# LibSBGN Current Status and Future Plans

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**Background Context & Motivation** 

#### WHY LIBSBGN?

#### Many tools support SBGN

- Arcadia
- Athena
- BiNoM
- BioModels Database
- BioPAX
- BioUML
- ByoDyn
- CellDesigner
- Dunnart
- Edinburgh Pathway Editor

- JWS Online
- Mayday
- Netbuilder (Apostrophe)
- PANTHER
- PathVisio
- PathwayLab
- Reactome
- Vanted
- VISIBIOweb
- ... 19 tools (and still counting)

See http://

sbgn.org/SBGN Software

#### The problem with SBGN tools

- No interchange of maps
- No reuse of code
  - Useful features (e.g. validation, layout) are scattered across tools, and code is duplicated.

#### Solution? LibSBGN

- Goals
  - Improve Interoperability
  - Encourage code re-use
  - Help development of SBGN compliant tools

#### Solution? LibSBGN

#### **LibSBGN** consists of 2 parts

- Exchange format: SBGN-ML
  - XML Schema based
  - express semantics, relationships and geometry
- Software library: LibSBGN
  - Java and C++
  - key features: reading, writing, validation, conversion and layout

#### Why SBGN-ML?

PNG / SVG BioPAX

GML / GraphML not standard

SBML-Layout

you lose biological network

you lose the layout

you lose SBGN semantics

Development Methods & Infrastructure

#### **HOW IT'S DONE**

# Community project

- Mirit Aladjem (MIM)
- Frank Bergmann (SBML Layout)
- Michael Blinov (BioNetGen)
- Sarah Boyd (Dunnart)
- Tobias Czauderna (VANTED)
- Emek Demir (Pathway Commons)
- Ugur Dogrusoz (Patika)
- Akira Funahashi (CellDesigner)
- Hiroaki Kitano (CellDesigner)

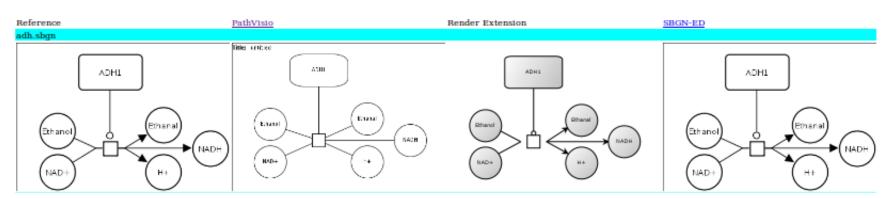
- Nicolas Le Novère (BioModels Database)
- Augustin Luna (MIM)
- Yukiko Matsuoka (CellDesigner)
- Huaiyu Mi (PANTHER Pathway)
- Stuart Moodie (EPE)
- Falk Schreiber (VANTED)
- Anatoly Sorokin (EPE)
- Martijn van Iersel (PathVisio)
- Martina Kutmon (PathVisio)
- Alice Villéger (Arcadia)
- Gael Jalowicki (Biomodels)

### Organization

- Mailing list: sbgn-libsbgn@lists.sourceforge.net
- Monthly online meetings
  - minutes and announcement on mailing list
  - on EVO: http://evo.caltech.edu
- SourceForge project: http://libsbgn.sourceforge.net
  - Wiki: documentation, road map, "how to", useful links, ...
  - Tracker: "to do" list (bugs and missing features)
  - SVN repository: test suite, specs, XSD, validation rules
- Quality control
  - Rendering comparison pipeline http:// libsbgn.sourceforge.net/rendering\_comparison

#### Development infrastructure

- Test suite: test cases (so far):
  - 25 for PD
  - 17 for ER
  - 8 for AF
  - SBGN map in PNG format
  - corresponding SBGN-ML file
- Rendering comparison pipeline



#### **Current Status**

#### WHERE WE ARE

#### SBGN-ML Roadmap

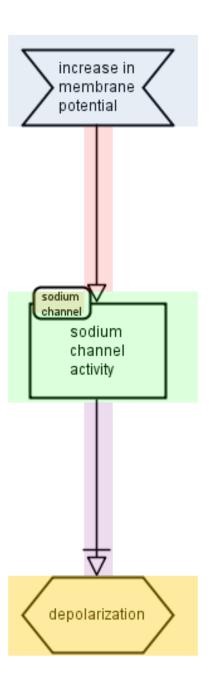
- Milestone 1 released (Jan. 2011)
  - Only support for SBGN PD
  - Only high-level graphics specification
  - Basic validation using XML Schema
- Milestone 2 (planned for Oct. 2011)
  - Implement semantics for all 3 languages: SBGN PD, ER and AF
  - Extra validation using Schematron
  - Third-party extensibility
- Milestone 3
  - Complete graphical specification
  - Submaps...
- Milestone 4
  - Linking, MIRIAM compatibility, ...

#### What is new (since Harmony)

- More test cases
- Schematron rulesets
- Third-party extensibility
- AF support
- compartmentRef and compartmentOrder
- Id's for Arcs are compulsory
- Arcgroups

#### Brief SBGN-ML overview

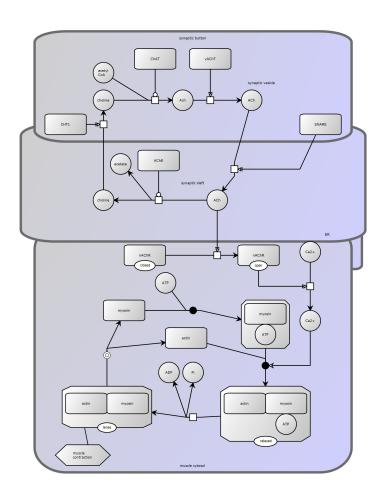
- Main requirements
  - Easy to draw (explicit coordinates)
  - Easy to interpret (network and semantics)
- Top level: Map element
- Most important elements: Glyph and Arc
  - "class" attribute determines semantics, e.g. "macromolecule"
- Glyph geometry: bounding box only
- Arcs refer to glyph or glyph ports (network connectivity)

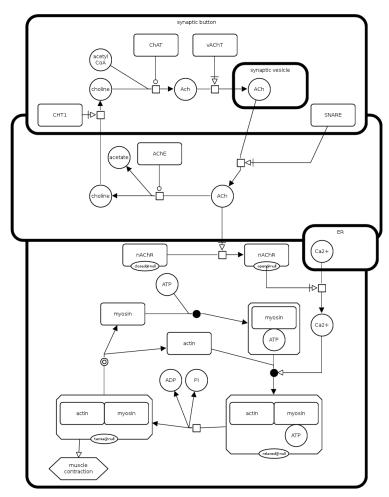


```
<?xml version="1.0" encoding="UTF-8"?>
 2
     -<sbgn xmlns="http://sbgn.org/libsbgn/0.2">
 3
           <map language="activity flow">
 4
 5
               <qlyph class="perturbation" id="q1">
                   <label text="increase in&#xA;membrane&#xA;potential"/>
 6
 7
                   <bbox x="30" y="30" w="120" h="60"/>
8
               </glyph>
9
10
               <qlyph class="biological activity" id="g2">
11
                   <label text="sodium&#xA;channel&#xA;activity"/>
12
                   <bbox x="36" y="232" w="108" h="75"/>
13
                   <qlyph class="unit of information" id="q2.1">
14
                       <label text="sodium&#xA;channel"/>
15
                       <entity name="macromolecule"/>
                       <bbox x="39" y="219" w="46" h="26"/>
16
                   </qlyph>
17
               </glyph>
18
19
               <qlyph class="phenotype" id="q3">
20
21
                   <label text="depolarization"/>
22
                   <bbox x="30" y="450" w="120" h="60"/>
23
               </glyph>
24
25
               <arc class="positive influence" source="g1" target="g2" id="a1">
26
                   <start x="90" y="90" />
27
                   <end x="90" v="232" />
28
               </arc>
29
30
               <arc class="necessary stimulation" source="g2" target="g3" id="a2">
31
                   <start x="90" y="307" />
32
                   <end x="90" y="450" />
33
               </arc>
34
35
           </map>
36
       </sbqn>
37
```

```
increase in
                             <?xml version="1.0" encoding="UTF-8"?>
 membrane
                            -<sbqn xmlns="http://sbqn.org/libsbqn/0.2">
 potential
                                <map language="activity flow">
                         4
                                   <qlyph class="perturbation" id="q1">
                                       <label text="increase in&#xA;membrane&#xA;potential"/>
                                       <bbox x="30" y="30" w="120" h="60"/>
                                   </glyph>
                <glyph class="biological activity" id="g2">
                      <label text="sodium&#xA;channel&#xA;activity"/>
                      <bbox x="36" y="232" w="108" h="75"/>
                      <glyph class="unit of information" id="g2.1">
sodium
channel
                            <label text="sodium&#xA;channel"/>
   sodium
                            <entity name="macromolecule"/>
   channel
   activity
                            <bbox x="39" y="219" w="46" h="26"/>
                     </qlyph>
                </glyph>
                                       <end x="90" y="232" />
                        28
                                    </arc>
                        29
                        30
                                   <arc class="necessary stimulation" source="q2" target="q3" id="a2">
                        31
                                       <start x="90" y="307" />
                                      <end x="90" v="450" />
                        32
                        33
                                    </arc>
                        34
                        35
                                </map>
                        36
                             </sbqn>
depolarization
```

# compartmentOrder & compartmentRef





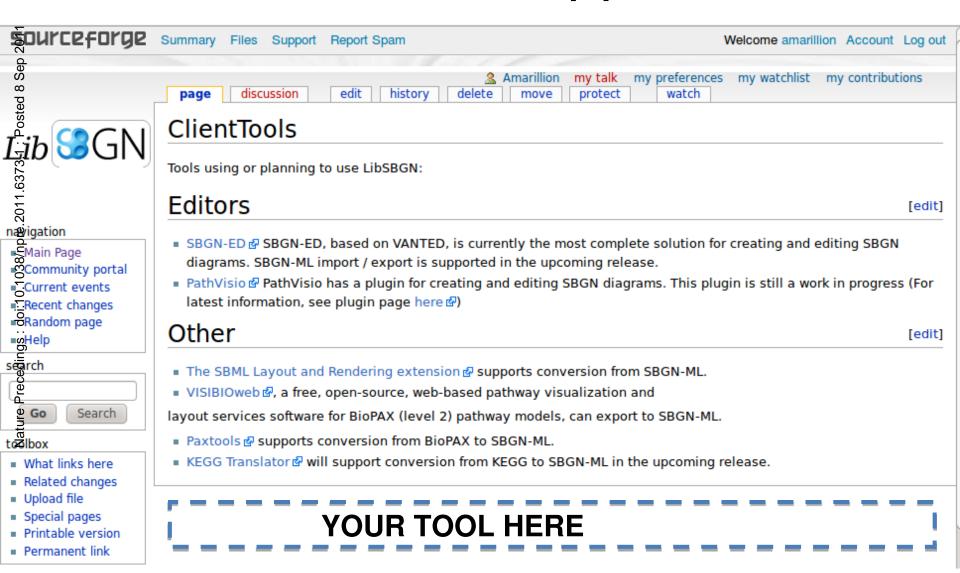
#### Extensions

```
<map language="process description">
   <extension>
      <renderInformation id="example" programName="SBML Layout"</pre>
          programVersion="3.0"
          xmlns="http://projects.eml.org/bcb/sbml/render/level2">
          <colorDefinition id="yelloComp" value="#ffffccff" />
          </renderInformation>
   </extension>
```

#### Future Plans

#### **WHAT NEXT?**

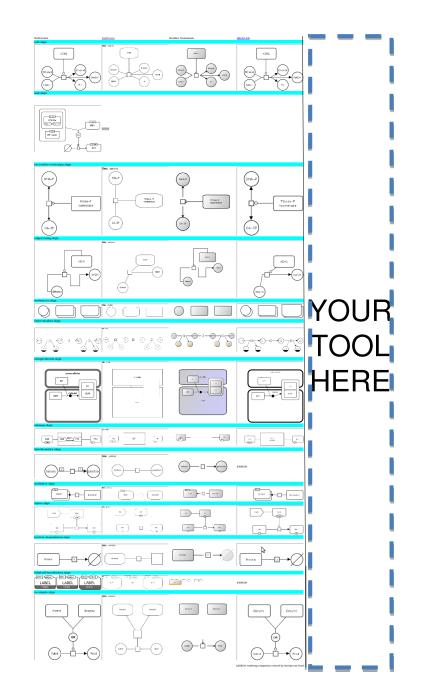
# Software support



#### Software support

 Conversion SBGN-ML -> PNG

- PathVisio (Martijn van Iersel)
- 2. SBGN-ED (Tobias Czauderna)
- 3. SBML Layout (Frank Bergmann)



#### What's next

- Release (Soon October 2011)
- More detailed graphics
  - Roundness of rounded rectangles
  - Arrow-glyph size
  - Line thickness
  - **—** . . .
- Better handling of submaps

#### THANK YOU

- To everyone involved so far: GOOD JOB TEAM
- To all developers supporting SBGN (or planning to):
  - feel free to join the club!
  - Use the **library** and support the **schema**
  - Take part in online discussions
  - Contribute content to the SourceForge project

http://libsbgn.sourceforge.net