LibSBGN: electronic exchange of SBGN maps


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What is SBGN?

The Systems Biology Graphical Notation (SBGN, See also Le Novère et al., 2009) is a standard notation for the visual representation of biochemical and cellular processes. SBGN maps can be used to exchange complex biological knowledge in a clear, concise and unambiguous manner. See figure 1 for an example of the SBGN Process Description (PD) language.

What is LibSBGN?

As SBGN is becoming adopted more widely, there is a need for exchanging maps electronically between the various systems biology tools. Exchange using graphics-only file formats (such as SVG) is often insufficient, because biological meaning of elements is lost. There is a need for a toolset to exchange maps while preserving biological meaning and relations.

Roadmap

Milestone 1:
- Implement semantics of Process Description language Level 1 Version 1.1.
- Only high-level graphics specification.
- XML Schema available for validation.

Milestone 2:
- Implement semantics for all three languages: PD, ER and AF

Milestone 3:
- Support for detailed graphics specification

Future plans
- Complete validation
- Conversion to and from SBML (with layout extension)
- Conversion to and from BioPAX
- Implementation of LibSBGN (object model & API) in C++

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References


Implementation

To meet this need, we are defining a new markup language named SBGN-ML. This file format is based on an XML Schema definition (XSD), and currently only covers the Process Description language. See figure 2 for an example.

In addition we are developing a supporting software library called LibSBGN. Besides reading and writing SBGN-ML files, this library will also be used to validate SBGN maps against the specifications, and convert to and from related systems biology standards, such as SBML (with layout extension) and BioPAX. LibSBGN is currently implemented in Java, a parallel C++ version is planned for the future. LibSBGN is still under development, but it is already being adopted by several tools (see the project wiki for an up-to-date list).

A test suite has been created: it consists of dozens of reference maps covering every aspect of SBGN PD. Corresponding reference documents have been encoded in XML. To test the adherence of supporting tools to the SBGN-ML specification, a rendering comparison pipeline was set up (see figure 3); it automatically renders SBGN maps through different programs, thus enabling comparison against the reference map.

Some features are optional, for example, not all tools can draw arrows. The biological meaning of the map is the same regardless.

Figure 1: Example SBGN map

Figure 2: SBGN-ML example

Figure 3: Renderer comparison

Reference maps have been made for all aspects of SBGN.

By comparing these implementations, we can spot ambiguities and tool-specific artifacts.

Some features are optional, for example, not all tools can draw arrows. The biological meaning of the map is the same regardless.

Figure 3: Renderer comparison

There are only two top level elements: glyph and arc.

Both arcs and glyphs have a class attribute, which determines both the biological meaning and the appearance of that glyph.

In the current version, only the bounding box of glyphs is stored. Further details, such as e.g. the roundness of corners, are left for future versions.

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