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Universität Tübingen, WSI, Andreas Dräger, Sand 1, 72076 Tübingen
To the editors of Oxford Bioinformatics

The submission of our manuscript about the software library JSBML

Dear Sir or Madam,

The modeling language SBML has become the most popular and most frequently used file format for storing and exchanging mathematical models of biological processes. Much of this success has been due to the very early availability of the supporting software library libSBML. The programming language Java has also become very popular and is amongst the most frequently used programming languages in research and university education. One of the advantages of Java is the free availability of run time environments on practically any platform. The library libSBML provides a Java binding around its internal C++ core to allow users to implement programs using SBML in Java as well and to avoid a duplication of effort. However, this strongly limits the platform independence of Java, makes internal states of the program almost invisible when doing debugging, and makes Java Web Start applications almost impossible. For these reasons, some groups mounted their own re-implementations of parts of libSBML in Java according to the individual needs of the particular research group.

In May 2009 the SBML team conducted a survey on the web site sbml.org, in which it was asked, among other questions, what kind of software development would be useful for the future of SBML. As one result, the community wished the development of an entirely Java-based implementation of libSBML. Around this time, different work groups combined their existing code. After almost two years of development, we can now present the result, JSBML. Instead of a simple code porting from C++ to Java, JSBML was entirely designed from scratch with respect to the Java programming library. In this way, JSBML tries to satisfy two important needs: it should feel like other Java libraries and also be compatible to libSBML. We believe that many other research groups will benefit from this effort. Since its first release in February 2011, JSBML has already been downloaded 138 times by users in 19 different countries.

For these reasons, we believe, this work should be published in Bioinformatics. This would increase the visibility of the software library JSBML and also reduce duplications of effort.

Best wishes

Andreas Dräger and colleagues