

CellDesigner 3.0

Akira Funahashi
Kitano Symbiotic Systems
Project, ERATO-SORST, JST

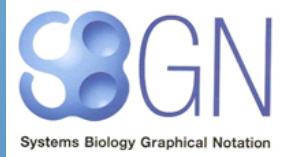
Oct 23, 2005



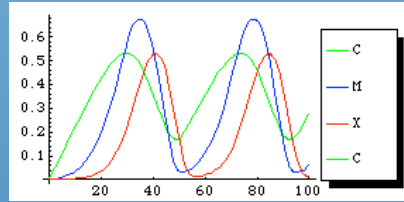
CellDesigner



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MYO1/YHR023W Summary

MYO1 BASIC INFORMATION

- Standard Name: MYO1
- Systematic Name: YHR023W
- Feature Type: ORF, Verified
- Description: Type II myosin heavy chain, required for wild-type cytokinesis and cell separation; localizes to the actomyosin ring; binds to myosin light chains Mlc1p and Mlc2p through its ICI and I2z motifs respectively (1, 2, 3, 4 and see [Summary Paragraph](#))

GO Annotations

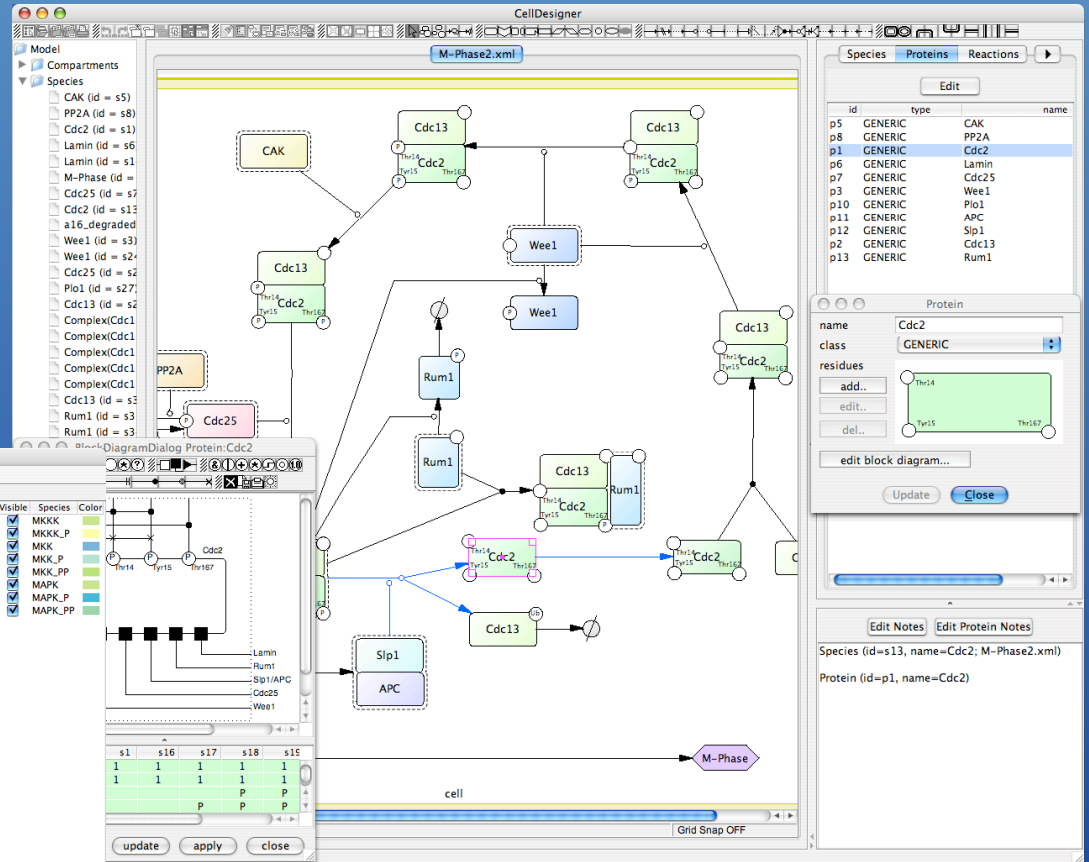
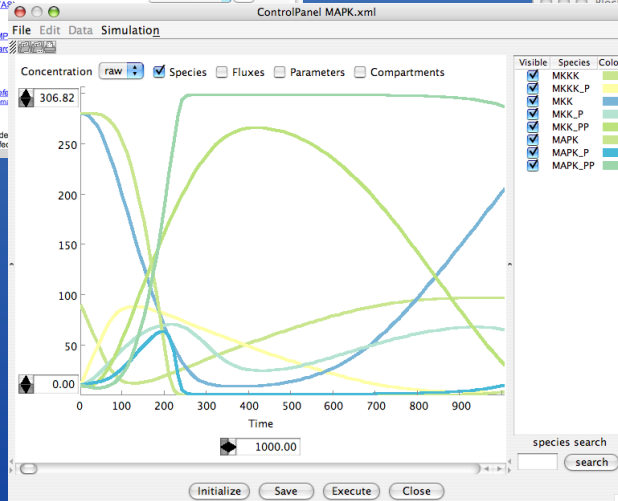
- Molecular Function:
 - microfilament motor activity (CTAP)
 - axial bud site selection (MB)
 - cytokinesis (IMP)
 - response to osmotic stress (IMP)
 - contractile ring (yeast) Saccharomyces cerevisiae

Cellular Component

- MYO1in

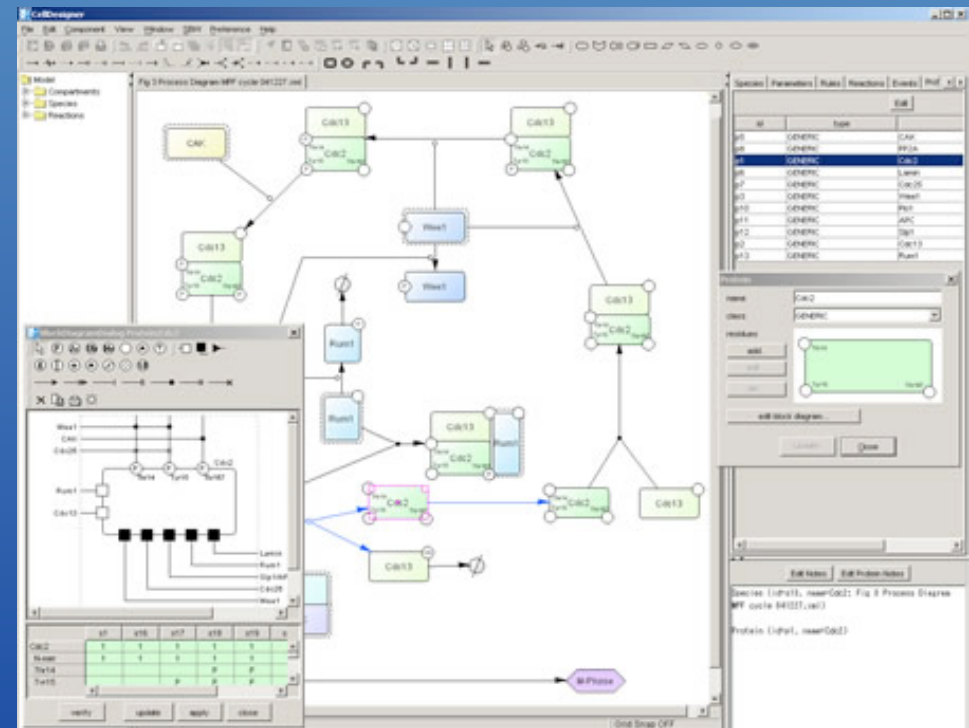
Mutant Phenotype

- class II myosin
- MYO1 Phenotype details and references
- Other mutant strains used in the system:
 - inviable
 - inviable
 - viable, but has severe growth defects
 - viable, but has mild growth defects



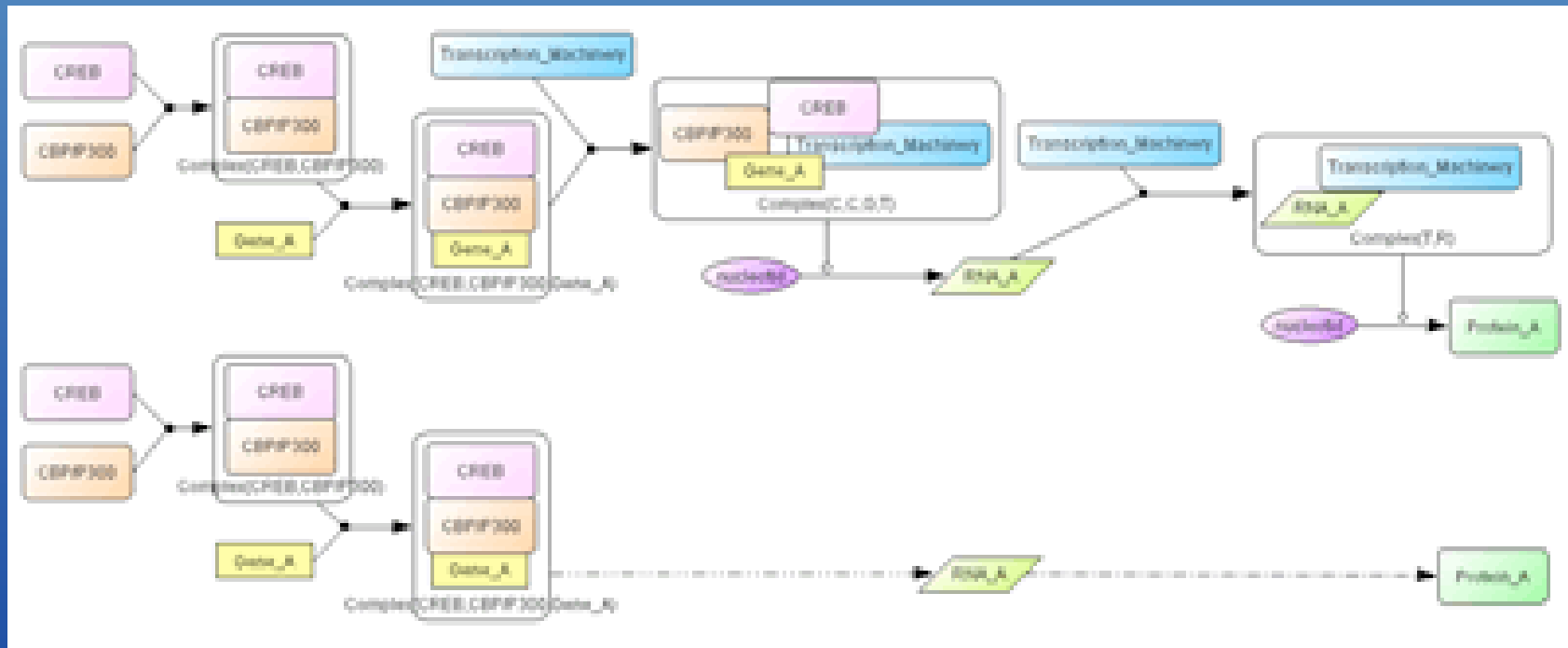
CellDesigner

- Graphical notation (SBGN)
- Built-in simulator (SBML ODE Solver)
- Integrate with Analysis tool, other simulators through SBW
- Database connection
- Export to PNG, SVG, etc.
- Freely available
- Supported Environment
 - Windows (98 or later)
 - Mac OS X
 - Linux



<http://celldesigner.org>

- Graphical Notation for representing biological interactions
- protein-protein interaction, gene regulatory networks



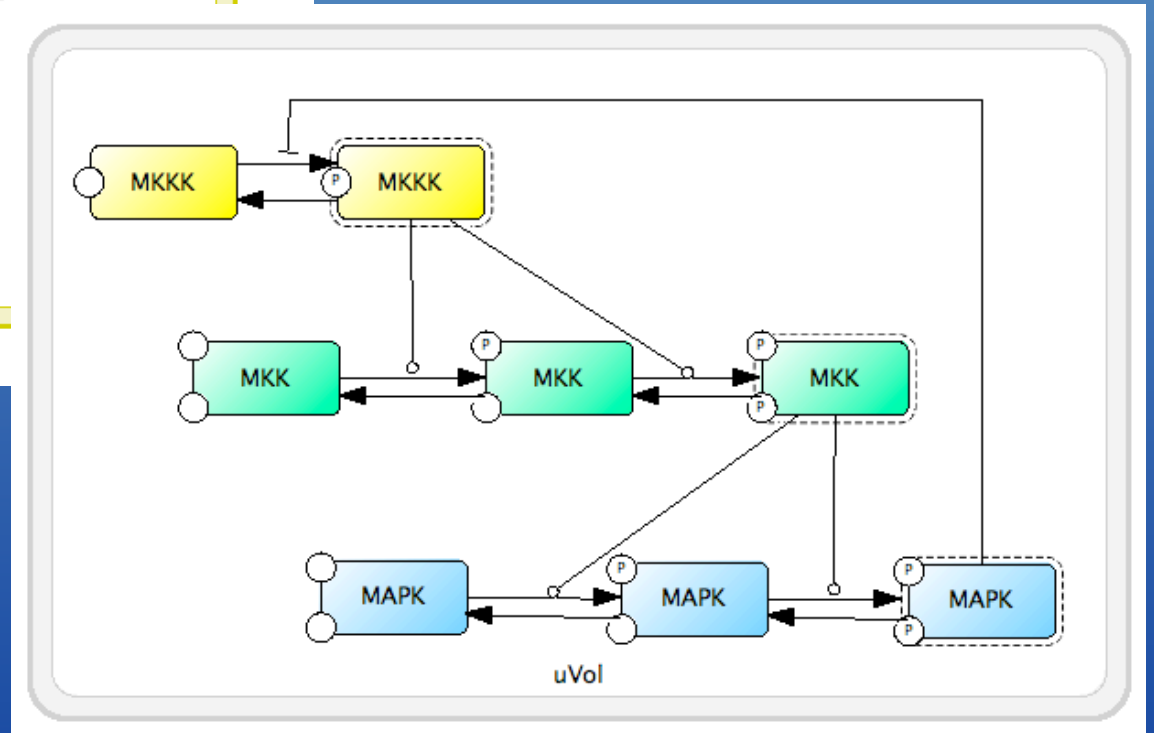
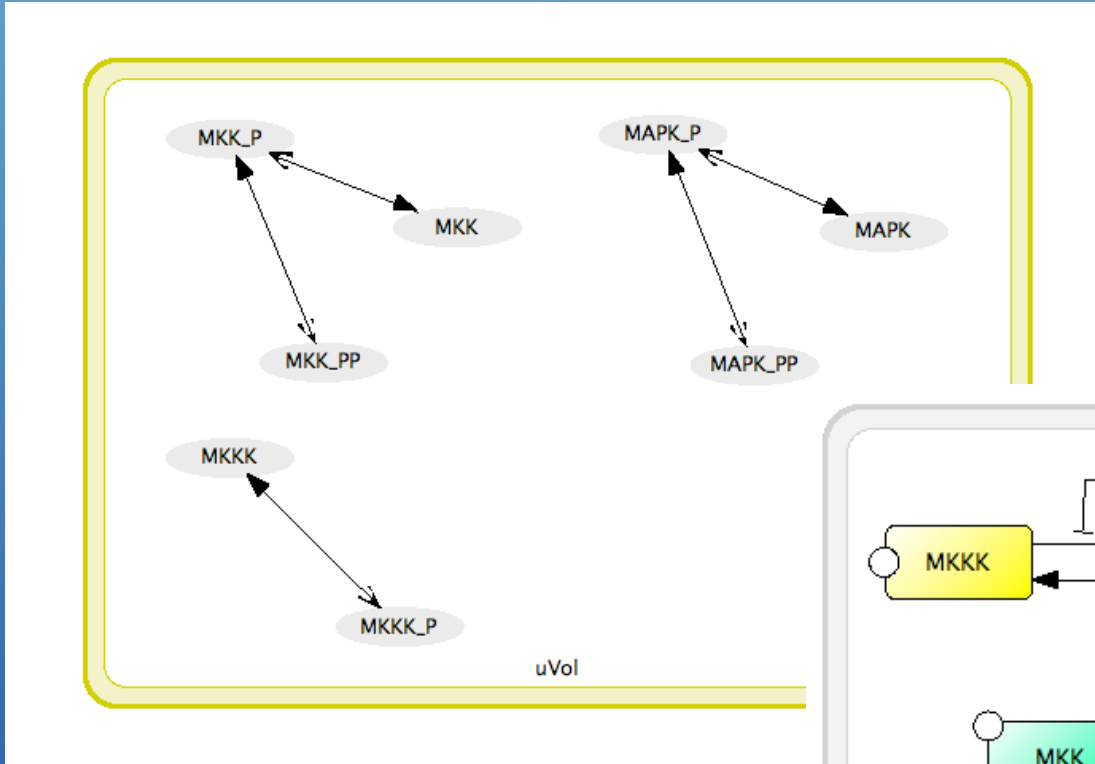
Kitano, H. et al. "Using process diagrams for the graphical representation of biological networks", *Nature Biotechnology* **23**(8), 961 - 966 (2005)

- Species type, Reaction type is stored in `<annotation>` for each species, reactions
- Layout information is stored separately (just as same as SBML layout extension)

```
<sbml>
  <model>
    <annotation>
      layout information
    </annotation>
    <listOfSpecies>
      <species>
        <annotation>species type</annotation>
      </species>
    </listOfSpecies>
  </model>
</sbml>
```

Pure SBML (w/o annotation)

Pure SBML (w/o annotation)



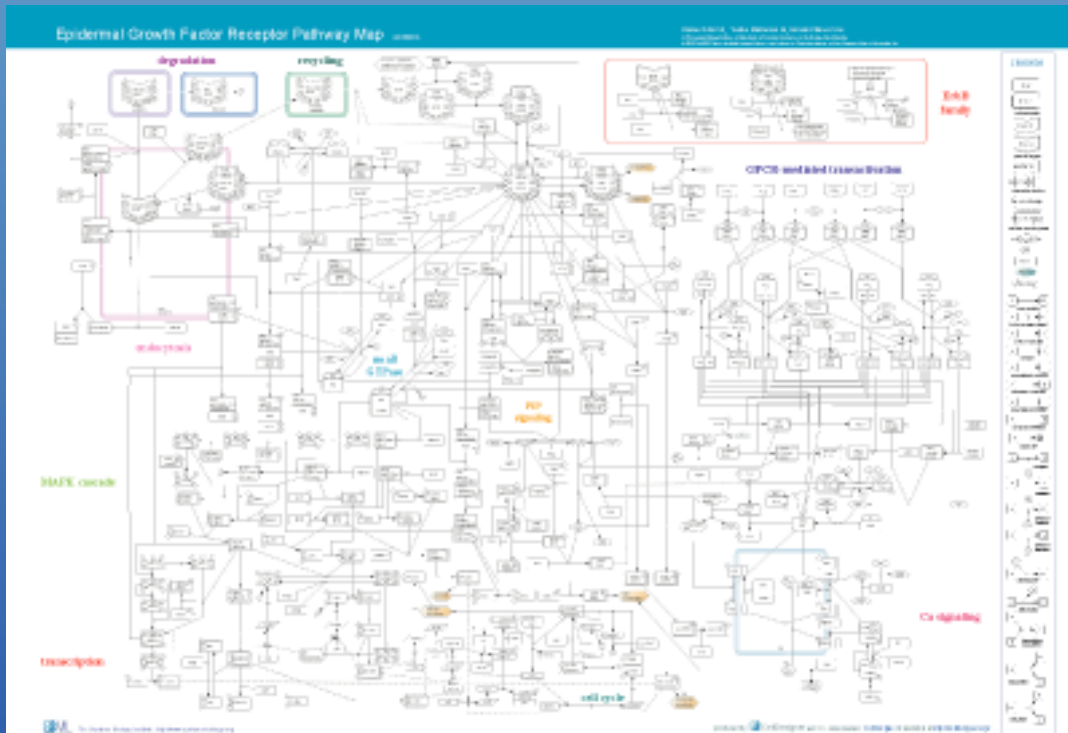
w/ CellDesigner annotation

Graphical notation (SBGN)

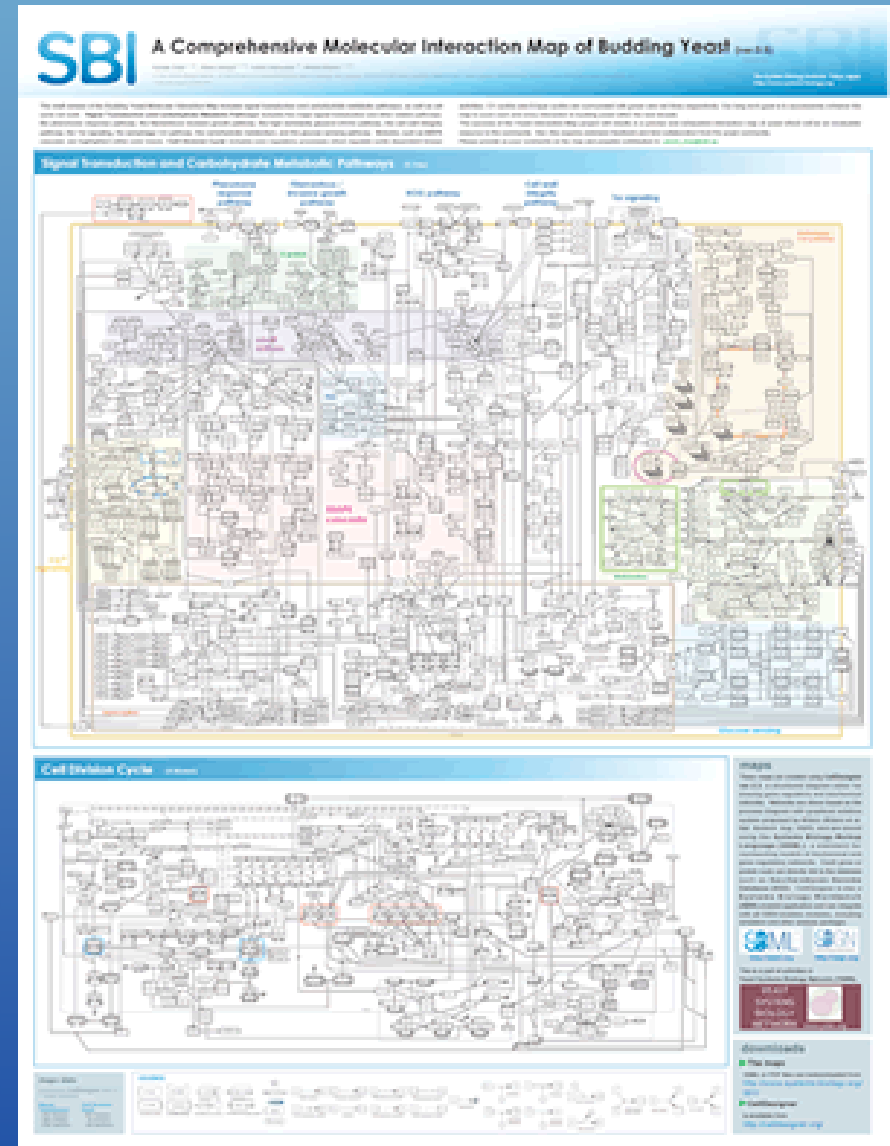
```
<celldesigner:speciesAlias compartmentAlias="ca3" id="a3" species="s3">  
  <celldesigner:activity>active</celldesigner:activity>  
  <celldesigner:bounds h="40.0" w="80.0" x="559.0" y="184.0">  
  </celldesigner:bounds>  
  <celldesigner:singleLine width="1.0"></celldesigner:singleLine>  
  <celldesigner:paint color="ffb3d2ff" scheme="Gradation">  
  </celldesigner:paint>  
</celldesigner:speciesAlias>
```

SBML Layout Extension

```
<speciesGlyph id="SpeciesGlyph_a3" species="s3">  
  <boundingBox id="SpeciesBB_a3">  
    <position x="559" y="184"/>  
    <dimensions width="80" height="40"/>  
  </boundingBox>  
</speciesGlyph>
```



EGFR Pathway (222 reactions, 330 species)
 Oda, K., Matsuoka, Y., et al.



Yeast Molecular Interaction Map (528 reactions, 864 species and 199 reactions, 264 species)
 Oda, K., Moriya, H., et al.

Current direction

- Use Java wrapping of libSBML
- Import SBML layout extension
- Improve auto-layout
- Performance improvement
- API, Open source
- Integrate with ReCSiP
- Integrate with Taverna

- **SBML ODE Solver**
 - **Rainer Machne**
 - **Christoph Flamm**
 - **Andrew Finney**
- **SBW library**
 - **Frank Bergmann**
 - **Herbert Sauro**