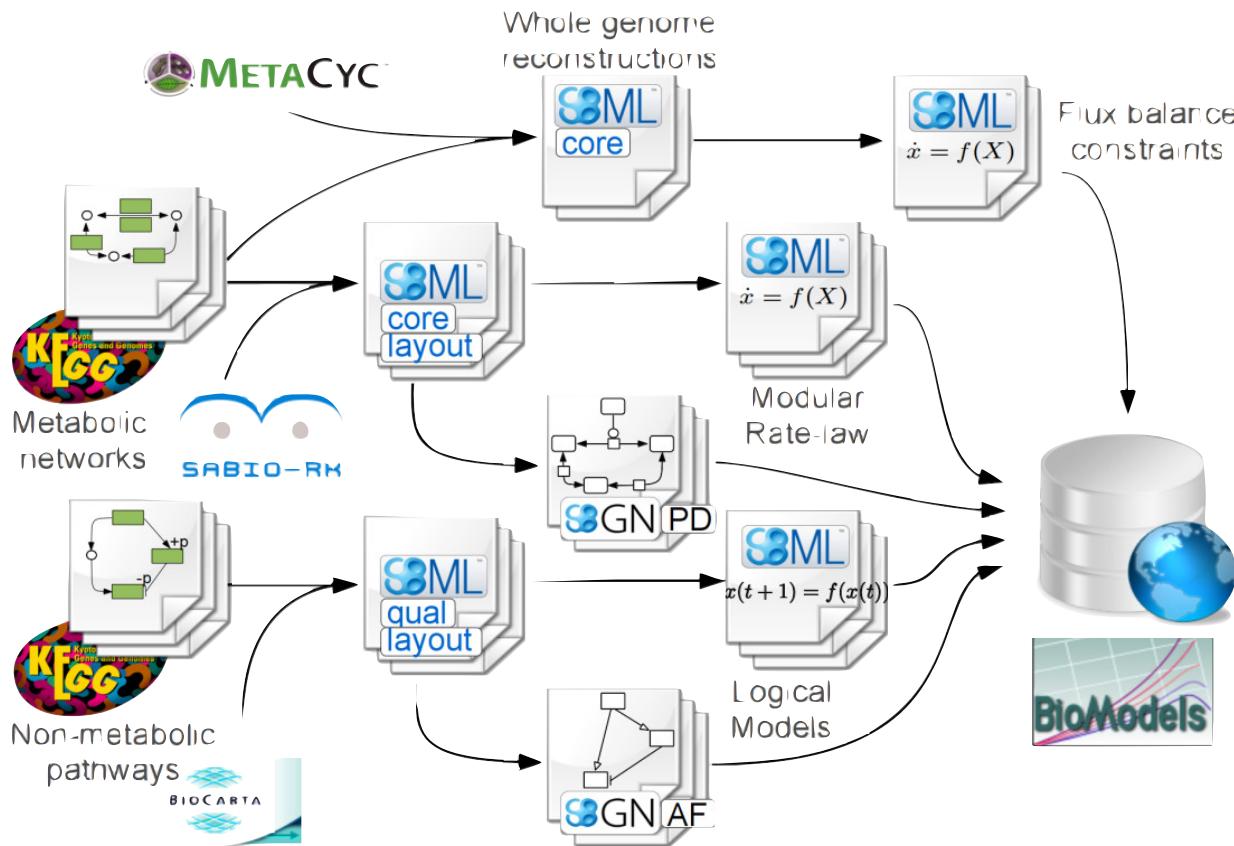


Data structures and parsers



Dräger A, Zielinski DZ, Keller R, Rall M, Eichner J, BØ Palsson, Zell A. Context-sensitive creation of kinetic equations in biochemical networks, *BMC Systems Biology* 2015.

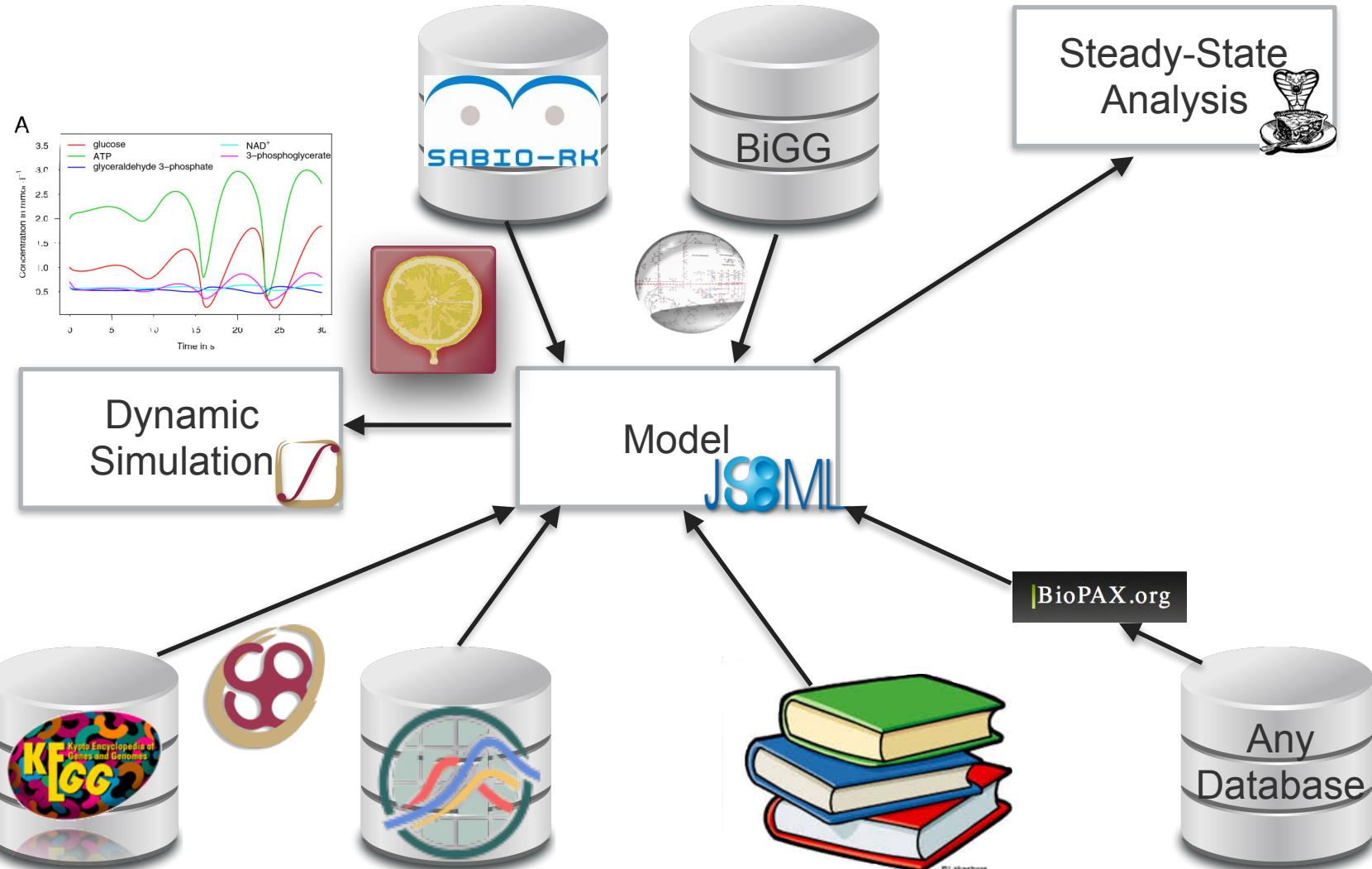
Large-scale generation of computational models from biochemical pathway maps



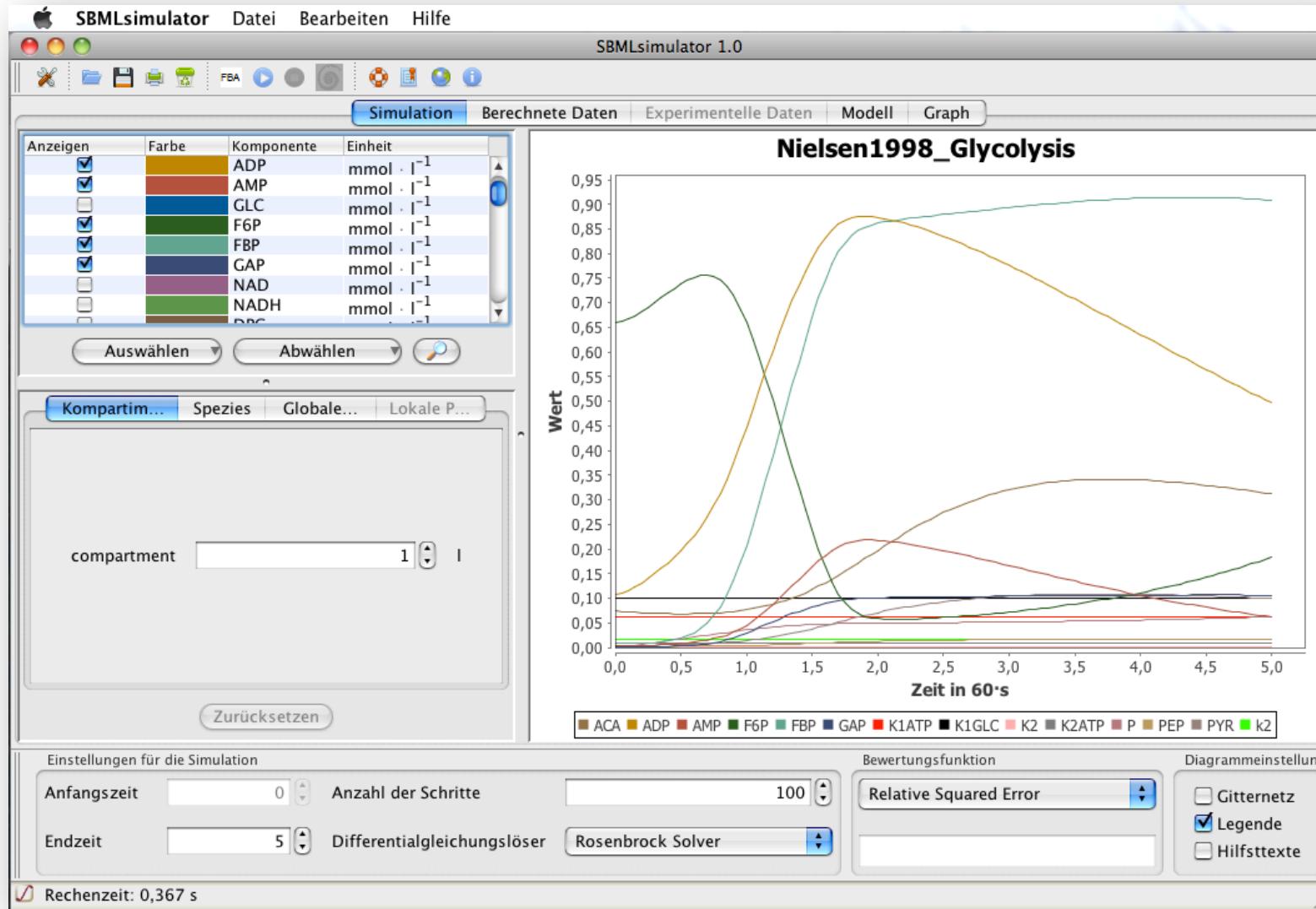
Büchel F, Rodriguez N, Swainston N, Wrzodek C, Czauderna T, Keller R, Mittag F, Schubert M, Glont M, Golebiewski M, van Iersel M, Keating SM, Rall M, Wybrow M, Hermjakob H, Hucka M, Kell DB, Müller W, Mendes P, Zell A, Chaouiya C, Saez-Rodriguez J, Schreiber F, Laibe C, **Dräger A**, and Le Novère N. Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, 7(1):116, November 2013.

Wrzodek C, Büchel F, **Dräger A**, Ruff M, and Zell A. Precise generation of systems biology models from KEGG pathways. *BMC Systems Biology*, 7(1):15, January 2013.

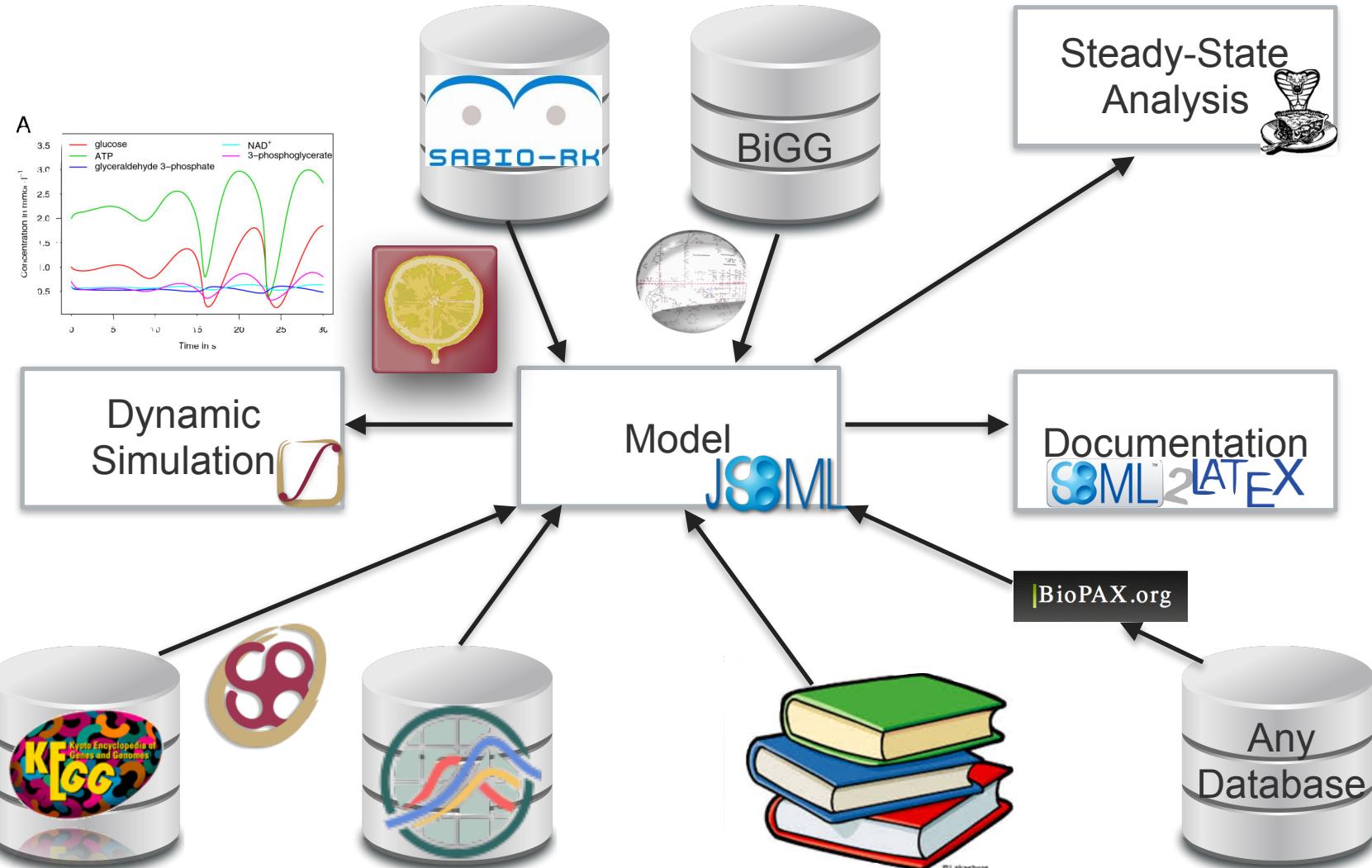
Frequent tasks in systems biology



SBMLsimulator



Frequent tasks in systems biology





- Extension with TiKz



```

1 <?xml version="1.0" encoding="UTF-8"?>
2 <sbml level="2" version="1" id="1" xmlns="http://www.sbml.org/sbml/level2/version1" level2="2" version="1">
3   <model id="Example" sbmlVersion="2009030393">
4     <listOfCompartments>
5       <compartment id="membrane">
6         <listOfSpecies>
7           <species id="Ca2_ion" units="molar" name="Ca2+ in membrane" species="Ca2+"/>
8           <species id="ATP" units="molar" name="ATP in membrane" species="ATP"/>
9           <species id="ADP" units="molar" name="ADP in membrane" species="ADP"/>
10          <species id="Pi" units="molar" name="Pi in membrane" species="Pi"/>
11        </listOfSpecies>
12        <listOfCompartments>
13          <compartment id="cytosol" volume="1e-10" units="Volume" sbmlType="SBV0000290"/>
14        </listOfCompartments>
15        <listOfSpecies>
16          <species id="Ca2_cytosol" compartment="cytosol" initialAmount="0.2" hasInitialSubstanceUnits="molar"/>
17          <species id="ATP_cytosol" compartment="cytosol" initialAmount="0.1" hasInitialSubstanceUnits="molar"/>
18          <species id="ADP_cytosol" compartment="cytosol" initialAmount="0.1" hasInitialSubstanceUnits="molar"/>
19          <species id="Pi_cytosol" compartment="cytosol" initialAmount="0.1" hasInitialSubstanceUnits="molar"/>
20        </listOfSpecies>
21        <reaction id="R1" reversible="false" sbmlType="SBR00000393">
22          <listOfReactants>
23            <speciesReference sbmlType="SBR0000015" species="Ca2_cytosol"/>
24          </listOfReactants>
25          <listOfProducts>
26            <speciesReference sbmlType="SBR0000011" species="Ca2_ion"/>
27          </listOfProducts>
28          <listOfModifiers>
29            <modifier speciesReference sbmlType="SBR0000011" species="Pi_cytosol"/>
30            <modifier speciesReference sbmlType="SBR0000002" species="ADP_cytosol"/>
31          </listOfModifiers>
32          <kineticLaw id="KL1" sbmlType="SBK0000037">
33            <math xmlns="http://www.w3.org/1998/Math/MathML">
34              <apply>
35                <divide/>
36                <apply>
37                  <div/>
38                  <ci value="1.5" type="constant"/>
39                </apply>
40                <apply>
41                  <times/>
42                  <ci value="0.001" type="constant"/>
43                  <apply>
44                    <times/>
45                    <ci value="0.001" type="constant"/>
46                  </apply>
47                </apply>
48                <divide/>
49                <ci value="0.001" type="constant"/>
50                <ci value="0.001" type="constant"/>
51              </apply>
52            </math>
53          </kineticLaw>
54        </listOfReactions>
55      </model>
56    </sbml>

```

The screenshot shows the Bioinformatics Toolbox interface with four tabs open:

- BioPAX2SBML**: A tool for converting BioPAX format to SBML. It includes a search bar, a file upload section, and a history panel.
- SBMLsqueezer**: A tool for generating kinetic rate equations for biochemical networks. It includes a search bar, a file upload section, and a history panel.
- SBML2LaTeX**: A tool for converting SBML files into human-readable reports. It includes a search bar, a file upload section, and a history panel.
- TFpredict**: A tool for identifying and characterizing transcription factors. It includes a search bar, a file upload section, and a history panel.

SBML Model Report
Model identifier: "Example"
May 30, 2009

1 General Overview
This is a document in SBML Level 2 Version 4 format. The SBO concept of this model is a production. An SBO item is 00000393. See Section A for the definition. Table 1 gives an overview of the quantities of all components of this model.

Table 1: The SBML component statistics.			
Element	Quantity	Element	Quantity
component types	0	compartments	1
species types	3	events	0
reactions	1	constraints	0
global parameters	0	function definitions	0
rules	0	initial conditions	0
		initial assignments	0

2 Unit Definitions
This is an overview of all unit definitions. The units molar, volume, area, length, and time are predefined by SBML and not mentioned in the model.

2.1 Unit mol_per_s

Definition mol/s

Produced by SBML2TeX

1

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

Dräger A, Planatscher H, Wouamba DM, Schröder A, Hucka M, Endler L, Golebiewski M, Müller W, and Zell A. SBML2L^AT_EX:
Conversion of SBML files into human-readable reports.
Bioinformatics, 25(11):1455-1456, April 2009.



- All tools freely available under open-source licenses
- Download of stand-alone versions from <http://www.cogsys.cs.uni-tuebingen.de/software/>
- Online versions at <http://webservices.cs.uni-tuebingen.de>
- Use of tools in numerous research projects and community efforts (e.g., the path2models project)
- Also driving force for further community projects, such as JSBML, see <https://github.com/sbmlteam/jsbml>

JSBML

Acknowledgments



University of Tuebingen

- Johannes Eichner
- Mirjam Gutekunst
- Roland Keller
- Florian Mittag
- Sebastian Nagel
- Hannes Planatscher
- Matthias Rall
- Fabian Schwarzkopf
- Clemens Wrzodek
- Finja Wrzodek
- Andreas Zell

UC San Diego

- Bin Du
- Ali Ebrahim
- Zachary A. King

- Nathan E. Lewis
- Justin S. Lu
- Bernhard Ø. Palsson
- Nikolaus Sonnenschein
- Alex Thomas
- Laurence Yang
- James T. Yurkovich
- Daniel C. Zielinski

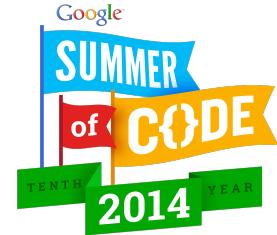
Further institutes

- Frank T. Bergmann
- Akira Funahashi
- Michael Hucka
- Sarah M. Keating
- Nicolas Le Novère
- Nicolas Rodriguez

UC San Diego



Google
Summer of Code



National Institutes
of Health



Baden-Württemberg



References

1. Michael Römer, Johannes Eichner, Andreas Dräger, Clemens Wrzodek, Finja Wrzodek, and Andreas Zell. ZBIT Bioinformatics Toolbox: a Web-Platform for Systems Biology and Expression Data Analysis. *PLoS ONE*, 11(2):e0149263, February 2016.
2. Andreas Dräger, Daniel C. Zielinski, Roland Keller, Matthias Rall, Johannes Eichner, Bernhard O. Palsson, and Andreas Zell. SBMLsqueezer 2: Context-sensitive creation of kinetic equations in biochemical networks. *BMC Systems Biology*, 9(1):1-17, September 2015.
3. Nicolas Rodriguez, Alex Thomas, Leandro Watanabe, Ibrahim Y. Vazirabad, Victor Kofia, Harold F. Gómez, Florian Mittag, Jakob Matthes, Jan D. Rudolph, Finja Wrzodek, Eugen Netz, Alexander Diamantikos, Johannes Eichner, Roland Keller, Clemens Wrzodek, Sebastian Fröhlich, Nathan E. Lewis, Chris J. Myers, Nicolas Le Novère, Bernhard Ø. Palsson, Michael Hucka, and Andreas Dräger. JSBML 1.0: providing a smorgasbord of options to encode systems biology models. *Bioinformatics*, June 2015.
4. Alexander Dörr, Roland Keller, Andreas Zell, and Andreas Dräger. SBMLsimulator: a Java tool for model simulation and parameter estimation in systems biology. *Computation*, 2(4):246-257, December 2014.
5. Johannes Eichner, Florian Topf, Andreas Dräger, Clemens Wrzodek, Dierk Wanke, and Andreas Zell. TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. *PLoS ONE*, 8(12):e82238, December 2013.
6. Finja Büchel, Nicolas Rodriguez, Neil Swainston, Clemens Wrzodek, Tobias Czauderna, Roland Keller, Florian Mittag, Michael Schubert, Mihai Glont, Martin Golebiewski, Martijn van Iersel, Sarah M. Keating, Matthias Rall, Michael Wybrow, Henning Hermjakob, Michael Hucka, Douglas B Kell, Wolfgang Müller, Pedro Mendes, Andreas Zell, Claudine Chaouiya, Julio Saez-Rodriguez, Falk Schreiber, Camille Laibe, Andreas Dräger, and Nicolas Le Novère. Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, 7(1):116, November 2013.
7. Roland Keller, Alexander Dörr, Akito Tabira, Akira Funahashi, Michael J. Ziller, Richard Adams, Nicolas Rodriguez, Nicolas Le Novère, Noriko Hiroi, Hannes Planatscher, Andreas Zell, and Andreas Dräger. The systems biology simulation core algorithm. *BMC Systems Biology*, 7:55, July 2013.
8. Clemens Wrzodek, Finja Büchel, Manuel Ruff, Andreas Dräger, and Andreas Zell. Precise generation of systems biology models from KEGG pathways. *BMC Systems Biology*, 7(1):15, January 2013.
9. Finja Büchel, Clemens Wrzodek, Florian Mittag, Andreas Dräger, Johannes Eichner, Nicolas Rodriguez, Nicolas Le Novère, and Andreas Zell. Qualitative translation of relations from BioPAX to SBML qual. *Bioinformatics*, 28(20):2648-2653, August 2012.
10. Andreas Dräger, Hannes Planatscher, Dieudonné Motsou Wouamba, Adrian Schröder, Michael Hucka, Lukas Endler, Martin Golebiewski, Wolfgang Müller, and Andreas Zell. SBML2L^AT_EX: Conversion of SBML files into human-readable reports. *Bioinformatics*, 25(11):1455-1456, April 2009.