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 [Waltemath et al., 2011]) is 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 MVC¹ and provide a web based interface to simulation studies using the SED-ML format. They are based on libSedML², 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

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¹www.asp.net/mvc
²libsedml.sf.net
resource identifier (URN). Once 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 CSim³. 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’ API⁴ demonstrates how to use the Web Tool within your application.

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³ get.readthedocs.io
⁴ 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.

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