

Systems Biology Graphical Notation

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Systems Biology has become an essential part of XXIst century biological research. It is an approach that has been accepted internationally everywhere from academic research departments to industrial pharmaceutical companies. A cornerstone of this movement is the use of computational modeling, a crucial tool for helping us cope with the vast size and complexity of natural organisms. The use of quantitative computational models by experimental scientists promises to pave the way for more rigorous analyses of biological functions, and ultimately will lead to new and better treatments for disease. But for this to happen, the computational models themselves must reach a wider audience.

An important first step is to reach agreement on how to communicate models. For models at the level of cellular biochemical reaction networks, the Systems Biology Markup Language (<http://sbml.org/>) has become a *de facto* machine-readable format for exchanging models between software tools. SBML is a critical enabler of research in computational systems biology, but it works at the software level; is not intended for humans to read and write. Humans find visual representations of models more appealing. However, today, there is no standard visual notation for computational models of biological systems, despite the increasing number of software tools offering visual diagrammatic interfaces. Experience in other fields such as electrical engineering has demonstrated the essential need for standardizing the visual notation for diagrams of models.

Our team has been developing a new visual notation aimed at addressing exactly this need. Similar to the SBML effort, we have initiated a Systems Biology Graphical Notation (SBGN) project (<http://www.sbgn.org/>). The goal of the SBGN effort is to help standardize a graphical notation for computational models in systems biology. Such a standard notation will have broad impact. For example, it will add rigor and consistency to the usually ad hoc diagrams that often accompany research articles in publications. It will also help bring consistency to the user interfaces of different software tools and databases. SBGN is a natural complement to SBML, but also to other standards such as BioPAX (<http://www.biopax.org/>).

Our ambition is that the SBGN project will produce a new standard leading to new industrial development in software tools for systems biology. The real payoff for SBGN will come when more people and software adopt such a common visual notation and it becomes as familiar to them as circuit schematics are to computer engineers. When researchers are saved the time and effort required to familiarize themselves with different notations, they can spend more time thinking about the underlying networks being depicted.

Currently, the SBGN team is working with the community on defining a Level 1 Version 1 standard that should be made available soon. It is our current expectation that SBGN Level 1 will allow to represent both State Transition diagrams—where several nodes represent different states of an entity, and Entity Relationship diagrams—where a unique node represent a given entity. A summary of the proposed glyphs to be used in state-transition diagrams is presented in Figure 1.

I: State / Entity Nodes

	glyph	example
Simple chemical		
Unspecified entity		
Source/sink		
unit of information		
State variable		
Macromolecules		
Multimer		
Complex		

II: Container Nodes

	glyph	example
Compartment		
Module		

III: Transition Nodes

	glyph	example
Transition		
Omitted process		
uncertain process		
Association (Bind)		
Dissociation		

IV: Connecting Arcs

	glyph	
Source		*SEN = State / Entity Node
Yield		*TRN = Transition Node
Modulation		Target TRN
Stimulation		Target TRN
Catalysis		Target TRN
Inhibition		Target TRN
Trigger		Target TRN

Figure 1: Summary of the symbols currently agreed-upon by the SBGN consortium, and that will be part of SBGN Level 1 Version 1.