# SBML Frequently Asked Questions

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# FAQ Contents

## 7.2   Who are the "SBML Editors"?

# 1 SBML Introduction and Background

## 1.1 What is SBML?

The Systems Biology Markup Language (SBML) is a machine-readable format for describing qualitative and quantitative models of biochemical networks. It can also be used to express the interactions of biochemical networks with other phenomena. By a "biochemical network", we mean a system consisting of biochemical entities linked by chemical reactions that alter, transport and/or transform the entities.

The primary encoding of SBML is

**Table 2:** Table of software libraries for SBML.

| Library | Language | SBML Level 1 | | SBML Level 2 | |
|---------|----------|------|-------|------|-------|
| | | Read | Write | Read | Write |
| libsbml | C/C++ | | | | |

**3.5  What is the point of having a Level 1 Version 2?  Why not forget about it now that Level 2 is out?**

First, please refer to the previous question about why it is important to have both Level 1 and Level 2

- SBML Level 1 Version 1

```
            </cmeta:identifier>
        </cmeta:bio-entity>
      </rdf:Description>
</rdf:RDF>

...
```

### 6.10.8 Discontinuities

Avoid the use of discontinuous operators like piecewise.

### 6.10.9 Delay

Avoid the use of the built-in delay operator.

### 6.10.10 Events

Avoid the use of the events.

### 6.10.11 Units

Do not expect tools to interpret units. Ensure your tool can parse models which use entirely default units.

### 6.11 How much effort should I invest in preserving the SBML form when round-tripping models through my software?

The first priority should be to support as much of the SBML standard as possible both for reading and writing. You should write using the most interoperable form as possible as described in Question 6.10. To maximize interoperability beyond this requires trying to include as much of an imported SBML model as possible when rewriting it in SBML. This includes preserving annotation data and avoiding mangling id and name fields. The order of structures, other than rules, and the white space between elements do not require preservation.

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## 7  Organization

### 7.1 What is the overall SBML development process?

SBML development has been and continues to be motivated and directed by the systems biology community. The process is managed by the *SBML Editors* (see next question), but they do so under the control of the community. The editors collect proposals forp3852gest izeThe uThefwrrk(d)-280(2497Gize)-up  The reading anize358-1

## 7.4 What are "SBML Forum" Meetings?

**7.8  I have identified a feature or features that are missing from SBML. How to do I start a working**

The I3C doesn't create standards; instead, it encourages their development and then makes recommendations on standards to its members. I3C has a close relationship with OMG.

**7.12  Why isn't SBML being developed under the auspices of a standards body like the OMG?**

# 9 Help

## 9.1 My question is not answered in this FAQ list. Who should I contact?