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To the editors of Oxford Bioinformatics

**The submission of our manuscript about the
Simulation Core Library for quantitative
biology**

Dear Sir or Madam,

In recent years the dynamic simulation of biological networks has become an integral part of research in biology. National and international research projects, such as the Virtual Liver Network in Germany, try to find organ-wide mathematical descriptions of all processes within biological entities. For a successful implementation of ambitious efforts like this, bioinformaticians require two important tools: First, well-defined and standardized interfaces between the different working groups. The availability of standards such as SBML, CellML, or SBGN satisfies these needs. Second, customized software must be developed in order to evaluate the systems encoded in these data formats, thereby integrating various kinds of biological data.

The growing complexity due to the ongoing development of these description languages makes it hardly possible to create customized software from scratch within the regular PhD period or the average duration of a systems-biology oriented research project.. Existing implementations are mostly only available in conjunction with graphical user interfaces, depend on commercial licenses, or are written in platform-dependent programming languages. All this makes re-use in customized applications very difficult. To overcome these limitations and to provide the research community with a flexible library for the numerical simulation of even complex differential equation systems, an international effort was implemented with the aim to develop a new Java-based API library. Its development took almost five years because the effort started based on libSBML, but it became soon evident that the Simulation Core Library would emerge as one of the driving forces for the development of the library JSBML. During this time, collaboration with teams from the CellML community has been established to open the door for the implementation of a real community-driven, platform independent, internationally maintained library that is not bound to a particular data structure.

By also supporting the emerging standard SED-ML that facilitates re-use and reproducibility of simulation experiments, the library provides up-to date standards and will be of great benefit for the systems biology community.

For these reasons, we believe, this work should be published in Bioinformatics. Its publication would increase the visibility of the Simulation Core Library and also reduce duplications of effort.
Best wishes

Andreas Dräger and colleagues