

# SED-ML Web Tools: Generate, modify and export standard-compliant simulation studies.

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## ABSTRACT

The Simulation Experiment Description Markup Language (SED-ML) is a standardized format for exchanging simulation studies independently of software tools. We present the SED-ML Web Tools, a software that supports SED-ML Level 1 Version 2, including complex modifications and co-simulation of SBML and CellML models. This online application allows for creating, editing, simulating and validating SED-ML documents. It lowers the bar on working with SED-ML documents and helps users create valid simulation descriptions for models in CellML and SBML formats.

**Availability and Implementation:** [sysbioapps.dyndns.org/SED-ML\\_Web\\_Tools](http://sysbioapps.dyndns.org/SED-ML_Web_Tools).

**Further information:** [sysbioapps.dyndns.org/SED-ML\\_Web\\_Tools/Services/SedMLService.asmx](http://sysbioapps.dyndns.org/SED-ML_Web_Tools/Services/SedMLService.asmx).

## INTRODUCTION

In 2011, the *Simulation Experiment Description Markup Language* (SED-ML [Waltemath et al., 2011]) was proposed as an exchange format to improve the reproducibility of simulation experiments in systems biology. Today, SED-ML is used as a *de facto* standard for machine-readable simulation descriptions. SED-ML descriptions typically consist of five major blocks of information: nomination of the models of interest; initialisation of a model's variables; specification of the simulation algorithm; post-processing of the obtained results; and definition of the desired plots and numerical reports [Bergmann et al., 2015]. Libraries to read and write SED-ML are provided by the community and some software tools already consume and export SED-ML files, e.g. BioUML [Kolpakov, 2002], COPASI [Hoops et al., 2006], JWS Online [Olivier and Snoep, 2004], or Tellurium [Sauro et al., 2016]. However, tool support is still limited and it remains challenging to derive simulation descriptions given a model, to update a SED-ML file to describe a different experimental setup, and to quickly investigate the behaviour of a model that is shared on the internet.

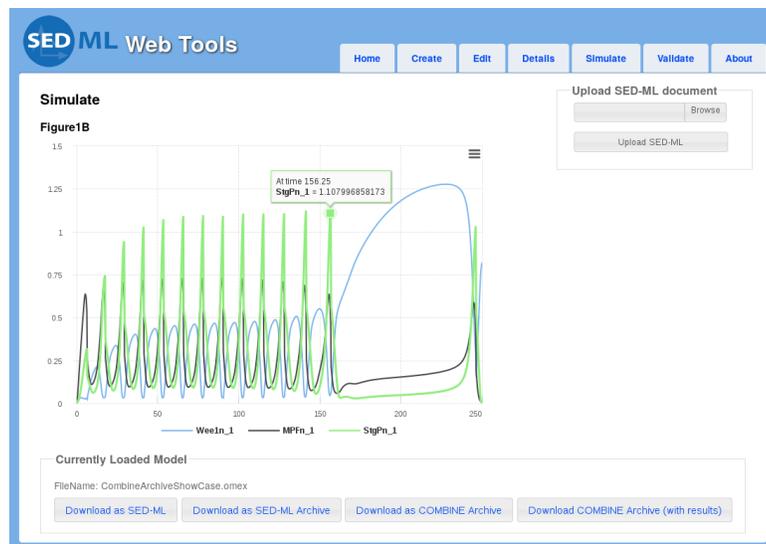
## RESULTS AND DISCUSSION

The SED-ML Web Tools are an online suite of tools for creating, editing, simulating and validating standard-compliant simulation studies. The tools are implemented in ASP.NET MVC<sup>1</sup> and provide a web based interface to simulation studies using the SED-ML format. They are based on libSedML<sup>2</sup>, a .NET library that is also available independently.

Users of the SED-ML Web Tools can easily *create* initial SED-ML files for a given model encoded in SBML format [Hucka et al., 2003]. A model can be specified by (i) uploading it to the portal, (ii) providing a link to a web server delivering the model file, or (iii) providing a unique

<sup>1</sup>[www.asp.net/mvc](http://www.asp.net/mvc)

<sup>2</sup>[libsedml.sf.net](http://libsedml.sf.net)



**Figure 1.** Screenshot of the SED-ML Web Tools simulating a cell cycle model published by Calzone et al. [2007]. The model and other information that is necessary to run the study are provided through a link to a fully featured COMBINE archive published on figshare [Scharm and Touré, 2016]. The figure can be reproduced in SED-ML Web Tools by clicking on the following link: [sysbioapps.dyndns.org/SED-ML\\_Web\\_Tools/Home/SimulateUrl?url=http://ndownloader.figshare.com/files/5370005](http://sysbioapps.dyndns.org/SED-ML_Web_Tools/Home/SimulateUrl?url=http://ndownloader.figshare.com/files/5370005).

resource identifier (URN). Once the the model is obtained, the SED-ML Web Tools scan the model's structure for parameters, derive initial values and generate a working SED-ML file using a default configuration (e.g., for a time course simulation). The integrated *editor* then allows for revising and updating the simulation description. For example, it is sometimes necessary to modify simulation descriptions in order to study an alternative behaviour of the system or to generate plots for different parametrisations of the model. The built-in editor supports the SED-ML XML format and a Python-based Script Language [Bergmann, 2011]. Using libSedML, SED-ML files can immediately be *simulated* on the server and the results are presented in the web browser (Figure 1). The SED-ML Web Tools run SBML models using RoadRunner [Bergmann and Sauro, 2006], Gillespie, and LPsolve. CellML models [Cuellar et al., 2003] are run using CSim<sup>3</sup>. Developed simulation studies can be exported as (i) standalone SED-ML descriptions; (ii) SED-ML archives; COMBINE archives [Bergmann et al., 2014] (iii) with or (iv) without simulation results. COMBINE archives are zip-based containers to bundle all files relevant for a virtual experiment. They facilitate the handling of complex simulation studies while ensuring reproducibility of research results. Moreover, the Web Tools are able to read and understand simulation studies encoded in COMBINE archives. Provided COMBINE archives are extracted and the simulations as defined in the simulation description are run immediately.

The SED-ML Web Tools can be integrated with other tools. For example, the CombineArchive Web application (WebCAT, [Scharm et al., 2014]), an online application to work on COMBINE archives, uses the API of the SED-ML Web Tools. WebCAT provides links to the SED-ML Web Tools to realise instantaneous simulation of studies. A click on the link launches the SED-ML Web Tools, triggers the download of the corresponding archive from WebCAT's web server, and executes the simulation study encoded in the COMBINE archive. Using the API, simulation studies may even be executed without any human interaction. For example, the M2CAT tool [Scharm and Waltemath, 2015] enriches studies via the addition of simulation results generated using the SED-ML Web Tools. The documentation of the Web Tools' API<sup>4</sup> demonstrates how to use the Web Tool within your application.

<sup>3</sup>[get.readthedocs.io](http://get.readthedocs.io)

<sup>4</sup>[sysbioapps.dyndns.org/SED-ML\\_Web\\_Tools/Home/API](http://sysbioapps.dyndns.org/SED-ML_Web_Tools/Home/API)

## DISCUSSION

The reuse of simulation studies is essential in collaborative and responsible research. The SED-ML format and the COMBINE archive are two pioneering approaches to exchange simulation experiments in computational biology and beyond. To support researchers in developing simulation studies that comply with the SED-ML standard, we introduced the SED-ML Web Tools. The Web Tools are an online tool to generate, modify, run, and export simulation studies in SED-ML format. The API is accessible for external services, for example, to generate simulation descriptions and COMBINE archives remotely, or to execute simulation studies online.

## ACKNOWLEDGMENTS

FTB thanks H.M. Sauro for the generous support.

**Funding:** This work was funded by the German Federal Ministry of Education and Research (BMBF) as part of the e:Bio SEMS project (FKZ 031 6194) and by the National Institute of General Medical Sciences (grant number GM081070).

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