



## 5 Implementing SBML support

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### 5.1 Which level of SBML should I use in my software?



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## 2 SBML Support

### 2.1 Which applications support SBML?

The following matrix (Table [1](#)



reactions, or other components of a model are meant to be interpreted in certain ways (e.g., to be simulated in a stochastic framework).

*Spatial features:* Support for describing 2-D and 3-D spatial characteristics of models, the geometry of compartments, the diffusion properties of species, and the specification of different species concentrations across different regions of a cell.

*Alternative reaction representations:* Extension of SBML reactions to support more directly the expression of stochastic

*Dynamic structures:* Support for enabling model structures to vary during simulation. One









- 5.5 How much effort should I invest in preserving the SBML form when round-tripping models through my software?
- 5.6 What do I do about the fact that SBML does not encode all the information that I need to encapsulate in a model?
- 5.7 How should I structure annotations?
- 5.8 What should I do when I encounter an incorrect SBML file or stream?
- 5.9 There are several different ways in which I could encode my models in SBML. Which forms are more interoperable?
- 5.10 How do I interpret SBML for stochastic simulation purposes?

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## 6 Organization

- 6.1 SBML doesn't encode all the types of representation that are being used in Systems Biology modelling. What is being done to address this problem?

- 6.2 What is the SBML development process?

All SBML development is and has been motivated and directed by the System Biology community.

- 6.3 What do SBML Editors do?

significant work has been required to write the standards documents, organize meetings, perform outreach around the world.

6.4 How do members of the working groups communicate?

6.5 I have identified a feature or features that are missing from SBML.

