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ONTOLOGICAL REPRESENTATION + SBGN PROGRESS

CellML, MIASE, SBO, SBGN 2009

Accessing Semantic Information

- SBO + Miriam Web Services as well as KEGG / ChEBI / OntologyQuery are available to Modules of the Systems Biology Workbench

- One (C#)library / SBW module, provides querying, as well as centralized caching to other modules

- Thus all programming languages can now access those features.

Displaying Information
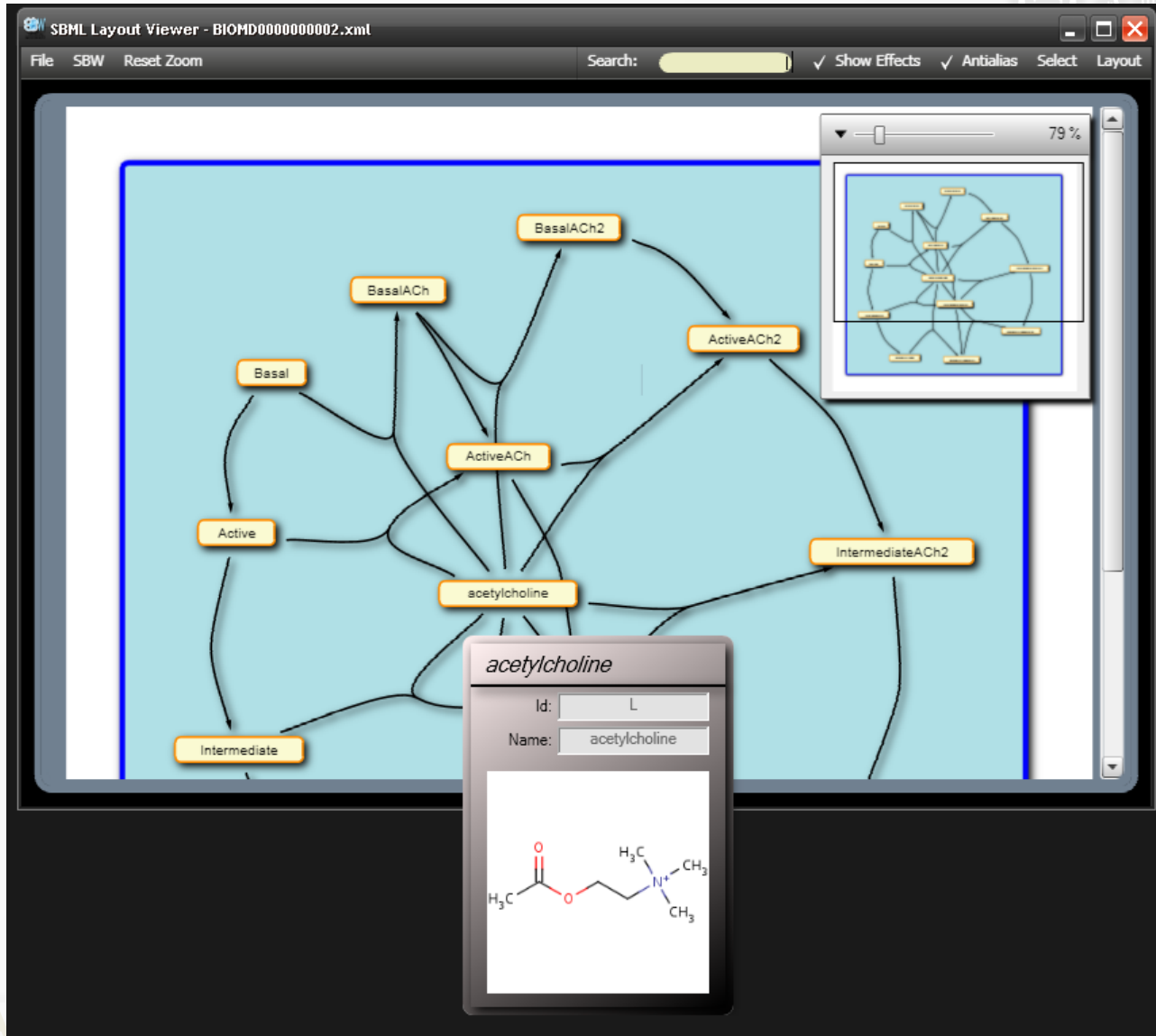
Need Exchange Format

- If we still seriously think about a 'libSBGN', with:
    - support for multiple model exchange languages
    - support for automated VALIDATION of a map
    - semi-automated Translation between graph types
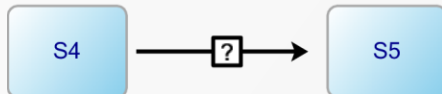   - auto layout routines

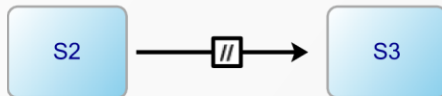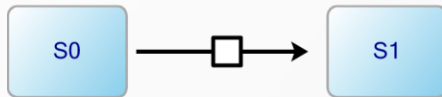- Need Exchange Format

Example

- Our tools use the SBML Layout / Render Extension to actually store position / dimensions + glyphs. Which is sufficient for us to exchange maps between tools.

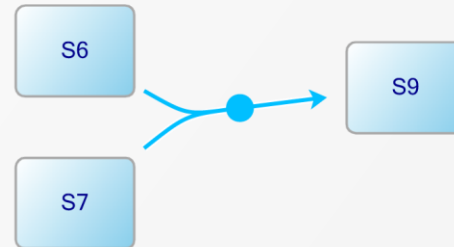- Render Extension Style sheet, which can be applied to SBML Layout based on SBO terms.
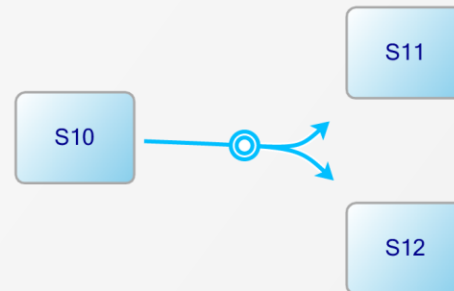
Style Sheet

Transition SBO:0000167

Associaton SBO:0000177

Disassociaton SBO:0000180
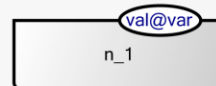
Style Sheet

Unspecified Entity: SBO:0000285

S0

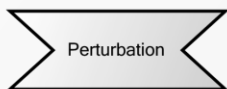Simple Chemical: SBO:0000247

S1

Macromolecule: SBO:0000245

val@var   info

S2

Genetic Entity: SBO:0000354
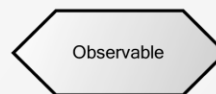
val@var

n_1

Multimer: SBO:0000286

N:5

S3

val@var

Source / Sink: SBO:0000291

Perturbation: SBO:0000357

Perturbation

Observable: SBO:0000358

Observable

Tag   Tag_0

Clonemarker

N:5   val@var

S4

N:2
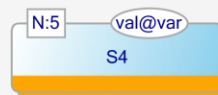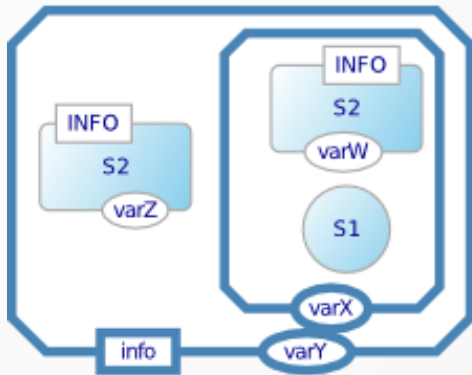
S5
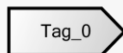
Style Sheet

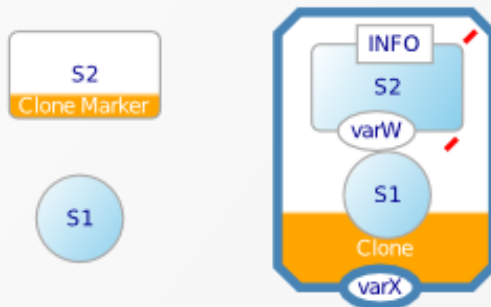

Complex: SBO:0000253

Compartment: SBO:0000289

More Clonemarkers

However

- Layout + RenderExtension do not make it possible to VALIDATE a given map

    - For that we need to store the actual graph

Problems (?)

- Some glyphs will never be (automatically) assigned:
  - Logical Operators,
  - Tag, Logic arc, Equivalence arc, aubmap
  - Omitted / unknown process
  - ➤ They are available in Athena, but probably not in the automated viewer.

- No support for the submap feature with automated collapsing as indicated by the SBGN spec, for that we wait for Sarah ☺

Questions

Funding