

SBMLsqueezer 2: a context-sensitive rate law generator for biochemical networks with access to SABIO-RK

Journal:	<i>Bioinformatics</i>
Manuscript ID:	BIOINF-2014-1303.R1
Category:	Applications Note
Date Submitted by the Author:	n/a
Complete List of Authors:	Dräger, Andreas; University of California, San Diego, Bioengineering; University of Tuebingen, Center for Bioinformatics Tuebingen (ZBIT) Keller, Roland; University of Tuebingen, Center for Bioinformatics Tuebingen (ZBIT) Rall, Matthias; University of Tuebingen, Center for Bioinformatics Tuebingen (ZBIT) Eichner, Johannes; University of Tuebingen, Center for Bioinformatics Tuebingen (ZBIT) Palsson, Bernhard; University of California, San Diego, Bioengineering Zell, Andreas; University of Tuebingen, Center for Bioinformatics Tuebingen (ZBIT)
Keywords:	Biological networks, Information extraction, Mathematical modeling, Metabolic engineering, Regulatory networks, Software engineering

SCHOLARONE™
Manuscripts

ew

SBMLsqueezer 2: a context-sensitive rate law generator for biochemical networks with access to SABIO-RK

Andreas Dräger^{1,2}, Roland Keller², Matthias Rall², Johannes Eichner², Bernhard Ø. Palsson¹, Andreas Zell²

¹Systems Biology Research Group, University of California, San Diego, La Jolla, CA, USA, ²Center for Bioinformatics Tuebingen (ZBIT), University of Tuebingen, Tübingen, Germany

Dear Editor and Reviewers,

Thank you for giving us the chance to take up position on the criticisms of the reviewers. The software presented in this article is by far not just an update note for an original program. We here describe significantly upgraded software. In the publication from 2008, SBMLsqueezer was described as a pure plug-in for CellDesigner that was only able to interpret the CellDesigner-specific nomenclature and to suggest a limited set rate equations based on this information without caring about units or annotation of elements.

The new release presented here describes a totally new program with a large amount of improvements:

- **Several new built-in rate laws:** The selection of rate equations has been drastically extended. The now included five modular rate laws by Liebermeister *et al.* were proposed in 2010, i.e., 2 years after the first paper and not available in the first version, and belong to the most recent developments in the field of kinetic equations. Ten specific rate laws for gene-regulatory processes have been added:

- Hill-Hinze equation
- Hill-Radde equation
- Linear additive network models (general form and NetGenerator form)
- Non-linear additive network models (general form, NetGenerator form, Vorhadský's equation, Weaver's equation)
- S-systems
- H-systems

None of those was provided in the original publication.

- **Experimental rate law download:** The connection to the rate law database SABIO-RK has been added and allows users to directly insert experimentally obtained rate laws from this database instead of deriving generic equations.
- **Unit derivation capability:** In contrast to the original program, SBMLsqueezer now derives units for all new parameters. This feature belongs to the most complex capabilities of the program, because numerous aspects of the model need to be taken into account in order to ensure unit consistency. This comprises, for instance, the

1
2
3 diverse fallback units in the model (depending on level/version combination of the SBML
4 file), if the species involved are declared in concentration or amount units together with
5 size and unit of their compartment, if reaction participants reside in different
6 compartments etc. The program needs to set units off against each other in order to
7 cancel out terms, which is not trivial.
8
9

- 10 ● **Annotation:** The program is now entirely based on Systems Biology Ontology (SBO)
11 annotations rather than on CellDesigner-specific information. This massive change was
12 necessary in order to create a stand-alone version of the program. SBMLsqueezer now
13 does not only understand annotations, it also annotates created objects (parameters,
14 kinetic equations, units etc.) with SBO terms and where possible also with MIRIAM
15 (Minimal Information Required in the Annotation of Models) controlled vocabulary terms.
16 Once again, this new feature significantly increases quality and reusability of models.
17
18 ● **Program usage:** The CellDesigner plug-in mode is now only one of many ways to use
19 the program. SBMLsqueezer is probably one of very few scientific programs that run in
20 so many diverse use-case scenarios and can therefore be inspiring for other tool
21 developers. The program can be used as a command-line tool (with full access to all
22 functions), as a stand-alone GUI program, through a web service, as a Garuda gadget,
23 as a Java™ Web Start program, and also as plug-in for CellDesigner, and through its
24 fully documented application programming interface (API) even as a software library for
25 rate law creation. The comprehensive Users' Guide gives code examples and details
26 how to benefit from all program features in each described environment.
27
28 ● **Improved SBML support:** Since it is no longer just a plug-in for CellDesigner,
29 SBMLsqueezer can now deal with all levels and versions of the SBML format, including
30 Level 1 Version 1 and Level 3, whereas CellDesigner is restricted from SBML Level 1
31 Version 2 up to Level 2 Version 4.
32
33 ● **Inspiring data structure:** The internal data structure of SBMLsqueezer has become a
34 separate large-scale community effort and led to the development of JSBML, which is
35 now an NIH-funded project and used by numerous other research groups.
36
37

38
39 Summarizing, with this new version of SBMLsqueezer, it is possible to create high-quality large-
40 scale kinetic models with minimal human interaction. In particular, the access to SABIO-RK now
41 enables the program to contribute to bottom-up knowledge-based model development as a
42 complementary feature to the extended top-down rate law generation. The capability to derive
43 units further enhances precision and usability of its results. The large number of ways to use
44 the program allows researchers to benefit from the program's functionality in diverse potential
45 use-case scenarios. Bug fixes and updates are only a small fraction of the improvements that
46 are described in this article.
47
48

49
50 We believe that this applications note will have a high impact and is worth being published in
51 Bioinformatics. The paper about the first CellDesigner plug-in version of SBMLsqueezer was
52 downloaded almost 9,000 times and cited more than 40 times. It belongs to the 100 most
53 viewed papers of BMC Syst. Biol. This new applications note about a significantly improved new
54 version should therefore gain even higher attention.
55
56

Please find below our specific responses to the reviewers' comments.

Best regards
Andreas Dräger and colleagues

Reviewer: 1

Comments to the Author

The work describes a piece of software with clear relevance to the system biology field. Furthermore, while I did not try the software myself, it seems to have many good features & ability to be run/interface with other programs in different ways. The paper is clearly written, with good motivation, discussion of related work, and some technical details of the program and its benefits. I have only a few small critiques:

(1) The figure quality might be improved. When I zoomed in, it looked quite pixelated.

Thank you for pointing this out. The problem was the LaTeX compiler. We have now uploaded our original input files and this problem should no longer happen.

(2) In section 3, "platform, for" should be just "platform for" -- i.e., no comma.

Corrected.

(3) In section 4, the last sentence "Based on SBMLsqueezer 2 complex..." is a bit confusing. I think the authors should put a comma after "(Drager, 2011)", so that "in which ... (Drager, 2011)," becomes a subordinate clause, with the main clause being "try-and-evaluate cycles now become possible". Assuming I understand well, that would clarify the grammar.

Corrected.

Reviewer: 2

Comments to the Author

General Comments

This paper describes an update to the previously published SBMLsqueezer software that has already been used in a number of modelling studies (Pathak 2013, Dolan 2013, Autiero 2009). The software aims to generate parameterised kinetic equations in a semi-automated manner to allow for more rapid (and accurate) production of models derived from SBML. It has been delivered so as to be accessible to a range of expert and non-expert users through Galaxy, stand alone software, plug-in (CellDesigner) or Garuda gadget. It's entirely Java and in principle

platform independent. This new version offers direct connection to the kinetic rates database, SABIO-RK.

Specific Comments

I have no additional comments.

Thank you.

We like to point out that the paper is not just about an update of SBMLsqueezer. This new version comprises a large amount of new features, such as the access to SABIO-RK (as you describe), but also the ability to automatically derive units for parameters, the annotation of created elements, the improved support for SBML (no longer bound to CellDesigner's restrictions), a large variety of use-cases (command-line, graphical user interface, Galaxy web service, Garuda gadget, API library), and many other features. Since the original publication, SBMLsqueezer's internal data structure has inspired many other groups and developed to a separate, international, NIH funded software project, namely JSBML. Bug fixes und updates are only a small portion of the article.

The previous publication from 2008 only described the CellDesigner plug-in SBMLsqueezer. This is now only one small aspect of the current version. A new publication is required in order to describe all the new features and capabilities of the program and to give users an up-to-date reference to be cited.

Reviewer: 3

Comments to the Author

This paper is well written and easy to understand. Authors present their new version of a tool to generate automatically some kinetic equation.

I think that authors have to choose if they want to present their method to do it and in this case to give the details of their algorithm or if they want to present some original results obtained with the help of the tool. In the paper we have nor algorithm nor concrete results. The problem of finding the right rate law is a crucial one as the author told but they analyze this problem very roughly and just evoke generalities that are well-known - it could be interesting to develop an example of such automatic valuation of pathway reaction to show how they solve ambiguous cases or conflicts. To conclude, I suggest to the authors to review their paper in the way to give more details about the informatics developements or biological using.

Thank you for this important comment. In this paper we intended to describe the application itself and the method behind it. Due to space limitations and the complexity of the algorithms, we have now thoroughly extended the Users' Guide. The completely new chapter 6 gives details about the

- architecture of the program
- algorithms for finding all applicable and the most relevant rate laws for a reaction

- 1
2
3 • matching of reactions to entries in SABIO-RK in order to find rate laws for all or
4 selected reactions.
5
6 In the paper we refer to the Users' Guide, which is at the same time also supplementary
7 material. We agree that the publication now gives much better insights about how the
8 program works.

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

For Peer Review

SBMLsqueezer 2: a context-sensitive rate law generator for biochemical networks with access to SABIO-RK

Andreas Dräger^{1,2,*}, Roland Keller², Matthias Rall², Johannes Eichner², Bernhard Ø. Palsson¹, Andreas Zell²

¹Systems Biology Research Group, University of California, San Diego, La Jolla, CA, United States

²Center for Bioinformatics Tuebingen (ZBIT), University of Tuebingen, Tübingen, Germany

Received on XXXXX; revised on XXXXX; accepted on XXXXX

Associate Editor: XXXXXXXX

ABSTRACT

Summary: Modeling metabolic networks belongs to the most laborious and error-prone tasks in systems biology. Size and complexity of published reconstructions are steadily increasing. In order to simulate the dynamics of quantitative models, kinetic equations need to be derived for each reaction. Parameters and units also need to be specified. The manual assignment of these equations is not practicable for large numbers of reactions. Complex test-and-evaluation cycles require automated methods for rate law assignment. The program SBMLsqueezer 2 is a generator for kinetic equations, parameters, and units. It distinguishes between multiple types of reactions and selects only suitable rate laws. The user can influence all choices made by the program in order to assign the desired type of rate law to each reaction. Experimentally derived rate laws can be obtained through a connection to the kinetics database SABIO-RK. This platform-independent program can be used in a large variety of ways, enabling flexible solutions and use-case scenarios.

Availability: Program, source code, and documentation can be obtained under the terms of the GPL version 3 from the website <http://www.cogsys.cs.uni-tuebingen.de/software/SBMLsqueezer/>.

Contact: sbmlsqueezer@googlegroups.com

1 INTRODUCTION

The reconstruction of genome-scale networks has been recognized as a highly laborious long-term effort, which requires several iterations of curation (Thiele and Palsson, 2010). However, for the creation of dynamic network simulations, the formulation of such a structural network is just the first step. For each reaction within the network, a specific kinetic equation, a so-called rate law, needs to be derived. These rate laws typically contain parameters, such as Michaelis constants, or even plain numbers, which are not always intended to be dimensionless quantities. Reactive species in these models may cross compartments through transport reactions. Hence, their reaction space may change and consequently their molarity with the volume differences of each compartment. Ensuring unit consistency for the entire network requires careful consideration. When a model is finally used as the basis for technical applications, inconsistent units could compromise therapeutic procedures or even endanger health and safety of patients.

*to whom correspondence should be addressed

Manually deriving both, kinetic equations and all units, brings several problems with it, because it a) is highly error-prone, b) very time-consuming, and c) cannot be applied in large-scale or automated approaches. For these reasons, automatic procedures are required for the assembly of rate laws. Programs, such as COPASI (Hoops *et al.*, 2006), CellDesigner (Funahashi *et al.*, 2007), the MASS-Toolbox (<http://opencobra.github.io/MASS-Toolbox/>), and Cellerator (Shapiro *et al.*, 2002), provide pre-defined lists of kinetic equations and also allow the user to modify these rate laws or to even create customized equations. CellDesigner 4.4 provides a dialog that assists the user to obtain rate laws from the kinetics database SABIO-RK (Wittig *et al.*, 2012). The MASS-Toolbox focuses on the creation of elementary rate laws and automatically derives pseudo-elementary rate constants with their units. Inference programs, such as NetGenerator (Weber *et al.*, 2013), estimate a topology and generate specific rate laws for gene-regulatory processes. Odefy (Krummsiek *et al.*, 2010) converts discrete Boolean networks into quantitative differential equation systems by applying Hill-type rate laws to each transition.

In contrast, SBMLsqueezer 2 applies several criteria to automatically select appropriate equations for each reaction. The user can influence these criteria and choose which rate law to apply. The aims of this approach are a) to ensure that only applicable rate laws can be selected and thus the consistency of the model, and b) to reduce the required human interaction to a minimum. SBMLsqueezer 2 is intended to be useful for modeling not only metabolic networks but also signal transduction processes and gene-regulatory mechanisms.

2 RESULTS

Originally, SBMLsqueezer has been developed as a plug-in for CellDesigner (Dräger *et al.*, 2008). It was then extended to a stand-alone tool (Dräger *et al.*, 2010). SBMLsqueezer 2 can be used as a) on-line program, b) stand-alone tool via graphical user interface or command-line, c) plug-in for CellDesigner, d) Garuda gadget, and e) through its API in complex workflows and algorithms.

The vast majority of biochemical reactions can be categorized into a limited number of classes. SBMLsqueezer 2 takes several features of the reaction into account in order to discriminate these classes. For each class it either determines all kinds of principally applicable rate laws, or the most suitable rate law. The user can influence how rate laws are picked. An equation preview assists the

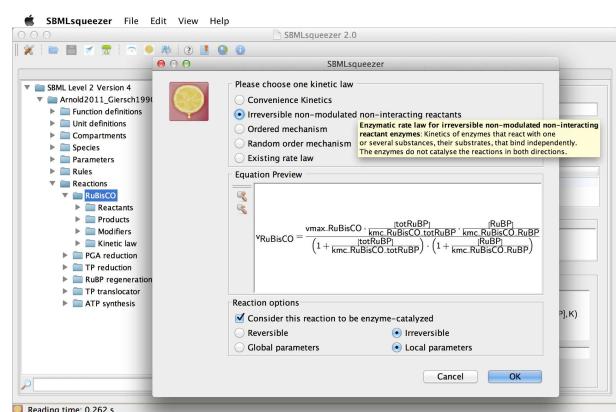


Figure 1: Reaction context dialog of SBMLSqueezer 2.

user to make this decision. The program equips all newly generated parameters with units in order to ensure consistency. It should be noted that for some levels and versions of SBML numbers cannot be associated with units and that some rate laws can under certain conditions not be evaluated in reaction extend per time units.

The dialog for access to SABIO-RK is similar to the on-line database service and uses the annotation of the reaction and its components to identify the best match in SABIO-RK. When successful, rate laws, parameters, units, and annotations will be transferred from SABIO-RK to the local model. Rate law generation and extraction from SABIO-RK can be performed for individual reactions (fig. 1) or for the entire model in a single step. Optionally, SBMLSqueezer 2 can remove unused variables and units from the model (cleaning) and update annotations where required. The content of models can be summarized in a comprehensive human-readable PDF report.

3 IMPLEMENTATION

SBMLSqueezer 2 is based on the data format SBML (Hucka *et al.*, 2004). It is entirely implemented in JavaTM and runs on every platform for which a JVM is available. Reading and writing of SBML files is done with JSBML (Dräger *et al.*, 2011), which also acts as the internal data structure. SBMLSqueezer 2 can also be launched using a libSBML (Bornstein *et al.*, 2008) back-end. The on-line program version is based on the command-line interface of the stand-alone tool, which is wrapped in a Galaxy (Goecks *et al.*, 2010) framework. For writing model reports, SBMLSqueezer 2 contains a development release of SBML2L^AT_EX (Dräger *et al.*, 2009). The Garuda gadget (Ghosh *et al.*, 2011) is implemented based on the back-end API for JavaTM. The CellDesigner plug-in uses the communication interface between CellDesigner's plug-in API and JSBML. Changes made by SBMLSqueezer 2 are synchronized with CellDesigner through a change listener interface. SBMLSqueezer 2 determines the type of reaction by interpreting SBO and MIRIAM annotations (Courtot *et al.*, 2011) of all components as well as the number and kind of reaction participants. Access to SABIO-RK (Wittig *et al.*, 2012) requires an active Internet connection and uses the RESTFUL API provided by SABIO-RK through a JavaTM URL connection. For detailed description of the algorithms, see the Users' Guide.

4 CONCLUSION

With SBMLSqueezer 2 a mature and stable application has been released, which can be applied in diverse ways. It can easily be integrated into versatile workflows and complex procedures. The Users'

Guide at the project web-site explains in detail how to exploit all program functions and provides several sample use-cases.

The path2models project (Büchel *et al.*, 2013) has demonstrated the usefulness of automated rate law assignment. Based on SBMLSqueezer 2 complex try-and-evaluate cycles, in which the most suitable rate law for a certain reaction needs to be identified in repeated simulation runs (Dräger, 2011), now become possible.

ACKNOWLEDGMENTS

The authors are grateful to Meike Aichele, Hannes Borch, Alexander Dör, Martin Golebiowski, Nadine Hassis, Marcel Kronfeld, Oliver Kohlbacher, Wolfgang Müller, Sarah R. Müller vom Hagen, Sebastian Nagel, Leif J. Pallesen, Alexander Peltzer, Julianus Pfeuffer, Sandra Saliger, Simon Schäfer, Adrian Schröder, Jochen Supper, Dieudonné M. Wouamba, Shaowu Yang, Michael J. Ziller.

Funding: Thanks to the Federal Ministry of Education and Research (BMBF, Germany) for funding the Virtual Liver Network (grant number 0315756) and to the 7th EU Framework Program for Research and Technological Development for AD's Marie Curie International Outgoing Fellowship (project AMBiCon, 332020).

Conflict of Interest: none declared.

REFERENCES

- Bornstein *et al.* (2008). LibSBML: an API library for SBML. *Bioinformatics*, **24**(6), 880–881.
- Büchel *et al.* (2013). Large-scale generation of computational models from biochemical pathway maps. *BMC Syst Biol*, **7**(1), 116.
- Courtot *et al.* (2011). Controlled vocabularies and semantics in systems biology. *Mol Syst Biol*, **7**, 543.
- Dräger, A. (2011). *Computational Modeling of Biochemical Networks*. Ph.D. thesis, University of Tuebingen.
- Dräger, *et al.* (2008). SBMLSqueezer: a CellDesigner plug-in to generate kinetic rate equations for biochemical networks. *BMC Syst Biol*, **2**(1), 39.
- Dräger *et al.* (2009). SBML2L^AT_EX: Conversion of SBML files into human-readable reports. *Bioinformatics*, **25**(11), 1455–1456.
- Dräger *et al.* (2010). *Systems Biology for Signaling Networks*, volume 2, chap. Automating mathematical modeling of biochemical reaction networks. Springer.
- Dräger *et al.* (2011). JSBML: a flexible Java library for working with SBML. *Bioinformatics*, **27**(15), 2167–2168.
- Funahashi *et al.* (2007). Integration of CellDesigner and SABIO-RK. *In Silico Biology*, **7**(2 Suppl), S81–S90.
- Ghosh *et al.* (2011). Software for systems biology: from tools to integrated platforms. *Nat Rev Genet*, **12**(12), 821–832.
- Goecks *et al.* (2010). Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biol*, **11**(8), R86.
- Hoops *et al.* (2006). COPASI-a COmplex PAthway SImulator. *Bioinformatics*, **22**(24), 3067–3074.
- Hucka *et al.* (2004). Evolving a *lingua franca* and associated software infrastructure for computational systems biology: the Systems Biology Markup Language (SBML) project. *Systems Biology, IEE*, **1**(1), 41–53.

- 1
2
3
4
5 Krumsiek *et al.* (2010). Odefy—from discrete to continuous models.
6 *BMC Bioinformatics*, **11**, 233.
7 Shapiro *et al.* (2002). Cellerator: extending a computer algebra system to include biochemical arrows for signal transduction
8 simulations. *Bioinformatics*, **19**(5), 677–678.
9 Thiele, I. and Palsson, B. Ø. (2010). A protocol for generating a
10 high-quality genome-scale metabolic reconstruction. *Nat Protoc*,
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
- 5(1), 93–121.
Weber *et al.* (2013). Inference of dynamical gene-regulatory networks based on time-resolved multi-stimuli multi-experiment data applying NetGenerator v2.0. *BMC Syst Biol*, **7**(1), 1.
Wittig *et al.* (2012). SABIO-RK—database for biochemical reaction kinetics. *Nucleic Acids Res*, **40**(Database issue), D790–D796.

For Peer Review



15 **Users' Guide**
16
17
18

19 **SBMLsqueezer 2**
20
21

22 **A context-based generator of kinetic equations**
23
24

25 Andreas Dräger^{1,2,*} Roland Keller² Matthias Rall²
26 Johannes Eichner² Bernhard Ø. Palsson¹ Andreas Zell²
27
28

29 Monday 27th October, 2014
30
31
32
33
34



35
36 **Institutional affiliations:**
37
38

39 ¹Systems Biology Research Group, University of California, San Diego, La Jolla, CA, USA
40
41

42 ²Center for Bioinformatics Tuebingen (ZBIT), University of Tuebingen, Tübingen, Germany
43
44
45
46
47
48
49
50
51
52
53

54 *Corresponding author: andraeger@eng.ucsd.edu
55
56
57
58
59
60

For Peer Review

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

The tool SBMLsqueezer facilitates the task of assigning kinetic equations to reactions within biochemical network models that are given in SBML format. It analyzes each reaction of interest, selects applicable equations, and derives appropriate units of all parameters contained in these equations. If possible, components that SBMLsqueezer adds to your model are annotated with Systems Biology Ontology (SBO) and Minimal Information Required In the Annotation of Models (MIRIAM) tags. Besides *de-novo* creation of rate equations, SBMLsqueezer also offers online access to the reaction kinetics database System for the Analysis of Biochemical Pathways – Reaction Kinetics (SABIO-RK), where you can extract experimentally determined rate laws for your model. In both modes (*de-novo* creation and database lookup), you can assign kinetic equations to all reactions of the model in one single step, or select individual reactions of interest. Several settings allow you to customize the behavior of the program. In particular, all choices made by SBMLsqueezer can be changed or influenced. The program can be used in multiple ways: as a plug-in for the program CellDesigner, as a gadget for Garuda, as a stand-alone tool via its graphical user interface, or as a command-line based tool. Furthermore, the application programming interface allows you to integrate SBMLsqueezer as an equation generating core into your end-user application. An export function based on the integrated program **SBML2LATEX** allows you to generate a comprehensive model report for scientific writing or further processing.

Contents

1	Introduction	1
19	1.1 Overview	1
20	1.2 General program features	3
2	Installation	5
24	2.1 Requirements	5
25	2.2 Stand-alone application	6
26	2.3 Plug-in for CellDesigner	8
27	2.4 Integration into Garuda	9
28	2.5 Online program	9
3	How to get started	10
31	3.1 Starting the application	10
32	3.2 Adjusting the preferences	11
33	3.3 Open a model	13
34	3.4 Equation generation one by one	15
35	3.5 Generate kinetic equations in a single step	17
36	3.6 Extraction of rate laws from SABIO-RK	20
37	3.7 Viewing and saving the results	24
38	3.8 Interaction with further Garuda gadgets	29
39	3.9 Using SBMLsqueezer as an online program	30
4	Advanced program features	33
44	4.1 Using SBMLsqueezer as an equation generator library	33
45	4.2 Querying SABIO-RK and merging the results into a local SBML document	38
46	4.3 Command-line arguments	40
5	Supported rate laws	59
50	5.1 Rate laws for metabolic processes	59
51	5.2 Rate laws for gene-regulatory processes	60
6	Algorithms and software design	62

Contents

6.1	Software architecture	62
6.2	Rate law selection	63
6.3	Extraction of rate laws from SABIO-RK	71
7	FAQ and troubleshooting	74
8	License	76
8.1	Disclaimer	76
8.2	Included third-party libraries	76
9	Acknowledgments	77
9.1	Core developers	77
9.2	Principal Investigators	77
9.3	Alumni	77
9.4	Collaborators and partners	78
A	Release Notes	79
A.1	Version 1.0	79
A.2	Version 1.1	79
A.3	Version 1.2	80
A.4	Version 1.2.1	82
A.5	Version 1.3	83
A.6	Version 2.0	88
A.7	Version 2.0.1	90
B	Acronyms	91
Bibliography		93
Index		100
Figures		
3.1	Basic configuration	11
3.2	Rate law selection	12
3.3	SABIO-RK search options	13
3.4	SABIO-RK search preferences	14
3.5	L ^A T _E X options	15
3.6	Reaction context menu in CellDesigner	16
3.7	Generating a kinetic equation for a single reaction	16
3.8	Launching SBMLsqueezer in CellDesigner	18
3.9	Generating kinetic equations in one single step with the kinetic law wizard	18

Contents

3.10	Results of the kinetics wizard displayed in a table	19
3.11	Changing selected rate laws in the kinetics wizard	19
3.12	Starting the SABIO-RK wizard	20
3.13	Selection of reactions in the SABIO-RK wizard	21
3.14	Selection of search terms for SABIO-RK	21
3.15	Removal of search terms for SABIO-RK	22
3.16	Window with kinetic equations found for all reactions	22
3.17	Summary of necessary changes	23
3.18	Starting the SABIO-RK application for a selected reaction	24
3.19	Selection of search terms	25
3.20	Window with two search terms	25
3.21	Window with kinetic equations found for a single reaction	26
3.22	Window for matching elements in the equation to model elements	27
3.23	Summary of necessary changes	27
3.24	Viewing SBMLsqueezer's results	28
3.25	Selecting a Garuda gadget	29
3.26	Starting the online version of SBMLsqueezer	30
3.27	Adjusting preferences in the online version	31
3.28	Obtaining the results from the online version	32
6.1	Architecture of SBMLsqueezer	63
6.2	Examples for general reaction categories	66
6.2	Examples for general reaction categories (continued)	67
6.3	Abstract syntax tree for an irreversible mass-action rate law	70

Tables

5.1	KEGG Identifiers (IDs) of small molecules and ions	61
6.1	Kinds of species that can potentially act as enzymes and their top-level SBO terms	64
6.2	SBO terms with relevance for the categorization of reactions	68

Listings

2.1	Example Bash script that launches SBMLsqueezer with a libSBML back-end	7
4.1	Generating rate laws for all reactions in a model via the API of SBMLsqueezer 2	34
4.2	Loading preferences in SBMLsqueezer 2	35

Contents

4.3	Initializing SBMLsqueezer 2 with a libSBML back-end	36
4.4	Assignment of a kinetic law to a reaction via the API of SBMLsqueezer 2	37
4.5	SABIO-RK query for the reactions of a model	38
4.6	Calling the SABIO-RK wizard	39
4.7	Launching SBMLsqueezer from the command-line	40
4.8	Launching SBMLsqueezer from the command-line with increased heap size	41
4.9	Launching SBMLsqueezer with an alternative language pack	41
A.1	Usage of SBMLsqueezer 1.3 via its API	84

1 Introduction

The program SBMLsqueezer is a versatile tool for the assembly and assignment of complex kinetic equations of reactions and processes in biochemical networks (Dräger *et al.*, 2008, 2010; Dräger, 2011). The purpose of SBMLsqueezer is hence to assist you when creating kinetic equations for a biochemical network, whose structure is already defined. SBMLsqueezer can add missing information, such as undefined initial concentration values or set some reacting species that represent genes to the boundary of the reaction system. But its main purpose is the creation of rate laws, parameter objects, and their units. The integrated **SBML2LATEX** can create an exhaustive model report that highlights all model features. A list of currently implemented rate laws that can be used for the *de novo* creation of kinetic laws can be found in chapter 5 on page 59.

1.1 Overview

The data format understood by SBMLsqueezer is the Systems Biology Markup Language (SBML)¹ in all of its levels and versions (Hucka *et al.*, 2001, 2003a,b, 2007, 2008, 2010; Finney and Hucka, 2003; Finney *et al.*, 2006). When using SBML Level 1 (not recommended), all generated equations are stored in form of infix formula strings. For all other versions of SBML, the generated equations are stored in form of MathML (Buswell *et al.*, 1999) expressions.

Kinetic equations contain a set of parameters, whose units must be derived to ensure that the overall equation can be interpreted in units of the extent of the respective reaction per time units. To give an example for the most common scenario, you can assume that the units of the rate law will simplify to a substance unit per time unit, for instance, mole per second. Other constellations, however, are possible, too. When using SBMLsqueezer you do not have to care much about units because the program does this for you. Since Level 3, the MathML subset understood by SBML has been extended and also supports units for actual numbers (integers or real values, which are not parameter values in this sense). When using a model in this more recent format, SBMLsqueezer will also assign units to numbers where necessary.

The program also annotates all created equations and parameters with appropriate terms from the SBO² (Systems Biology Ontology) and also with MIRIAM-compliant³ controlled vocabulary terms (Minimal Information Required In the Annotation of Models), where appropriate (Le Novère *et al.*, 2005; Le Novère *et al.*, 2006; Laible and Le Novère, 2007; Courtot *et al.*, 2011).

¹Various information about SBML can be found at <http://sbml.org>.

²For more information about SBO see <http://www.ebi.ac.uk/sbo/main/>.

³The MIRIAM registry is described at <http://combine.org/standards/miriam>.

1 2 3 4 1 Introduction 5 6

7 The selection of the kinetic equations is done automatically by the program, where several settings
8 allow users to influence the algorithm's choice. In many cases, SBMLsqueezer suggests
9 multiple equations for the same process, from which the user can choose as desired. This behavior
10 of the program is important to ensure that only appropriate equations can be selected at any time.
11

12 In order to decide, which equations can be applied to a reaction of interest, SBMLsqueezer
13 analyzes several properties, such as the number and type of reactants, products, and modifiers,
14 if the reaction is reversible, etc. Here, reaction of interest means that the user can either select
15 individual reactions from a larger model and equip these with kinetic equations, or rate equations
16 can be created in one go for the entire model. Thereby, already existing equations can either be
17 kept or overwritten, depending on your choice. You can influence and change all choices of the
18 program, even in the single-step-mode.
19

20 If you are connected to the Internet, you can also use SBMLsqueezer to extract experimentally
21 determined kinetic equations from the rate law database SABIO-RK⁴ (Wittig *et al.*, 2006; Rojas
22 *et al.*, 2007; Krebs *et al.*, 2007; Wittig *et al.*, 2012). To this end, SBMLsqueezer provides several
23 settings, such as the organism, temperature, or pH value under which the reaction's rate was deter-
24 mined. Again, you can extract equations from SABIO-RK for an entire network in one single step,
25 or individually select reactions of interest.
26

27 The program itself can be customized and used in several ways. It remembers your last opened
28 files, the window's size, your rate law selection and so forth. You can run it as a stand-alone tool, or
29 as a plug-in for the well-known program CellDesigner⁵ (Funahashi *et al.*, 2003, 2006, 2007, 2008).
30 By default, the stand-alone version is based on the JSBML back-end (Dräger *et al.*, 2011), but you
31 can also use libSBML (Bornstein *et al.*, 2008) as its SBML back-end instead if this library's more
32 elaborated off-line model validation matters.
33

34 If you neither like to download SBMLsqueezer, nor to install any software on your local com-
35 puter, you can even use SBMLsqueezer as a Galaxy-based web service⁶ Goecks *et al.* (2010). This
36 web-service runs on the servers of the University of Tuebingen and therefore do not require any
37 local installation. In this setting, you can benefit from Galaxy's capability to easily combine SB-
38 MLsqueezer with other programs in a more complex work-flow. You can, for instance, convert a
39 BioPAX file to SBML using the also included program BioPAX2SBML (Büchel *et al.*, 2012) and
40 populate the model with kinetic equations afterwards. Another option would be to launch it as
41 a Java™ Web Start application directly from your web browser⁷. In this case, your browser will
42 download the executable program SBMLsqueezer as a temporary file and run it locally on your
43 computer.
44

45 In addition, SBMLsqueezer implements the Garuda specification and can therefore also be used
46 as a gadget within this powerful framework for systems biology (Ghosh *et al.*, 2011). In this
47 configuration, the output of tools that assist you to create your models, such as KEGGtranslator
48

50 ⁴You can access SABIO-RK at <http://sabio.h-its.org>.
51

52 ⁵For more information about CellDesigner see <http://www.celldesigner.org>.

53 ⁶Galaxy web service available at <http://webservices.cs.uni-tuebingen.de>.

54 ⁷You can use SBMLsqueezer as a Java™ Web Start application by clicking on <http://www.cogsys.cs.uni-tuebingen.de/software/SBMLsqueezer/downloads/SBMLsqueezer.jnlp>.
55
56
57
58 2
59
60

1.2 General program features

(Wrzodek *et al.*, 2011, 2013) can directly be piped as the input to SBMLsqueezer. Furthermore, SBMLsqueezer's output can be forwarded to further programs, such as SBMLsimulator (Keller *et al.*, 2013, 2014) for further analysis.

Finally, the command-line mode of SBMLsqueezer provides all capabilities of the program without any restriction. Furthermore, the fully accessible Application Programming Interface (API) can be used to integrate SBMLsqueezer as an equation generating core into your end-user program. You can hence equip a large number of files with kinetic equations without the need to open each file in a Graphical User Interface (GUI). The usefulness of this approach has recently been demonstrated as part of the path2models project⁸, in which more than 142,000 SBML models have been processed with SBMLsqueezer (Büchel *et al.*, 2013).

For the documentation of your model, SBMLsqueezer includes the program **SBML2LATEX**⁹, which generates a comprehensive report of your model, including a detailed description of all components and equations (Dräger *et al.*, 2009b; Dräger *et al.*, 2010). These reports can be very handy to support scientific writing, because you can easily copy the formulas into your scientific paper.

1.2 General program features

Depending on in which variant you use SBMLsqueezer and your preferences (see section 3.2 on page 11), SBMLsqueezer can

- ✓ generate kinetic equations for all reactions in your model, or only for those reactions that are currently lacking a rate law. This gives you the option to replace existing rate laws with new ones. Thereby, you can define a number of arbitrary chemicals (usually small molecules or ions) that you like to exclude from the rate law generation process in order to keep the generated equation simple. The program offers you a large variety of generic and specific rate laws for several standard cases and allows you to create all rate laws in a reversible manner if desired.
- ✓ detect reactive species, whose annotation indicates that these are genes. Since usually the concentration or amount of genes does not change, SBMLsqueezer offers you to set the boundary condition of these species to true. This means that even if these species participate in reactions, their amount or concentration will always remain constant, irrespective of their participation in reactions.
- ✓ assume that all reactions in your network are enzymatically catalyzed and hence change the selection of rate laws. This means that even reactions without explicit catalyst can be modeled with an enzymatic rate law. Hence, a simplified model structure can be recognized by SBMLsqueezer and interpreted as a more complex structure. For catalyzed reactions, you have the choice of a large variety of species types to be interpreted as enzymes.

⁸You can access and download all pathway models of the path2models project from <http://www.ebi.ac.uk/biomodels-main/path2models>.

⁹Download **SBML2LATEX** at <http://www.cogsys.cs.uni-tuebingen.de/software/SBML2LaTeX/>.

1 1 Introduction

- 2 ✓ define the units of all species and compartments if necessary and derive the units for all
3 newly created local and global parameters and numbers in order to ensure unit consistency
4 of the entire model. Thereby you can choose if species should be brought to amount or
5 concentration units. This influences if in rate equations division by the compartment sizes or
6 multiplication with the compartment will be performed where this is necessary.
- 7 ✓ check the model for global and local parameters as well as unit definitions that are never
8 used and addressed. SBMLsqueezer can automatically remove these from the model, i.e.,
9 perform *model cleaning*.
- 10 ✓ import experimentally determined rate equations from SABIO-RK and include them into
11 your model. To this end, it offers you several options to make the lookup of rate laws as
12 precise as possible and to narrow down the database entries as much as possible.
- 13 ✓ equip your model with default values where no values are defined. For instance, if it was
14 forgotten to define the spatial dimensions or the size of a compartment, SBMLsqueezer will
15 insert a default value for you. The same is also done for species and all newly created (local)
16 parameters.
- 17 ✓ summarize all features of the model in an exhaustive L^AT_EX-based model report. To this end,
18 SBMLsqueezer brings with it a full version of the model documentation tool SBML2L^AT_EX
19 including all of its options.

20 This document is intended to guide you through installation and use of SBMLsqueer by intro-
21 ducing its various interfaces to you. In the following, we will describe how you can benefit from
22 the features of SBMLsqueez and how to customize the program. The next chapter describes how
23 you can install and access SBMLsqueez on your operating system (see p. page 5). Chapter 3
24 introduces the GUI of the stand-alone version of SBMLsqueez to you and explains how to ac-
25 cess all of its functions. If you are interested to run SBMLsqueez in a batch or shell script, the
26 command-line interface will be interesting for you, which is described in section 4.3 on page 40.

27 Just as every other scientific software, also SBMLsqueez is work in progress. If you encounter
28 any difficulties or bugs, please do not hesitate to contact the mailing list, [✉ sbmlsqueez@google-](mailto:sbmlsqueez@google-groups.com)
29 groups.com.

2 Installation

To obtain a local copy of SBMLsqueezer, you can download it in form of a Java™ Archive (JAR) file from the project's website¹.

In the most common scenario, you might want to launch the program as a stand-alone tool and access its GUI. To do so, start SBMLsqueezer with a simple double click on the icon of the downloaded JAR file. Provided that a Java™ Virtual Machine (JVM) is installed on your system (see section 2.1.2 on the next page), you will see the main window of SBMLsqueezer as soon as the splash screen has finished.

2.1 Requirements

SBMLsqueezer can be used in multiple ways, depending on your preferences:

- As a stand-alone tool
 - via its GUI (see chapter 3 on page 10)
 - via its command-line interface (see section 4.3 on page 40)
- In both cases, you can choose between JSBML or libSBML as your backend for SBML (see section 2.2 on the following page).
- As a plug-in for CellDesigner (see section 2.3 on page 8)
- As a gadget for Garuda (see section 2.4 on page 9)
- As an online program embedded in the Galaxy web service environment Goecks *et al.* (2010)
- As a Java™ Web Start application
- As a rate law core in an end-user application via its API

Depending on how you like to use SBMLsqueezer, different requirements must be fulfilled before launching the program for the first time.

Note that the extraction of kinetic equations from SABIO-RK requires an active Internet connection. For this program features, the security settings of your operating system must also allow SBMLsqueezer to establish a connection to this online database.

¹Project website of SBMLsqueezer: <http://www.cogsys.cs.uni-tuebingen.de/software/SBMLsqueezer/>.

2 Installation

When launching SBMLsqueezer, it will connect to the program homepage in order to check if a newer version of the program is available. This feature can also only be used if an Internet connection is available and if your operating system allows SBMLsqueezer to establish such a connection. Note that no further information is transmitted. SBMLsqueezer only compares the version number of the local program with the version number of the latest release. If you do not want to use this feature, you can switch it off. See section 4.3 on page 40 for instructions how to do so.

2.1.1 Hardware

With at least 1 GB main memory, you should be able to perform most tasks without any problem. For large models, you should have at least 2 GB of main memory. An active Internet connection is required for some program features, but not mandatory to run the program.

2.1.2 Software

SBMLsqueezer is entirely implemented in Java™ and runs on any operating system, where a suitable Java™ Virtual Machine (JVM), Java™ Development Kit (JDK) version 1.6 or newer, is installed. For instructions how to obtain an up-to-date Java™ Virtual Machine (JVM) for your system, see, for example, the Java™ SE download page².

SBMLsqueezer has successfully been tested with

- Microsoft Windows 7 Professional (64 bit),
- Microsoft Windows 7 Professional (SP1, 64 bit),
- Mac OS X (versions 10.8.2 through 10.10), and
- Ubuntu Linux (version 12.04, 64 bit).

See chapter 7 on page 74 if you encounter any problems.

2.2 Stand-alone application

Besides what is explained above, no further requirements are necessary if you like to use SBMLsqueezer as a stand-alone application. The program SBMLsqueezer does not have to be installed in order to be executed. Just copy the JAR file of SBMLsqueezer to your preferred path on your hard-disk to launch the application. On Mac OS X, you may like to copy the JAR file into your `Macintosh HD` `Applications` folder. On Microsoft Windows systems, the preferred position for the JAR file could be, for instance, `C:\Program Files`. For Linux, we propose to copy the JAR file to the `opt` folder.

²<http://www.oracle.com/technetwork/java/javase/downloads/>

2.2 Stand-alone application

Using the JSBML back-end

No special actions are necessary if you like to use JSBML, because this is the default and JSBML is already included in the JAR file that you have downloaded.

Launching SBMLSqueezer with libSBML as back-end

Follow the installation instructions of the JavaTM binding for libSBML for your platform, which you can find at the website of libSBML³. On some platforms, you may have to define an environment variable pointing to the installation directory of libSBML before being able to use its JavaTM binding. On the most Unix and Linux platforms, this variable is called LD_LIBRARY_PATH. On Mac OS X, you should instead define the variable DYLD_LIBRARY_PATH. Follow the instructions at libSBML's website⁴ before launching SBMLSqueezer. On Windows you should add the libSBML directory to the PATH environment in the Control Panel. The following script can help you to run SBMLSqueezer on your Unix platform:

```
1 #!/bin/bash
2
3 VM_ARGS="-Xms32M -Xmx512M -Djava.library.path="
4 # The following lines depend on your system's configuration;
5 # so here is just an example:
6 VM_ARGS="${VM_ARGS}\n"
7 /usr/lib/jvm/java-6-sun/jre/lib/i386/client:\n
8 /usr/lib/jvm/java-6-sun/jre/lib/i386:\n
9 /usr/lib/jvm/java-6-sun/lib:\n
10 /usr/local/lib"\n
11 #:[path to xerces]/xerces/lib\n
12 CLASS_PATH="/usr/local/share/java/libsbmlj.jar:\n
13 [path\u2014to\u2014]SBMLSqueezer_v2.0.1.jar"\n
14
15 # Set the environment variable; under Linux or most Unix systems this is
16 LD_LIBRARY_PATH="${LD_LIBRARY_PATH}:/usr/local/lib"\n
17 # On Mac OS you have to use the following code instead:
18 #DYLD_LIBRARY_PATH="${DYLD_LIBRARY_PATH}:/usr/local/lib"\n
19
20 # Start SBMLSqueezer using the command-line options:
21 MAIN_CLASS=org.sbml.squeezer.SBMLSqueezer\n
22 java ${VM_ARGS} -cp ${CLASS_PATH} ${MAIN_CLASS} --try-loading-libsbml=true \
23 [further options]
```

Listing 2.1: Example Bash script that launches SBMLSqueezer with a libSBML back-end

In the example above the arguments for the JavaTM Virtual Machine (JVM) define an initial heap space of 32 MB (-Xms32M) and a maximal heap size of 512 MB (-Xmx512M). For more information about the program usage from the command line see section 4.3.1 on page 40.

³<http://sbml.org/Software/libSBML>

⁴For information about how to execute a libSBML-based JavaTM application, see the section about Java at <http://sbml.org/Software/libSBML/docs/cpp-api/libsbml-accessing.html>

2 Installation

2.3 Plug-in for CellDesigner

If you like to use SBMLsqueezer as a plug-in for the popular graphical model editor CellDesigner (Funahashi *et al.*, 2003, 2006, 2007, 2008), you can do this by following four installation steps:

1. Download and install CellDesigner from the project's website⁵.
2. Locate, where your copy of CellDesigner is installed.
3. Open the `plugin` folder in your installation of CellDesigner and copy the file `SBML-squeezer_v2.0.1_incl-libs.jar` into this folder.
4. Open the `lib` folder in your installation of CellDesigner and replace the JSBML JAR file that is redistributed by CellDesigner with the JAR file `jsbml-1.0-a1-with-dependencies.jar` that you can download at <http://www.cogsys.cs.uni-tuebingen.de/software/SBMLsqueezer/downloads/>.

Some more information about this installation procedure: Depending on your operating system, CellDesigner will be installed in different folders. In Microsoft Windows it is usually `C:\Program Files\CellDesigner4.4`. In Linux you might find it in `/opt/CellDesigner4.4`, and in Mac OS X CellDesigner will be installed under `/Macintosh HD/Applications/CellDesigner4.4`, where 4.4 is the version number with which SBMLsqueezer 2.0.1 has been tested. Note that the version numbers 4.4 and 2.0.1 of CellDesigner and SBMLsqueezer might change in the future, but the procedure will remain the same.

When replacing CellDesigner's version of JSBML with the one downloaded from the download site of the SBMLsqueezer project, make sure that the name of the new JSBML file will be identical to the name of the JSBML file distributed with CellDesigner. Otherwise, you will have to change some start script of CellDesigner. Even though this is not difficult and can be done on each operating system, we prefer to avoid that for the sake of simplicity. Alternatively, you can also download JSBML from the official sourceforge page. However, you must make sure that the downloaded JAR file includes the package `org.sbml.jsbml.celldesigner`. Without this package, SBMLsqueezer cannot be launched in CellDesigner. Another possible solution is to checkout the development trunk of JSBML and run the antscript by yourself, thus building the latest version of JSBML. If you like to go this way, please read the documentation about JSBML⁶ first.

It should be noted that SBMLsqueezer might produce different results when using it as a plug-in of CellDesigner from the results of all other ways to use the program. The reason is that CellDesigner models can contain a rich tool-specific annotation, which can only be understood by SBMLsqueezer in the plug-in mode for this program. In contrast, all other variants of SBMLsqueezer described herein depend on SBO terms to indicate the roles of modifiers (e.g., enzymatic catalysts) when it is not used as a plug-in for CellDesigner. Again, the reason is that the CellDesigner plug-in has different ways to receive this information. Applying SBMLsqueezer to a model exported

⁵<http://celldesigner.org>

⁶<http://sbml.org/Software/JSBML/docs>

2.4 Integration into Garuda

from CellDesigner and opened in the stand-alone version might therefore yield different results compared to when directly running it as a plug-in from CellDesigner.

2.4 Integration into Garuda

When downloading Garuda, a functioning copy of SBMLsqueezer will be included. Hence, no special installation steps are required. Just follow the instructions of how to install Garuda⁷ (Ghosh *et al.*, 2011).

2.5 Online program

In order to use SBMLsqueezer as an online program, it is necessary to install a recent web browser for your specific operating system, such as Mozilla Firefox, Google Chrome, Apple Safari, Microsoft Internet Explorer, Opera, or any other browser that you prefer and that is able to render up-to-date web sites. See the documentation of Galaxy web services⁸ (Goecks *et al.*, 2010), on which the online version of SBMLsqueezer is based, for precise software requirements.

When using the online version, no specific installation of SBMLsqueezer is necessary. Note, however, that an active Internet connection is essential in order to use SBMLsqueezer as an online program. Just use your regular web browser and go to <http://webservices.cs.uni-tuebingen.de> to use the program. See section 3.9 on page 30 for further information.

⁷<http://www.garuda-alliance.org/>

⁸<http://galaxyproject.org>

3 How to get started

In this chapter you will learn how the GUI of the program SBMLsqueezer is designed and intended to work, how you can launch, configure, and use the program. We will systematically go through all program features and explain what can be done and how. Where possible, keystroke combinations will be introduced that can be used to simplify the work with the program. All special scenarios of the diverse ways of using SBMLsqueezer (as a stand-alone tool, online program, plug-in in CellDesigner, Java™ Web Start application, as a gadget of Garuda, etc.) will be highlighted and discussed.

More experienced users might want to skip several parts of this chapter and be more interested in the description of the command-line interface (see section 4.3 on page 40) or examples for how to use the API (see section 4.1 on page 33) in custom applications.

3.1 Starting the application

 If you downloaded a ZIP file, you need to unzip it before starting the application. Launch SBMLsqueezer by double-clicking on the Java™ icon, which might look like the image next to this text, in a file browser of your operating system. This will start the GUI (see chapter 3 for further details).

You can also start SBMLsqueezer from the command line. Depending on your preference and your operating system, it might be helpful for you to write a short shell or bash scripts for starting the application. You might name this, for instance, `start.sh` for Linux or Mac OS X, and `start.bat` for Microsoft Windows. Within those scripts you could specify several command-line options (see section 4.3 on page 40) and hence customize the behavior of SBMLsqueezer. How to do that is described in section 4.3.1 on page 40. If you are using libSBML as your SBML parsing engine, writing such a script is highly recommended. You can find a sample script for this purpose in section 2.2 on page 7.

If you are using SBMLsqueezer as a plug-in for CellDesigner, just open a model that you like to edit. You can then launch all functions of SBMLsqueezer by clicking on one of the options within the menu `Plugin > SBMLsqueezer 2.0.1` in CellDesigner.

 To start SBMLsqueezer in Garuda, simply double-click on SBMLsqueezer's program icon (see the symbol that is printed next to this text). Alternatively, you can also launch SBMLsqueezer there by sending an SBML file to it from any other Garuda gadget. For more information about that, see the documentation of Garuda.

When using SBMLsqueezer as an online program, just open a browser of your choice and go to <http://webservices.cs.uni-tuebingen.de> and select the tool SBMLsqueezer in the

3.2 Adjusting the preferences

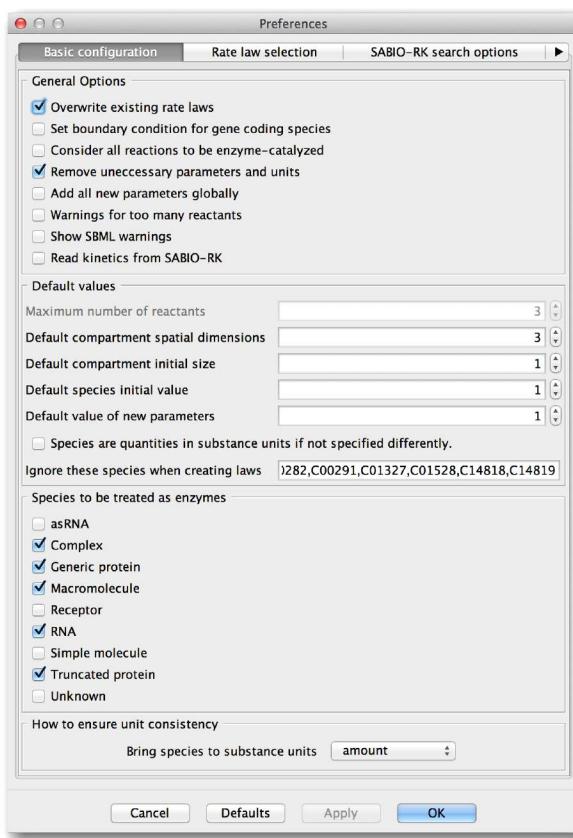


Figure 3.1: Basic configuration. All preferences in this tab correspond to the command line options described in section 4.3.3. You can specify if already existing rate laws should be replaced with newly generated ones, if a SABIO-RK search should be performed, etc. Taking small molecules and ions into account may lead to complex kinetic equations. You can here give a list of KEGG identifiers for those species to be ignored when creating rate laws (see table 5.1). If values are missing in the model, this tab allows you to specify default values to be inserted. You can decide how SBMLSqueezer should ensure unit consistency, by either bringing all species to amount units, or to concentration units. For situations, in which the role of modifiers is unclear, you can here select types of species to be considered enzymes.

overview of tools. You do not have to execute any further software besides your web browser.

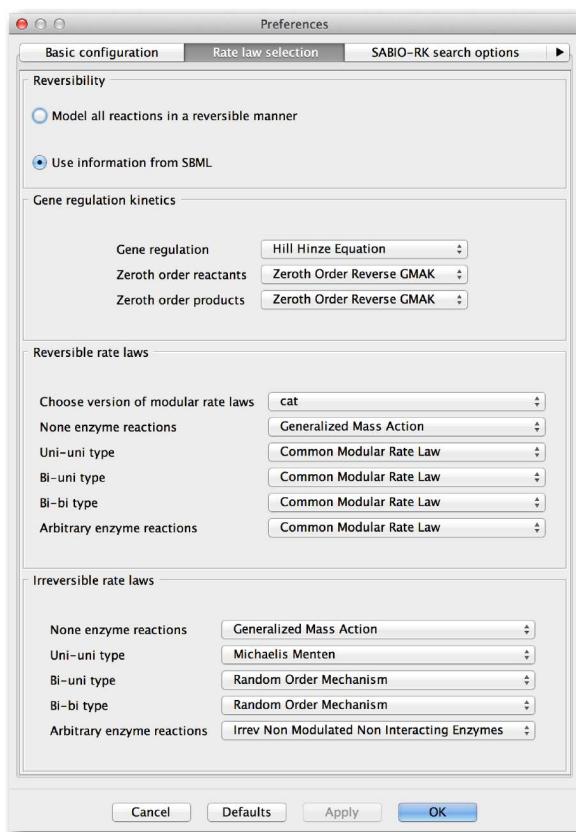
3.2 Adjusting the preferences

The program SBMLSqueezer offers a large number of options to configure how kinetic equations are generated. All options described in this section can also be applied using SBMLSqueezer's command-line interface (see section 4.3 on page 40 for details). This means that you can already upon launching the program define with which options it should be initialized. Your configuration can always be set back to the default options if desired. SBMLSqueezer stores its configuration in the system's preferences of your operating system. This means that when launching the program for the next time, you can directly continue with your previous configuration. Furthermore, there are no configuration files generated by SBMLSqueezer in addition to those maintained by your operating system. Hence, SBMLSqueezer integrates well into your working environment.

We will now take a closer look at the options and describe what you can influence and which choices the program offers to you. In order to configure your preferences, you can click on the

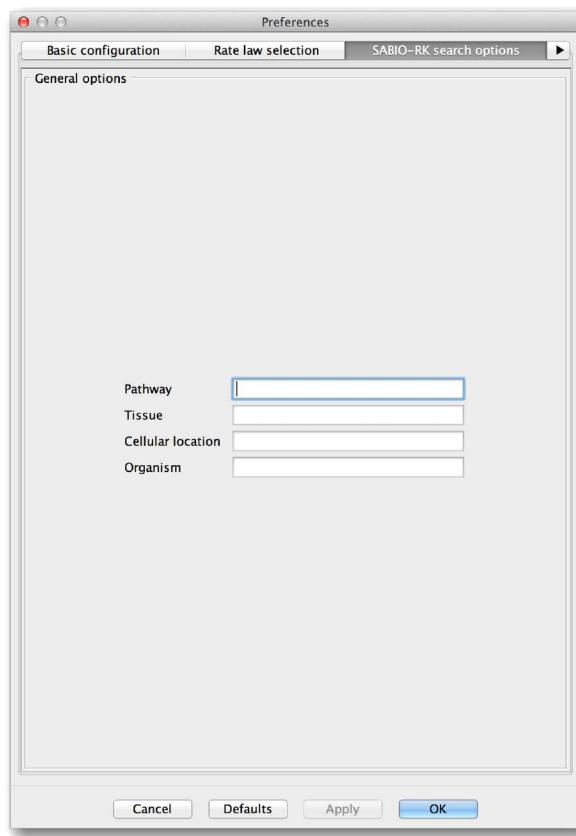
3 How to get started

Figure 3.2: Rate law selection. It has been observed that irreversible rate laws are often too restrictive and cannot capture the dynamics of complex reaction systems. For this reason, SBMLsqueezer can create all kinetic equations in a reversible manner and will then also update the property *reversible* in affected reactions. Depending on this setting, you will be able to select default types of irreversible rate laws. The other sections of this tab allow you to select which type of rate law should be primarily selected when generating equations for an entire network in one single step. If you create equations for individual reactions only, as shown in fig. 3.2, these settings do not have an effect. For more information about your choices in this tab, see also the description of its corresponding command-line options in section 4.3.4 on page 45.



tool icon in the tool-bar (see the icon next to this text), or select the corresponding entry in the menu bar. Under Microsoft Windows and Linux, you can access the preferences menu under **Edit** **Preferences**, whereas under Mac OS X, these can be found under **SBMLsqueezer** **Preferences...** or by using the keystroke combination **⌘ + ,**.

 On the bottom panel of the preferences dialog you can see the four buttons **Cancel**, **Defaults**, **Apply**, and **OK** as this is displayed in figs. 3.1 to 3.5 on pages 11–15. The **Cancel** button has the same effect as a click on the close button on the top of the window or hitting the **Esc** key: all of your changes will be disregarded and the window will be closed. The **Defaults** button restores the standard settings of SBMLsqueezer. With **Apply** you can persistently save your current settings. The **OK** button is a combination of **Apply** and close, i.e., it makes your settings persistent and closes the window. Hitting the **Esc** key has the same effect as clicking on the **OK** button. Note that the dialog is structured with multiple tabs. When clicking on **Defaults** the preferences in all tabs will be restored, even if those are not active at the time when you hit that button.



3.3 Open a model

Figure 3.3: SABIO-RK search options. The options in this tab correspond to the command-line options that are described in section 4.3.5 on page 52. You can specify general features of the reaction for which you want to look up appropriate rate laws in SABIO-RK, such as the pathway, in which the reaction occurs, the tissue, in which it was observed, even the cellular location. Of course, you can also restrict your search to an organism of choice.

3.3 Open a model

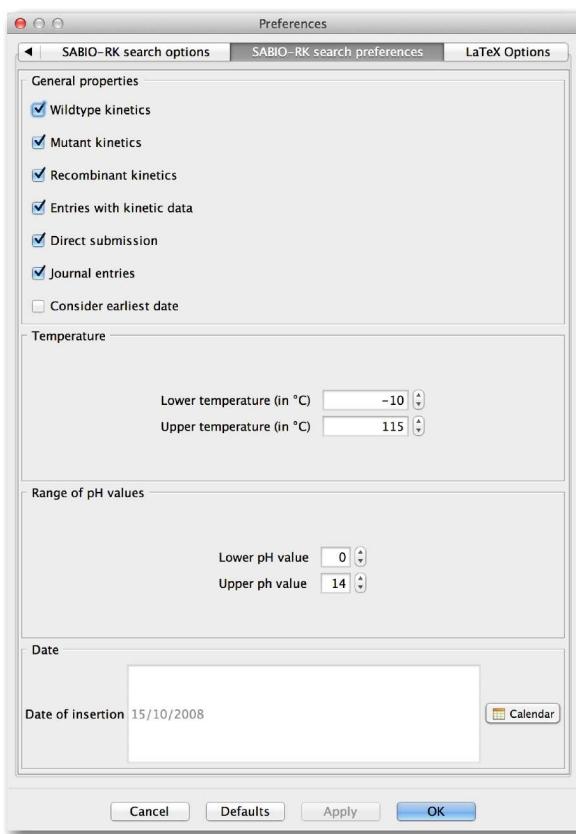
The simplest way to open an SBML file is to click on **File** **Open** in the menu bar, or at the folder icon (see the icon next to this text) in the tool bar. If you prefer keystroke combinations, you can use **⌘ + O** on Mac OS X or **Ctrl + O** on Microsoft Windows and Linux computers. The GUI can open multiple SBML files in parallel. SBMLsqueezer arranges these SBML documents in tabs, whose order can be changed by dragging and dropping the tabs. Furthermore, you can also open one ore multiple models in SBMLsqueezer via drag and drop, i.e., just select one or multiple SBML files in an arbitrary file browser of your operating system and drag these into SBMLsqueezer's GUI.

When starting SBMLsqueezer from the command line, you can directly pass a model file to it, which will then be opened in the GUI. To this end, use the option **--sbml-in-file=<File>**, where **<File>** is the absolute or relative path to the SBML file you want to open (see section 4.3.2 on page 41). Note, however, that the command line option allows you to specify just one file to open. If you like to open further files, you need to do this in the GUI.

In case that you use libSBML as SBML back-end, SBMLsqueezer will conduct a model valida-

3 How to get started

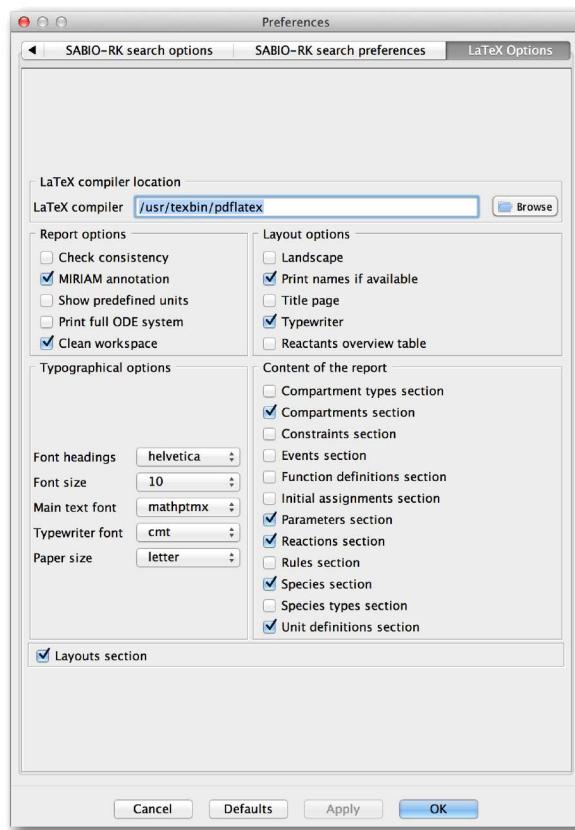
Figure 3.4: SABIO-RK search preferences. All preferences in this tab can also be changed through the command line. See section 4.3.6 on page 52 for details. Here you can define more fine-grained search properties for looking up kinetic equations in SABIO-RK, such as the minimal and maximal temperature and pH value, under which the reaction proceeds, the currentness of the entry in SABIO-RK, and several boolean switches that influence which type of database entry can be considered. These features are mainly important when extracting rate laws for all reactions in the network in a bulk. When you search for kinetics of individual reactions, you may want to also apply more appropriate settings for just this reaction.



tion upon opening the file. The result of the validation will then be displayed in a dialog window. This feature is not available when using JSBML as SBML back-end, because the JSBML library does currently not implement an off-line validation for SBML documents.

SBMLSqueezer remembers up to ten files you have already worked with. Once you have opened one or more models, these are accessible in the menu bar, where you can click on **File > Recent files**. This sub-menu will display the names of the files and their absolute path as tool-tip. You can open one of these files by just clicking on its entry in the menu, or you can apply one of the keystroke combinations **⌘ + 0** to **⌘ + 9** on Mac OS X or **Alt + 0** to **Alt + 9** on Linux and Microsoft Windows. Here, the number keys are used to sort the previously opened models according to when you last accessed the file. The most recently opened file will always have number 0 and the model number 9 is the model that was opened a longer time ago. Note that this order will change as soon as you open one model from this list or any other model.

If you are working with CellDesigner, open the model with this program's menu item or keystroke combination. When launching the SBMLSqueezer as CellDesigner plug-in, it will always use the currently selected model. This means that, in case that you are working with multiple models in CellDesigner, this model will be passed to SBMLSqueezer, whose tab is currently selected.



3.4 Equation generation one by one

Figure 3.5: \LaTeX options. All options in this tab are also available as command-line options (see section 4.3.8 on page 54). You can specify where your \LaTeX compiler is located in your operating system and what to include into the model report. This tab also gives you several style options that influence how the generated document will look like. As a new feature, it now also supports the Layout extension for SBML (Gauges *et al.*, 2006). You can here decide if a figure of your network should be generated and included into the report, given that layout information is provided in your file. For more information about SBML2\LaTeX see the documentation of this project.

In Garuda, SBMLSqueezer can receive files from other gadgets and will open these whenever this is requested. SBMLSqueezer will automatically open accepted files. There is hence nothing further to do. If SBMLSqueezer is not running when a file is sent to it from another gadget, Garuda will automatically launch the program and the file will be opened upon start.

3.4 Equation generation one by one

You can add a kinetic equation to individual reactions. To this end, SBMLSqueezer provides a specialized context menu and dialog window, which enable you to select the type of rate law that seems appropriate for your purposes. This dialog window is available whenever using SBMLSqueezer as a plug-in for CellDesigner or in the stand-alone version (also in the Garuda version). In all cases, the same dialog window will appear, which offers you a selection of appropriate rate laws for the particular reaction and gives you the opportunity to choose between those, or to discard the dialog. No change will be performed to your model when canceling the dialog (either by pushing [Esc] or by clicking on [Cancel]).

We here use model № 390 from BioModels database (Li *et al.*, 2010; Arnold and Nikoloski,

3 How to get started

Figure 3.6: Reaction context menu in CellDesigner. After installing SBML-squeezer as a plug-in, its functionality will be incorporated into CellDesigner's reaction context menu. If you right-click on an arbitrary reaction, it allows you to create a kinetic equation for this reaction (with the dialog in fig. 3.7), or to generate a LATEX model report that only involves the details relevant for the selected reaction.

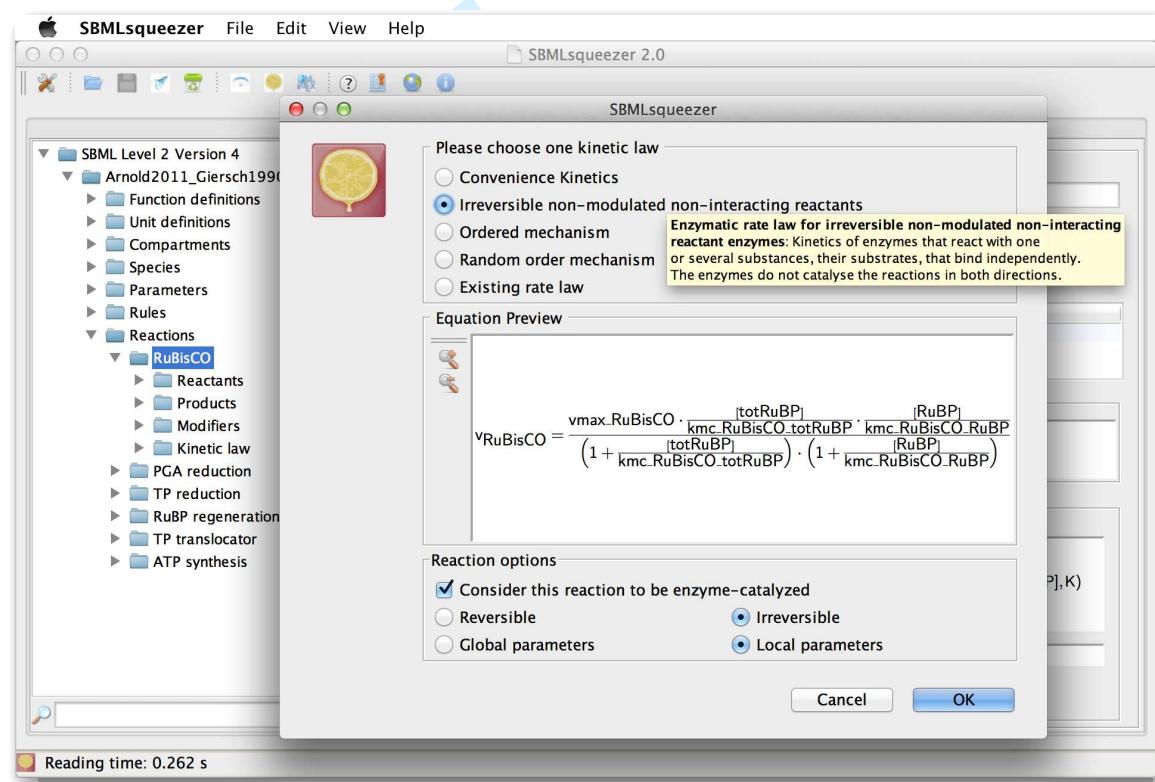
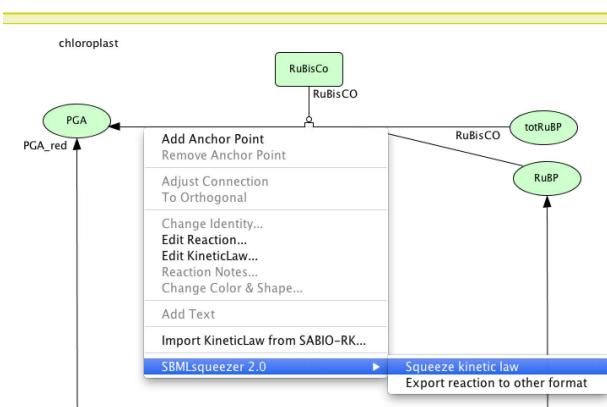


Figure 3.7: Generating a kinetic equation for a single reaction. This dialog can be opened by right-clicking on an individual reaction in your active model and selecting **Squeeze** in the pop-up menu. The directionality of the reaction and the enzyme property can be altered. Both options possibly influence the selection of rate laws. To abort this dialog, click on **Cancel** or hit the **Esc** key.

3.5 Generate kinetic equations in a single step

2011) as an illustrative example.

In case that you are working with CellDesigner (Funahashi *et al.*, 2003, 2006, 2007, 2008), right-click on the reaction of interest as this is displayed in fig. 3.6 on page 16 and select the menu item **Squeeze kinetic law**. When using SBMLsqueezer as a stand-alone program, you can generate kinetic equations for a selected reaction by right-clicking on the reaction of interest. An example is given in fig. 3.7 on page 16. SBMLsqueezer analyzes the currently selected reaction according to various properties and displays a selection of suitable rate laws, of which you can select the most appropriate one.

The equation preview, where you can zoom in and out of the rendered formula, helps you to choose a rate law. If a corresponding SBO entry can be found for a rate law, a tool-tip will be displayed with further information about this equation. You can also decide if the reversibility of the reaction should be changed. This would also alter the list of applicable kinetic equations. The other options, if newly created parameters should be locally attached to the kinetic law object or globally to the model, influences the internal structure of the model, but not its behavior. Just note, that there are some parameters, which cannot be stored locally because they represent recurrent properties of some reactive species and are needed across several rate laws (e.g., energy constants).

3.5 Generate kinetic equations in a single step

SBMLsqueezer can create rate laws for all reactions in one single step without the need of further human interaction or manual selection of rate laws for any reaction. This option can be useful if you are working with a large model and want to create a first draft of a kinetic system, or if you are interested to apply the same type of approximative rate law to each reaction. To see how to use this program feature, have a look at fig. 3.9 on the next page.

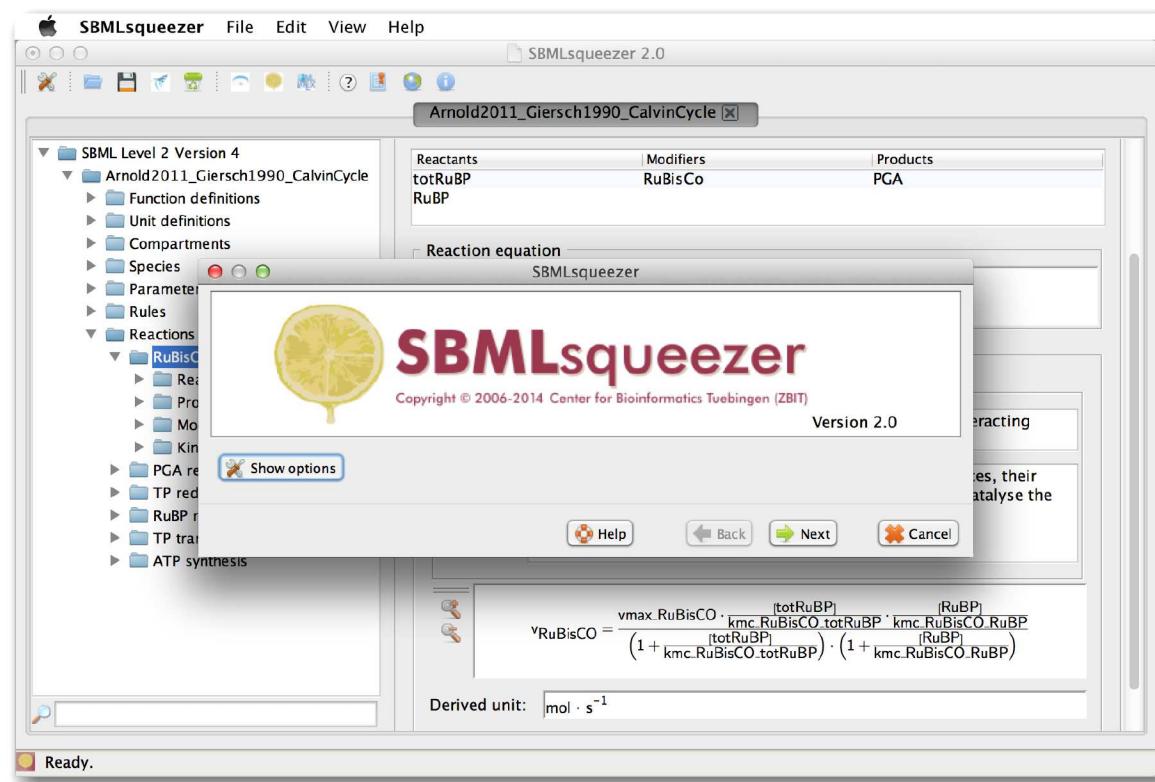
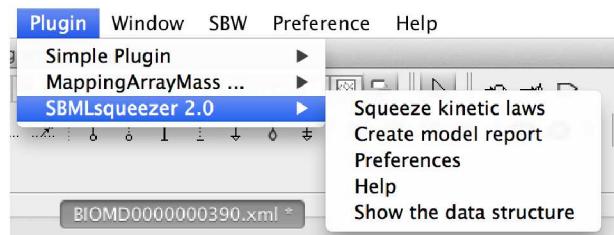
Just like in the case of the reaction context menu (section 3.4 on page 15), the same kinetics wizard can be used in stand-alone mode and when working with the CellDesigner plug-in version. Various options allow you to customize how this is done. The most important options decide if already existing rate laws should either be kept or overwritten, if all reactions can be modeled in a reversible manner, or as currently defined in the model. In the CellDesigner plug-in version, just click on **Plugin > SBMLsqueezer 2.0.1 > Squeeze kinetic laws** to launch the kinetics wizard. In the stand-alone version, you can either right-click on the model in the SBML tree, the lemon icon in the tool bar (icon next to this text), or **Edit > Squeeze** in the menu bar.

The usage of the kinetics wizard is identical, irrespective of how you launched it. You can see how this wizard looks like in fig. 3.9 on the next page. You can always discard all your changes by either clicking on the **Cancel** button or by hitting the **Esc** key. The **Help** button opens a browser window that gives you more information about SBMLsqueezer. If you click on **Show options**, the preference dialog will be displayed, which is described in section 3.2 on page 11. In this way, SBMLsqueezer gives you the option to make sure that the selection of kinetic equations for all distinguished cases will be done as if you pick those individually.

When you hit the **Next** button, kinetic equations will be created according to your settings and

1
2
3
4 **3 How to get started**
5

6
7 Figure 3.8: Launching SBMLsqueezer in
8 CellDesigner. The menu item **Plugin**
9 **SBMLsqueezer 2.0.1** gives you access to
10 nearly all functions of the program. You
11 can launch the kinetics wizard, adjust
12 your preferences, export a **LATEX** report,
13 open a help browser, or just look at how
14 SBMLsqueezer internally represents Cell-
15 Designer's data structure.
16
17



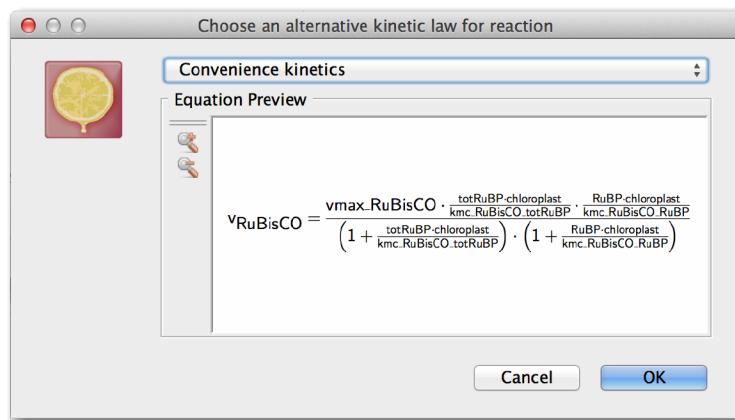
49 Figure 3.9: Generating kinetic equations in one single step with the kinetic law wizard. This
50 screen-shot shows the Kinetic Law Wizard (here shown under Mac OS X). When launched, this
51 wizard allows you to generate kinetic equations for all reactions in the active model. From this
52 wizard, you can directly access and alter all program options, see the online help, and go back and
53 forth between all steps through which the wizard will guide you.
54
55
56
57
58

3
4
5
6
7
8
9 3.5 Generate kinetic equations in a single step

Kinetic Equations		Number of warnings (red): 2		
Reaction	Kinetic Law	Reactants...	Products...	Formula
RuBisCO	enzymatic rate law for multireactant enzymes	2	0	vmax_RuBisCO*RuBP*chloroplast*totRuBP*chloroplast/((kmc_RuBisCO*totRuBP)+(kmc_RuBisCO*RuBP))
PGA_red	common modular rate law	2	3	(vmax_PGA_red*(PGA*chloroplast/kmc_PGA_red_PGA))/((totPGA*chl)+(totPGA*chl*kmc_PGA_red_PGA))
TP_red	enzymatic rate law for multireactant enzymes	5	0	vmax_TP_red*(TP*chloroplast/kmc_TP_red_TP)^5/(1+(TP*chloroplast/kmc_TP_red_TP)^5)
RuBP regeneration	enzymatic rate law for multireactant enzymes	2	0	vmax_RuBP_reg*ATP*chloroplast*Ru5P*chloroplast/((kmc_RuBP_Reg*ATP*chl)+(kmc_RuBP_Reg*Ru5P))
TPT	common modular rate law	2	2	(vmax_TPT*(TP*chloroplast/kmc_TPT_TP))^hco_TPT*(1+(TP*chloroplast/kmc_TPT_TP)^hco_TPT))
ATP_S	irreversible Michaelis-Menten rate law for two substrates	2	0	vmax_ATP_S*Pi*chloroplast*ADP*chloroplast/(kic_A*Pi*chl+ADP*chl)

17 Buttons: Export changes, Help, Back, Finish, Cancel

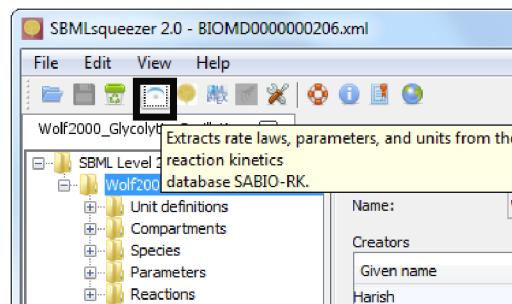
22 Figure 3.10: Results of the kinetics wizard displayed in a table. We again use model № 390 from
23 BioModels database (Li *et al.*, 2010; Arnold and Nikoloski, 2011) as an example. Two rows are
24 highlighted in red. The reason is that these reactions involve an unrealistically high number of
25 reactant molecules, or are reversible with a high number of products, respectively. These warnings
26 indicate that the generated rate law might neglect several intermediate steps. In this table, you
27 can review all generated rate law. Note that these will not be transferred to your original model
28 before you hit the Finish button. You can alter each rate law by double- or right-clicking on an
29 entry in the column “Kinetic Law,” or hit the Back button and change your preferences for the rate
30 law selection. You can already generate a LATEX report about the changed model (hit the button
31 Export changes), which can help you to make your decision if you want to apply or discard your
32 changes.
33
34



35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60 Figure 3.11: Changing selected rate laws in the kinetics wizard. This dialog window appears when you double-click on an entry in the column “Kinetic Law” of the kinetics wizard. You can here select and apply an alternative rate equation. If you want to change the criteria for the creation of equations, you need to go back to a previous step in the wizard.

3 How to get started

Figure 3.12: Starting the SABIO-RK wizard. After opening a model in SBML-squeezer, the SABIO-RK button will become active in the tool-bar (see the black fringe). A tool-tip will display more information about this button when moving the mouse over it. You can click on this button to launch the SABIO-RK wizard. Alternatively, you can also click on **Edit > SABIO-RK**.



displayed in a summary table (see fig. 3.10 on page 19). You can change individual rate laws by double-clicking or right-clicking on a specific entry in this table. A pop-up window will then appear asking you to choose an alternative rate law (see fig. 3.11 on page 19). When applying the change, the selection will be updated. When you hit the button **Finish**, the created rate equations, units, and parameter objects will be incorporated into your original model.

3.6 Extraction of rate laws from SABIO-RK

Instead of deriving kinetic equations *de novo* for your model, you can also use SBML-squeezer to automatically obtain experimentally determined equations from SABIO-RK. To this end, SBMLsqueezer compares the reactions of interest to reaction signatures in this online database and allows you to select the most appropriate reactions or to restrict your search by using several parameters, such as pH, temperature, etc. Note that this feature does not apply for the CellDesigner plug-in variant, because CellDesigner brings already with it its own SABIO-RK interface, which you can use directly in CellDesigner. Furthermore, this feature requires an active Internet connection and can therefore not be used in an off-line mode.

This section describes how to use the GUI to extract information from SABIO-RK. You can also do this on the command line, which allows for batch processing of multiple SBML files as this has been done by Büchel *et al.* (2013). For more information about the command-line options for SABIO-RK see section 4.3 on page 40. You can directly use SBMLsqueezer's API to benefit from this functionality. Section 4.1 provides an elaborated description of how to use this feature.

3.6.1 Rate laws from SABIO-RK for an entire network

Figures 3.12 to 3.17 show how you can add kinetic equations from SABIO-RK to several reactions at once. As an example model we pick model № 206 from BioModels database (Li *et al.*, 2010; Wolf *et al.*, 2000). A wizard guides you through the selection of relevant reactions (fig. 3.13 on the facing page) and provides several options to restrict the search in SABIO-RK (fig. 3.14 on page 21),

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

3.6 Extraction of rate laws from SABIO-RK



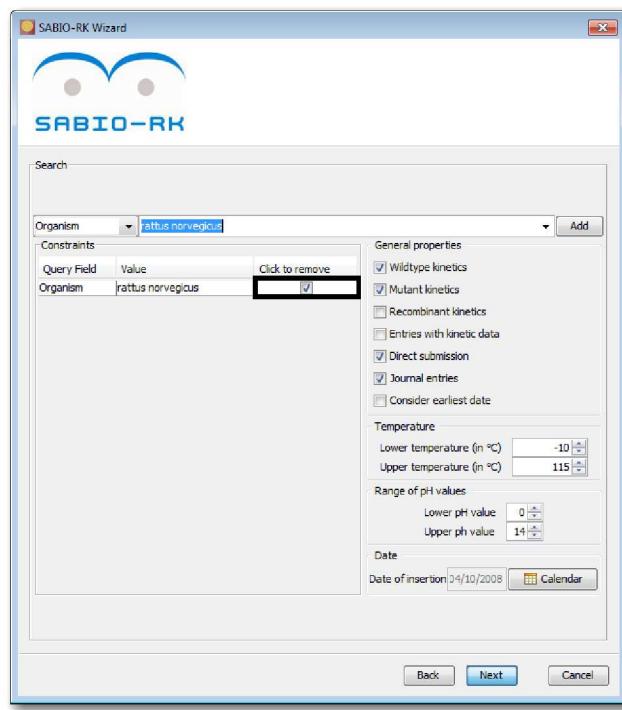
Figure 3.13: Selection of reactions in the SABIO-RK wizard. On the first window you can select which reactions you want to equip with kinetic equations from SABIO-RK. It is possible to directly select the reactions with some property (such as reactions not yet containing a kinetic law or fast reactions). Furthermore, you can select the desired reactions by holding the **Ctrl** key pressed while clicking on the desired reactions. You can abort the wizard by either clicking on the **Cancel** button or by hitting the **Esc** key. When finished click on the button **Next**.



Figure 3.14: Selection of search terms for SABIO-RK. On the next window you can add categories for search terms together with their values. These terms are used to select only reactions and rate laws from SABIO-RK, whose annotation contains these terms. An example is the organism, in which this reaction takes place. You can choose “organism” from the provided terms and type the desired name as value of the term in the text field. By clicking on button **Add** (black fringe), the term will be added to the table on the left-hand side of the dialog window. See fig. 3.15 on the next page for an example how to remove a term again.

3 How to get started

Figure 3.15: Removal of search terms for SABIO-RK. You can remove a query field again by clicking on the check box button in the right-most column. When you are done with selecting appropriate search terms, click on button [Next] to see the results of your query. Figure 3.16 displays an example who this overview can look like. The [Back] button allows you to return to the selection of reactions as displayed in fig. 3.13 on page 21. As before, you can abort the dialog by either hitting the key [Esc] or by clicking on the [Cancel] button.



Results						
Reaction	Selected Reaction [SABIO-RK]	Matching Entries	Entry ID [SABIO-RK]	Partial / Non-Matching Entries	Total Entries	
Glucose + 2 ATP ⇌ F16P		0		0	0	
F16P ⇌ 2 Triose_Gly3Phos_DHAP	beta-D-Fructose 1,6-bisphosphate $\xrightarrow{\text{fructose-bisphosphatase(Enzyme) wildtype}}$ G	1	3467	0	1	
Triose_Gly3Phos_DHAP + NAD \rightleftharpoons 3PG + ATP		0		0	0	

Figure 3.16: Window with found kinetic equations. A reaction is highlighted in green if a matching rate equation was found, yellow if the found equations do not exactly fit to your model (there is no straightforward matching of all elements in the equation to elements in your model), and red if no matching rate equation was found. If you are satisfied with the results, click [Next].

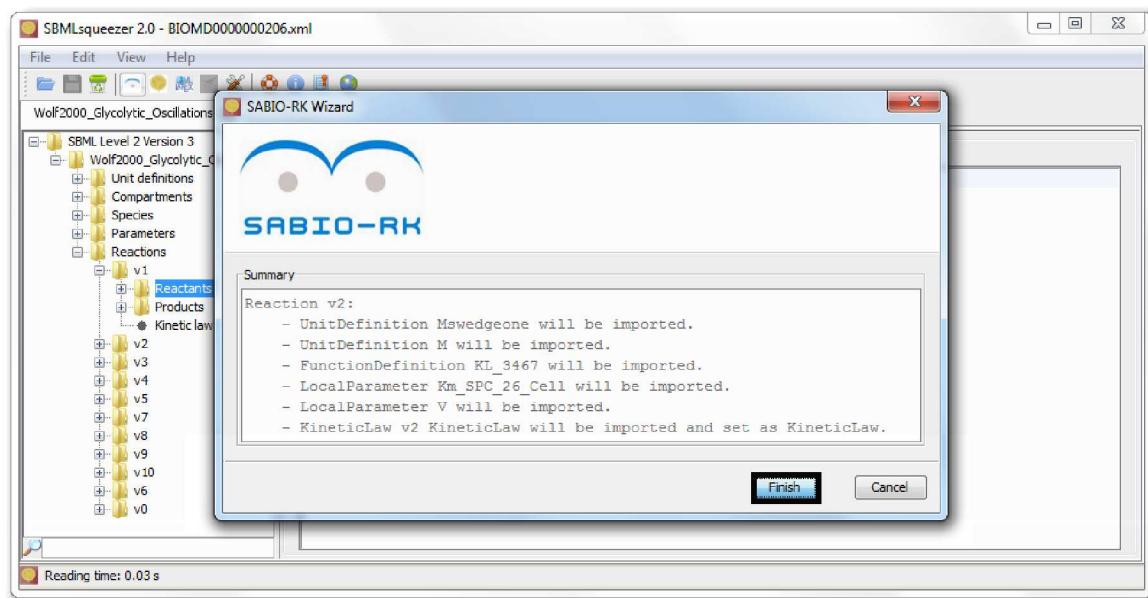


Figure 3.17: Summary of necessary changes. The wizard summarizes all changes to the model that are required if you want to transfer the identified rate laws from SABIO-RK to your model. This summary lists only changes related to reactions that have been highlighted in green in the previous step (fig. 3.16 on page 22). Upon clicking on [Finish] a pop-up dialog will finally ask you to either confirm these changes to be made or to disregard all results. If you confirm, the rate equations will be transferred to your model and all changes will be applied as stated in this summary.

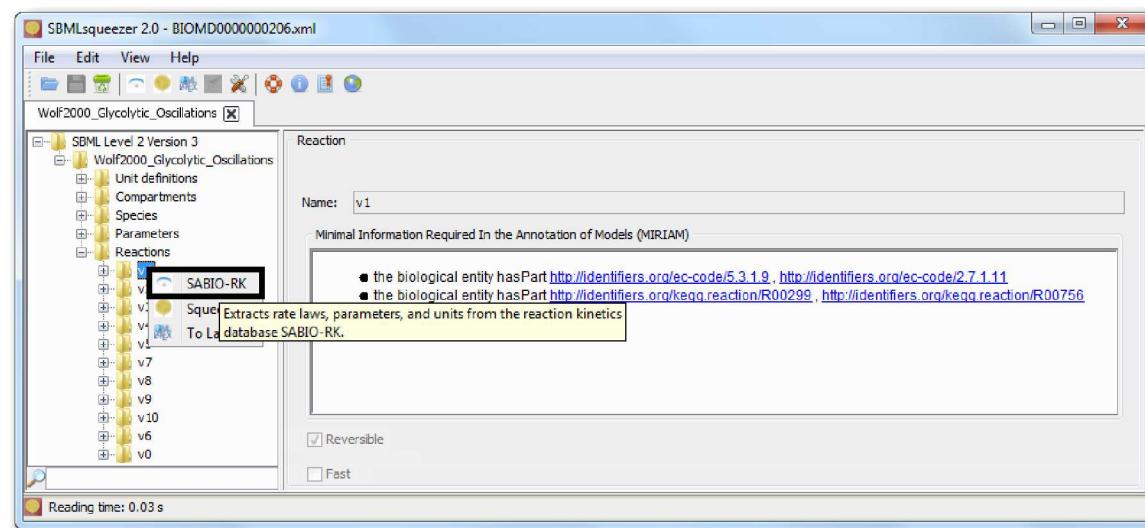
whose interface is similar to the database front end of SABIO-RK¹. To ensure that entries for the reactions of interest can be found in SABIO-RK, it is important to annotate these reactions with IDs from the Kyoto Encyclopedia of Genes and Genomes (KEGG) database (Kanehisa and Goto, 2000) using the MIRIAM registry (Juty *et al.*, 2012). The KEGG reaction ID is then always included in the respective search in order to avoid adding kinetic laws referring to other reactions. To further restrict your search, change the bounds of pH, temperature, etc. in the right panel (see fig. 3.14 on page 21).

3.6.2 SABIO-RK for a selected reaction

As an alternative you can add kinetic equations from SABIO-RK to a selected individual reaction. How to do this is shown in figs. 3.18 to 3.23 on pages 24–27. We here use model № 206 from BioModels database (Li *et al.*, 2010; Wolf *et al.*, 2000) as an example network. You should first select the reaction, for which you want to obtain a rate law from SABIO-RK (fig. 3.18 on the next

¹<http://sabio.h-its.org>

1
2
3
4 **3 How to get started**
5



26 Figure 3.18: Starting the SABIO-RK application for a selected reaction. To find a reaction of
27 interest, you can use the search function at the bottom of the SBML tree. Just click on the text field
28 and type a part of the reaction's name or ID. The tree will be updated while you type and reduced
29 to elements that contain the text you are typing. Alternatively, you can just scroll to the entry of
30 interest. Once you have found a reaction of interest, right-click on it. Then click on the SABIO-RK
31 item in the pop-up menu and the SABIO-RK wizard will be started. The reaction is shown again
32 in the first window and you can just click on **Next**. This will bring you to the selection of search
33 terms that is described in fig. 3.19 on the facing page.
34

35
36 page). All subsequent steps of the procedure are essentially the same as described before. The only
37 difference is that the SABIO-RK wizard will be launched for one selected reaction of interest only
38 instead of having all reactions in the model.
39

42 3.7 Viewing and saving the results

43 When using the stand-alone version of SBMLsqueezer, you can see a tree representation
44 of the SBML document you are working with on the left-hand side of the GUI. Figure 3.24
45 displays how model № 390 from BioModels database (Li *et al.*, 2010) looks like after SB-
46 MLsqueezer has modified one reaction's rate law. The program recognizes if an SBML document
47 has been modified by one of its functions. You can see this because the title bar of the program
48 will change, and the save actions in tool-bar and menu-bar will become active. In Microsoft Win-
49 dows and Linux an asterisk will be added to the file name in the title bar. In Mac OS X, the red
50 "close" button on the top-left most corner of the program will no longer display a cross, but a
51 circle (you can see this in fig. 3.24 on page 28). You can save the modified file either by clicking
52
53
54

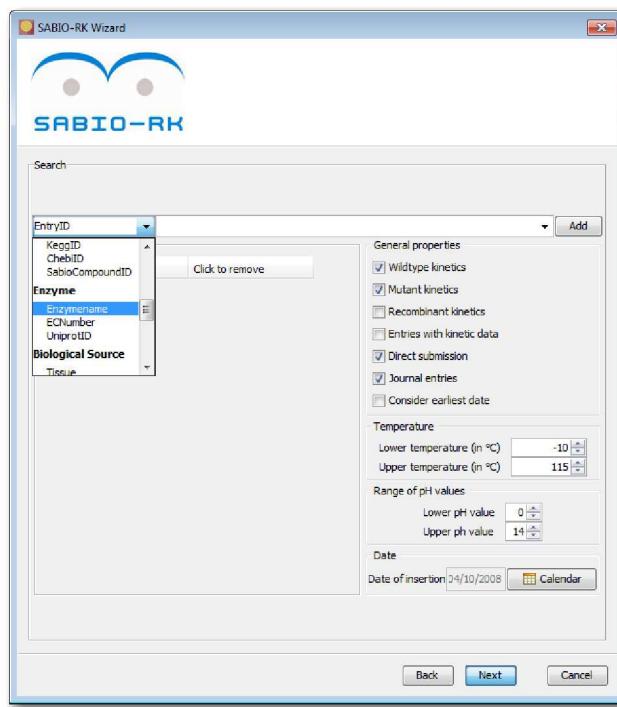
 3.7 Viewing and saving the results


Figure 3.19: Selection of search terms. You can add search terms such as the organism by choosing from the provided terms and typing in the value of the term. The search can be further restricted by changing the bounds of pH, temperature, etc. in the right panel. You can remove a query field by clicking on the checkbox button in the table on the left-hand side. This dialog is just the same what has been described in figs. 3.14 to 3.15 on pages 21–22 when adding kinetic laws to several reactions in a single step. The example continues in fig. 3.20.



Figure 3.20: Window with two search terms. Here a search for an organism and an enzyme name has been specified and will be combined to a query when clicking on **Next**. You will then see the list of reactions as it is displayed in fig. 3.21 on the following page.

3 How to get started

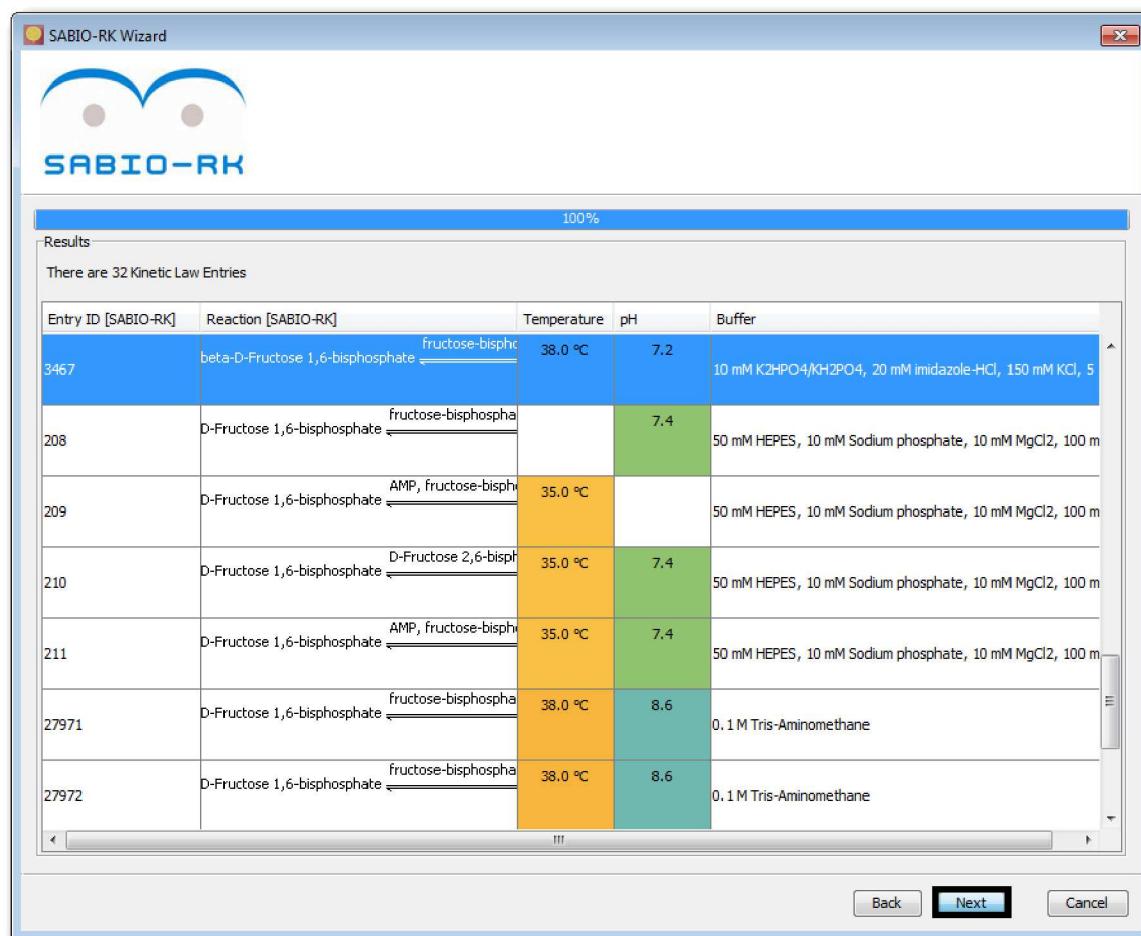


Figure 3.21: Window with kinetic equations found for a single reaction. The rate equations that match your search criteria are displayed here. You can select a reaction and click on **Next**, which will bring you to fig. 3.22 on the facing page. Alternatively, you can click on **Back** and change your search criteria (see fig. 3.20 on page 25).

on **File** **Save** or by clicking on the disk symbol in the tool-bar. Alternatively, you can also use the keystroke combination **Ctrl** + **S** (under Microsoft Windows and Linux) or **⌘** + **S** (under Mac OS X).

You can always select **File** **Save as...** in order to save the active SBML document under a different file name. The keystroke combination **↑** + **Ctrl** + **S** (Microsoft Windows and Linux) **↑** + **⌘** + **S** (Mac OS X) will also open a file chooser to save a copy of the active SBML document. In Mac OS X you have a further options to save the currently selected document elsewhere: you can drag the file symbol in the title bar into an arbitrary folder of a file browser.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

3.7 Viewing and saving the results

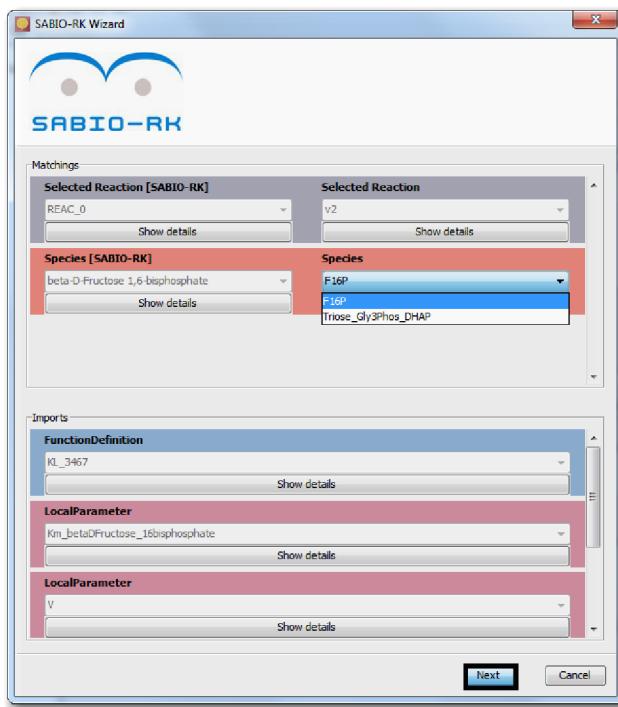


Figure 3.22: Window for matching elements in the equation to model elements. If kinetic laws are added to an entire network simultaneously, a straightforward matching of all elements (e.g., the species) contained in each rate equation to SBML elements in your model will be necessary. In contrast to that, if you only add a rate law to one reaction at a time, the application presents you a suggestion for the matching and enables you to change it if desired. The necessary elements to import, such as function definitions contained in the rate equation to add, are also shown in this window.

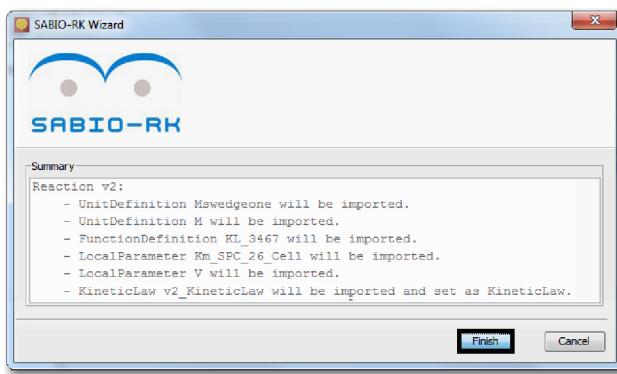


Figure 3.23: Summary of necessary changes. This overview summarizes how your model will be changed when adding the selected rate equation. Now click on **Finish** and afterwards a dialog pops up asking you to confirm the changes. After this confirmation the rate equation will be transferred and these changes will be applied to your model.

3 How to get started

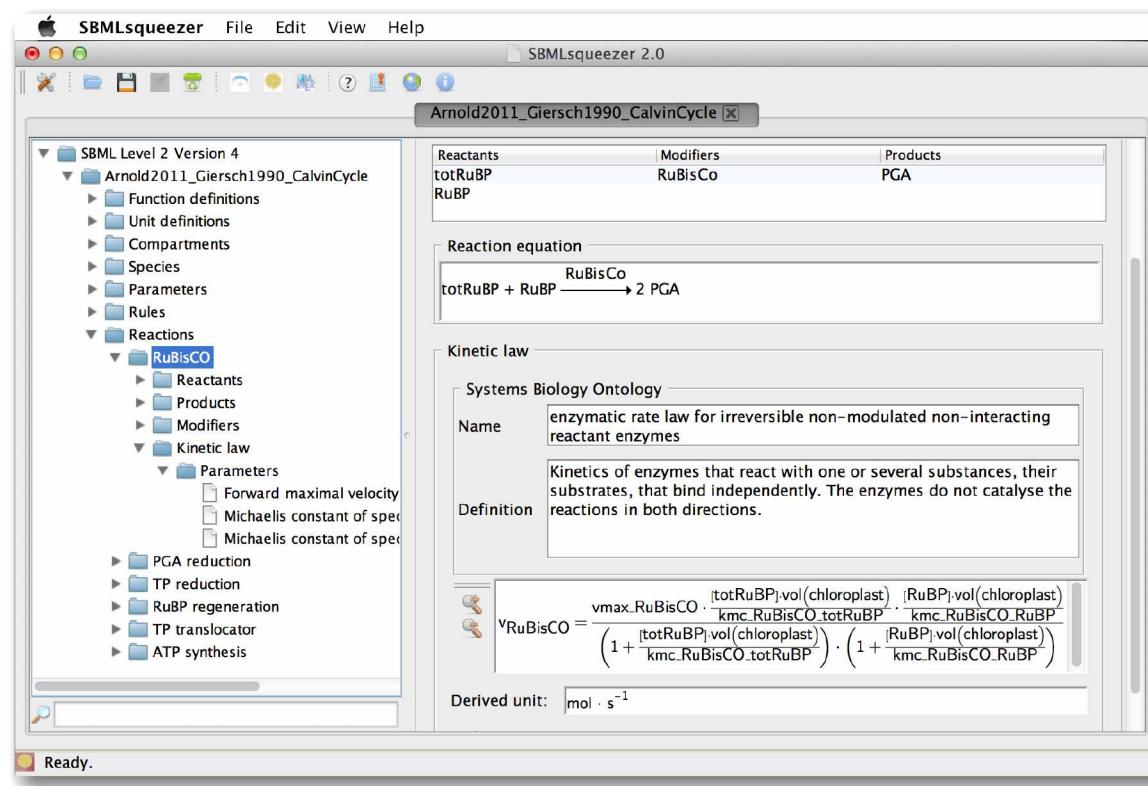


Figure 3.24: Viewing SBMLsqueezer's results. SBMLsqueezer provides a two-part view that displays the details of the model's structure. On the left you can see the hierarchical SBML data structure. By clicking on selected elements within this tree, details about the element will be displayed on the right. If you select a reaction or a kinetic law directly, the rate equation, parameters, etc. will be displayed. You can search for elements within the model by using the text field on the left-bottom corner. This text field reacts to your input while typing and will immediately reduce the number of selectable items in the tree. Exact hits will be highlighted in a bold font.

Now, let us assume, you have used SBMLsqueezer to assign kinetic equations to the reactions in your model (either by extracting those from SABIO-RK or with the *de novo* equation generator). When expanding that tree and clicking on individual components, the program enables you to view the generated kinetic equations. Just expand "Reactions" and afterwards the desired reaction. Then you can click on "Kinetic law" and the rate equation is displayed on the right in detail. A convenient search function at the bottom of the window helps you to quickly find reactions and other model components of interest.

When using SBMLsqueezer as a plug-in for CellDesigner, you can either see the results by looking through the tables and overviews provided by CellDesigner itself, or you can click on **Plugin > SBMLsqueezer 2.0.1 > Show the data structure**. This will open a similar view as the stand-alone



3.8 Interaction with further Garuda gadgets

Figure 3.25: Selecting a Garuda gadget. This dialog window shows you all available Garuda gadgets that support the file type you are sending. Upon hitting the **OK** button, the model in the currently selected tab will be sent to the selected application.

version provides. SBMLSqueezer automatically synchronizes all of its changes with CellDesigner. This means that CellDesigner will be notified about these changes and incorporate these into its in-memory model. You can hence directly use its save functions or also save a copy of your model.

3.8 Interaction with further Garuda gadgets

After having kinetic equations assigned to reactions of interest, it might be useful to pass the resulting SBML document to further gadgets in Garuda for subsequent analysis. SBMLSqueezer is automatically connected to Garuda core if it has been launched inside of Garuda. Otherwise, SBMLSqueezer will also connect to Garuda if you launch your installation of Garuda before starting SBMLSqueezer. If SBMLSqueezer is already running when you launch Garuda, no new connection will be established, you would need to restart SBMLSqueezer.

Now let us assume, your connection to Garuda has been successfully established. In this case, SBMLSqueezer can both, receive and send SBML files from or to further gadgets. SBMLSqueezer will notify you when it is connected to Garuda by displaying a message in its status bar (at the bottom of the main window). You do not have to do anything in SBMLSqueezer when you want to receive a file from another gadget. The program will automatically be notified as soon as it receives the file and will directly open it in a new tab, so that you can work with the file as if you have just regularly opened it within the application.

It might, for instance, be an interesting idea to create a draft for a dynamic model directly based on information from the KEGG database (Kanehisa and Goto, 2000) using KEGGtranslator (Wrzodek *et al.*, 2011, 2013) and to pass the model to SBMLSqueezer in order to assign kinetic equations. This model can then be forwarded to the application SBMLsimulator (Keller *et al.*, 2013, 2014) that can be used to estimate the parameter values within the newly created kinetic laws, given that reference data are available. A similar approach has been suggested for the generation of draft genome-scale metabolic models (Büchel *et al.*, 2013).

As soon as at least one SBML file has been opened, SBMLSqueezer will activate the Garuda icon in the tool-bar (which you can see next to this text) as well as the menu item **File > Send current file to Garuda**. By clicking on that icon or selecting this entry in the menu bar, you can send the active file, i.e., the file that belongs to the currently selected tab in

3 How to get started

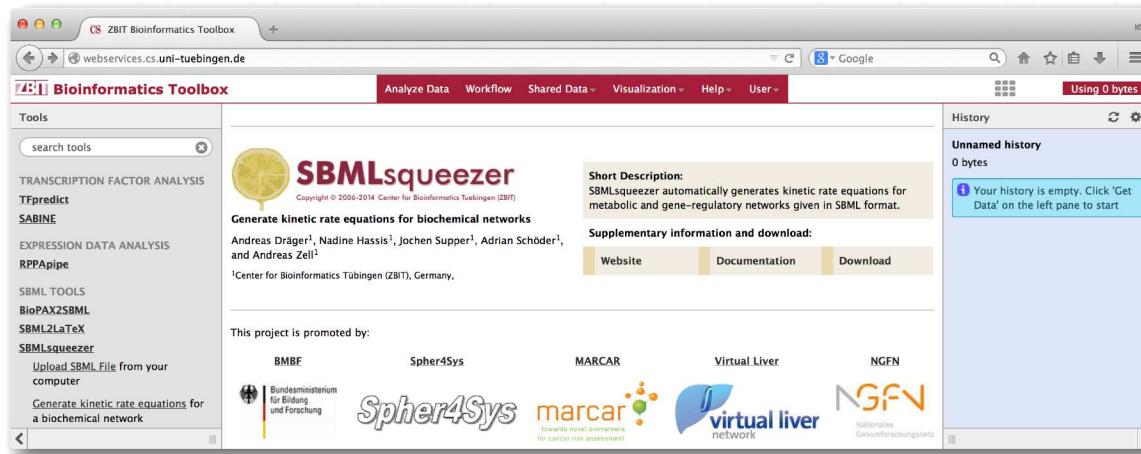


Figure 3.26: Starting the online version of SBMLsqueezer. This figure displays the Galaxy framework in the browser Firefox (version 29.0.1) under Mac OS X (version 10.9.3). You can start working with SBMLsqueezer by either clicking on the program's icon or the link "Upload SBML file".

SBMLsqueezer, to another gadget. To this end, SBMLsqueezer will display the dialog window that is shown in fig. 3.25 on page 29. If the model in the selected tab has been modified and not yet saved, SBMLsqueezer will create a temporary file in your operating system's directory for temporary files and send this file to the selected gadget.

3.9 Using SBMLsqueezer as an online program

SBMLsqueezer can also be used via the Galaxy web service facility (Goecks *et al.*, 2010) of the University of Tuebingen². Since the user interface of this variant greatly differs from all other use-case scenarios, we here give a description of options and functions of the web interface.

In order to use the online version of SBMLsqueezer, open a browser of your choice. Go to the main portal of all web services provided by the Universitiy of Tuebingen² and scroll down until you find the tool SBMLsqueezer and click on the the program's logo, or you can click on the link in the list of tools on the left. Alternatively, you can directly go to the service SBMLsqueezer³. Figure 3.26 displays the web interface of the Galaxy framework (Goecks *et al.*, 2010).

The first step is now to upload your SBML file of interest to the online program. To this end, you can either click on the link "Upload SBML file" on the left-hand side of the browser window, or click on the icon of SBMLsqueezee. In both cases you should see a browse button that allows you to select an Extended Markup Language (XML) or SBML file from your local file system. After

²<http://webservices.cs.uni-tuebingen.de>

³http://webservices.cs.uni-tuebingen.de/tool_runner?tool_id=sbmlupload2

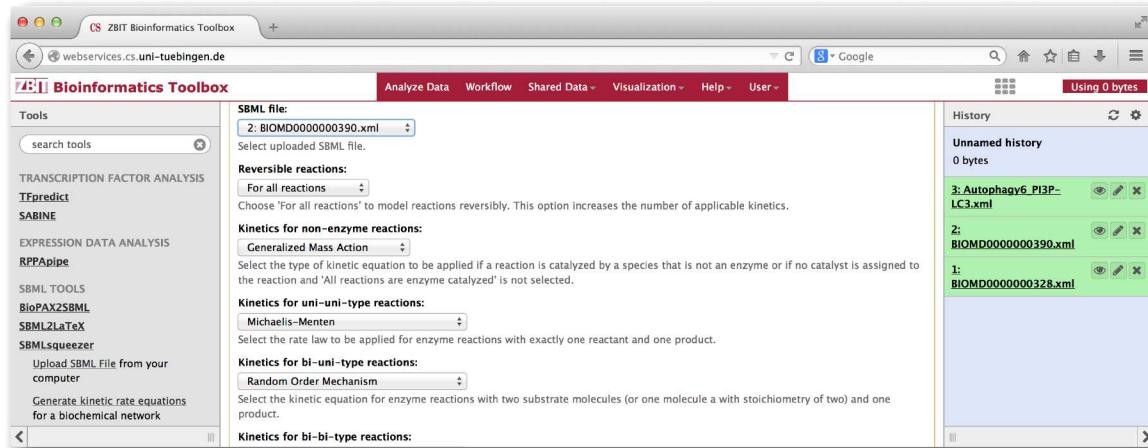


Figure 3.27: Adjusting preferences in the online version. In this example, three models have been uploaded to the Galaxy service and are shown in the history column in the right-hand side of the browser window. You can now choose for which file SBMLsqueezer should generate kinetic equations by altering the selected entry in the combo box at the top of the center column. In the center column, this view offers you all options of the stand-alone version of SBMLsqueezer.

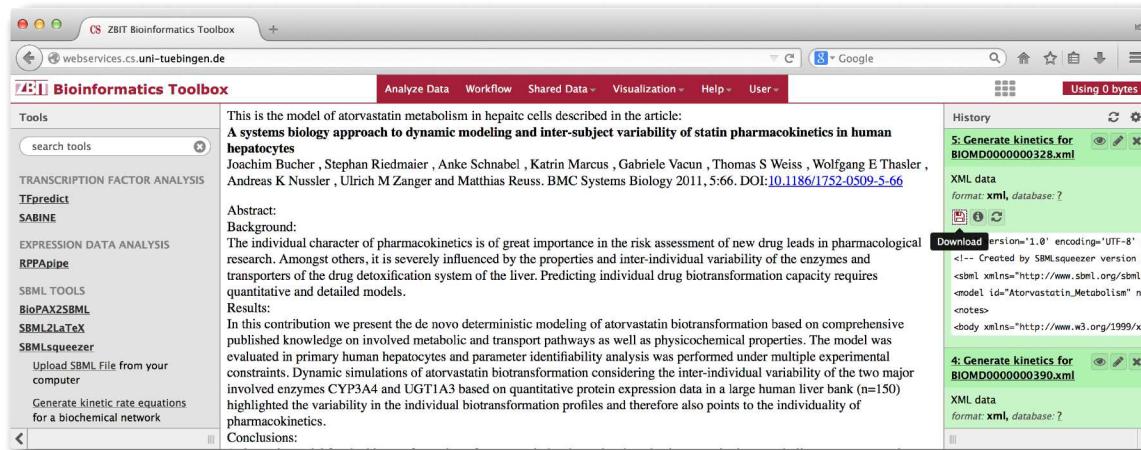
selecting the file, hit the button “Execute” in order to actually upload the file to the Galaxy service. Galaxy informs you about the progress of the upload in the “History” column at the right-hand side of the browser window. You can upload further files if you like, but at least one file is required in order to run SBMLsqueezer. Please note that uploaded models and files will be deleted after the job has been executed and are not accessible to any third-parties, i.e., data security is guaranteed.

Second, click on the link “Generate kinetic rate equations” on the left-hand side of the browser window. You should see a view similar to what is displayed in fig. 3.27. Scroll down to see all available options. At the bottom of this page, there is also a descriptive text explaining how to proceed. Each option has descriptive text as well. The online version presents all options of the program just as the stand-alone version. You can therefore go back in this tutorial and look-up the meaning of individual options either in section 3.2 on page 11 about the GUI of the stand-alone version or in section 4.3 on page 40 where the command-line options are described. When you scroll down, you can see that this online program also offers you to obtain rate laws from SABIO-RK. Just one option group is missing, namely **SBML^{LATEX}**. The reason is because the Galaxy framework of the University of Tuebingen provides **SBML^{LATEX}** as a separate online program (Dräger *et al.*, 2009b).

When you are happy with the settings, scroll down until you see the “Execute” button. When you hit this button, SBMLsqueezer will create kinetic equations for your model according to your preferences. To this end, a new job will be scheduled that will be displayed in your history.

When the job is done, you can obtain the results by first clicking on the link “Generated kinetics for [file name],” which will appear in the history column. You can then click on the disk icon below

1
2
3
4
5 **3 How to get started**



23 Figure 3.28: Obtaining the results from the online version. The history column contains an
24 overview of all files for which kinetic equations have been generated. You can view the details
25 of each file by clicking on the eye icon, or download the file by first clicking on the link in the
26 headline of the respective entry (“Generated kinetics for...”) and then clicking on the disk icon.
27

28
29 in order to download the SBML file that contains your results. If you click on the eye icon, the
30 central column will display a rendered version of your SBML file, which is the view at all Extended
31 HTMl (XHTML) notes within your file.
32

4 Advanced program features

This chapter discusses how more experienced users can benefit from SBMLsqueezer's capabilities. In the first two sections we will have a look behind the scenes and explain how you can directly access and use the API of SBMLsqueezer in a programming environment. In the next section we will list and explain all possible command-line options. All program features that have been described in the previous chapter can also be addressed through the command-line and programming interface, making SBMLsqueezer a versatile tool that can be used in diverse, customized applications.

4.1 Using SBMLsqueezer as an equation generator library

We will now discuss how to use the API of SBMLsqueezer directly in order to generate kinetic equations as part of more complex operations. This function could already be used in version 1.3 of SBMLsqueezer (see listing A.1 on page 84). Since then, the API has been greatly modified and improved. We will now discuss important aspects of the new API of SBMLsqueezer and give examples of particularly important use-case scenarios.

4.1.1 Assignment of kinetic equations to all reactions in an SBML file

Listing 4.1 gives you an example for a simple application that takes the paths to two SBML files as input and proceeds as follows:

1. It changes the preferences of the program by defining several options.
2. It creates an instance of SBMLsqueezer with type parameter `org.sbml.jsbml.Model`, i.e., it will use JSBML as its parsing library.
3. By calling the `squeeze` method, it will then use JSBML to read the first file into an SBML-Document data structure and generate kinetic equations for all reactions within the document according to the current preferences.
4. The result will be written into the second file, i.e., the original file will remain unchanged unless the two arguments point both to the identical file.

The paths in this example can also point to a directory instead of a particular file. If this is the case, SBMLsqueezer will recursively traverse all acceptable SBML files in the given input folder and create a corresponding file with newly created or obtained kinetic equations in the output folder.

4 Advanced program features

```
1 /**
2  * This program takes the absolute paths to an input file and an output
3  * file as arguments, configures several preferences for
4  * {@link SBMLsqueezer}, generates kinetic equations, units, parameters
5  * etc. and saves the result in the given output file in SBML format.
6  *
7  * @param args absolute or relative paths to two SBML files (in and out)
8  * @throws Throwable if either user preferences cannot be made
9  *         persistent or the creation of rate laws fails.
10 */
11 public static void main(String[] args) throws Throwable {
12     /*
13      * Configure user preferences of SBMLsqueezer
14      */
15     // General preferences
16     SBPreferences prefs =
17         SBPreferences.getPreferencesFor(OptionsGeneral.class);
18     prefs.put(OptionsGeneral.ALL_REACTIONS_AS_ENZYME_CATALYZED, true);
19     prefs.put(OptionsGeneral.DEFAULT_COMPARTMENT_SIZE, 1d);
20     prefs.put(OptionsGeneral.POSSIBLE_ENZYME_RNA, true);
21     prefs.flush();
22
23     // Rate law selection
24     prefs = SBPreferences.getPreferencesFor(OptionsRateLaws.class);
25     prefs.put(OptionsRateLaws.KINETICS_REVERSIBLE_UNI_UNI_TYPE,
26             MichaelisMenten.class);
27     prefs.put(OptionsRateLaws.KINETICS_REVERSIBLE_ARBITRARY_ENZYMEREACTIONS,
28             ConvenienceKinetics.class);
29     prefs.flush();
30
31     // Initialize SBMLsqueezer with JSBML as its internal SBML library
32     SBMLsqueezer<Model> squeezer = new SBMLsqueezer<Model>();
33     // Create kinetic equations, parameters, units etc. and save the result
34     squeezer.squeeze(args[0], args[1]);
35 }
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
```

Listing 4.1: Generating rate laws for all reactions in a model via the API of SBMLsqueezer 2

4.1.2 Adjusting configuration and user preferences

While the previous version of SBMLsqueezer stored its preferences in configuration files within the user's home directory, SBMLsqueezer now makes use of the preferences of your operating system. The keywords for the individual options have been slightly changed, but are still very similar. In general, the names of the command-line options (see section 4.3 on page 40) are very similar to the names of the options that you can use when hacking SBMLsqueezer's API. Furthermore, the grouping of the preferences is identical to the grouping of options you have in the tabs of the preferences dialog (see figs. 3.1 to 3.5 on pages 11–15) and also the groups of command-line

4.1 Using SBMLsqueezer as an equation generator library

options. You can therefore read through the command-line options in order to get a description of potential options to be used in the API. The Java™ API documentation, which you can find online on the project's homepage¹, will also be helpful to gain an understanding of available options.

The options of SBMLsqueezer are each gathered in specialized interfaces, which all extend the interface KeyProvider. Each option is a constant field variable. If you are using an Integrated Development Environment (IDE), such as Eclipse, an auto-complete function will directly show you which options are provided within a particular sub-class of KeyProvider. Such an IDE will also display the Java documentation to you. You can load the preferences by calling

```
SBPreferences prefs =
    SBPreferences.getPreferencesFor(MyOptionsClass.class);
```

Listing 4.2: Loading preferences in SBMLsqueezer 2

Here, MyOptionsClass acts as a placeholder for your actual instance of KeyProvider for which you want to load preferences. SBMLsqueezer gathers its specific options in the following interfaces:

org.sbml.squeezer.OptionsGeneral See the command-line options described in section 4.3.3 on page 41.

org.sbml.squeezer.io.IOOptions These options are described in section 4.3.2 on page 41.

org.sbml.squeezer.kinetics.OptionsRateLaws Corresponds to the command-line arguments in section 4.3.4 on page 45.

org.sbml.squeezer.sabiork.SABIORKOptions See the description in section 4.3.5 on page 52.

org.sbml.squeezer.sabiork.SABIORKPreferences See section 4.3.6 on page 52.

Each option has a specific data type associated with it. You can hence use a call of the put method on your instance of SBPreferences to alter the value for an option. Thereby, the option is used as the key in the preferences object. In the same way, you can also obtain the current value for an option. Just read the documentation about preferences of the standard Java™ distribution². The only difference is that SBMLsqueezer uses an extended version of the regular preferences implementation, which allows you to directly store and retrieve more complex data structures besides Strings, such as File or Class objects. In particular, when selecting a specific kind of rate law for a certain type of reaction, SBMLsqueezer expects the class object of that KineticLaw. Note that this is in contrast to version 1.3, which expected the name of the class.

¹<http://www.cogsys.cs.uni-tuebingen.de/software/SBMLsqueezer/doc/api/SBMLsqueezer2.0.1/>

²<http://docs.oracle.com/javase/6/docs/api/java/util/prefs/Preferences.html>

1
2
3
4 4 Advanced program features
5
6
7
8

4.1.3 Using SBMLsqueezer with a libSBML back-end

9
10 Let us now discuss how you can use SBMLsqueezer's API with a libSBML back-end instead of
11 pure JSBML. To this end, you only have to change the way how you initialize your instance of
12 SBMLsqueezer:

```
13 SBMLsqueezer<org.sbml.libsbml.Model> squeezer = new
14   SBMLsqueezer<org.sbml.libsbml.Model>(
15     new org.sbml.jsbml.xml.libsbml.LibSBMLReader(),
16     new org.sbml.jsbml.xml.libsbml.LibSBMLWriter());
```

17
18 Listing 4.3: Initializing SBMLsqueezer 2 with a libSBML back-end
19
20

21 Everything else of listing 4.1 on page 34 can be left unchanged. Here, we are initializing SBML-
22 squeezer based on a libSBML Model data structure. It is important to use the correct reader and
23 writer from the package `org.sbml.jsbml.xml.libsbml`, and not to confuse these with the `Lib-`
24 `SBMLReader` and `LibSBMLWriter` from the `org.sbml.jsbml.celldesigner.libsbml` pack-
25 age in JSBML. Otherwise, your application will not function, because the classes in this package
26 are very basic implementations needed for the interface between JSBML and CellDesigner.

27 Please note that SBMLsqueezer can internally only work with the JSBML data structure. The
28 libSBML back-end is used to parse and write SBML files and also allows for off-line model valida-
29 tion. However, SBMLsqueezer will convert libSBML's data structure to JSBML and synchronize
30 its changes to the original data structure. When run-time is crucial for your application, this proce-
31 dure should hence be avoided.
32

4.1.4 Assignment of specific rate laws to selected reactions

33 Instead of reading and writing entire files or recursively walking through a directory structure, it
34 can also be desirable to perform more customized calls to create rate laws for individual reactions
35 only. To this end, a deeper understanding about the functioning of SBMLsqueezer is required.
36 There are a few particularly important classes for the *de novo* creation of kinetic equations, which
37 are all located in the package `org.sbml.squeezer`:

38 **KineticLawGenerator** This class contains the actual algorithms to build a rate law and to syn-
39 chronize changes between models.
40

41 **ParameterFactory** Here all (local) parameters are generated. The implementation follows the
42 factory pattern, but it requires an instance of the model for which the parameters are created
43 because of numerous dependencies between objects and IDs. It uses the unit factory (see
44 below) to derive the units of new parameters. This class also annotates all newly created
45 parameter objects with SBO terms.
46

47 **SubmodelController** SBMLsqueezer never modifies the original model data structure. Inter-
48 nally, this controller creates a minimal copy of the model, only comprising those reactions
49 with dependent model components (required species, compartments, parameters, units, etc.)
50
51
52
53
54
55
56
57
58
59
60

4.1 Using SBMLsqueezer as an equation generator library

that are needed to work with the currently selected set of reactions. In the GUI, the user can typically select one or all reactions of a model. This class is more powerful, as it could potentially generate a sub-model for an arbitrary set of reactions with all required other components of the model. It hence generates a restricted clone of the model.

ReactionType This class determines the base type of a given reaction and contains the algorithms that select appropriate rate laws or the most suitable rate law. It also removes substances from the reaction if these belong to the group of substances from the ignore list (see table 5.1 on page 61).

UnitFactory This factory class generates unit definition objects and IDs for unit definitions, which are to be assigned to parameters and numbers in kinetic expressions.

With these classes at hand, new kinetic equations can be created for arbitrary reactions. The example in listing 4.1 on page 34 demonstrates how a convenience rate law (Liebermeister and Klipp, 2006) can be assigned to a selected reaction in an SBML file. This type of rate equation can be applied to reversible as well as to irreversible enzyme-catalyzed reactions and has been found to be particularly useful when no specific information about reaction mechanisms is known (Dräger *et al.*, 2007a, 2009a; Dräger, 2011).

```
1  /**
2   * Reads a given SBML file, creates a convenience rate law for the first
3   * reaction within that file, and stores the result in the second file.
4   *
5   * @param args absolute or relative paths to two SBML files (in and out)
6   * @throws Throwable
7   */
8  public static void main(String args[]) throws Throwable {
9      // Select an SBML reaction object from your SBML document
10     SBMLDocument doc = SBMLReader.read(new File(args[0]));
11     Model model = doc.getModel();
12     Reaction reaction = model.getReaction(0);
13
14     // Create and run the kinetic law generator
15     KineticLawGenerator klg = new KineticLawGenerator(model);
16     // This operates on a copy of the model that only contains one reaction
17     klg.createKineticLaw(
18         reaction,                      // the selected reaction
19         ConvenienceKinetics.class,    // the type of rate law to be created
20         false,                        // whether to set the reaction reversible
21         TypeStandardVersion.cat,     // type parameter for modular rate laws
22         UnitConsistencyType.amount,  // how to ensure unit consistency
23         1d);                         // the value for new parameters
24
25     // Transfer the rate law from the model copy to the original model
26     klg.storeKineticLaws();
27
28     // Save the result in another file
```

4 Advanced program features

```
29     SBMLWriter.write(doc, new File(args[1]), '□', (short) 2);  
30 }
```

Listing 4.4: Assignment of a kinetic law to a reaction via the API of SBMLSqueezer 2

4.2 Querying SABIO-RK and merging the results into a local SBML document

The command-line mode for the interface to SABIO-RK is implemented in the class `ConsoleWizard`. This class is located in the package `org.sbml.squeezer.sabiork.wizard.console`. The following example shows how to query for rate equations in SABIO-RK by using SBMLSqueezer's API. The search can either comprise all reactions or just the reactions in a model. All search terms that can be applied to the model are listed at the beginning of the source-code example. The KEGG (Kanehisa and Goto, 2000) ID of a reaction is automatically added to the search terms (compare section 3.6.1 on page 20). A found kinetic law is added to a reaction if all contained elements can be matched to SBML elements in the model.

```
1  /**  
2   * Reads a given SBMLDocument and runs the console mode. The reactions  
3   * are searched by their KEGG term and additional search terms.  
4   *  
5   * @param args  
6   *         absolute or relative paths to two SBML files (input and output)  
7   */  
8  public static void main(String[] args) throws Throwable{  
9      // The different search terms can be set here (null means that the term  
10     // is not used).  
11     String pathway = null;  
12     String tissue = null;  
13     String organism = null;  
14     String cellularLocation = null;  
15     Boolean isWildtype = true;  
16     Boolean isMutant = true;  
17     Boolean isRecombinant = false;  
18     Boolean hasKineticData = true;  
19     Double lowerpHValue = 7.9d;  
20     Double upperpHValue = 14d;  
21     Double lowerTemperature = -10d;  
22     Double upperTemperature = 115d;  
23     Boolean isDirectSubmission = true;  
24     Boolean isJournal = true;  
25     Boolean isEntriesInsertedSince = false;  
26     String dateSubmitted = "15/10/2008";  
27  
28     boolean overwriteExistingRateLaws = true;  
29 }
```

```
1  
2  
3  
4       4.2 Querying SABIO-RK and merging the results into a local SBML document  
5  
6  
7       30     // Read the SBMLDocument  
8       31     SBMLDocument doc = SBMLReader.read(new File(args[0]));  
9  
10      32     // Run the console mode  
11      33     SABIORKWizard.getResultConsole(doc, overwriteExistingRateLaws,  
12           pathway, tissue, organism,  
13           cellularLocation, isWildtype, isMutant, isRecombinant,  
14           hasKineticData, lowerpHValue, upperpHValue, lowerTemperature,  
15           upperTemperature, isDirectSubmission, isJournal,  
16           isEntriesInsertedSince, dateSubmitted);  
17  
18      39     // Save the changed document  
19      40     SBMLWriter.write(doc, new File(args[1]), '□', (short) 2);  
20      41     }  
21
```

Listing 4.5: SABIO-RK query for the reactions of a model

You can also launch the GUI of the SABIO-RK wizard by using SBMLsqueezer's API. The following source-code example demonstrates how to do so.

```
1       /**  
2        * Runs the wizard  
3        *  
4        * @param input the input file  
5        * @param output the output file  
6        */  
7      public static void runGUI(final File input, final File output) {  
8       try {  
9        UIManager.setLookAndFeel(UIManager.getSystemLookAndFeelClassName());  
10      } catch (Exception exc) {  
11       exc.printStackTrace();  
12      }  
13      final JFrame frame = new JFrame("SBMLsqueezer");  
14      frame.setLayout(new BorderLayout());  
15      frame.setMinimumSize(new Dimension(300, 300));  
16  
17      JButton buttonWizard = new JButton("Open SABIO-RK Wizard");  
18      buttonWizard.addActionListener(new ActionListener() {  
19       @Override  
20       public void actionPerformed(ActionEvent e) {  
21        SBMLDocument result = null;  
22        try {  
23          result = SABIORKWizard.getResultGUI(frame,  
24           ModalityType.APPLICATION_MODAL,  
25           SBMLReader.read(input), true).getSBMLDocument();  
26        } catch (XMLStreamException e1) {  
27          e1.printStackTrace();  
28        } catch (IOException e1) {  
29          e1.printStackTrace();  
30        }  
31        try {  
32          
```

1
2
3
4 *4 Advanced program features*
5
6

```

7
8         if (result != null) {
9             SBMLWriter.write(result, output, '□', (short) 2);
10       }
11      } catch (SBMLError e1) {
12         e1.printStackTrace();
13      } catch (XMLStreamException e1) {
14         e1.printStackTrace();
15      } catch (IOException e1) {
16         e1.printStackTrace();
17      }
18     }
19   });
20
21   frame.add(buttonWizard, BorderLayout.NORTH);
22   frame.setVisible(true);
23 }
```

23 *Listing 4.6: Calling the SABIO-RK wizard*
24
25
26

27 **4.3 Command-line arguments**
28
29

30 All functions of the program SBMLSqueezer are also available as command-line arguments. SB-
31 MLSqueezer is therefore fully functional even if you do not use its GUI. This can be useful if you
32 like to generate kinetic equations, units, and parameter objects for a large number of SBML files
33 in a loop or in a more complex schedule. To benefit from this functionality, just open a command
34 line window on your operating system, e.g., execute the cmd.exe in Microsoft Windows or open a
35 terminal window in Unix (incl. Linux and Mac OS X).

36 It should also be noted that the command line options impact the GUI. It is hence possible
37 to use command-line options in order to launch SBMLSqueezer with a pre-defined configuration.
38 However, you should note that if you pass a command-line argument to SBMLSqueezer, it might
39 assume that you intend to use the program in the pure command-line mode and hence will not
40 launch the GUI. In this case, you will need to also pass the command-line option --gui=true or
41 just --gui to the program.

42 **4.3.1 Program usage**
43
44

45 You can start the application on all operating systems by typing
46

```
47     java -jar SBMLSqueezer.jar [options]
```

48 *Listing 4.7: Launching SBMLSqueezer from the command-line*
49
50

51 on your command prompt. Please note that you might have to change SBMLSqueezer.jar for the
52 real name of the JAR file, e.g., SBMLSqueezer_v2.0.1_incl-libs.jar. For future versions of
53
54
55
56
57

4.3 Command-line arguments

SBMLsqueezer the name of the JAR file could also change, because it usually includes the version number.

In most cases, SBMLsqueezer needs more than 128 MB memory, so it might be convenient to create a shortcut and start the application with as much memory as available. If you have 2 GB RAM, for example, you might want to start the application with the following command:

```
java -Xms128m -Xmx1400M -jar SBMLsqueezer.jar [options]
```

Listing 4.8: Launching SBMLsqueezer from the command-line with increased heap size

How much memory you actually need strongly depends on the size of your input datasets. Under Microsoft Windows you might want to type `javaw` instead of `java` in order to be able to close the command-line window while the program is running. This feature is particularly useful when writing a batch script to launch SBMLsqueezer with your favorite command-line arguments.

Use the following program parameters to lists all available options of SBMLsqueezer: `--help` or `-?`. The subsequent sections describe all available options of SBMLsqueezer version 2.0.1.

SBMLsqueezer's entire user interface (the GUI as well as the command line) is equipped with language packs for German and English, and partially for Chinese (Mandarin). By default the program checks your system's configuration and loads the language pack of your operating system. The fallback language is English. You can also purposely choose the language of the user interface by passing the language parameter as an argument to the Java™ Virtual Machine (JVM). To this end use the following launch command

```
java -Xms128m -Xmx1400M -Duser.language=en -jar SBMLsqueezer.jar [options]
```

Listing 4.9: Launching SBMLsqueezer with an alternative language pack

if you want to launch the program with an English user interface. For German use `de`, and `zh` for Chinese.

4.3.2 Input/output options

`--sbml-in-file[|=]<File>` Specifies the SBML input file. Default value: none

`--sbml-out-file[|=]<File>` Specifies the file where SBMLsqueezer writes its SBML output. Default value: none

`--try-loading-libsbml` If selected, the application will try to load the library libSBML for reading and writing SBML files, otherwise everything will be done with JSBML only, i.e., pure Java™ and therefore platform independent. Default value: `false`

4.3.3 Basic configuration

With the options introduced in this section, you can specify which assumptions SBMLsqueezer should make when values or information are missing, i.e., if the model is lacking more informa-

4 Advanced program features

tion than just kinetic equations. You can also specify how to interpret the model and when error messages should be displayed.

General Options

The behavior of SBMLSqueezer can be specified by the following options, for instance, to decide if error messages should be displayed under certain circumstances.

--overwrite-existing-rate-laws[|=]<Boolean> If this flag is set to true, a new rate law will be created for each reaction irrespective of whether there is already a rate law assigned to this reaction or not. If false, new rate laws are only generated if missing in the SBML file. Note that if this option is checked, already existing kinetic laws will be overwritten. Default value: true

--set-boundary-condition-for-genes[|=]<Boolean> If true, the boundary condition of all species that represent gene-coding elements, such as genes or gene-coding regions, will be set to true. Default value: true

--all-reactions-as-enzyme-catalyzed[|=]<Boolean> If true, all reactions within the network are considered to be enzyme-catalyzed reactions. If false, an explicit enzymatic catalyst must be assigned to a reaction to obtain this status. Default value: true

--remove-unnecessary-parameters-and-units[|=]<Boolean> If true, parameters and units that are never referenced by any element of the model are automatically deleted after creating kinetic equations. Default value: true

--new-parameters-global If true, all parameters are stored globally for the whole model. Otherwise the majority of parameters is stored locally for the respective kinetic equation they belong to. Note that some parameters represent global properties of the entire model and should therefore be always stored in the global list of parameters. In this way, these parameters are valid within the entire model. Default value: false

--warnings-for-too-many-reactants[|=]<Boolean> If true, warnings will be displayed for reactions with an unrealistic number of reactants. The maximal number of reactants that are believed to be still realistic can be defined if this option is selected. Default value: true

--show-sbml-warnings[|=]<Boolean> If true, SBML warnings are displayed. These warnings are mainly the result of a syntactical model check and do not give much information about the semantic correctness of your model. Since the SBML library performs this check, SBMLSqueezer cannot influence the content of the syntax check. Note that this option only works properly if you use libSBML as your SBML back-end, because JSBML does not provide a full validity check for SBML models. Default value: true

4.3 Command-line arguments

7 **--read-from-sabio-rk[|=]<Boolean>** This option lets the user choose whether to search
8 for experimentally obtained rate laws in the reaction kinetics database SABIO-RK. Note
9 that performing this search requires an active Internet connection. Default value: true
10
11

12 Default values

13
14 The options in this group allow you to specify several default values to be applied for components
15 of the model. This is done in addition to the actual rate law generation, such as the default com-
16 partment size, etc., and to define model wide settings to be taken into account when creating rate
17 equations.
18
19

20 **--max-number-of-reactants[|=]<Integer>** A simultaneous collision of a high number of
21 reactants just by chance is very unlikely. Usually, these reactions proceed in a sequence of
22 separate steps, each involving only very few molecules. Here you can specify the maximal
23 number of reactants so that the reaction is still considered plausible. Note that this option is
24 only available if you decide that this kind of warning should be displayed. Default value: 3
25
26

27 **--default-compartment-spatial-dim[|=]<Double>** If no spatial dimensions are defined
28 for a compartment, the value defined by this option will be used as a default. Default value:
29 3.0
30

31 **--default-compartment-size[|=]<Double>** For compartments that are not yet initialized,
32 SBMLsqueezer will use this value as the default initial size. Default value: 1.0
33

34 **--default-species-init-val[|=]<Double>** If species are not yet initialized, SBMLsqueezer
35 will use this value as initial amount or initial concentration of the species. Which kind of
36 quantity is used, depends on whether the species has only substance units. This means, for
37 species that are to be interpreted in terms of concentration, an initial concentration will be set,
38 whereas an initial amount will be set if the species is to be interpreted in terms of molecule
39 counts. Default value: 1.0
40
41

42 **--default-new-parameter-val[|=]<Double>** Here you can specify the default value that is
43 set for newly created parameters. Default value: 1.0
44

45 **--default-species-has-only-substance-units[|=]<Boolean>** This option allows users
46 to specify that the numerical value of a species should be interpreted as a value given in
47 substance units in cases where this has not yet been defined. If not selected, species with
48 undefined meaning will be conceived as a quantity in concentration units. Default value:
49 true
50
51

52 **--ignore-these-species-when-creating-laws[|=]<String>** This option allows the user
53 to ignore species that are annotated with the given compound IDs when creating rate laws
54 for reactions that involve these species. For instance, water or single protons can often be
55
56
57
58
59
60

4 Advanced program features

ignored when creating rate equations, hence simplifying the resulting rate equations. Pre-selected are the KEGG (Kanehisa and Goto, 2000) compound IDs for several ions and small molecules, including water and protons. See table 5.1 on page 61 for details. Default value: C00001, C00038, C00070, C00076, C00080, C00175, C00238, C00282, C00291, C01327, C01528, C14818, C14819

Species to be treated as enzymes

In many situations, it is not clear, which kinds of chemical species can be considered an enzyme. The following options allow you to select, which kind of species SBMLSqueezer should interpret as an enzyme when acting as a catalytic modifier of a reaction.

--possible-enzyme-antisense-rna[|=]<Boolean> If this is set to true, anti-sense Ribonucleic Acid (RNA) molecules are treated as enzymes when catalyzing a reaction. If false anti-sense RNA molecule catalyzed reactions are not considered to be enzyme-catalyzed reactions. Default value: false

--possible-enzyme-complex[|=]<Boolean> If checked, complex molecules are treated as enzymes when catalyzing a reaction. Otherwise, complex-catalyzed reactions are not considered to be enzyme reactions. Default value: true

--possible-enzyme-generic[|=]<Boolean> If true, generic proteins are treated as enzymes when catalyzing a reaction. Otherwise, generic protein-catalyzed reactions are not considered to be enzyme reactions. Default value: true

--possible-enzyme-macromolecule[|=]<Boolean> If this option is selected, species that are annotated as macromolecules are treated as enzymes when catalyzing a reaction. Otherwise, macromolecule-catalyzed reactions are not considered enzyme reactions. If a modifier of a reaction that is annotated as an enzymatic catalyst refers to a macromolecule but this option is not active, SBMLSqueezer will reduce the modifier to a simple catalyst. Default value: true

--possible-enzyme-receptor[|=]<Boolean> If true, receptors are treated as enzymes when catalyzing a reaction. If false, receptor-catalyzed reactions are not considered to be enzyme reactions. Default value: false

--possible-enzyme-rna[|=]<Boolean> If true, RNA is treated as an enzyme when catalyzing a reaction. Otherwise RNA-catalyzed reactions are not considered to be enzyme-catalyzed reactions. Default value: true

--possible-enzyme-simple-molecule If true, simple molecules are treated as enzymes when catalyzing a reaction. If false, simple molecule-catalyzed reactions are not considered to be enzyme reactions. Default value: false

4.3 Command-line arguments

```
1  
2  
3  
4  
5  
6  
7 --possible-enzyme-truncated[ |=]<Boolean> If true, truncated proteins are treated as  
8 enzymes when catalyzing a reaction. Otherwise, truncated protein-catalyzed reactions are  
9 not considered to be enzyme reactions. Default value: true  
10  
11 --possible-enzyme-unknown If true, unknown molecules are treated as enzymes when cat-  
12 alyzing a reaction. If false, unknown molecule-catalyzed reactions are not considered to  
13 be enzyme reactions. Default value: false  
14  
15
```

16 How to ensure unit consistency

```
17  
18 Unit consistency is an important property for kinetic models. In SBML, the kinetics of all reactions  
19 should be defined so that these can be evaluated to units of substance per time. Since Level 3, the  
20 extend units of a model can be defined. Since then, evaluating reactions should result in extend  
21 units per time units. The main difficulty when dealing with units are transport reactions and the  
22 ability to specify reactive species in terms of molecule counts (amounts) or concentration units,  
23 which is amounts per size. In addition, the sizes of compartments do not necessarily have to be  
24 three dimensional. In SBML, the spatial dimensions do not have to be integers either. However,  
25 SBMLSqueezer contains several complex algorithms to determine appropriate units for newly gen-  
26 erated parameters and to incorporate the sizes of surrounding compartments into the generated rate  
27 laws. Here you can specify how to do that.  
28  
29
```

```
30  
31 --type-unit-consistency[ |=]<UnitConsistencyType> This option ensures unit consis-  
32 tency and can attain two different values: Choose amount to bring each occurrence of a par-  
33 ticipating species to a substance unit. Depending on whether the species has only substance  
34 units or not it might be necessary to multiply the species with the size of its surrounding com-  
35 partment. Choose concentration to bring each participating species to concentration units. In  
36 this case the species will be divided by the surrounding compartment size in a kinetic equa-  
37 tions if it is defined to have only substance units. The units of parameters are set accordingly.  
38 All possible values for type <UnitConsistencyType> are: amount and concentration.  
39 Default value: amount  
40  
41
```

42 4.3.4 Rate law selection

```
43  
44 The options in this group allow you to define the rate laws with highest priority when generating  
45 kinetic equations in one single step for an entire network. To this end, SBMLSqueezer defines  
46 several basic types of reactions and provides a list of applicable generic equations for each type.  
47 Special cases of these equations have to be derived for each individual case, also depending on  
48 unit consistency, compartment dimensions, etc. The actual selection of a rate law means that you  
49 can specify, which class of the program SBMLSqueezer should be used to generate a rate law of  
50 this type. You do not need to have deep programming skills for this. All you need to know here  
51 is that the names of the rate laws are a bit more complicated than the actual human-readable  
52 names, because you must specify, how SBMLSqueezer internally names these rate laws. For more  
53  
54
```

4 Advanced program features

advanced users, it might be interesting to know that SBMLsqueezer uses the concept known as *reflection* to select its kinetic equations.

Furthermore, you can decide how to deal with information about reversible or irreversible reactions.

Reversibility

These two options are mutually exclusive and their values must not contradict. Use either one of both.

--treat-all-reactions-reversible If true, all reactions are set to reversible before creating new kinetic equations. Otherwise, the information given by the SBML file will be left unchanged. Default value: false

--treat-reactions-reversible-as-given[|=]<Boolean> If checked, the information about reversibility will be left unchanged. Default value: true

Gene regulation kinetics

--kinetics-gene-regulation[|=]<Class> Please specify the default kinetic law to be applied for reactions that are identified to belong to gene-regulatory processes (reactions involving genes, RNA, and proteins), such as transcription or translation. All possible values for type <Class> are:

- org.sbml.squeezer.kinetics.AdditiveModelLinear (general form linear additive model),
- org.sbml.squeezer.kinetics.AdditiveModelNonLinear (general form of the non-linear additive model),
- org.sbml.squeezer.kinetics.NetGeneratorLinear (NetGenerator form of the linear additive model),
- org.sbml.squeezer.kinetics.HillEquation (generalized Hill equation),
- org.sbml.squeezer.kinetics.HillHinzeEquation (Hill-Hinze equation),
- org.sbml.squeezer.kinetics.HillRaddeEquation (Hill-Radde equation),
- org.sbml.squeezer.kinetics.HSystem (H-system equation by Spieth *et al.*, 2006),
- org.sbml.squeezer.kinetics.NetGeneratorNonLinear (NetGenerator form of the non-linear additive model),
- org.sbml.squeezer.kinetics.SSystem (S-System-based kinetic),
- org.sbml.squeezer.kinetics.Vohradsky (Non-linear additive model by Vu and Vohradský, 2007), and

1
2
3
4 **4.3 Command-line arguments**
5
6
7 • org.sbml.squeezer.kinetics.Weaver (non-linear additive model by Weaver *et al.*,
8 1999).
9
10 Default value: org.sbml.squeezer.kinetics.HillHinzeEquation
11
12 **--kinetics-zero-reactants[|=]<Class>** Default rate law with zeroth order reactants. All
13 possible values for type <Class> are:
14 • org.sbml.squeezer.kinetics.AdditiveModelLinear (general form of the lin-
15 ear additive model),
16 • org.sbml.squeezer.kinetics.AdditiveModelNonLinear (general form of the
17 non-linear additive model),
18 • org.sbml.squeezer.kinetics.HillHinzeEquation (Hill-Hinze equation),
19 • org.sbml.squeezer.kinetics.HillRaddeEquation (Hill-Radde equation),
20 • org.sbml.squeezer.kinetics.HSystem (H-system equation by Spieth *et al.*, 2006),
21 • org.sbml.squeezer.kinetics.NetGeneratorLinear (NetGenerator form of the
22 linear additive model),
23 • org.sbml.squeezer.kinetics.NetGeneratorNonLinear (NetGenerator form of
24 the non-linear additive model),
25 • org.sbml.squeezer.kinetics.SSystem (S-System-based kinetic),
26 • org.sbml.squeezer.kinetics.Vohradsky (Non-linear additive model by Vu and
27 Vohradský, 2007),
28 • org.sbml.squeezer.kinetics.Weaver (non-linear additive model by Weaver *et al.*,
29 1999),
30 • org.sbml.squeezer.kinetics.ZerothOrderForwardGMAK (zeroth order forward
31 mass action kinetics), and
32 • org.sbml.squeezer.kinetics.ZerothOrderReverseGMAK (zeroth order reverse
33 mass action kinetics).
34
35 Default value: org.sbml.squeezer.kinetics.ZerothOrderReverseGMAK
36
37 **--kinetics-zero-products[|=]<Class>** Default rate law with zeroth order products All
38 possible values for type <Class> are:
39 • org.sbml.squeezer.kinetics.AdditiveModelLinear (general form of the lin-
40 ear additive model),
41 • org.sbml.squeezer.kinetics.AdditiveModelNonLinear (general form of the
42 non-linear additive model),
43 • org.sbml.squeezer.kinetics.HillHinzeEquation (Hill-Hinze equation),
44 • org.sbml.squeezer.kinetics.HillRaddeEquation (Hill-Radde equation),
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

4 Advanced program features

- org.sbml.squeezer.kinetics.HSystem (Hill-Radde equation),
- org.sbml.squeezer.kinetics.NetGeneratorLinear (NetGenerator form of the linear additive model),
- org.sbml.squeezer.kinetics.NetGeneratorNonLinear (NetGenerator form of the non-linear additive model),
- org.sbml.squeezer.kinetics.SSystem (S-System-based kinetic),
- org.sbml.squeezer.kinetics.Vohradsky (Non-linear additive model by Vu and Vohradský, 2007),
- org.sbml.squeezer.kinetics.Weaver (non-linear additive model by Weaver *et al.*, 1999),
- org.sbml.squeezer.kinetics.ZerothOrderForwardGMAK (zeroth order forward mass action kinetics), and
- org.sbml.squeezer.kinetics.ZerothOrderReverseGMAK (zeroth order reverse mass action kinetics).

Default value: org.sbml.squeezer.kinetics.ZerothOrderReverseGMAK

Reversible rate laws

--type-standard-version[|=]<TypeStandardVersion> This option declares the version of the modular rate laws and can attain the three different values *cat*, *hal*, and *weg* as described in the publication of Liebermeister *et al.* (2010). This option can only be accessed if all reactions are modeled reversibly. All possible values for type <TypeStandardVersion> are: *cat*, *hal*, and *weg*. Default value: *cat*

--kinetics-reversible-non-enzyme-reactions[|=]<Class> Determines the key for the standard kinetic law to be applied for reactions that are catalyzed by non-enzymes or that are not catalyzed at all. The value may be any rate law that implements InterfaceNonEnzymeKinetics All possible values for type <Class> are:

- org.sbml.squeezer.kinetics.GeneralizedMassAction (the generalized mass-action rate law),
- org.sbml.squeezer.kinetics.ZerothOrderForwardGMAK (zeroth order forward mass action kinetics), and
- org.sbml.squeezer.kinetics.ZerothOrderReverseGMAK (zeroth order reverse mass action kinetics).

Default value: org.sbml.squeezer.kinetics.GeneralizedMassAction

--kinetics-reversible-uni-uni-type[|=]<Class> This key defines the default kinetic law to be applied to enzyme-catalyzed reactions with one reactant and one product. All possible values for type <Class> are:

4.3 Command-line arguments

- org.sbml.squeezer.kinetics.CommonModularRateLaw (CM: the common modular rate law),
- org.sbml.squeezer.kinetics.ConvenienceKinetics (convenience kinetics),
- org.sbml.squeezer.kinetics.DirectBindingModularRateLaw (DM: the direct binding modular rate law),
- org.sbml.squeezer.kinetics.ForceDependentModularRateLaw (FM: the force-dependent modular rate law),
- org.sbml.squeezer.kinetics.HillEquation (generalized Hill equation),
- org.sbml.squeezer.kinetics.MichaelisMenten (Michaelis-Menten),
- org.sbml.squeezer.kinetics.PowerLawModularRateLaw (PM: the power-law modular rate law), and
- org.sbml.squeezer.kinetics.SimultaneousBindingModularRateLaw (SM: the simultaneous binding modular rate law).

Default value: org.sbml.squeezer.kinetics.MichaelisMenten

--kinetics-reversible-bi-uni-type[|=]<Class> Choose the type of the default kinetic law for reversible bi-uni reactions (two reactants, one product). All possible values for type <Class> are:

- org.sbml.squeezer.kinetics.CommonModularRateLaw (CM: the common modular rate law),
- org.sbml.squeezer.kinetics.ConvenienceKinetics (convenience kinetics),
- org.sbml.squeezer.kinetics.DirectBindingModularRateLaw (DM: the direct binding modular rate law),
- org.sbml.squeezer.kinetics.ForceDependentModularRateLaw (FM: the force-dependent modular rate law),
- org.sbml.squeezer.kinetics.OrderedMechanism (ordered mechanism),
- org.sbml.squeezer.kinetics.PowerLawModularRateLaw (PM: the power-law modular rate law),
- org.sbml.squeezer.kinetics.RandomOrderMechanism (random order mechanism), and
- org.sbml.squeezer.kinetics.SimultaneousBindingModularRateLaw (SM: the simultaneous binding modular rate law).

Default value: org.sbml.squeezer.kinetics.RandomOrderMechanism

--kinetics-reversible-bi-bi-type[|=]<Class> Select the type of the default kinetic law for reversible bi-bi reactions (two reactants, two products). All possible values for type <Class> are:

4 Advanced program features

- org.sbml.squeezer.kinetics.CommonModularRateLaw (CM: the common modular rate law),
- org.sbml.squeezer.kinetics.ConvenienceKinetics (convenience kinetics),
- org.sbml.squeezer.kinetics.DirectBindingModularRateLaw (DM: the direct binding modular rate law),
- org.sbml.squeezer.kinetics.ForceDependentModularRateLaw (FM: the force-dependent modular rate law),
- org.sbml.squeezer.kinetics.OrderedMechanism (ordered mechanism),
- org.sbml.squeezer.kinetics.PingPongMechanism (Ping-Pong mechanism),
- org.sbml.squeezer.kinetics.PowerLawModularRateLaw (PM: the power-law modular rate law),
- org.sbml.squeezer.kinetics.RandomOrderMechanism (random order mechanism), and
- org.sbml.squeezer.kinetics.SimultaneousBindingModularRateLaw (SM: the simultaneous binding modular rate law).

Default value: org.sbml.squeezer.kinetics.RandomOrderMechanism

--kinetics-reversible-arbitrary-enzyme-reactions[|=]<Class> Arbitrary reversible enzyme reactions. All possible values for type <Class> are:

- org.sbml.squeezer.kinetics.CommonModularRateLaw (common modular rate law, CM),
- org.sbml.squeezer.kinetics.ConvenienceKinetics (convenience kinetics),
- org.sbml.squeezer.kinetics.DirectBindingModularRateLaw (direct binding modular rate law, DM),
- org.sbml.squeezer.kinetics.ForceDependentModularRateLaw (force-dependent modular rate law, FM),
- org.sbml.squeezer.kinetics.PowerLawModularRateLaw (power-law modular rate law, PM), and
- org.sbml.squeezer.kinetics.SimultaneousBindingModularRateLaw (simultaneous binding modular rate law, SM).

Default value: org.sbml.squeezer.kinetics.CommonModularRateLaw

Irreversible rate laws

--kinetics-irreversible-non-enzyme-reactions[|=]<Class> Determines the key for the standard kinetic law to be applied for reactions that are catalyzed by non-enzymes or

4.3 Command-line arguments

7
8 that are not catalyzed at all. The value may be any rate law that implements the inter-
9 face `org.sbml.squeezer.kinetics.InterfaceNonEnzymeKinetics`. All possible val-
10 ues for type `<Class>` are:

- 11 • `org.sbml.squeezer.kinetics.GeneralizedMassAction` (the generalized mass-
12 action rate law),
13
- 14 • `org.sbml.squeezer.kinetics.ZerothOrderForwardGMAK` (zeroth order forward
15 mass action kinetics), and
16
- 17 • `org.sbml.squeezer.kinetics.ZerothOrderReverseGMAK` (zeroth order reverse
18 mass action kinetics).

19 Default value: `org.sbml.squeezer.kinetics.GeneralizedMassAction`

20
21 **--kinetics-irreversible-uni-uni-type[|=]<Class>** This key defines the default kinetic
22 law to be applied to enzyme-catalyzed reactions with one reactant and one product. All pos-
23 sible values for type `<Class>` are:
24

- 25 • `org.sbml.squeezer.kinetics.ConvenienceKinetics` (convenience kinetics),
26
- 27 • `org.sbml.squeezer.kinetics.IrrevCompetNonCooperativeEnzymes` (the irre-
28 versible non-exclusive non-cooperative competitive inhibition),
29
- 30 • `org.sbml.squeezer.kinetics.IrrevNonModulatedNonInteractingEnzymes` (a
31 rate law for irreversible non-modulated non-interacting reactant enzymes),
32
- 33 • `org.sbml.squeezer.kinetics.HillEquation` (generalized Hill equation), and
34
- 35 • `org.sbml.squeezer.kinetics.MichaelisMenten` (Michaelis-Menten).

36 Default value: `org.sbml.squeezer.kinetics.MichaelisMenten`

37
38 **--kinetics-irreversible-bi-uni-type[|=]<Class>** Choose the type of the default ki-
39 netic law for irreversible bi-uni reactions (two reactants, one product). All possible values
40 for type `<Class>` are:
41

- 42 • `org.sbml.squeezer.kinetics.ConvenienceKinetics` (convenience kinetics),
43
- 44 • `org.sbml.squeezer.kinetics.IrrevNonModulatedNonInteractingEnzymes` (a
45 rate law for irreversible non-modulated non-interacting reactant enzymes),
46
- 47 • `org.sbml.squeezer.kinetics.OrderedMechanism` (the ordered mechanism), and
48
- 49 • `org.sbml.squeezer.kinetics.RandomOrderMechanism` (the random order mech-
anism).

50 Default value: `org.sbml.squeezer.kinetics.RandomOrderMechanism`

51
52 **--kinetics-irreversible-bi-bi-type[|=]<Class>** Select the type of the default kinetic
53 law for irreversible bi-bi reactions (two reactants, two products). All possible values for type
54 `<Class>` are:
55

4 Advanced program features

- org.sbml.squeezer.kinetics.ConvenienceKinetics (convenience kinetics),
- org.sbml.squeezer.kinetics.IrrevNonModulatedNonInteractingEnzymes (a rate law for irreversible non-modulated non-interacting reactant enzymes),
- org.sbml.squeezer.kinetics.OrderedMechanism (ordered mechanism),
- org.sbml.squeezer.kinetics.PingPongMechanism (Ping-Pong mechanism), and
- org.sbml.squeezer.kinetics.RandomOrderMechanism (random order mechanism).

Default value: org.sbml.squeezer.kinetics.RandomOrderMechanism

--kinetics-irreversible-arbitrary-enzyme-reactions[|=]<Class> Arbitrary irreversible enzyme reactions All possible values for type <Class> are:

- org.sbml.squeezer.kinetics.ConvenienceKinetics (convenience kinetics) and
- org.sbml.squeezer.kinetics.IrrevNonModulatedNonInteractingEnzymes (a rate law for irreversible non-modulated non-interacting reactant enzymes).

Default value: org.sbml.squeezer.kinetics.IrrevNonModulatedNonInteractingEnzymes

4.3.5 SABIO-RK search options

For querying the content of the SABIO-RK database for experimentally determined kinetic equations, SBMLsqueezer provides a large set of options in order to customize your search.

General options

With these options you can define key options to restrict the results of your search for reaction kinetics in SABIO-RK.

--pathway[|=]<String> Define the pathway for which the kinetics are to be determined.

--tissue[|=]<String> Define the tissue for which the kinetics are to be determined.

--cellular-location[|=]<String> Define the cellular location for which the kinetics are to be determined.

--organism[|=]<String> Define the organism for which the kinetics are to be determined.

4.3.6 SABIO-RK search preferences

General properties

--is-wildtype[|=]<Boolean> Search for wild-type kinetics. Default value: true

--is-mutant[|=]<Boolean> Search for kinetics of mutants. Default value: true

1
2
3
4 4.3 Command-line arguments
5
6
7 **--is-recombinant** Search for kinetics of recombinant organisms. Default value: **false**
8
9 **--has-kinetic-data[|=]<Boolean>** Search for entries containing kinetic data. Default value:
10 **true**
11
12 **--is-direct-submission[|=]<Boolean>** Search for entries directly submitted. Default value:
13 **true**
14
15 **--is-journal[|=]<Boolean>** Search for entries referring to journal publications. Default
16 value: **true**
17
18 **--is-entries-inserted-since** Consider only entries inserted after the specified date. Default
19 value: **false**
20
21
22
23 **Temperature**
24
25 **--lowest-temperature-value[|=]<Double>** The lowest possible temperature for entries (in
26 °C). Arguments must fit into the range [-271.15, 1000]. Default value: -10.0
27
28 **--highest-temperature-value[|=]<Double>** The highest possible temperature for entries
29 (in °C). Arguments must fit into the range [-271.15, 1000]. Default value: 115.0
30
31
32 **Range of pH values**
33
34 **--lowest-ph-value[|=]<Double>** The lowest possible pH value for entries. Arguments must
35 fit into the range [0, 14]. Default value: 0.0
36
37 **--highest-ph-value[|=]<Double>** The highest possible pH value for entries. Arguments
38 must fit into the range [0, 14]. Default value: 14.0
39
40
41 **Date**
42
43 **--lowest-date[|=]<Date>** Define the earliest acceptable date when the entries have been in-
44 serted into SABIO-RK. Default value: Wed Oct 15 00:00:00 PDT 2008
45
46 **4.3.7 Options for the Graphical User Interface**
47
48 The options in this group allow you to influence the behavior of the GUI. This means that you can
49 directly launch SBMLsqueezer with your preferred configuration.
50
51 **--check-for-updates[|=]<Boolean>** Decide whether or not this program should search for
52 updates at start-up. Default value: **true**
53
54 **--gui** If this option is given, the program will display its GUI. Default value: **false**
55
56
57
58
59
60

4 Advanced program features

7
8 **--log-level[|=]<String>** Change the log-level of this application. This option will influence
9 how fine-grained error and other log messages will be that you receive while executing this
10 program. Log messages whose level exceeds the given threshold will also be displayed in
11 the status bar of the GUI. All possible values for type <String> are:

- 12 • ALL: all log messages will be displayed,
- 13 • CONFIG: those log messages related to configuration of the program and less fine-
14 grained will be displayed,
- 15 • FINE: displays simple debugging messages and less fine-grained messages,
- 16 • FINER: the messages that will be displayed are already relevant for more extensive
17 debugging purposes and less fine-grained messages,
- 18 • FINEST: information relevant for intensive debugging the program and less fine-grained
19 will be displayed,
- 20 • INFO: information messages and less fine-grained messages, such as warning messages,
21 will be displayed,
- 22 • OFF: no log messages will be displayed at all,
- 23 • SEVERE: only serious error messages will be displayed, and
- 24 • WARNING: only warnings and serious error messages will be displayed.

25 Default value: INFO

4.3.8 **LaTeX** options

35 The program SBMLsqueezer brings with it a full version of the latest development release of **SBML2**
36 **LaTeX**. Hence, all options provided by this report generator for SBML models can also be applied
37 to SBMLsqueezer. For more information, see the project web site of **SBML2LaTeX**³ and the corre-
38 sponding publication (Dräger *et al.*, 2009b).

LaTeX compiler location

43 **--load-latex-compiler[|=]<File>** The path to the **LaTeX** compiler to generate PDF, DVI or
44 other files from the created **LaTeX** report file. Accepts all files (*). Default value: <current
45 directory>

Report options

50 **--check-consistency** If true, the automatic model consistency check is performed and the
51 results are written in the appendix of the model report file. Note that this might require an
52 active Internet connection. Default value: false

54 ³<http://www.cogsys.cs.uni-tuebingen.de/software/SBML2LaTeX/>

1
2
3
4
5
6
7 **--miriam-annotation[|=]<Boolean>** If true, MIRIAM annotations are included into the
8 model report if there are any. In this case, SBML^{LATEX} generates links to the resources for
9 each annotated element. Default value: true
10
11
12 **--show-predefined-units[|=]<Boolean>** If true, all the predefined unit declarations of
13 the model are made explicit in the report file as these are defined by the corresponding SBML
14 Level and Version. Otherwise only unit definitions from the model are included. Note that
15 this option is only available if the option --include-section-unit-definitions is ac-
16 tive. Default value: true
17
18
19 **--print-full-ode-system** If set to true, the entire rate of change will be written for each
20 species. By default, SBML^{LATEX} only prints the sum of the individual reaction rates, which
21 are hyper-linked but displayed at a different position of the report. Note that this option
22 is only available if the option --include-section-reactions is active. Default value:
23 false
24
25
26 **--clean-workspace** If this option is set to true, all temporary files will be deleted after running
27 SBML^{LATEX}. In case of PDF creation, for instance, this will cause even the T_EX file to be
28 deleted. However, this option can be meaningful to remove all the temporary files created by
29 your system's L^AT_EX compiler. Default value: false
30
31
32

Layout options

33
34 **--landscape** This option decides whether to set the L^AT_EX document in landscape or portrait
35 mode. By default most pages are in portrait format. Default value: false
36
37
38 **--print-names-if-available** If selected, the names of SBML elements (NamedSBase) are
39 displayed instead of their IDs. This can only be done if the element has a name. Default
40 value: false
41
42 **--title-page** If true, a separate title page will be created. By default the title is written as a
43 simple heading on the first page. Default value: false
44
45
46 **--typewriter[|=]<Boolean>** This option decides whether a typewriter font should be applied
47 to highlight SBML IDs. This is particularly important when these occur in mathematical
48 equations. Default value: true
49
50
51 **--reactants-overview-table** If true, the details (ID and name) of all reactants, modifiers
52 and products participating in a reaction are listed in one table. By default a separate table is
53 created for each one of the three participant groups including its SBO term. Note that this
54 option is only available if the option --include-section-reactions is active. Default
55 value: false
56
57
58
59
60

1
2
3
4 4 Advanced program features
5
6
7
8

Typographical options

9 **--font-headings[|=]<SansSerifFont>** Allows to select the font of captions and other (by
10 default sans serif) text. All possible values for type <SansSerifFont> are:

- `avant` (sample in Avant Garde),
- `cmss` (sample in Computer Modern Sans Serif), and
- `helvetica` (sample in Helvetica).

16 Default value: `helvetica`

18 **--font-size[|=]<Short>** This option allows you to select the size of the standard text font.
19 Headings appear with a larger font. All possible values for type <Short> are: 8, 9, 10, 11,
20 12, 14, and 17. Default value: 11

22 **--font-text[|=]<SerifFont>** Allows to select the font of continuous text. Choosing `times`
23 is actually not recommended because in some cases equations might not look as nicely as
24 they do when using `mathptmx`. All possible values for type <SerifFont> are:

- `chancery` (*sample in Chancery*),
- `charter` (sample in Charter),
- `cmr` (sample in Computer Modern Roman),
- `mathptmx` (sample in Times for math),
- `palatino` (sample in Palatino),
- `times` (sample in Times), and
- `utopia` (sample in Utopia).

37 Default value: `mathptmx`

39 **--font-typewriter[|=]<String>** Select a typewriter font that can be used for IDs if option
40 'TYPEWRITER' is selected. URLs and other resources are also marked with this font. All
41 possible values for type <String> are:

- `cmt` (sample in Computer Modern Typewriter) and
- `courier` (sample in Courier).

46 Default value: `cmt`

48 **--paper-size[|=]<PaperSize>** The paper size for L^AT_EX documents. With this option the
49 paper format can be influenced. Default paper size: DIN A4. All sizes a?, b?, c? and d? are
50 European DIN sizes. Letter, legal and executive are US paper formats. All possible values
51 for type <PaperSize> are: letter, legal, executive, a0, a1, a2, a3, a4, a5, a6, a7, a8,
52 a9, b0, b1, b2, b3, b4, b5, b6, b7, b8, b9, c0, c1, c2, c3, c4, c5, c6, c7, c8, c9, d0, d1, d2,
53 d3, d4, d5, d6, d7, d8, and d9. Default value: letter

4.3 Command-line arguments

Content of the report

```
1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60
```

--include-section-compartment-types[|=]<Boolean> This option decides whether or not a section about compartment types should be included in the resulting model report. Note that this option only causes an effect if the model contains compartment type declarations. Default value: true

--include-section-compartments[|=]<Boolean> This option decides whether or not a section about compartments should be included in the resulting model report. Note that this option only causes an effect if the model contains compartment declarations. Default value: true

--include-section-constraints[|=]<Boolean> This option decides whether or not a section about constraints should be included in the resulting model report. Note that this option only causes an effect if the model contains constraint declarations. Default value: true

--include-section-events[|=]<Boolean> This option decides whether or not a section about events should be included in the resulting model report. Note that this option only causes an effect if the model contains event declarations. Default value: true

--include-section-function-definitions[|=]<Boolean> This option decides whether or not a section about function definitions should be included in the resulting model report. Note that this option only causes an effect if the model declares any function definitions. Default value: true

--include-section-initial-assignments[|=]<Boolean> This option decides whether or not a section about initial assignments should be included in the resulting model report. Note that this option only causes an effect if the model declares any initial assignments. Default value: true

--include-section-parameters[|=]<Boolean> This option decides whether or not a section about parameters should be included in the resulting model report. Note that this option only causes an effect if the model declares any parameters. Default value: true

--include-section-reactions[|=]<Boolean> This option decides whether or not a section about reactions should be included in the resulting model report. Note that this option only causes an effect if the model declares any reactions. Furthermore, this option also decides if a summary of the differential equation system that is implied by the given model should be generated. Again, this will only cause an effect if the model contains any species. Default value: true

--include-section-rules[|=]<Boolean> This option decides whether or not a section about rules should be included in the resulting model report. Note that this option only causes an effect if the model declares any rules, no matter if these are of algebraic, assignment or rate rule type. Default value: true

4 Advanced program features

1
2
3
4
5
6
7 **--include-section-species[|=]<Boolean>** This option decides whether or not a section
8 about the species in the given model should be included in the resulting model report. Note
9 that this option only causes an effect if the model declares any species. Default value: true
10
11 **--include-section-species-types[|=]<Boolean>** If this option is selected, a section about
12 species types will occur in the model report. Otherwise, this section will be excluded from
13 the report. Default value: true
14
15 **--include-section-unit-definitions[|=]<Boolean>** This option decides whether or not
16 a section about the unit definitions of the given model should be included in the resulting
17 model report. Note that this option only causes an effect if the model declares any unit def-
18 initions. However, in some level/version combinations SBML models contain predefined
19 unit definitions which might be included in the model report if this option is active. Default
20 value: true
21
22
23

24 Additional options

25
26 **--include-section-layouts[|=]<Boolean>** Include a section with images of model lay-
27 outs if these are available. Default value: true
28
29

30 4.3.9 Garuda options

31 Garuda is a software framework that allows multiple applications (gadgets) to communicate with
32 each other by sharing data files. In addition, you can launch an application from Garuda, query for
33 tools with specific aims and much more. Since version 2.0, SBMLSqueezer can also be used as a
34 gadget in Garuda.
35

36
37 **--connect-to-garuda[|=]<Boolean>** Decides whether or not the current application should
38 attempt to connect to the Garuda Core. Default value: true
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

5 Supported rate laws

The kinds of equations supported by the program are numerous, including traditional approaches (Guldberg and Waage, 1879; Michaelis and Menten, 1913) just like very recent equations (Liebermeister and Klipp, 2006; Liebermeister *et al.*, 2010). It provides equations for gene-regulatory processes (Hinze *et al.*, 2007; Radde and Kaderali, 2007; Töpfer *et al.*, 2007; Vu and Vohradský, 2007; Weaver *et al.*, 1999) and approximative rate laws (Savageau, 1969). In addition, SBMLsqueezer covers a large variety of standard rate laws for biochemical reactions from relevant text books (Segel, 1993; Heinrich and Schuster, 1996; Bisswanger, 2000; Cornish-Bowden, 2004). Here, we give a short overview of all equations that are currently implemented in SBMLsqueezer, ordered by the categories metabolic or gene-regulatory. For a detailed description of all rate laws, see the PhD thesis of Dräger, 2011. However, the actual algorithm that suggests applicable rate laws is more complex and considers several features of the reaction. It can therefore happen that SBMLsqueezer suggests multiple different rate equations for the same reaction.

5.1 Rate laws for metabolic processes

- (Generalized) mass-action rate law with numerous orders (Guldberg and Waage, 1879; Heinrich and Schuster, 1996, p. 16), a rate law that has also been shown to be useful as an approximation for more complex mechanisms (Dräger *et al.*, 2007b, 2009a)
- Uni-uni Michaelis-Menten kinetics (Michaelis and Menten, 1913)
- Irreversible non-modulated non-interacting reactant enzymes (see SBO)
- Bi-uni enzyme mechanisms (Segel, 1993; Bisswanger, 2000; Cornish-Bowden, 2004)
 - Random-order mechanism
 - Ordered mechanism
- Bi-bi enzyme reactions (Segel, 1993; Bisswanger, 2000; Cornish-Bowden, 2004)
 - Random-order mechanism (Cornish-Bowden, 2004, p. 169)
 - Ordered mechanism
 - Ping-pong mechanism
- Modular rate laws for enzymatic reactions (Liebermeister *et al.*, 2010)

5 Supported rate laws

- Power-law modular rate law (PM)
- Common modular rate law (CM)
- Direct binding modular rate law (DM)
- Simultaneous binding modular rate law (SM)
- Force-dependent modular rate law (FM)
- Convenience kinetics (Liebermeister and Klipp, 2006)
 - Thermodynamically dependent form
 - Thermodynamically independent form
- (Generalized) Hill equation (Hill, 1910; Cornish-Bowden, 2004, p. 314)

5.2 Rate laws for gene-regulatory processes

- Hill-Hinze equation (Hinze *et al.*, 2007)
- Hill-Radde equation (Radde and Kaderali, 2007; Radde, 2007)
- Linear additive network models
 - General form
 - NetGenerator form (Töpfer *et al.*, 2007)
- Non-linear additive network models
 - General form
 - NetGenerator form (Töpfer *et al.*, 2007)
 - Vohradský's equation (Vu and Vohradský, 2007)
 - Weaver's equation (Weaver *et al.*, 1999)
- S-systems (Savageau, 1969; Spieth *et al.*, 2004; Tournier, 2005; Spieth *et al.*, 2006; Hecker *et al.*, 2009)
- H-systems (Spieth *et al.*, 2006)

5.2 Rate laws for gene-regulatory processes

Table 5.1: KEGG IDs of small molecules and ions. This table gives the default list of all small molecules and ions that are ignored by SBMLsqueezer when creating kinetic equations. This list was created according to Blum (2009).

Chemical formula	Common name	KEGG ID
H ₂ O	Water	C00001
Zn ²⁺	Zinc ion	C00038
Cu ²⁺	Copper ion	C00070
Ca ²⁺	Calcium ion	C00076
H ⁺	Proton	C00080
Co ²⁺	Cobalt ion	C00175
K ⁺	Potassium ion	C00238
H ₂	Hydrogen	C00282
Ni ²⁺	Nickel ion	C00291
Cl ⁻	Chloride ion	C00698
HCl	Hydrochloric acid	C01327
H ₂ Se	Hydrogen selenide	C01528
Fe ²⁺	Iron (II) ion	C14818
Fe ³⁺	Iron (III) ion	C14819

6 Algorithms and software design

This chapter describes aspects of the algorithmic concepts in SBMLSqueezer (Dräger, 2011). The focus is not on source code or concrete implementation. The purpose of this chapter is rather to explain *a*) how the program's architecture is designed; *b*) how it makes its choices in order to select applicable rate equations for reactions of interest; *c*) which criteria the program uses in order to compare reactions in the local model to the content of SABIO-RK (Wittig *et al.*, 2012) and subsequently extracts further information. For a correct use of the program an understanding of these methods is recommendable.

6.1 Software architecture

SBMLSqueezer has been planned and implemented as a modular program that follows established software design patterns, such as the Model-View-Controller pattern, and hence strictly discriminates between its (graphical or command-line) user interface, its data model, algorithms, etc. A schematic of the program's design can be seen in fig. 6.1 on the next page.

SBMLSqueezer consists of a core package that provides a general infrastructure for the program. The core deals with user preferences and command-line arguments (see section 4.3 on page 40), and searches for online updates. Furthermore, the core is responsible to launch the program. This can be done in diverse ways, e.g., in command line mode, as a plug-in of CellDesigner, as a gadget in Garuda, etc.

The internal data structure of the program is provided by JSBML (Dräger *et al.*, 2011). Converters can read and write input SBML documents through libSBML (Bornstein *et al.*, 2008) or CellDesigner's API (Funahashi *et al.*, 2008), or JSBML can directly parse these files. In this way, JSBML acts as an abstraction layer between diverse forms of input and synchronizes all changes made by the program back to the original source. In case that JSBML is being directly used, the synchronization step can be omitted.

A graphical user interface can be launched from the core and has then control over all functions of the program. For details about which functions are available and how to use the user interface, see chapter 3 on page 10.

All implemented rate laws are gathered in the kinetics package and are grouped by twelve interfaces that are described in section 6.2 on the facing page. For version 2, a new SABIO-RK package has been implemented that obtains kinetic equations from the rate law database SABIO-RK (Wittig *et al.*, 2012). A mathematics package contains an implementation of the Gaussian rank calculation, which is required for convenience rate laws (Liebermeister and Klipp, 2006).

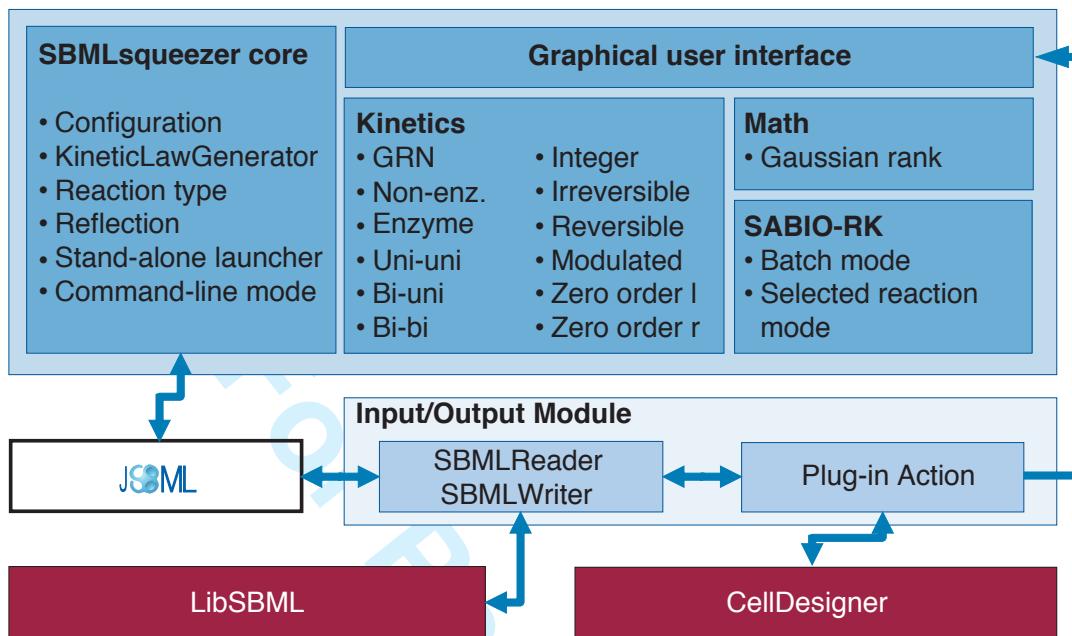


Figure 6.1: Architecture of SBMLSqueezer. The program is organized in several modules that use JSBML as internal data structure. A compatibility layer enables the program to be used based on libSBML, CellDesigner, or as a stand-alone tool (also embedded in Garuda, an online program, etc.). Modified and updated from Dräger (2011).

6.2 Rate law selection

MIRIAM (Le Novère *et al.*, 2005; Laible and Le Novère, 2007; Juty *et al.*, 2012, 2013) and SBO annotations (Courtot *et al.*, 2011) constitute the main sources of information for SBMLSqueezer in order to make its choices. Models can also be evaluated if no such information is given. However, in these cases the program will most likely make different assignments compared to a fully annotated model. When used as CellDesigner plug-in, SBO terms are inferred from the CellDesigner-specific annotations of modifiers and further elements.

At first, the algorithm creates a submodel that only comprises those reactions for which rate laws are to be created. All relevant model components, such as species, compartments, units, etc. are copied into this submodel. Operating on this trimmed copy of the full model has the advantage that changes of the algorithm do not affect the original data structure and can be easily disregarded. When creating this submodel, the algorithm also checks if fall-back units are defined for all components. This is crucial in order to avoid problems in later steps. Depending on which units are missing, it generates units for area, reaction extend, length, substance, time, and volume just as the default units in SBML Level 2 Version 4 (Hucka *et al.*, 2008) would be defined. All subsequent steps can hence assume that every model component has a defined unit.

1
2
3
4
5
6 6 Algorithms and software design

7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
Table 6.1: Kinds of species that can potentially act as enzymes and their top-level SBO terms. These SBO terms correspond to the annotation of the actual species and therefore define the material classes of potential enzymes. The terms given in this table represent the top-level terms, i.e., the algorithm also accepts each more specialized term for a specific category. Note that the user can exclude elements from this list and therefore influence the algorithm's choices.

Material entity	SBO term
Antisense RNA (asRNA)	SBO:0000317
Complex	SBO:0000253
Generic protein	SBO:0000252
Macromolecule	SBO:0000245
Receptor	SBO:0000244
RNA	SBO:0000250
Simple molecule	SBO:0000247
Truncated protein	SBO:0000248
Unknown molecule	SBO:0000285

The algorithm then iterates through all reactions within the submodel and performs several pre-processing steps, before an appropriate type of rate law can be selected:

1. If the user defines a list of KEGG (Kanehisa and Goto, 2000) IDs for species whose contribution to rate laws should be neglected, species with such terms in their MIRIAM annotation (Le Novère *et al.*, 2005) are removed. Table 5.1 shows the predefined list of those entities.
2. Based on their SBO term (Courtot *et al.*, 2011) attribute all modifiers of the reaction are grouped into the following sets: *a*) enzymes; *b*) activators; *c*) inhibitors; and *d*) non-enzyme catalysts. Since it is not always clear if a catalyst of a reaction is an enzymatic catalyst, the user can define, which kinds of species may be considered enzymes in the specific context. Table 6.1 presents a list of all kinds of species that the algorithm can potentially accept as enzymes of a reaction. The algorithm checks if any modifier of the reaction corresponds to a species with one of the SBO terms in this list. If the modifier is annotated as *catalyst* (SBO:0000013) and its corresponding species belongs to the list of potential enzymes, the algorithm assigns the SBO term *enzymatic catalyst* (SBO:0000460) to the modifier. Based on the user's selection the algorithm hence solves contradictions between the SBO term of a modifier and the corresponding species.
3. The stoichiometry of each reaction participant is analyzed in order to obtain the accumulated stoichiometry of reactants and products and to answer the question if all values are integers. In this step the algorithm also analyzes the SBO term (Courtot *et al.*, 2011) attribute of each reaction participant. Further top-level SBO terms with relevance to the algorithm can be found in Table 6.2. The aim of this step is to get hints if the reaction represents a transcription or translation:
 - If a reactant represents a gene or gene-coding region, the reaction could be a transcription.
 - If the reaction involves a reactant that stands for an RNA or Messenger RNA (mRNA) molecule it could be a translation.

6.2 Rate law selection

- If at least one modifier represents a gene or RNA molecule, the reaction could represent a translation.

Figure 6.2b depicts these processes in a simple schematic based on the Systems Biology Graphical Notation (SBGN) recommendations. The algorithm recognizes these reaction patterns only based on the stoichiometry and SBO term annotation of all participants.

4. In order to ensure that the algorithm can process each reaction within the submodel, it checks the following semantic rules:

- If a reaction involves a gene or gene-coding region as reactant or its set of reactants is *empty* and all products are RNA molecules, the reaction is recognized as transcription.
- If the substrate species of a reaction are RNA molecules or the reaction does not have any reactants and all products are forms of protein or poly-peptide chains, the reaction is recognized as translation.
- If the stoichiometry of reactants and products is unity, the reaction can only be categorized as transcription if the only reactant is a gene or gene-coding region and it is only a valid translation if the only reactant is an RNA molecule. Depending on user preferences, the algorithm can set the boundary condition for each gene as part of this step.

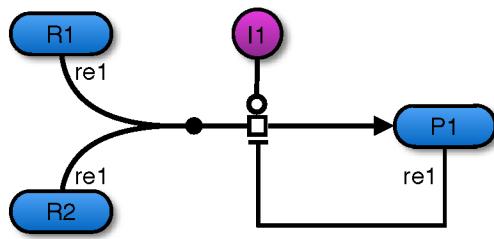
Note that a list of reactants or products is said to be *empty* if either *a*) no such list exists; *b*) no element has been assigned to this list; *c*) the stoichiometry of each element within the list is zero; or *d*) if each element in the list is annotated with an SBO term derived from the term for *empty set* (SBO:0000291).

After having reaction preprocessing and semantic checking completed, the algorithm assigns a list of applicable categories to each reaction within the submodel. The algorithm distinguishes between the following twelve such categories, which are not necessarily exclusive:

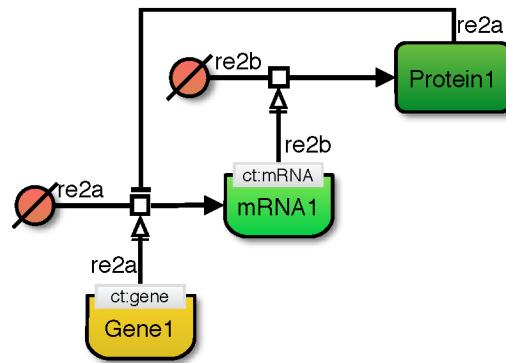
1. Non-enzyme reactions (fig. 6.2a)
2. Gene-regulatory processes (fig. 6.2b)
3. Uni-uni enzyme reactions (fig. 6.2c)
4. Bi-uni enzyme reactions (fig. 6.2d)
5. Bi-bi enzyme reactions (fig. 6.2e)
6. Arbitrary enzyme reactions (fig. 6.2f)
7. Integer stoichiometry reactions (fig. 6.2g)
8. Irreversible reactions (fig. 6.2h)
9. Modulated reactions (fig. 6.2i)
10. Reversible reactions (fig. 6.2j)
11. Zeroth reactant order reactions (fig. 6.2k)
12. Zeroth product order reactions (fig. 6.2l)

All kinetic equations are also assigned to one or multiple of these categories. The algorithm may now either collect all appropriate rate laws for the obtained reaction categories (types) or just the one rate law with highest priority. While the first method allows users to interactively

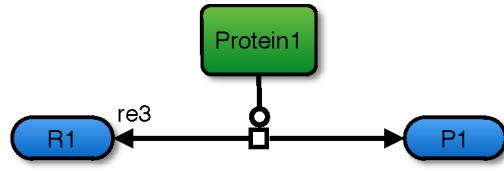
6 Algorithms and software design



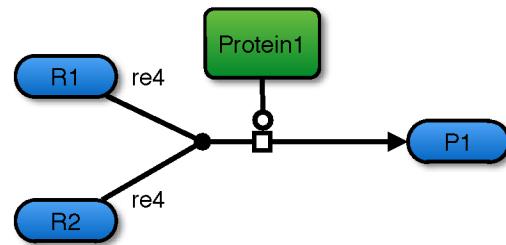
(a) A non-enzyme reaction. The ion “I1” catalyzes this association reaction, which can therefore not be considered enzyme catalyzed. In addition, this reaction is also modulated in a feedback inhibition loop, has an integer stoichiometry, and two reactants.



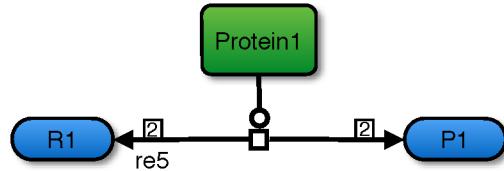
(b) Gene-regulatory processes. Reaction re2a assembles an mRNA molecule from a source of bases (transcription), enabled by the a specific gene. This mRNA in turn (re2b) enables the assembly of a protein from a source of amino acids (translation). In a feedback inhibition loop, the protein interferes with the transcription of its own gene.



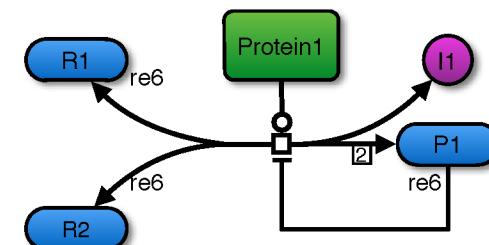
(c) Uni-uni enzyme reaction. This schematic conforms the classical Michaelis-Menten mechanism.



(d) Bi-uni enzyme reaction. This association reaction has an integer stoichiometry.

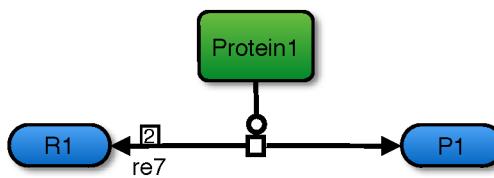


(e) Bi-bi enzyme reaction. In this example, two molecules of identical type act as reactants and also as products, respectively.

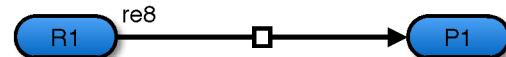


(f) Arbitrary enzyme reaction. This reversible reaction involves a feedback inhibition and a complex stoichiometry, in which an ion and two identical molecules are created from two distinct reactants.

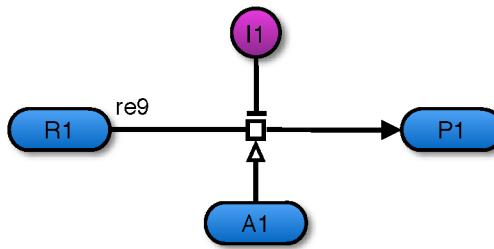
Figure 6.2: Examples for general reaction categories. This figure displays example reactions in SBGN for each of the twelve categories that are used to determine applicable rate equations.



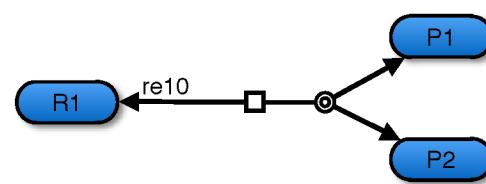
(g) Integer stoichiometry. This reversible, enzyme-catalyzed reaction has two identical reactants and one product.



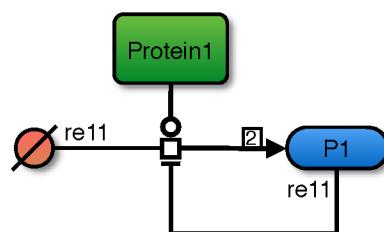
(h) Irreversible reaction. This reaction has no explicit catalyst assigned to it. Depending on user-settings, the algorithm can still consider this an enzyme-catalyzed reaction, assuming that the omission of the catalyst is for the sake of simplicity.



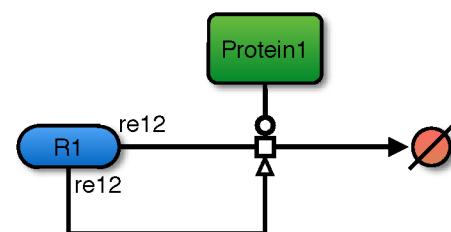
(i) Modulated reaction. Both, a stimulator and an inhibitor interfere with this reaction.



(j) Reversible reaction. This dissociation reaction can also be seen as an association when the equilibrium shifts to the reverse reaction.



(k) Zeroth reactant order reaction. The two product molecules lower the velocity of their own creation.



(l) Zeroth product order reaction. The reactant stimulates its own degradation.

Figure 6.2: Examples for general reaction categories (continued)

6 Algorithms and software design

Table 6.2: SBO terms with relevance for the categorization of reactions. The algorithm uses the SBO terms listed in this table in order to distinguish between different types of species and modification in order to categorize each reaction in the submodel as well as the role of individual reaction participants. This also includes further relevant material entities of reaction participants. Note that the algorithm always checks if the SBO term of an element is a child of a certain reference term in order to also include all more specific sub-terms.

Definition	SBO term
catalyst	SBO:000013
empty set	SBO:0000291
enzymatic catalyst	SBO:0000460
gene	SBO:0000243
gene-coding region	SBO:0000335
generic	SBO:0000252
inhibition	SBO:0000169
inhibitor	SBO:0000020
mRNA	SBO:0000278
necessary stimulation	SBO:0000171
protein	SBO:0000297
RNA	SBO:0000250
stimulation	SBO:0000170
stimulator	SBO:0000021
transcriptional activation	SBO:0000459
transcriptional inhibition	SBO:0000020
translational activation	SBO:0000459
trigger	SBO:0000461
translation	SBO:0000184
transcription	SBO:0000183

select rate laws of choice, the latter option is important for the automatic selection of the most appropriate equation. The selection of one or multiple appropriate categories and in turn suitable kinetic equations for a reaction is based on a set of defined rules, which are here summarized and simplified for the sake of better comprehensiveness. The algorithm distinguishes the following three basic cases, which are not necessarily exclusive:

1. The list of reactants is *empty* or the reaction is reversible and the list of products is *empty*. If the reaction does neither involve genes, gene-coding regions, nor RNA molecules, then the algorithm can assign it to the zeroth reactant order reactions if also the list of reactants is *empty*, and to the zeroth product order reactions if it is reversible with an empty list of products. If it does involve genetic components, it can be assigned to the gene-regulatory reactions depending on its directionality.
2. The reaction has at least one reactant and if it is reversible also at least one product. If the reaction does neither have any enzymatic catalyst nor any non-enzymatic catalyst, it is assigned to the category of non-enzyme reactions with respect to its directionality. In case of unity stoichiometry on both sides of the reaction, and if the reaction follows the pattern of transcription or translation reactions, it is added to the category of gene-regulatory reactions.

6.2 Rate law selection

The pattern is satisfied if the reactant is a genetic element or an empty set and the product is an RNA molecule or protein.

3. The preprocessing has revealed that the reaction belongs to enzyme kinetics. Depending on user preferences, a reaction can also be recognized as enzyme-catalyzed process if no catalytic modifier is assigned to it. If the reaction is reversible with at least one product, the category of arbitrary enzyme reactions is assigned. Next, the stoichiometry and directionality of the reaction are taken into account in order to determine if the reaction also belongs to the uni-uni, bi-uni, or bi-bi reactions.

Each reaction category is represented with one interface that can be implemented by rate laws that are applicable for this category. Since one rate law can be useful for multiple categories, rate laws can also implement several of these interfaces. For all categories that can be applied to a reaction, the algorithm then compiles a list of concrete kinetic equations using a concept known as *reflection*. The list of applicable kinetic equations is hence generated on the fly and only based on the general reaction categories. In this way, the program can easily be extended, because additional kinetic equations only need to declare the categories to which they can be applied and will automatically be available when the program is executed.

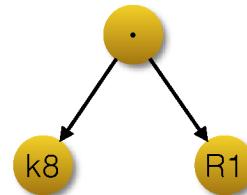
Additional rules apply when the algorithm compiles the list of rate laws based on reaction categories, because some rate laws can only be applied to certain combinations of categories. For instance, the *enzymatic rate law for irreversible non-modulated non-interacting uni-reactant enzymes* (SBO:0000150) can only be applied to irreversible reactions with integer but arbitrary stoichiometry, but does not allow stimulators or inhibitors. Thus, some categories exclude certain rate laws from being assigned to a reaction.

The user can select one default rate law for almost all categories. No specific default rate law can be selected for the categories irreversible or reversible reactions, modulated reactions, or integer stoichiometry, because these cases mainly refine the other categories. Instead, the selection of default rate laws is split into three major groups: *a*) gene-regulatory reactions (including reactions with zeroth order reactants or products); *b*) reversible reactions; and *c*) irreversible reactions. This is necessary because some rate laws can only be applied to reversible reactions, others only to irreversible reactions.

The identification of the category with highest priority works very similar. For reactions with empty list of reactants a gene-regulatory reaction has higher priority than the zeroth reactant order (but requires that the reaction follows the right pattern). Similarly, the algorithm first tries to assign a reaction to the gene-regulation category if it is reversible with an empty list of products, before assigning it to the zeroth product order reactions. Non-enzymatic reactions have higher priority than any enzymatic reaction. If the reaction is enzyme-catalyzed, the algorithm tries to first assign the most detailed category before it chooses an arbitrary enzyme reaction category. Hence, the algorithm determines one category for each reaction and applies the default rate law from this category to the reaction. In case of conflicts there are two final fall-back rate laws that can be applied if not other rate law can be selected: *a*) for non-enzyme reactions, the generalized mass-action rate law (Guldberg and Waage, 1879; Heinrich and Schuster, 1996); and *b*) the convenience rate law

6 Algorithms and software design

Figure 6.3: Abstract syntax tree for an irreversible mass-action rate law. This tree represents the rate law $v_8 = k_8 \cdot [R_1]$. The program internally constructs all equations in form of syntax trees, which can contain references to objects in the SBML document.



(Liebermeister and Klipp, 2006) for any kind of enzyme-catalyzed reaction. Both rate laws can be applied to reversible and irreversible reactions with arbitrary stoichiometry and can be combined with pre-factors for modification (activation or inhibition) as needed. When creating rate laws for individual reactions, a complete list of all applicable rate laws for the reaction of interest is compiled.

When convenience rate laws are used, the algorithm prefers the simple form and applies the thermodynamically independent form only if the system does not have full column rank. To this end, the program calculates the rank of the stoichiometric matrix using the Gaussian algorithm. This rank check is performed only once for the given model and only executed if at least one reaction exists, for which a convenience rate law is selected. Note that the algorithm calculates the rank for the full stoichiometric matrix and not just for the current submodel. This is crucial, because in many cases submodels would only contain one reaction, and thus the rank would be full.

Applying a rate law to the reaction means that the algorithm has to construct an abstract syntax tree, which symbolically represents the kinetic equation for the reaction. To this end, the reaction needs to be analyzed again and all of its components need to be taken into account as relevant for the selected rate law (irreversible equations, for instance, tend to ignore effects of products). An example for such a syntax tree can be seen in fig. 6.3, which has been created for the reaction schematic displayed in fig. 6.2h on page 67.

In order to ensure unit consistency of the equation, it can be necessary to multiply or divide reactive species with/by their surrounding compartment. User preferences and the units of the species determine if and which of those operation is required, because in SBML, each reaction should yield units of extent per time. Two cases need to be distinguished:

1. If a species has only substance units and the user decides to bring all species to concentration units, the species must be divided by its surrounding compartment.
2. If a species is given in concentration units and the user wants to bring all species to substance units, then a multiplication of the species with its surrounding compartment is required.

Depending on the type of rate law that is being created and the structural composition of the reaction, a certain number of parameters needs to be constructed. This can include forward or

6.3 Extraction of rate laws from SABIO-RK

backward rate constants, limiting velocity rates, inhibition or stimulation constants, thermodynamic properties, and many more. These parameters can be incorporated as local or global parameters. To this end, the algorithm first collects all parameters in a separate list and transfers them to the submodel only when a rate law is to be applied. Just as for species, parameter objects need to be equipped with appropriate units. The units of many parameters also depend on the structure of the reaction, for instance, the number and units of all reactants. Because of this connection, it can be necessary to also take the units of compartments into account when deriving the units of parameters in order to obtain extend by time units for the overall rate law. The algorithm equips each newly created parameter with a meaningful name and identifier as well as an appropriate SBO term.

If during this step additional units or unit definitions need to be added to the submodel, these are simplified as much as possible, annotated with a MIRIAM identifier pointing to the Units Ontology, and equipped with meaningful names and identifiers as appropriate. The algorithm avoids creating duplicate unit definitions by checking the model for identical existing unit definitions before adding a new one. If possible, the newly created kinetic equation is also annotated with a corresponding SBO term. Due to the large number of SBO terms that can be created by the algorithm, a comprehensive list of all cases is omitted in this document.

Whenever a kinetic equation that involves stoichiometry values is created for models in SBML Level 3, the algorithm inserts the ID of the corresponding species reference rather than the actual numerical value of the stoichiometry into the rate law. This gives the advantage that model changes can be directly reflected in the rate law, hence increasing the consistency of models. At the same time, it avoids the problem that units and meaning of single numerical values might not always be clear.

Finally, all relevant changes in the submodel are synchronized to the original model. This includes all newly created units and unit definitions, local and global parameters, annotations, mathematical equations, reversibility flags, and boundary condition flags. If species have been deleted from reactions, because their MIRIAM annotation was on the ignore list, this change is skipped and not synchronized, so that the structure of the model will remain identical. In the graphical user interface, the user can also disregard the changes. When being used as a CellDesigner plug-in, a special observer class synchronizes all changes from the submodel to the data model of CellDesigner.

6.3 Extraction of rate laws from SABIO-RK

The extraction of rate laws from the database SABIO-RK requires an SBML document and search terms as input. All possible values for the search terms can be found in section 4.3.5 on page 52.

The algorithm first generates a Uniform Resource Locator (URL) that is used to query the SABIO-RK database. This URL comprises the search terms and the respective KEGG reaction ID. The URL begins with the prefix `http://sabio.h-its.org/sabioRestWebServices/searchKineticLaws/sbml?q=`. Each search term and its given value extend this base URL with `keyword:value`. If a search term is associated with a range (e.g., the temperature), the

6 Algorithms and software design

URL is extended with keyword: [min..T0..max]. The keywords for the terms are presented here: <http://sabio.h-its.org/layouts/content/docuRESTfulWeb/SearchKeyVoc.gsp>. The operator `AND` connects multiple keyword-value pairs in the query.

The URL for querying points to an XML document for download. In the case of success, the XML document will be an SBML document with all kinetic laws found for the query. Otherwise, SABIO-RK returns an XML document with an error message and the algorithm terminates with a user message.

Just like for the *de novo* creation of rate laws the algorithm can either process all reactions within the SBML document or one particular reaction. To this end, the algorithm creates one query URL for each reaction, for which a rate law should be extracted from SABIO-RK. After obtaining an SBML document from SABIO-RK, the algorithm extracts all kinetic laws from the SBML document and tries to match all elements contained in a kinetic law to elements in the input network. This matching is based on the MIRIAM annotations of model components and involves the search for one corresponding

- species in the local model for each species that participates in the kinetic law.
- compartment in the local model for each compartment addressed in the kinetic law (this can be the compartment of a participating species or the reaction itself can have a compartment assigned to it).
- reaction in the local model for each reaction in the kinetic law.
- species reference for each species reference in the kinetic law within each such identified local reaction. This species reference needs to refer to a species with an annotation similar to that of the species referenced by the species reference in the found rate law.

In this context, an annotation of two SBML elements is considered similar and hence these elements are considered a *match* if both have *controlled vocabulary terms* in common that are linked through qualifiers *has version* or *is*.

In the batch mode, the algorithm always selects the first kinetic law in the query results for which all elements can be matched to respective elements in the model. The algorithm adds this rate law to the reaction. This merging involves

1. substituting all elements in the found kinetic law with the matched elements in the model; and
2. adding unit definitions, function definitions, global and local parameters contained in the kinetic law to the model.

Since this algorithm mainly operates on models obtained from SABIO-RK it is not necessary to create a submodel copy of the local model beforehand (as this is done for the *de novo* creation of rate laws). Changes are only applied upon user agreement or in batch mode. This is done by

1
2
3
4 *6.3 Extraction of rate laws from SABIO-RK*
5
6
7
8
9

merging required components from the downloaded model into the local model. For this reason, the local model does not change, before rate laws are applied.

When rate laws are obtained from SABIO-RK for individual reactions, the algorithm presents a list of all rate laws found for the given query to the user, who can then select the most appropriate equation. In cases when the selection of the first law with a successful matching does not lead to a satisfying result, the single reaction mode might yield better results.

15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

For Peer Review

7 FAQ and troubleshooting

Where can I get help for a certain component, option, check-box, etc.?

Most elements in SBMLsqueezer have tool-tips. If you do not understand an option, you can get help in the first place by just pointing the mouse cursor over it and wait for the tool-tip to show up (~3 seconds).

I'm getting a "java.lang.OutOfMemoryError: Java heap space"

Some operations need a lot of memory. If you simply start SBMLsqueezer, without any Java™ Virtual Machine (JVM) parameters, only 64 MB of memory are available. Please append the argument -Xmx1024M to start the application with 1 GB of main memory. See section 4.3.1 on page 40 for a more detailed description of how to start the application with additional memory. If possible, you should give the application 2 GB of main memory. A minimum of 1 GB main memory should be available to the application.

Is an Internet connection required to run SBMLsqueezer?

The vast majority of SBMLsqueezer's functions run in off-line mode. Features that require an active Internet connection are the online check for updates, the extraction of rate laws from the online database SABIO-RK, and following external links within online help.

Where can I obtain the latest version?

Go to <http://www.cogsys.cs.uni-tuebingen.de/software/SBMLsqueezer/>.

Which Java™ version must be installed on my computer to launch SBMLsqueezer?

SBMLsqueezer requires at least Java™ 1.6. Please see <http://www.java.com/de/download/> to download the latest Java™ version.

Why does SBMLsqueezer not start on my Mac with Mac OS X prior to 10.6 Update 3?

If you try to launch SBMLsqueezer, but the application does not start and you receive the following error message on the command-line or Java™ console of your Mac, you need to update your Java™ installation:

```
Exception in thread "AWT-EventQueue-0" java.lang.NoClassDefFoundError:  
    com/apple/eawt/AboutHandler  
    at java.lang.ClassLoader.defineClass1(Native Method)  
    at java.lang.ClassLoader.defineClass(ClassLoader.java:703)  
    ...
```

The interface `com.apple.eawt.AboutHandler` was introduced to Java™ for Mac OS X 10.6 Update 3. If you have an earlier version of Mac OS X or Java™, please update your OS or Java™ installation. Also see the Mac OS X documentation about the `AboutHandler` for more information. On a Mac, you can update your Java™ installation through the Software Update menu item in the main Apple menu.

How can I report bugs or get help?

Please contact the mailing list using the e-mail address ✉ sbmlsqueezer@googlegroups.com.

8 License

8.1 Disclaimer



SBMLsqueezer is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License (GPL) as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but **without any warranty**; without even the implied warranty of **merchantability** or **fitness for a particular purpose**. See the GNU General Public License for more details.

Each distributed version of SBMLsqueezer should contain a copy of the GNU General Public License. If not, please see <http://www.gnu.org/licenses/>.

8.2 Included third-party libraries

SBMLsqueezer includes and re-distributes the following third-party software libraries.

- JSBML (1.0 β 1, revision 1697) including all of its third-party libraries, see <http://sbml.org/Software/JSBML>.
- JUnit (version 4.8, Eclipse Public License), see <http://junit.org/>.
- SBML2^{LaTeX} (build 20140410-1447, GPL), see <http://sourceforge.net/projects/sbml2latex/> and <http://www.cogsys.cs.uni-tuebingen.de/software/SBML2LaTeX/>.
- libSBML (version 5.9.0, GNU Lesser General Public License (LGPL)), see <http://sbml.org/Software/libSBML>.
- Quaqua filechooser (version 9, LGPL), see <http://www.randelshofer.ch/quaqua/>.
- Garuda (version 1.0 β 1) including all of its third-party libraries, see <http://www.garuda-alliance.org>.
- jlatexmath (version 1.0.0, GPL), see <http://forge.scilab.org/index.php/p/jlatexmath/>.

All version numbers are given with respect to the latest release of SBMLsqueezer.

9 Acknowledgments

This work has been funded by a Marie Curie International Outgoing Fellowship awarded to Andreas Dräger within the EU 7th Framework Program for Research and Technological Development (project AMBiCon, 332020) and by the Federal Ministry of Education and Research (BMBF, Germany) in the projects Virtual Liver Network (project number 0315756), National Genome Research Network (NGFN-Plus, project number 01GS08134), and Spher4Sys (grant number 0315384C).

9.1 Core developers

The following people implemented wide parts of SBMLsqueezer:

- Andreas Dräger, University of California, San Diego, La Jolla, California, USA and University of Tuebingen, Germany andraeger@eng.ucsd.edu
- Roland Keller, University of Tuebingen, Germany roland.keller@uni-tuebingen.de
- Johannes Eichner, University of Tuebingen, Germany johannes.eichner@uni-tuebingen.de

9.2 Principal Investigators

- Bernhard Ø. Palsson, University of California, San Diego, La Jolla, California, USA palsson@ucsd.edu
- Andreas Zell, University of Tuebingen, Germany andreas.zell@uni-tuebingen.de

9.3 Alumni

During the years, many people contributed to this project. We are grateful to each contribution, such as source code, advice, proof reading and much more. In particular, we like to thank our former scientific advisors, colleagues, and students, who are here listed all together in alphabetical order: Meike Aichele, Hannes Borch, Alexander Dörr, Nadine Hassis, Marcel Kronfeld, Oliver Kohlbacher, Sarah Rachel Müller vom Hagen, Sebastian Nagel, Leif J. Pallesen, Alexander Peltzer, Julianus Pfeuffer, Sandra Saliger, Simon Schäfer, Adrian Schröder, Jochen Supper, Dieudonné M. Wouamba, Michael J. Ziller

We also thank Shaowu Yang for providing the Chinese language pack for this program.

1
2
3
4 *9 Acknowledgments*
5
6
7 **9.4 Collaborators and partners**
8
9
10 The authors are grateful to the SABIO-RK team, in particular Martin Golebiewski and Wolfgang
11 Müller from the Heidelberg Institute of Technology (HITS).
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

For Peer Review

Appendix A

Release Notes

This chapter gives a brief overview of the main user-visible changes of SBMLsqueezer since its first release. As such, this chapter gives you an historic overview about the development of SBMLsqueezer as a large software project.

A.1 Version 1.0

Release date: April 28th 2008.

This is the initial release of the software that has been made available as a supplement to the original publication from in 2008. All features of this version are therefore described in the corresponding publication Dräger *et al.* (2008).

A.2 Version 1.1

Release date: February 9th 2009.

A.2.1 New features

- ✓ SBMLsqueezer now allows you to specify whether new parameters should be stored locally (only valid within the respective kinetic law) or globally (valid for the whole model). Both, the main window and the context menu contain switches to make this decision. Please note that the k_G parameters of the thermodynamically independent convenience kinetics are always stored globally because these do not belong to a specific reaction but to a specific reacting species.
- ✓ The context menu of SBMLsqueezer now also shows already existing kinetic equations and renders their formula. The name of the kinetic equation created by SBMLsqueezer is now written to the notes element of the newly created kinetic law.
- ✓ The L^AT_EX export function was improved:
 - Several choices allow for a customization of the output.
 - The context menu also allows you to export a LaTeX file for a specific kinetic equation.

Appendix A Release Notes

- It now includes HTML2 \LaTeX that converts notes elements from XHTML to \LaTeX . Therefore, SBMLsqueezer also includes your notes in its model report.

- ✓ SBMLsqueezer version 1.1 is distributed under the terms of the GNU General Public License (GPL).

Please note that SBMLsqueezer's \LaTeX export function is, however, still not comprehensive. For a fully-featured model report generator, we strongly recommend to have a look on our latest project: SBML2 \LaTeX on <http://webservices.cs.uni-tuebingen.de> and <http://www.cogsys.cs.uni-tuebingen.de/software/SBML2LaTeX>.

A.2.2 Bug fixes

- ✖ In some cases SBMLsqueezer's context menu did not offer the full list of available and applicable kinetic equations for certain reactions.
- ✖ If the number of products was higher than the number of reactants a null pointer exception was thrown in the thermodynamically independent form of the convenience kinetics due to an incorrect access to the list of products of a reaction.
- ✖ In the thermodynamically independent convenience kinetics the root function was called with only one argument. This is actually not incorrect but earlier versions of libSBML are unable to interpret such an implicit square root and require a 2 as the second argument.
- ✖ In the thermodynamically independent convenience kinetics the exponent of the anabolic term and the catabolic term were incorrect if the stoichiometry was not equal to one. In this case, a division of the exponent by two was missing.
- ✖ In the mass action kinetics a copy and paste error in the source code lead to incorrect pre-factors for activation and inhibition if both effects were assigned to the same reaction. Instead of receiving one activation function and one inhibition function there was the same activation twice.
- ✖ For several reasons null pointer exceptions could occur when trying to create \LaTeX code from a model.

A.3 Version 1.2

Release date: July 31st 2009.

A.3 Version 1.2**A.3.1 New features**

- ✓ SBMLsqueezer now automatically checks for updates. If a newer version of SBMLsqueezer is available online, the user is notified by a message window in the bottom right corner of the screen. Furthermore, the release notes of the most recent SBMLsqueezer version are shown to the user by clicking on [show release notes](#).
- ✓ In contrast to previous versions, SBMLsqueezer now indicates if a model already contains rate equations for all reactions or no reactions at all. In earlier versions SBMLsqueezer did not overwrite existing kinetic equations and did also not state why.
- ✓ SBMLsqueezer's complete internal data structure was improved: It has become much more efficient and simpler.

A.3.2 Improved Adaptation of SBMLsqueezer to CellDesigner 4.0.1

Due to the changes in CellDesigner, SBMLsqueezer only offered zeroth order mass action kinetics as available option to model transcription and translation processes. The reason for this was that the arrows for transcriptional/translational activation disappeared. These effects have now to be covered by trigger and physical stimulation. Unfortunately, CellDesigner maps the old arrows for transcriptional/translational activation to catalysis instead of "trigger". Therefore, we also have to cover the case of having a transcription or translation "catalyzed" by some stimulator. This has now been implemented and SBMLsqueezer therefore offers several kinetic rate equations for both processes. The same holds true for the "batch" mode of SBMLsqueezer: besides transcriptional-/translational activators also all kinds of catalysts and activators/inhibitors are accepted for the Hill equation.

We now apply the inhibition pre-factor from convenience kinetics also to reversible Michaelis-Menten kinetics with multiple inhibitors. In cases where the formulas of Michaelis-Menten and convenience kinetics are equal, only one of both is offered to the user:

- For reversible or irreversible uni-uni reactions without inhibition or activation only the Michaelis-Menten equation is selectable and
- in the case of reversible uni-uni reactions with multiple inhibitors only convenience kinetics can be applied.
- However, if the stoichiometric matrix of the reaction system does not have a full column rank, the thermodynamically independent form of the convenience kinetics can be selected as an alternative to the Michaelis-Menten equation.

Additionally, the activation pre-factor is now also applied for the mixed-type inhibition of irreversible enzymes by mutually exclusive inhibitors (SBO:0000275) if activators are assigned to the reaction.

Appendix A Release Notes

The new SBGN representation of transcription and translation uses the trigger symbol (for the gene or the RNA molecule, depending on the process) and a reaction from some source to RNA or from some source to a protein (Le Novère *et al.*, 2009). SBMLSqueezer did in these cases not suggest the Hill equation as a possible rate law because it still required the translation/transcription arrows that are going to be deprecated. Since this version, SBMLSqueezer also produces the identical form of the Hill equation for the old style of transcription/translation reaction and the new SBGN-compliant form.

A.3.3 Bug fixes

- ✖ Local parameters could not be removed completely if not necessary (this happened only in SBMLSqueezer version 1.1 because SBMLSqueezer version 1.0 did not create or delete local parameters at all).
- ✖ In Michaelis-Menten kinetics activators were multiplied incorrectly (only in the preview, not in the equation itself)
- ✖ The help browser could not be started in SBMLSqueezer version 1.1 because of a null pointer exception (an image could not be loaded correctly).
- ✖ Problems of the “batch mode”:
 - In some cases SBMLSqueezer did not show the correct SBO numbers (for “Hill equation” and “Henri-Michaelis-Menten equation”).
 - In the kinetics summary table SBMLSqueezer did not list the k_G parameters of the thermodynamically independent convenience kinetics in the column “parameters”.
 - Sometimes there was a problem with the equation preview.

A.4 Version 1.2.1

Release date: August 7th 2009.

A.4.1 New features

- ✓ In the context menu, SBMLSqueezer now remembers the rate law when switching the reaction from reversible to irreversible and automatically selects the corresponding equation if available.

A.4.2 Bug fixes

- ✖ In the Hill equation instead of inhibitors SBMLSqueezer accessed the list of activators to create an inhibition term (only in SBMLSqueezer 1.2).

A.5 Version 1.3

- ❖ When trying to remove unnecessary parameters from the model, SBMLsqueezer 1.2 deleted parameters, whose IDs contain upper case letters, no matter if these occur in kinetic equations because of an incorrect String comparison.
- ❖ The thermodynamically independent convenience kinetics was not created correctly in SBMLsqueezer 1.2: the integer one was subtracted in the denominator in cases where this was incorrect and the parameter k_V was not multiplied with the formula.

A.5 Version 1.3

Release date: April 2nd 2010.

Parts of the content in these release notes have been taken from the Ph.D. thesis of Dräger, 2011, where this section is much more elaborated.

A.5.1 New features**A new and purely Java™-based SBML data structure**

SBMLsqueezer's data structure was completely changed: Earlier versions were based on String concatenation to create kinetic formulas with all participating species and parameters. Now SBMLsqueezer is based on an abstract syntax tree representation of the formula and also creates Parameter objects rather than simply their ID.

This new data structure is actually an almost complete Java™ implementation of SBML and has therefore become a separate project, JSBML, available at <http://sourceforge.net/projects/jsbml>. On the SBML homepage, you can find a separate mailing list about this project: <http://sbml.org/Forums>

With JSBML at hand, SBMLsqueezer does no longer manipulate CellDesigner's plug-in Objects directly. If you start SBMLsqueezer from CellDesigner's plug-in menu or its reaction context menu, SBMLsqueezer will copy all required parts of the model into JSBML objects. Only this copy of the model is manipulated. By clicking on **OK** or **Apply**, all changes will be synchronized with CellDesigner's original data structures

Stand-Alone Mode

SBMLsqueezer now also runs in a stand-alone mode. With the help of libSBML, valid SBML files can be read and copied into the JSBML data objects. JSBML now mirrors the complete definition of SBML up to Level 2 Version 4. As in the CellDesigner plug-in mode, SBMLsqueezer only manipulates JSBML objects. By clicking on **Save**, changes are written into the SBML file.

Command-line mode: All features of SBMLsqueezer are now also available from the command line. This allows users to write shell or batch scripts that access SBMLsqueezer's functions.

The API of SBMLsqueezer has been simplified. There is now just one function, `squeeze` in the main class SBMLsqueezer that can be called to read in a model from a valid SBML file and to write

Appendix A Release Notes

the result, i.e., an SBML model including new KineticLaws, new Parameters, new or adapted UnitDefinitions, into the given out file. Before creating kinetic formulas for the model, the user probably wants to adjust SBMLSqueezer's configuration. To this end, the methodsset(CfgKey, <boolean|double|int|String>) in class SBMLSqueezer allow the programmer to set any configuration key and value pair, similar to the command-line mode. Here we give a minimal example of how to use this new API:

```

1 public static void main(String[] args) {
2     // Initialize SBMLSqueezer with appropriate SBML readers/writers
3     SBMLSqueezer squeezer = new SBMLSqueezer(new LibSBMLReader(), new
4         LibSBMLWriter());
5     // Configure SBMLSqueezer
6     squeezer.set(CfgKeys.OPT_ALL_REACTIONS_ARE_ENZYME_CATALYZED, true);
7     squeezer.set(CfgKeys.OPT_DEFAULT_COMPARTMENT_INITIAL_SIZE, 1.0);
8     squeezer.set(CfgKeys.POSSIBLE_ENZYME_RNA, true);
9     squeezer.set(CfgKeys.KINETICS_UNI_UNI_TYPE,
10        MichaelisMenten.class.getName());
11    squeezer.set(CfgKeys.KINETICS_OTHER_ENZYME_REACTIONS,
12        ConvenienceKinetics.class.getName());
13    try {
14        // Create kinetic equations, parameters, units etc. and save the result
15        // args contains paths to input file and output file
16        squeezer.squeeze(args[0], args[1]);
17    } catch (Throwable e) {
18        e.printStackTrace();
19    }
20 }
```

Listing A.1: Usage of SBMLSqueezer 1.3 via its API

Since SBMLSqueezer still requires an installation of libSBML on the user's system, which can sometimes become problematic, a more convenient way of using SBMLSqueezer has now been made available: the SBMLSqueezer web application does not require any local installation and is freely available at <http://webservices.cs.uni-tuebingen.de>. In this framework, workflows can be created in which SBMLSqueezer can directly be linked to the full version of **SBML2LATEX**. The full version of **SBML2LATEX** contains many additional features that are not included in SBMLSqueezer's version of **SBML2LATEX**. Hence, it is highly recommended to make use of the online version of **SBML2LATEX**.

Configuration

SBMLSqueezer now memorizes every setting and changed parameters from the GUI whether in CellDesigner plug-in or stand-alone mode. In the stand-alone case, SBMLSqueezer even memorizes given command-line arguments. These settings are read from a configuration file at the next start. This is especially convenient for open and save directories. At any time, the user can change all settings to the defaults by clicking on the designated button in the preferences dialog.

A.5 Version 1.3**Improved Systems Biology Ontology support**

SBMLsqueezer is now fully based on the Systems Biology Ontology (SBO). The JSBML copy of CellDesigner's plug-in data structures maps all CellDesigner-specific annotations to corresponding SBO terms. Afterwards these are mapped back. SBO term "enzymatic catalyst" (SBO:0000460) was created because it is required by SBMLsqueezer to distinguish enzymes and other catalysts, such as certain inorganic ions. SBMLsqueezer's stand-alone version interprets SBO terms that can be found in the model and changes the annotation of ModifierSpeciesReferences from "catalyst" (SBO:0000013) to "enzymatic catalyst" if the SBO term of the corresponding Species is one of those belonging to the family of materials considered as enzymes (SBMLsqueezer still offers check boxes to indicate certain kinds of species as enzymes).

Earlier versions of SBMLsqueezer indicated the SBO term IDs of newly created kinetic equations if these were already defined in SBO. However, this was more or less just for information to the user and could neither be saved nor be considered during any other processes. This version of SBMLsqueezer is able to not only take SBO terms into account while creating rate laws, but can even save SBO terms in the resulting SBML file. However, in CellDesigner plug-in mode, SBMLsqueezer is not yet able to save SBO term IDs in CellDesigner data objects due to the missing functionality in its API.

SBMLsqueezer now contains an own parser to identify the correct SBO term IDs and attributes that are required to annotate all newly created objects.

Whenever possible, SBMLsqueezer annotates newly created objects, such as Parameters or UnitDefinitions, with SBO IDs.

MIRIAM Support

In contrast to earlier versions, SBMLsqueezer now also interprets and uses MIRIAM tags. The new command-line and configuration key option `OPT_IGNORE_THESE_SPECIES_WHEN_CREATING_LAWS` takes a list of comma-separated MIRIAM IDs as value. Species annotated with `BQB_IS` and the given MIRIAM resource are then ignored when creating rate equations. This is, for instance, useful if small molecules such as water take part in a reaction. The concentration of water can hardly be measured and it is assumed to occur abundantly within the cell. By default, the list of species whose influence is to be neglected when creating new kinetic equations contains the KEGG compound IDs for the substances listed in table 5.1 on page 61.

New kinetic equations and extensibility

In earlier versions the inclusion of new kinetic equations into SBMLsqueezer was not an easy task. After writing a class that actually generates the new rate law, a rule had to be implemented of when to make this rate law available. Furthermore, the GUI had to be changed to include this new formula. Summarized, several changes in the program code were necessary to include additional rate laws.

Appendix A Release Notes

Now SBMLsqueezer is based on JavaTM reflection, i.e., initially SBMLsqueezer does not know any one of its available kinetic equations. These are all loaded when initializing SBMLsqueezer. Currently, twelve interfaces define the properties of all kinetic equations. The rules of when select which kind of rate equation only make use of the implemented interfaces. Hence, new kinetic equations can be incorporated into SBMLsqueezer simply by implementing designated interfaces. Since SBMLsqueezer is an open-source project, users can customize it easily and extend it with desired rate laws.

Much effort was put into the extension of SBMLsqueezer with additional rate laws for gene-regulatory processes. Earlier versions of SBMLsqueezer only provided the Hill equation variant suggested by Hinze *et al.* (2007). This equation has now been renamed to Hill-Hinze equation to highlight that it is actually a modification of the original rate law. Only in special cases this equation equals the traditional Hill equation (SBMLsqueezer will highlight these cases). Now nine additional rate equations were included:

Additive Model Linear A generalized super class of all other additive rate laws for gene-regulatory processes.

Additive Model Non-Linear defined in the paper “The NetGenerator Algorithm] Reconstruction of Gene Regulatory Networks” by Töpfer, Guthke, Driesch, Wötzel, and Pfaff, 2007

H-Systems Spieth, Hassis, Streichert, Supper, Beyreuther, and Zell, 2006 “Comparing Mathematical Models on the Problem of Network Inference”.

NetGenerator Linear Model “The NetGenerator Algorithm: Reconstruction of Gene Regulatory Networks” by Töpfer, Guthke, Driesch, Wötzel, and Pfaff, 2007

NetGenerator Non-Linear Model “The NetGenerator Algorithm] Reconstruction of Gene Regulatory Networks” by Töpfer, Guthke, Driesch, Wötzel, and Pfaff, 2007

S-Systems Tournier (2005): “Approximation of dynamical systems using S-systems theory: application to biological systems”

Hill-Radde equation “Modeling Non-Linear Dynamic Phenomena in Biochemical Networks” by Radde, 2007

Vohradsky “Neural network model of gene expression.” of Vu and Vohradský, 2007

Weaver “Modeling regulatory networks with weight matrices” by Weaver, Workman, and Stormo, 1999

The following new generalized kinetic equations for metabolic reactions were also implemented in SBMLsqueezer, which are all defined by Liebermeister *et al.* (2010):

- Common modular rate law (CM)

A.5 Version 1.3

- Direct binding modular rate law (DM)
- Force-dependent modular rate law (FM)
- Power-law modular rate law (PM)
- Simultaneous binding modular rate law (SM).

Each one of these equations is only available in a reversible mode and the user must choose one of the three possible versions that determine the degree of thermodynamic correctness. The *weg* version is the most complicated form but always thermodynamically correct. The *hal* version ensures thermodynamic correctness in most cases, whereas for the *cat* version thermodynamic properties cannot be guaranteed to be correct. The versions can be selected in the preferences dialog or provides as a command-line option.

Finally, the generalized form of Hill's equation as proposed by Cornish-Bowden (2004, in "Fundamentals of Enzyme Kinetics", p. 314) has been implemented and is now also available for metabolic reactions.

If the corresponding flag is set, boundary conditions are also set for species that represent empty sets, i.e., degraded species, sources, or sinks in a reaction.

Support and assignment of units and unit definitions

For multi-compartment models concentration versus molecule counts matters. SBMLSqueezer now provides two different ways of ensuring unit correctness. First, each species can be brought to units of concentration. To this end, SBMLSqueezer interprets the `hasOnlySubstanceUnits` attribute of each species. Depending on whether this is set to true, the species is divided by the size of the surrounding compartment. Otherwise the species already represents a concentration and nothing is done. Second, all species can be brought to molecule count units. This is again achieved with the help of the `hasOnlySubstanceUnits` attribute, but now SBMLSqueezer multiplies with the compartment size if this attribute is false.

In contrast to earlier versions, SBMLSqueezer now equips all newly created Parameter objects with units. To this end, SBMLSqueezer derives the correct units from the context. For instance, in the mass action kinetics the units of the catalytic constants depend on the order of the reaction and have therefore to be computed whenever such a rate law is created. Furthermore, SBMLSqueezer also considers the `hasOnlySubstanceUnits` property of each species and the way in which the surrounding compartment comes into play to derive the units of parameters.

To make models more realistic, SBMLSqueezer redefines the pre-defined SBML unit definition `substance` from mol to mmol and `volume` from l to ml.

If possible, SBMLSqueezer avoids creating new `UnitDefinition` objects. It first tries to find equivalent and already existing definitions in the model.

Appendix A Release Notes**A.5.2 Bug Fixes**

- In the original paper of Hinze *et al.* (2007), inhibition was expressed with 1 - product of all inhibition functions. Earlier versions of SBMLsqueezer created a product that run over all inhibitors with $(1 - \text{inhibition function})$ for each such function.
- In all gene-regulation kinetics, it is now assumed that degradation processes are distinct reactions that can be, e.g., modeled using a mass action rate law. Hence, no degradation terms can be found in gene-regulation kinetics anymore.
- The rate law corresponding to SBO:0000266 was not correct. Earlier versions of SBMLsqueezer produced the fraction $K_{Mjs}/K_{ibj} \cdot I$, but correct is $S \cdot I/K_{ibj}$ (see Equation 10 in the supplementary material “Kinetic Laws”; the correct version of this equation can be found at <http://www.ebi.ac.uk/sbo/main/SBO:0000266>).
- In case of an explicit enzyme catalysis, earlier versions of SBMLsqueezer did not multiply the numerator of equation SBO:0000273 with the enzyme. Therefore, it always produced the V_{max} version of the equation, but the parameter was called k_{cat} .

A.6 Version 2.0

Release date: June 30th 2014.

Many concepts that have been introduced with version 1.3 have been revised and updated. The entire handling of user settings has been massively changed and now uses the concept of user preferences instead of configuration files. The source code has been cleaned and re-factored in many positions and lots of development time has been invested into with the library JSBML.

A.6.1 New features

SBMLsqueezer can now be used in several different ways:

- As fully-featured stand-alone program without the need to install any further software, based on the official JSBML version 1.0β1
- As a stand-alone program based on a libSBML back-end, which means that real off-line SBML validation is possible.
- Irrespective of whether JSBML or libSBML is used as SBML library, the stand-alone version provides both, a GUI as well as a fully-featured command-line version. For large-scale rate law generation, this command-line interface has already proven to be useful (as part of the path2models project).
- SBMLsqueezer can be launched directly from the project’s website as a Java™ Web Start program without the need of any local installation.

A.6 Version 2.0

- As a plug-in for CellDesigner 4.3
- As a Garuda gadget, as which it can communicate with further Garuda gadgets

Hence, the usage of the program has been greatly simplified. Further new program features comprise:

- ✓ SBMLsqueezer fully supports all Levels and Versions of SBML up to the most recent specification Level 3 Version 1.
- ✓ A direct query wizard for SABIO-RK has been implemented and allows users to extract experimentally obtained rate laws from this database together with parameters, values, and units. The search engine provides several settings for experimental conditions.
- ✓ SBMLsqueezer includes now several JUnit test cases to check if the generated kinetic equations are correct.
- ✓ It includes now a full version of SBML2LATEX and can directly open Portable Document Format (PDF) files that are generated to document the content of the model.
- ✓ The renderer for equations and formula has been changed and provides more capabilities. SBMLsqueezer windows and context menus are now zoom-able and re-sizable.
- ✓ Improved user preferences menu and management for each individual operating system.
- ✓ The user interface (GUI and command-line) is fully bilingual (German and English), and partially also translated to Chinese, but models and their labels are only created in English for the sake of a better international re-usability.
- ✓ A new search function allows users to query the model data structure in the GUI.
- ✓ Lots of effort has been put to better adapt SBMLsqueezer to individual platforms. The support for Mac OS X has been greatly improved, the program now provides many features of native applications for Mac OS X.
- ✓ The documentation of the API has been improved.

A.6.2 Bug fixes

The communication between SBMLsqueezer and CellDesigner was very inefficient. The new plug-in interface in JSBML provides a much better performance. Errors in kinetic equations and units of parameters have been detected and solved:

- ✖ Sometimes SBMLsqueezer created invalid IDs for newly introduced units.

Appendix A Release Notes

- 1 ✗ The units of the association and dissociation constant in generalized mass action kinetics
2 could not be derived correctly if a catalyst interfered with the reaction, because the units of
3 the catalyst were not taken into account.
- 4 ✗ The units of the half saturation constant in the (generalized) Hill equation were not correctly
5 derived. The derivation of units of kinetic parameters has been improved.

6 Several minor issues with the GUI have been solved.
7

8 **A.6.3 Known Issues**

9 In SBML models, it should be possible to evaluate all kinetic equations to extend of reaction units
10 per time units. Usually, the extend of a reaction would be a variant of a substance unit. However, it
11 has been recognized that some kinetic equations cannot under all conditions be evaluated to extend
12 per time units. The reasons are often the structure of the definition of the rate law. Some equations
13 that have been defined for gene-regulatory networks, for instance, give a purely phenomenological
14 description of the system (e.g., S- or H-systems). In other equations, it is assumed that the
15 equilibrium constant is always dimensionless. If this is not the case, it cannot be guaranteed that
16 SBMLSqueezer will create correct units for these equations (e.g., modular rate laws and convenience
17 kinetics). It is therefore recommended to check the units of generated rate laws, even if in
18 the vast majority of cases these will be correct. Please note that in this version the general unit han-
19 dling has been extensively revised and improved and is in the vast majority of cases very reliable.
20 SBMLSqueezer displays the derived units of equations, so that problematic equations can be easily
21 identified.

22 **A.7 Version 2.0.1**

23 Release date: October 24th 2014.
24

25 This release has become necessary due to major changes in the Garuda backend and also includes
26 an updated version of JSBML.
27

Appendix B

Acronyms

API Application Programming Interface

asRNA Antisense RNA

BioPAX Biological Pathway Exchange Language

FAQ Frequently Asked Questions

GPL GNU General Public License

GUI Graphical User Interface

HTML Hypertext Markup Language

ID Identifier

IDE Integrated Development Environment

JDK JavaTM Development Kit

JVM JavaTM Virtual Machine

JAR JavaTM Archive

LGPL GNU Lesser General Public License

KEGG Kyoto Encyclopedia of Genes and Genomes

MIRIAM Minimal Information Required In the Annotation of Models

mRNA Messenger RNA

PDF Portable Document Format

RNA Ribonucleic Acid

SBGN Systems Biology Graphical Notation

1
2
3
4 *Appendix B Acronyms*
5

6

7 **SBML** Systems Biology Markup Language
8

9 **SABIO-RK** System for the Analysis of Biochemical Pathways – Reaction Kinetics
10

11 **SBO** Systems Biology Ontology
12

13 **URL** Uniform Resource Locator
14

15 **XHTML** Extended HTML
16

17 **XML** Extended Markup Language
18

19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Bibliography

- Arnold, A. and Nikoloski, Z. (2011). A quantitative comparison of calvin-benson cycle models. *Trends Plant Sci*, **16**(12), 676–683.
- Bisswanger, H. (2000). *Enzymkinetik – Theorie und Methoden*. Wiley-VCH, Weinheim, Germany, 3rd edition.
- Blum, T. (2009). *Computational Approaches for Analyzing Metabolic Pathways*. Ph.D. thesis, Eberhard-Karls-Universität Tübingen, Tübingen, Germany.
- Bornstein, B. J., Keating, S. M., Jouraku, A., and Hucka, M. (2008). LibSBML: an API Library for SBML. *Bioinformatics*, **24**(6), 880–881.
- Büchel, F., Wrzodek, C., Mittag, F., Dräger, A., Eichner, J., Rodriguez, N., Le Novère, N., and Zell, A. (2012). Qualitative translation of relations from BioPAX to SBML qual. *Bioinformatics*, **28**(20), 2648–2653.
- Büchel, F., Rodriguez, N., Swainston, N., Wrzodek, C., Czauderna, T., Keller, R., Mittag, F., Schubert, M., Glont, M., Golebiewski, M., van Iersel, M., Keating, S., Rall, M., Wybrow, M., Hermjakob, H., Hucka, M., Kell, D. B., Müller, W., Mendes, P., Zell, A., Chaouiya, C., Saez-Rodriguez, J., Schreiber, F., Laibe, C., Dräger, A., and Le Novère, N. (2013). Large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, **7**(1), 116.
- Buswell, S., Devitt, S., Diaz, A., Ion, P., Miner, R., Poppelier, N., Smith, B., Soiffer, N., Sutor, R., and Watt, S. (1999). Mathematical markup language (mathml™) 1.01 specification. Technical report, MIT, INRIA, Keio.
- Cornish-Bowden, A. (2004). *Fundamentals of Enzyme Kinetics*. Portland Press Ltd., 59 Portland Place, London, United Kingdom, 3rd edition.
- Courtot, M., Juty, N., Knüpfer, C., Waltemath, D., Zhukova, A., Dräger, A., Dumontier, M., Finney, A., Golebiewski, M., Hastings, J., Hoops, S., Keating, S., Kell, D. B., Kerrien, S., Lawson, J., Lister, A., Lu, J., Machne, R., Mendes, P., Pocock, M., Rodriguez, N., Villéger, A., Wilkinson, D. J., Wimalaratne, S., Laibe, C., Hucka, M., and Le Novère, N. (2011). Controlled vocabularies and semantics in systems biology. *Mol Syst Biol*, **7**, 543.
- Dräger, A. (2011). *Computational Modeling of Biochemical Networks*. Ph.D. thesis, University of Tuebingen, Tübingen, Germany.

Bibliography

- Dräger, A., Kronfeld, M., Supper, J., Planatscher, H., Magnus, J. B., Oldiges, M., and Zell, A. (2007a). Benchmarking Evolutionary Algorithms on Convenience Kinetics Models of the Valine and Leucine Biosynthesis in *C. glutamicum*. In D. Srinivasan and L. Wang, editors, *2007 IEEE Congress on Evolutionary Computation*, pages 896–903, Singapore. IEEE Computational Intelligence Society, IEEE Press.
- Dräger, A., Supper, J., Planatscher, H., Magnus, J. B., Oldiges, M., and Zell, A. (2007b). Comparing Various Evolutionary Algorithms on the Parameter Optimization of the Valine and Leucine Biosynthesis in *Corynebacterium glutamicum*. In D. Srinivasan and L. Wang, editors, *2007 IEEE Congress on Evolutionary Computation*, pages 620–627, Singapore. IEEE Computational Intelligence Society, IEEE Press.
- Dräger, A., Hassis, N., Supper, J., Schröder, A., and Zell, A. (2008). SBMLsqueezer: a Cell-Designer plug-in to generate kinetic rate equations for biochemical networks. *BMC Systems Biology*, **2**(1), 39.
- Dräger, A., Kronfeld, M., Ziller, M. J., Supper, J., Planatscher, H., Magnus, J. B., Oldiges, M., Kohlbacher, O., and Zell, A. (2009a). Modeling metabolic networks in *C. glutamicum*: a comparison of rate laws in combination with various parameter optimization strategies. *BMC Syst Biol*, **3**, 5.
- Dräger, A., Planatscher, H., Wouamba, D. M., Schröder, A., Hucka, M., Endler, L., Golebiewski, M., Müller, W., and Zell, A. (2009b). SBML2L^AT_EX: Conversion of SBML files into human-readable reports. *Bioinformatics*, **25**(11), 1455–1456.
- Dräger, A., Schröder, A., and Zell, A. (2010). *Systems Biology for Signaling Networks*, volume 1 of *Systems Biology*, chapter Automating mathematical modeling of biochemical reaction networks, pages 159–205. Springer-Verlag.
- Dräger, A., Rodriguez, N., Dumousseau, M., Dörr, A., Wrzodek, C., Le Novère, N., Zell, A., and Hucka, M. (2011). JSBML: a flexible Java library for working with SBML. *Bioinformatics*, **27**(15), 2167–2168.
- Finney, A. and Hucka, M. (2003). Systems biology markup language: Level 2 and beyond. *Biochem Soc Trans*, **31**(Pt 6), 1472–1473.
- Finney, A., Hucka, M., and Le Novère, N. (2006). Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. Technical report.
- Funahashi, A., Tanimura, N., Morohashi, M., and Kitano, H. (2003). CellDesigner: a process diagram editor for gene-regulatory and biochemical networks. *BioSilico*, **1**(5), 159–162.
- Funahashi, A., Matsuoka, Y., Jouraku, A., Kitano, H., and Kikuchi, N. (2006). CellDesigner: a modeling tool for biochemical networks. In *Proceedings of the 38th conference on Winter simulation*, WSC '06, pages 1707–1712, Monterey, California. Winter Simulation Conference.

Bibliography

- Funahashi, A., Morohashi, M., Matsuoka, Y., Jouraku, A., and Kitano, H. (2007). CellDesigner: A Graphical Biological Network Editor and Workbench Interfacing Simulator. In S. Choi, editor, *Introduction to Systems Biology*, chapter 21, pages 422–434. Humana Press.
- Funahashi, A., Matsuoka, Y., Jouraku, A., Morohashi, M., Kikuchi, N., and Kitano, H. (2008). CellDesigner 3.5: A Versatile Modeling Tool for Biochemical Networks. In *Proceedings of the IEEE*, volume 96, pages 1254–1265. IEEE.
- Gauges, R., Rost, U., Sahle, S., and Wegner, K. (2006). A model diagram layout extension for SBML. *Bioinformatics*, **22**(15), 1879–1885.
- Ghosh, S., Matsuoka, Y., Asai, Y., Hsin, K.-Y., and Kitano, H. (2011). Software for systems biology: from tools to integrated platforms. *Nature Reviews Genetics*, **12**(12), 821–832.
- Goecks, J., Nekrutenko, A., Taylor, J., and Team, G. (2010). Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biology*, **11**(8), R86.
- Guldberg, C. M. and Waage, P. (1879). Über die chemische affinität. *Journal für Practische Chemie*, **127**, 69–114.
- Hecker, M., Lambeck, S., Töpfer, S., Someren, E. v., and Guthke, R. (2009). Gene regulatory network inference: data integration in dynamic models-a review. *Biosystems*, **96**(1), 86–103.
- Heinrich, R. and Schuster, S. (1996). *The Regulation of Cellular Systems*. Chapman and Hall, New York, NY, USA.
- Hill, A. V. (1910). The possible effects of the aggregation of the molecules of haemoglobin on its dissociation curves. *Journal of Physiology*, **40**(4), iv–vii.
- Hinze, T., Hayat, S., Lenser, T., Matsumaru, N., and Dittrich, P. (2007). Hill Kinetics meets P Systems: A Case Study on Gene Regulatory Networks as Computing Agents *in silico* and *in vivo*. In G. Eleftherakis, P. Kefalas, and G. Paun, editors, *Proceedings of the Eight Workshop on Membrane Computing*, pages 363–381. SEERC.
- Hucka, M., Finney, A., Sauro, H., and Bolouri, H. (2001). Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions. Technical report, Systems Biology Workbench Development Group ERATO Kitano Systems Biology Project Control and Dynamical Systems, MC 107-81.
- Hucka, M., Finney, A., Sauro, H., and Bolouri, H. (2003a). Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions. Technical Report 2, Systems Biology Workbench Development Group JST ERATO Kitano Symbiotic Systems Project Control and Dynamical Systems, MC 107-81, California Institute of Technology, Pasadena, CA, USA.

Bibliography

- Hucka, M., Finney, A., Sauro, H. M., Bolouri, H., Doyle, J. C., Kitano, H., Arkin, A. P., Bornstein, B. J., Bray, D., Cornish-Bowden, A., Cuellar, A. A., Dronov, S., Gilles, E. D., Ginkel, M., Gor, V., Goryanin, I. I., Hedley, W. J., Hodgman, T. C., Hofmeyr, J.-H. S., Hunter, P. J., Juty, N. S., Kasberger, J. L., Kremling, A., Kummer, U., Le Novère, N., Loew, L. M., Lucio, D., Mendes, P., Minch, E., Mjolsness, E. D., Nakayama, Y., Nelson, M. R., Nielsen, P. F., Sakurada, T., Schaff, J. C., Shapiro, B. E., Shimizu, T. S., Spence, H. D., Stelling, J., Takahashi, K., Tomita, M., Wagner, J. M., Wang, J., and the rest of the SBML Forum (2003b). The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. *Bioinformatics*, **19**(4), 524–531.
- Hucka, M., Finney, A. M., Hoops, S., Keating, S. M., and Le Novère, N. (2007). Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. Technical Report 1.
- Hucka, M., Finney, A., Hoops, S., Keating, S. M., and Le Novère, N. (2008). Systems biology markup language (SBML) Level 2: structures and facilities for model definitions. Technical report, Nature Precedings.
- Hucka, M., Bergmann, F. T., Hoops, S., Keating, S. M., Sahle, S., Schaff, J. C., Smith, L., and Wilkinson, D. J. (2010). The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Technical report, Nature Precedings.
- Juty, N., Le Novère, N., and Laibe, C. (2012). Identifiers.org and MIRIAM Registry: community resources to provide persistent identification. *Nucleic Acids Research*, **40**(D1), D580–D586.
- Juty, N., Laibe, C., and Le Novère, N. (2013). Controlled annotations for systems biology. In M. V. Schneider, editor, *In Silico Systems Biology*, volume 1021, pages 227–245. Springer.
- Kanehisa, M. and Goto, S. (2000). KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Research*, **28**(1), 27–30.
- Keller, R., Dörr, A., Tabira, A., Funahashi, A., Ziller, M. J., Adams, R., Rodriguez, N., Le Novère, N., Hiroi, N., Planatscher, H., Zell, A., and Dräger, A. (2013). The systems biology simulation core algorithm. *BMC Syst Biol.*
- Keller, R., Dörr, A., Zell, A., and Dräger, A. (2014). SBMLsimulator: a Java tool for model simulation and parameter estimation in systems biology. *Bioinformatics*. Under revision.
- Krebs, O., Golebiewski, M., Kania, R., Mir, S., Saric, J., Weidemann, A., Wittig, U., and Rojas, I. (2007). SABIO-RK: A data warehouse for biochemical reactions and their kinetics. *Journal of Integrative Bioinformatics*, **4**(1).
- Laible, C. and Le Novère, N. (2007). MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology. *BMC Systems Biology*, **13**(58), 58–67.

Bibliography

- Le Novère, N., Finney, A., Hucka, M., Bhalla, U. S., Campagne, F., Collado-Vides, J., Crampin, E. J., Halstead, M., Klipp, E., Mendes, P., Nielsen, P., Sauro, H., Shapiro, B. E., Snoep, J. L., Spence, H. D., and Wanner, B. L. (2005). Minimum information requested in the annotation of biochemical models (MIRIAM). *Nature Biotechnology*, **23**(12), 1509–1515.
- Le Novère, N., Courtot, M., and Laibe, C. (2006). Adding semantics in kinetics models of biochemical pathways. In C. Kettner and M. G. Hicks, editors, *2nd International ESCEC Workshop on Experimental Standard Conditions on Enzyme Characterizations*. Beilstein Institut, Rüdesheim, Germany, pages 137–153, Rüdesheim/Rhein, Germany. ESEC.
- Le Novère, N., Hucka, M., Mi, H., Moodie, S., Schreiber, F., Sorokin, A., Demir, E., Wegner, K., Aladjem, M. I., Wimalaratne, S. M., Bergmann, F. T., Gauges, R., Ghazal, P., Kawaji, H., Li, L. M., Lu, Y., Villéger, A., Boyd, S. E., Calzone, L., Courtot, M., Dogrusoz, U., Freemann, T. C., Funahashi, A., Ghosh, S., Jouraku, A., Sohyoung, K., Kolpakov, F., Luna, A., Sahle, S., Schmidt, E., Watterson, S., Wu, G., Goryanin, I., Kell, D. B., Sander, C., Sauro, H., Snoep, J. L., Kohn, K., and Kitano, H. (2009). The Systems Biology Graphical Notation. *Nature biotechnology*, **27**(8), 735–741.
- Li, C., Donizelli, M., Rodriguez, N., Dharuri, H., Endler, L., Chelliah, V., Li, L., He, E., Henry, A., Stefan, M. I., Snoep, J. L., Hucka, M., Le Novère, N., and Laibe, C. (2010). Biomodels database: An enhanced, curated and annotated resource for published quantitative kinetic models. *BMC Syst Biol*, **4**, 92.
- Liebermeister, W. and Klipp, E. (2006). Bringing metabolic networks to life: convenience rate law and thermodynamic constraints. *Theor Biol Med Model*, **3**(42), 41.
- Liebermeister, W., Uhlendorf, J., and Klipp, E. (2010). Modular rate laws for enzymatic reactions: thermodynamics, sensitivities, and implementation. *submitted to Bioinformatics*.
- Michaelis, L. and Menten, M. L. (1913). Kinetik der Invertinwirkung. *Biochemische Zeitschrift*, **49**, 333–369.
- Radde, N. (2007). *Modeling Non-Linear Dynamic Phenomena in Biochemical Networks*. Ph.D. thesis, Faculty of Mathematics and Natural Sciences, University of Cologne, Germany.
- Radde, N. and Kaderali, L. (2007). *Bayesian Inference of Gene Regulatory Networks Using Gene Expression Time Series Data*, volume 4414/2007, chapter 1, pages 1–15. Springer Berlin/Heidelberg.
- Rojas, I., Golebiewski, M., Kania, R., Krebs, O., Mir, S., Weidemann, A., and Wittig, U. (2007). Storing and Annotating of Kinetic Data. *In Silico Biology*, **7**, 37–44.
- Savageau, M. A. (1969). Biochemical systems analysis. I. Some mathematical properties of the rate law for the component enzymatic reactions. *J Theor Biol*, **25**(3), 365–369.

Bibliography

- Segel, I. H. (1993). *Enzyme Kinetics—Behavior and Analysis of Rapid Equilibrium and Steady-State Enzyme Systems*. Wiley-Interscience, New York, NY, USA.
- Spieth, C., Streichert, F., Speer, N., and Zell, A. (2004). Optimizing Topology and Parameters of Gene Regulatory Network Models from Time-Series Experiments. In *Proceedings of the Genetic and Evolutionary Computation Conference (GECCO 2004)*, volume 3102 (Part I) of *LNCS*, pages 461–470.
- Spieth, C., Hassis, N., Streichert, F., Supper, J., Beyreuther, K., and Zell, A. (2006). Comparing Mathematical Models on the Problem of Network Inference. In *Proceedings of the 8th annual conference on Genetic and evolutionary computation*, GECCO '06, pages 279–286, New York, NY, USA. ACM.
- Töpfer, S., Guthke, R., Driesch, D., Wötzl, D., and Pfaff, M. (2007). The NetGenerator Algorithm: reconstruction of gene regulatory networks. In K. Tuyls, R. Westra, Y. Saeys, and A. Nowé, editors, *Knowledge Discovery and Emergent Complexity in Bioinformatics*, volume 4366 of *Lecture Notes in Computer Science*.
- Tournier, L. (2005). Approximation of dynamical systems using s-systems theory: application to biological systems. In *ISSAC '05: Proceedings of the 2005 international symposium on Symbolic and algebraic computation*, pages 317–324, New York, NY, USA. ACM press.
- Vu, T. T. and Vohradský, J. (2007). Nonlinear differential equation model for quantification of transcriptional regulation applied to microarray data of *saccharomyces cerevisiae*. *Nucleic Acids Res*, **35**(1), 279–287.
- Weaver, D. C., Workman, C. T., and Stormo, G. D. (1999). Modeling regulatory networks with weight matrices. In *Pacific Symposium on Biocomputing*, volume 4, pages 112–123. World Scientific Publishing.
- Wittig, U., Golebiewski, M., Kania, R., Krebs, O., Mir, S., Weidemann, A., Anstein, S., Saric, J., and Rojas, I. (2006). SABIO-RK: Integration and Curation of Reaction Kinetics Data. In U. Leser, F. Naumann, and B. Eckmann, editors, *Data Integration in the Life Sciences*, pages 94–103. Springer Berlin/Heidelberg.
- Wittig, U., Kania, R., Golebiewski, M., Rey, M., Shi, L., Jong, L., Algaa, E., Weidemann, A., Sauer-Danzwith, H., Mir, S., Krebs, O., Bittkowski, M., Wetsch, E., Rojas, I., and Müller, W. (2012). SABIO-RK—database for biochemical reaction kinetics. *Nucleic Acids Res*, **40**(Database issue), D790–D796.
- Wolf, J., Passarge, J., Somsen, O. J. G., Snoep, J. L., Heinrich, R., and Westerhoff, H. V. (2000). Transduction of intracellular and intercellular dynamics in yeast glycolytic oscillations. *Biophys J*, **78**(3), 1145–1153.

Bibliography

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

Wrzodek, C., Büchel, F., Ruff, M., Dräger, A., and Zell, A. (2013). Precise generation of systems biology models from kegg pathways. *BMC Syst Biol*, **7**(1), 15.

Index

Symbols

- Application Programming Interface* (API) .. 3, 5, 10, 20, 33–36, 38, 39, 62, 83–85, 89
Biological Pathway Exchange Language (BioPAX) 2
GNU General Public License (GPL) 76
Graphical User Interface (GUI) 3–5, 10, 13, 20, 24, 31, 37, 39–41, 53, 54, 84, 88–90
Integrated Development Environment (IDE) .. 35
Java™ Archive (JAR) 5–8, 40, 41
Java™ Development Kit (JDK) 6
Java™ Virtual Machine (JVM) 5–7, 41, 74
Kyoto Encyclopedia of Genes and Genomes (KEGG) . 23, 29, 38, 44, 61, 64, 71, 85
GNU Lesser General Public License (LGPL) 76
Minimal Information Required In the Annotation of Models (MIRIAM) 1, 23, 55, 63, 64, 71, 72, 85
Portable Document Format (PDF) 89
System for the Analysis of Biochemical Pathways – Reaction Kinetics (SABIO-RK) 2, 4, 5, 13, 14, 20–24, 28, 31, 38–40, 43, 52, 53, 62, 71–74, 78, 89
Systems Biology Graphical Notation (SBGN) 65, 66, 82
Systems Biology Ontology (SBO) ... 1, 8, 17, 36, 55, 59, 63–65, 68, 71, 85
Uniform Resource Locator (URL) 71, 72
Extended HTML (XHTML) 32, 80
Extended Markup Language (XML) 30, 72

A

- ant 8

B

- BioModels database 15, 19, 20, 23, 24
BioPAX2SBML 2

C

- CellDesigner .. 2, 5, 8–10, 14–18, 20, 28, 29, 36, 62, 63, 71, 81, 83–85, 89

E

- Eclipse 35

G

- Galaxy 30
Garuda . 2, 5, 9, 10, 15, 29, 58, 62, 63, 76, 89, 90
Gene 1, 3, 42, 46, 59, 60, 64, 65, 68, 69

J

- Java™ 2, 5–7, 10, 35, 41, 74, 75, 83, 86, 88
Java™ Web Start 2, 5, 10, 88
JSBML .. 2, 5, 7, 8, 14, 33, 36, 41, 42, 62, 63, 76, 83, 85, 88–90
JUnit 76, 89

K

- KEGGtranslator 2, 29

L

- Language pack
Chinese 41, 77, 89
English 41, 89
German 41, 89
libSBML .. 2, 5, 7, 10, 13, 36, 41, 42, 62, 63, 76, 80, 83, 84, 88

M

- MathML 1

N

- NetGenerator 46–48, 60

O

- Operating System . 4–6, 8–11, 13, 15, 30, 34, 40, 89
Linux 6–8, 10, 12–14, 24, 26, 40

	Index
1	
2	
3	
4	
5	
6	
7	
8	LD_LIBRARY_PATH 7
9	Ubuntu 6
10	Mac OS X .. 6–8, 10, 12–14, 18, 24, 26, 30, 40, 74, 75, 89
11	DYLD_LIBRARY_PATH 7
12	Microsoft Windows . 6, 8, 10, 12–14, 24, 26, 40, 41
13	PATH 7
14	Windows 7 6
15	Unix 7, 40
16	
17	
18	P
19	Path to models project 3
20	protein 65, 69
21	
22	R
23	RNA 44, 46, 64, 65, 68, 69, 82
24	
25	
26	
27	
28	
29	
30	
31	
32	
33	
34	
35	
36	
37	
38	
39	
40	
41	
42	
43	
44	
45	
46	
47	
48	
49	
50	
51	
52	
53	
54	
55	
56	
57	
58	
59	
60	

asRNA 64
mRNA 64, 68

S

SBML . 1–3, 5, 10, 13–15, 17, 20, 24, 26–30, 32,
33, 36–38, 40–42, 45, 46, 54, 55, 58,
62, 63, 70–72, 83–85, 87–90

SBML2LATEX .. 1, 3, 4, 15, 31, 54, 55, 76, 80, 84,
89

SBMLsimulator 3, 29

T

transcription 64, 65, 68

translation 64, 65, 68

Z

ZIP 10