

# CellDesigner2.0: A Process Diagram Editor for Gene-regulatory and Biochemical Networks

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**Keywords:** computational biology, systems biology, biochemical network, gene-regulatory network, SBML

## 1 Introduction

Systems biology is characterized by synergistic integration of theory, computational modeling, and experiment. Though software infrastructure is one of the most critical components of systems biology research, there has been no common infrastructure or standard to enable integration of computational resources. To solve this problem, the Systems Biology Markup Language (SBML) [2] and Systems Biology Workbench (SBW) have been developed. A number of simulation and analysis software packages already support SBML and SBW, or are in the process to support it.

An identification of logic and dynamics of gene-regulatory and biochemical networks is a major challenge of systems biology. We believe that such network building tools and simulation environments using standardized technologies play an important role in software platform of systems biology. As one of the approaches, we have developed CellDesigner [1], which is a process diagram editor for gene-regulatory and biochemical networks.

## 2 Features

Roughly classifying, current version of CellDesigner2.0 has following features:

- Representation of biochemical semantics
- Detailed description of state transition of protein
- SBML compliant (SBML Level-1 and Level-2 document)
- Integration with SBW-enabled simulation modules
- Block diagram support

The aim of the development of CellDesigner is to supply a process diagram editor with standardized technology for every computing platform so that it benefits the users as many as possible. By using the standardized technology, created model can be easily used with other applications which use standardized technology, thus it reduces efforts of users to create a model for each editing/simulation/analysis tools. The main features of standardized technology which CellDesigner supports are "Graphical notation", "Model description", and "Application integration environment".

### 2.1 Symbols and Expressions

CellDesigner supports graphical notation and listing of the symbols based on proposal by Kitano [3]. Although several graphical notation systems have been already proposed [4,5,6], each has their own obstacles to overcome to be a standard. Kitano proposed a graphical notation for biological networks [3] so that it will be powerful enough to express sufficient information in clearly visible and unambiguous way. CellDesigner supports graphical notation for state transition diagram, block diagram and residue state representation. Figure 1 shows a screenshot of CellDesigner describing a part of Yeast Cell Cycle process.

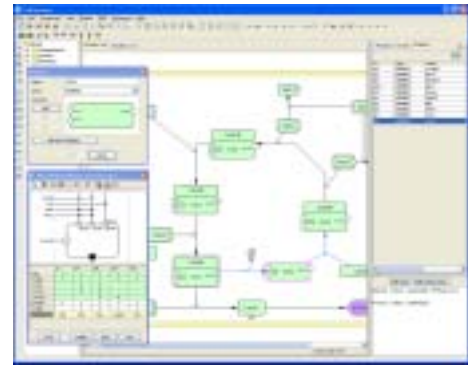


Figure 1: Screenshot of CellDesigner.

## 2.2 SBML Compliant

CellDesigner is an SBML compliant application. SBML is an open, XML-based format for representing biochemical reaction networks which is the standard model definition language in systems biology field. CellDesigner can read all SBML Level-1 and Level-2 documents. Users can import SBML models which are available from SBML model repository (<http://sbml.org/models/>). Also, users can use their own SBML model created by CellDesigner on over 60 SBML compliant applications. The complete list of SBML compliant applications is represented on <http://sbml.org/>.

## 2.3 SBW-enabled

CellDesigner is also an SBW-enabled application. SBW is a modular, broker-based, message-passing framework for simplified application intercommunications. CellDesigner can integrate with all SBW-enabled modules so that users can launch an ODE-based/stochastic simulator and analysis tools from CellDesigner. The SBW-enabled modules are freely available from <http://www.sbw-sbml.org/>.

## 3 Conclusion

We have introduced CellDesigner, which is a process diagram editor for gene-regulatory and biochemical networks. CellDesigner is based on standardized technologies, such as SBML and SBW; the model created by CellDesigner can be used in other SBML compliant applications and SBW-enabled modules. Also, CellDesigner aims to support standard graphical notation. CellDesigner runs on multiple platforms such as Windows, Linux and MacOS X and it is freely available from <http://www.systems-biology.org/>.

## References

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