Contribution to SBGN contest: best SBGN software support (1) - completeness, exactitude, validation

SBGN-ED for Editing, Validating, and Translating of SBGN Maps

Tobias Czauderna, Christian Klukas, Falk Schreiber

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany

Institute of Computer Sciences, Martin Luther University of Halle-Wittenberg, Germany

SBGN-ED is a tool which allows the creation of all three types of SBGN maps from scratch or editing of existing maps, the validation of these maps for syntactical and semantical correctness, the translation of networks from the KEGG and MetaCrop databases into SBGN, and the export of SBGN maps into several file and image formats. SBGN-ED is freely available from http://vanted.ipkgatersleben.

As required in this part of the competition, SBGN-ED is *complete* - it supports all types of SBGN maps in their current specifications, it is *exact* – it represents all glyphs as required and supports all types of connections, and it supports *validation* – the maps can be checked and errors / invalid elements are emphasized graphically. In addition, SBGN-ED also renders SBGN maps in a user friendly manner and supports the translation of metabolic pathways from two different sources into SBGN: KEGG and MetaCrop. All SBGN maps can be exported in different file and image formats such as GML, GraphML, PDF, SVG, PNG, PNG/HTML image maps, and JPG.

Included in this submission are

- A paper describing SBGN-ED (accepted for publication in Bioinformatics)
- Visual proofs that SBGN-ED software supports all of SBGN languages (maps and GML files for SBGN-ED, screenshots for all three maps types showing supported glyphs)
- Visual proofs that SBGN-ED uses the languages accurately and is able to catch or correct mistakes made by users (screenshots)
- The tool, tutorial files, and example files can be accessed at http://vanted.ipk-gatersleben.de/addons/sbgn-ed/