

Presentation by Michael Hucka at
COMBINE 2011

http://co.mbine.org/events/COMBINE_2011

Sunday, 4 September 2011

General updates about SBML and SBML Team activities

Michael Hucka and the rest of the SBML Team

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Outline

1. SBML.org Updates
2. SBML Development
3. SBML Team Software

SBML.org updates

SBML Software Guide changes

SBML Software Guide - SBML.org

http://sbml.org/SBML_Software_Guide

SBML.org The Systems Biology Markup Language

News Documents Downloads Forums Facilities Community Events About

Parent pages: [SBML.org](#)

SBML Software Guide

The following pages describe SBML-compatible software packages known to us. We offer different ways of viewing the information, all drawn from the same underlying data collected from the systems' developers via our [software survey](#). The *Matrix* provides a table listing all known software and a variety of their features; the *Summary* provides general descriptions of most of the software; and the *Showcase* provides a sequential slideshow of a subset of the software.

Number of software packages listed in the matrix today: **230**.

Go to the SBML Software Matrix

Go to the SBML Software Summary

Go to the SBML Software Showcase

Please [use the survey form](#) to notify us about additions and suggestions.

[\[edit\]](#) **Historical trend**

The following graph shows the total number of known SBML-compatible software packages each year, as counted by the SBML Team. The counts shown are for approximately the middle of each year.

Nature Precedings : doi:10.1038/npre.2011.6345.1 : Posted 6 Sep 2011

New version of the SBML software survey

SBML Software Guide/SBML Software Details Questionnaire - SBML.org

http://sbml.org/SBML_Software_Guide/SBML_Software_De Google

SBML.org The Systems Biology Markup Language

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Parent pages: [SBML.org](#) / [SBML Software Guide](#)

SBML Software Details Questionnaire

General information about your software

1 / 6

Please fill out this form to tell us about your SBML-compatible software. We will use this information to update the **SBML Software Guide**. We may also use the information to write **papers about SBML software**.

*What is **your name**? (This is to verify the info you enter in this form; your name will not be put in the SBML Software Guide.)*

*What is **your email address**? (Again, this is to verify the information you enter; your name will not be put in the Guide.)*

*What is the public **contact address** for the software? Generally this is an email address (possibly the same as the one above, if you wish), although it can be an online help form instead.*

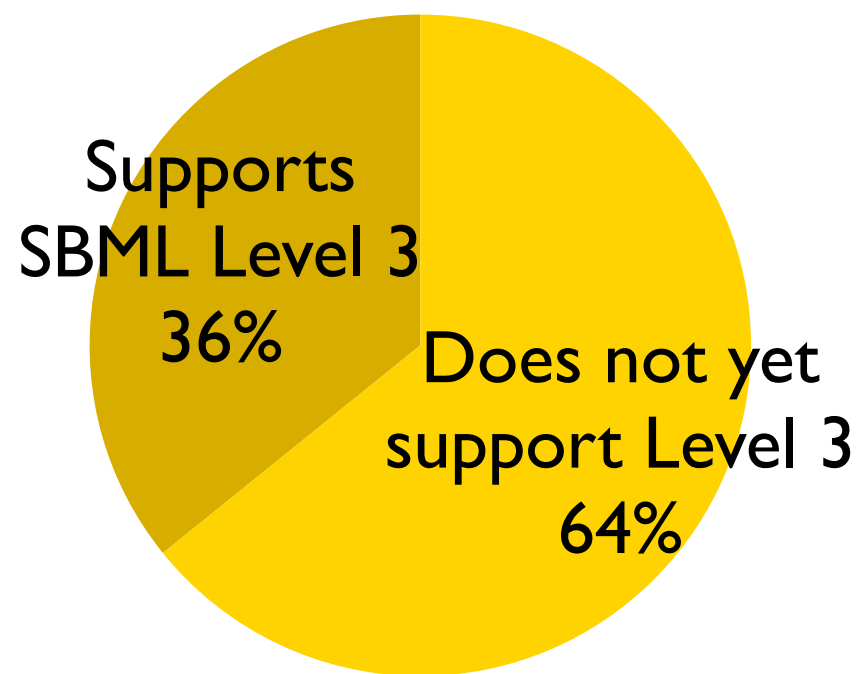
Forthcoming in the SBML Software Guide

More data about SBML software in the world

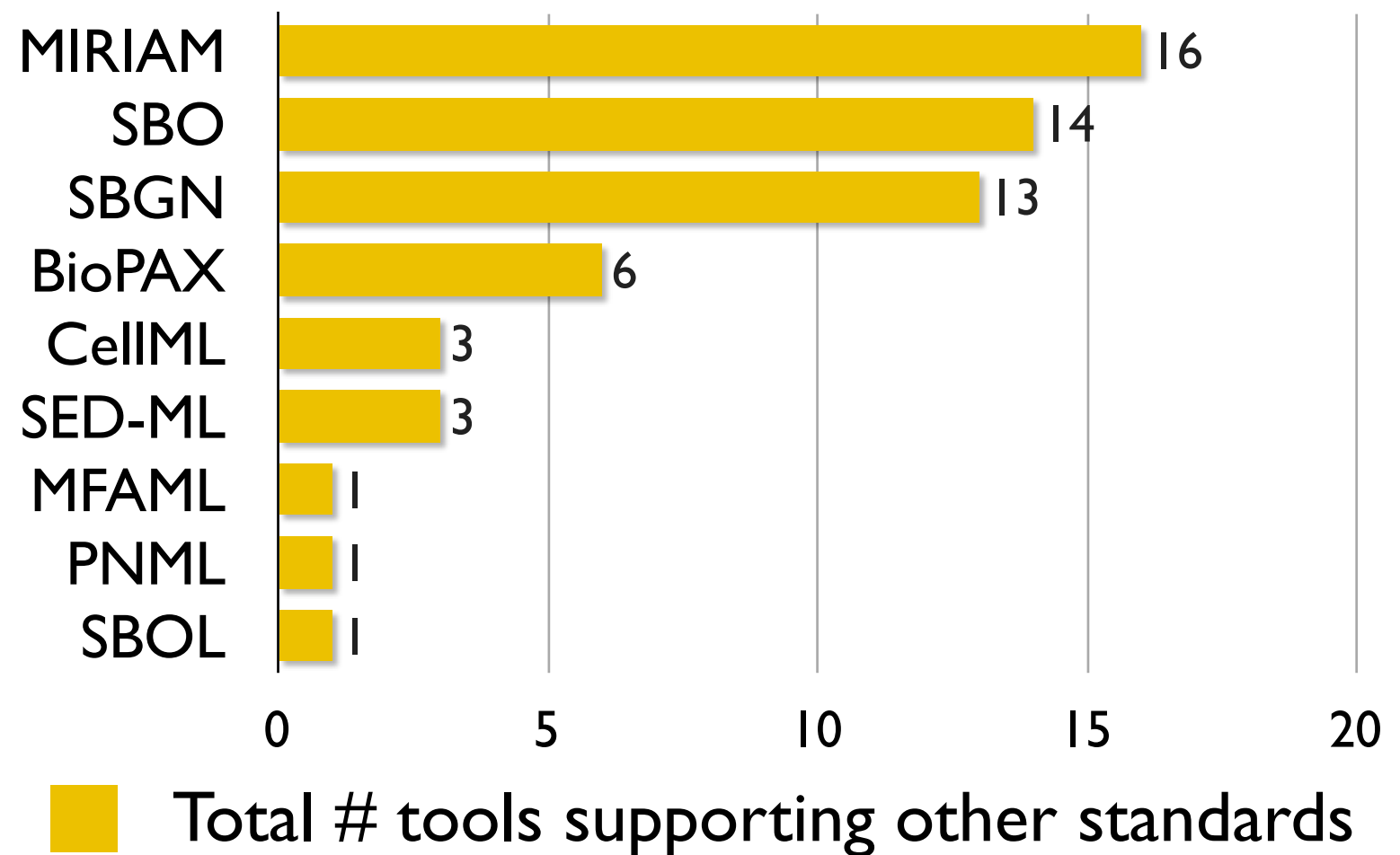
More *accurate* data about SBML software in the world

Statistics about SBML software in the world

- Examples: data on 81 software tools reported between May–July



Percentage supporting
SBML Level 3



Updated SBML Level 3 package activity table

Name	Label	Description	PWG list	Prop. Stat.	Spec. Stat.	libSBML
Level 3 Core	core	The core portion of SBML Level 3.	sbml-discuss			
Layout	layout	Support for storing the spatial topology of a model's network diagram. Adjunct to the <i>render</i> package, below.	sbml-layout			
Flux Balance Constraints	fbc	Support for constraint-based (a.k.a. steady-state) models.	sbml-flux			
Rendering	render	Support for defining the graphical symbols and glyphs used in a diagram of the model. Adjunct to the <i>layout</i> package above.	sbml-render			
Hierarchical Model Composition	comp	A means for defining how a model is composed from other models.	sbml-comp			
Qualitative Models	qual	Support for models wherein species don't represent quantity of matter & processes are not reactions per se. (E.g.: Boolean nets.)	sbml-qual			
Annotations	annot	Support for richer annotation syntax than the regular annotations in SBML Level 3 Core.	sbml-annot			
Spatial Processes	spatial	Support for describing processes that involve a spatial component, and describing the geometries involved.	sbml-spatial			
Groups	groups	Support for groups of SBML entities. This partially replaces the Level 2 SpeciesType and CompartmentType constructs with a	sbml-groups			
Required Elements	req	elements that have been changed by the	sbml-required			

<http://sbml.org/Community/Wiki>

SBML Development

SBML Development Process Progress

Documents/SBML Development Process - SBML.org

http://sbml.org/Documents/SBML_Development_F Reader Google

Process/SBML Development Proc... Development Process - SBML.org

SBML.org The Systems Biology Markup Language

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SBML Development Process

An intrinsic aspect of SBML's development has been the adoption of a participative, community-oriented approach. In the early years of SBML, this process was highly informal. The use of SBML has grown to the point where its original, informal approach to development is no longer sufficient to meet the needs of the SBML community and the continued evolution of SBML. Beginning in 2003, the SBML Team and SBML Editors have been working to put into place a more formal organization and systematic process, one that will be less ambiguous and subjective and more responsive to the needs of the SBML community. This page describes the plans for this *SBML Development Process*, and the current status of its implementation.

This SBML Development Process is being followed as of mid-2008.

The process described here evolved from previous proposals and discussions, and supercedes all previous SBML Development Process descriptions and proposals. (Previous proposals were presented at the following SBML Forum meetings: the **7th**, the **10th**, the **11th**, and the **12th**.) Some readers may recall that previous proposals involved additional components not described here (such as the formation of "Architectural Boards"; these ideas were dropped because they were too complex and would have complicated the process of simplifying the SBML Development Process as much as possible.

Contents [hide]

- 1 Goals and Motivations for SBML
- 2 Goals of the SBML Development Process
- 3 SBML Community Organization
 - 3.1 The SBML Forum
 - 3.1.1 Requirements for membership
 - 3.1.2 Conduct of meetings
 - 3.2 The SBML Editors
 - 3.2.1 Responsibilities of SBML Editors
 - 3.2.2 Terms for SBML Editors
 - 3.2.3 Election process for SBML Editors
 - 3.2.4 Selection of the Chair of the SBML Editors
 - 3.3 The SBML Team
- 4 SBML Development Procedures and Guidelines
 - 4.1 Development Roadmap
 - 4.2 General Procedures and Guidelines
 - 4.2.1 Public participation
 - 4.2.2 Communication and transparency
 - 4.2.3 Archiving proposals
 - 4.2.4 SBML Levels, Versions, and Releases
 - 4.2.5 Process for SBML Level 2

http://sbml.org/Documents/SBML_Development_Process

Elaboration of process for Level 3 packages

The screenshot shows a web browser window with the address bar containing the URL http://sbml.org/Documents/SBML_Development_Process/. The browser tabs show 'Process/SBML Development Proc...' and 'Development Process - SBML.org'. The page header features the SBML.org logo and the text 'The Systems Biology Markup Language'. A navigation menu includes links for News, Documents, Downloads, Forums, Facilities, Community, Events, and About, along with a search box labeled 'Google Site Search...'. The main content area has a breadcrumb trail: 'Parent pages: SBML.org / Documents / SBML Development Process'. The title is 'SBML Development Process for SBML Level 3'. The text explains that the overall process is on a separate page and that this page focuses on specific aspects of Level 3 development. It notes that SBML Level 3 is modular, with a core set of features and optional packages. Packages are developed in two stages: proposal and specification. A 'Contents' box on the right lists: '1 The package proposal development stage' and '2 The package specification development stage'. The text further explains that proposals can be produced at low cost, while specifications require more effort and software implementations. At the bottom, there is an '[edit] The package proposal development stage' section, which states that as of December 2008, a core specification for Level 3 was in development and no official packages existed yet.

[\[edit\]](#) Contents of the voting form

The voting form for package proposals will reflect the principles described in the section on **architectural principles**. To encourage thoughtful and thorough consideration of the proposed packages with respect to those **architectural principles**, the form will request voters to address the points individually, and ask for an overall assessment as a separate question. The following is an outline of the basic content of the voting form:

Utility: the package addresses a problem whose solution SBML users are likely to find useful.

Agree Disagree Insufficient information Abstain

Biological orientation: the package's overall aim is to support the description of biological processes and phenomena.

Agree Disagree Insufficient information Abstain

Coherence: the package extends SBML in a way that follows naturally from Level 3 Core and other packages.

Agree Disagree Insufficient information Abstain

Orthogonality: within reason, the package does not duplicate the purpose or data captured by other packages.

Agree Disagree Insufficient information Abstain

Overall assessment of the package proposal:

Accept: proposal addresses a need that SBML should cover, and the approach clearly follows the stated principles

Reject: proposal does not address a need that SBML should cover

Revise: approach either does not follow the stated principles, or there is insufficient information to tell if it does

Abstain: I cannot fully assess the proposal as given, or do not wish to state an opinion

In addition to the above, the voting form will include comment boxes that allow voters to provide more detailed feedback about the proposal and why they voted they way they did.

[\[edit\]](#) Formula for assessing the outcome

To assess the outcome of the vote, the SBML Editors will use only the question titled "Overall assessment of the package proposal" in the form **described above**. The formula to be used is as follows:

1. For the decision to be *accept*, 50% or more of the non-abstaining voters must have chosen the *accept* option.
2. For the decision to be *reject*, more than 50% of the non-abstaining voters must have chosen the *reject* option.

Further elaboration of package voting criteria

Writing L3 package specs

Proper draft spec. for Hierarchical Model Composition almost ready

New LaTeX templates for SBML package specifications

SBML Level 3 Package Specification

Hierarchical Model Composition

Lucian P. Smith
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Version 1 (Draft)

This is a working draft of the specification for the SBML Level 3 package "comp". It is not a normative document. Please send comments and other feedback to the Package Working Group mailing list, sbml-comp@lists.sourceforge.net.

The latest release, past releases, and other materials related to this specification are available at http://sbml.org/Documents/Specifications/Packages/Hierarchical_Model_Composition

This release of the specification is available at http://sbml.org/Documents/Specifications/Packages/Hierarchical_Model_Composition/Draft_Sep_2011



SBML Level 3 Package Specification

SBMLPACKAGE: A LaTeX Class for SBML Package Specifications


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18 August 2011

Version 1.0

The latest release, past releases, and other materials related to this specification are available at

This release of the specification is available at



SBML Editor vote coming up



Chris



Jim



Lucian



Sarah



Frank



Yours truly

One new editor being replaced

- Nominations & voting open to anyone on sbml-discuss mailing list

SBML Editor vote coming up



Chris



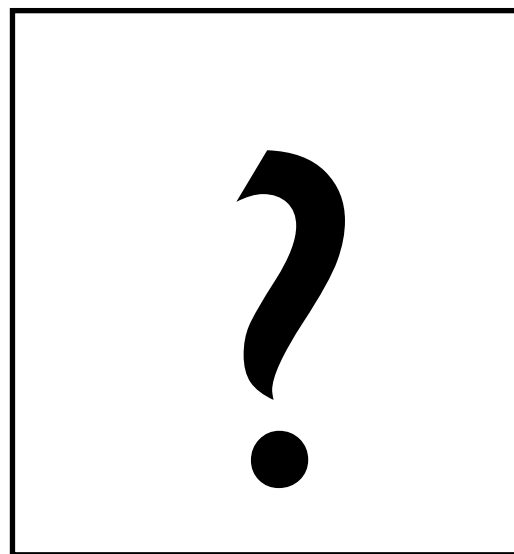
Jim



Lucian



Sarah



Frank



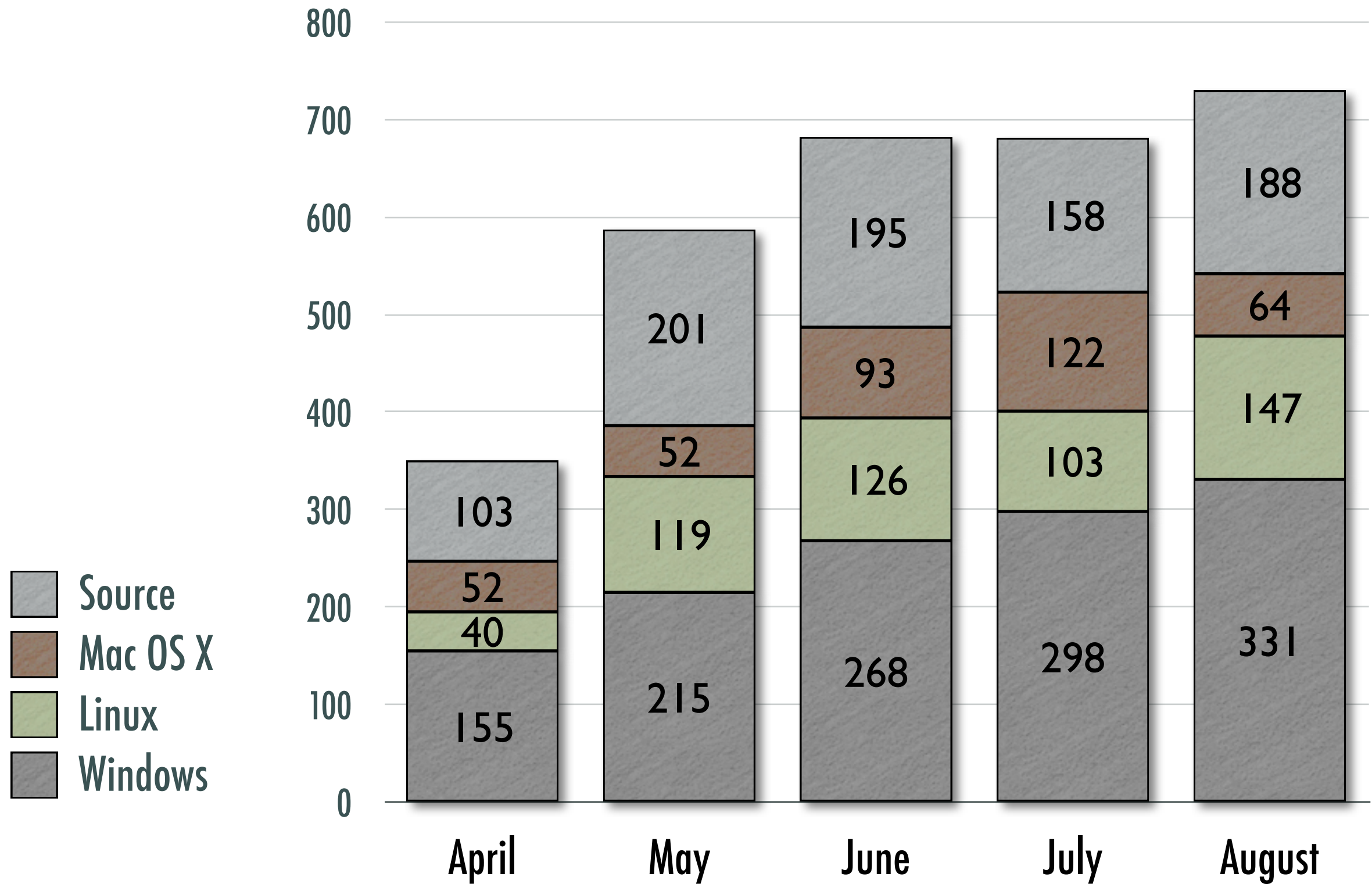
Yours truly

One new editor being replaced

- Nominations & voting open to anyone on sbml-discuss mailing list

SBML Team Software

libSBML 5.0.0: over 3400 downloads since April



Downloads of all libSBML 5.0.0 distributions since April

Other software news

LibSBML, JSBML, SBMLToolbox, Online SBML Validator, others...

... Listen to Sarah, Frank, Nico & Andreas