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To the editors of Oxford Bioinformatics

Submission of our manuscript about SBMLsqueezer 2

Dear Sir or Madam,

We like to submit an applications note about the latest version of the program SBMLsqueezer. This program has continuously been developed through the past eight years. It was the driving force for many developments in the field of systems biology and triggered various collaborative efforts. One recent large-scale community effort, in which this program was used, was the path2models project. In this effort kinetic draft models have been created for all pathways in the KEGG database and even more. Another prominent example for a successful offspring of the development of SBMLsqueezer is the library JSBML, which started as SBMLsqueezer's internal data structure and has now become an international community effort.

The original paper about SBMLsqueezer from 2008 has been downloaded more than 8,000 times and, according to Google Scholar, it was cited 39 times. Since the original release, the program has been completely changed. The most recent update publication about SBMLsqueezer 1.3 from 2010 does by far not cover all the improvements. The new version comes with a comprehensive Users' Guide (93 pages) and comprises diverse new features, which have never been described in any prior publication. For instance, the SABIO-RK access module is completely new, the Garuda interface is recent, unit consistency have been significantly improved and also have the kinetic equations. In addition to that, SBMLsqueezer can now again be used as a plug-in for CellDesigner, but also as a stand-alone program and a programming library (amongst other use-cases). This whole set of scenarios is new and has not been described before. In particular, the original publication from 2008 only focuses on CellDesigner's features, for which the software has been designed as a plug-in. Already the title of the previous work "SBMLsqueezer: a CellDesigner plug-in to generate kinetic rate equations for biochemical networks" is too restrictive and does not cover the capabilities of the program anymore.

With this rich set of possible use-cases and the comprehensive Users' Guide at hand, we believe that SBMLsqueezer has become a versatile and helpful tool for researchers working in kinetic modeling and related fields. This publication should make potential users aware of the capabilities of the program and also provide a citable resource, which is up to date.

With best regards


Dr. Andreas Dräger