SBML Frequently Asked Questions

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This Frequently Asked Q(e)-1(n)2stions (FAQ) document answers questions about the Systems Biology Markup Lang(e)-age (SBML). It is a non-normative document that does not appear as a spect of SBML; rathe2.98 raET842(r)1(aET842(r)/F89.cL9(t)-334(911dt)-1(84tor)/F8ptano)toi3(CA)-3/F8add33(T)i333(ne)-1/2012 from the content of the systems are content and the systems a

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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

2.2 Are software libraries available for programming with SBML?

The matrix in Table 2

Note that since all Level 1 models can be translated to SBML Level 2, tools that read SBML Level 2 can be made to support Level 1 reasonably easily. Moreover, the availability of libsbml makes it much easier

•	SBML	Level 1	Version	2. This	is the lat	est vers	sion of	SBML	Level 1	and su	percede	s the c	riginal	SBML
	Levei	i versior	ı i derin	ittion. A	As explair	ned eise	wnere	(Quest	ion 3.4,), Levei	2 and 1	Levei	i are ir	itenaea

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6.10.8 Discontinuities

Avoid the use of discontinuous operators like pi ecewi se.

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 e ort 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 i d and name fields. The order of structures, other than rules, and the white space between elements do not require preservation.

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 a	re missing	from S	BML.	How	to do l	start	a working	J

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?