biographer: web based editing and rendering of SBGN compliant biochemical networks

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1 INTRODUCTION

The web resource Pathguide (Bader et al., 2006) currently lists 35 databases for “Pathway Diagrams” of biochemical reaction networks, each using different means of visualization and containing at least a two digit number of network graphs. While other scientific areas have used universal visual languages for decades, e.g. circuit diagrams in electrical engineering or UML in software engineering, Systems Biology was missing unified network visualizations until the introduction of the Systems Biology Graphical Notation (SBGN) (Le Novère et al., 2009). SBGN provides standardized glyphs for the representation of cellular networks in three different languages: Activity Flow diagrams (AF), depicting the flow of information through a network, Entity Relationship diagrams (ER), showing possible interactions of network components, and Process Descriptions (PD), highlighting the temporal order of such interactions, all of which are fully supported by biographer.

Several tools supporting SBGN compliant visualization are already available. However, they suffer from limitations. Desktop applications like CellDesigner (Funahashi et al., 2003), PathVisio (van Iersel et al., 2008), and SBGN-ED (Czauderna et al., 2010) require the user to install them in their operating system, creating a barrier for their initial use. Web based visualization tools do not provide ready to use libraries (e.g. Reactome, Joshi-Tope et al., 2005) and/or do not adhere to representation standards (e.g. KEGG, Ogata et al., 1999). Such libraries would be of great help in the development of novel tools supporting SBGN-compliant visualizations. The libSBGN (van Iersel et al., 2012) enables basic manipulations of SBGN-ML files, a text-based exchange format for SBGN graphics, but it does not provide methods for interactive visualizations.

The biographer project is trying to address these needs by providing an open source web-based SBGN renderer and editor. It includes a web service for rendering SBGN and a core library based on HTML5 that can easily be integrated into other tools and web resources. Our software has been tested within different environments and works in up-to-date browsers like Firefox and Chrome.
2 SIMPLE USE CASE
The simplest method to use biographer is to visit its interactive editor tools at our website (see Fig.1). This editor allows users to create graphs from scratch by dragging glyphs onto a canvas and connecting them via arcs. Furthermore, it is possible to import existing models directly from BioModels Database, Reactome pathways, or from user-provided SBML, jSBGN, or SBGN-ML files. Since SBML documents by default do not contain information on glyph or arc types, these are guessed from MIRIAM annotations (Le Novère et al., 2005) and SBO terms (Le Novère, 2006).

After the network has been created or imported, the editor provides several tools to customize the visualization, e.g. to change the glyph color or to align and distribute nodes. Furthermore, it provides methods to layout networks using different algorithms. These algorithms include a force directed layout provided by the d3 JavaScript library (http://d3js.org/) and two novel methods, biographer-flow and biographer-grid.

Finally, the tool allows the export of the graph in the SBGN exchange format jSBGN and in the image document formats SVG, PDF, PNG, and TIFF for further editing.

3 USE OF BIOGRAPHER IN OTHER TOOLS
Software developers can use biographer for network visualizations on their own web sites. Given an input model in one of the above mentioned formats, our simple web service can provide SBGN compliant SVG images in an HTML Inlineframe.

The JavaScript API of biographer allows web applications to dynamically change the visualized network and its appearance. Applications using the library include our editor, semanticSBML (Krause et al., 2010), the NetworkExplorer (http://cheetah.biologie.hu-berlin.de/networkexplorer/ - a tool that allows users to interactively browse through subnetworks of a large reaction network, and rxcon (Tiger et al., 2012) - which is able to automatically create topological jSBGN documents for reaction network in SBGN-ER and SBGN-PD simultaneously and includes a boolean simulator with an interactive SBGN-AF visualization.

4 jSBGN
We have chosen to create our own JSON based exchange format, called jSBGN, to store and transmit SBGN images. Our web services require an exchange format that is compact enough to be transmitted fast over the internet and that can be easily interpreted in scripting languages. Furthermore, jSBGN avoids the “no computation” paradigm of SBGN-ML, which requires that all properties of all visible elements have to be declared in the exchanged file. For example in jSBGN arcs only need to provide the source and target glyph, while the start and end positions of the lines on the glyphs will be calculated. This concept makes the creation of jSBGN files simpler and lowers the barrier to integrate the biographer library into other software.

5 CONCLUSION
The visualization of biochemical networks, which includes metabolic, signaling, and regulatory networks, has become an important task in the field of biology. In particular with the emergence of electronic databases containing large interaction networks of biochemical species, the need for automatic or at least semi-automatic rendering of such information has increased drastically. Here we present a tool that allows visualizing and editing of network information in web-based environments as a stand-alone application as well as a library.

While software systems for rendering and editing SBGN images are available, biographer addresses several needs that these tools do not fulfill yet. We believe that the SBGN standard will be more widely used when its creation and usage is as simple as possible.

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