SBML tools in Python

Here I compare the different python tools for SBML manipulation

Website for collected packages/software information: https://biosimulators.org

Online tool to validate SBML model: http://constraint.caltech.edu:8888/validator_servlet/index.jsp

Status	Name of Package	Advantages	Disadvantages	Description
X, 1	Tellurium	Import successful, simulation up and running.	Crashes program when errors in matlab file.	Relies on Roadrunner
X, 0	SimpleSBML	Import successful. No simulation possible, use of tellurium in documentation.		Intended Use with tellurium.
X, 0	sbmlutils	Manipulation tool, Intended use is creating and manipulating sbml files. Great error messages.	No direct support to extract species or reaction data	Relies on https://sbmlutils.readthedocs.io/en/latest/notebooks/sbml_interpolation.html other packages for simulations
o	SBMLmod	Manipulation tool	Only intended for GUI use, code in component Pascal	
X, 1	SBMLtoODE	Manipulation tool, up and running, accessing species requires string of name of species.	Access to species ect. Requires exact names. Conversion from matlab export removes these name informations, thus making it very difficult to use.	Prints second file with “python readable” model file
X, 0	LibSBML	Manipulation tool, Import successful. Intended Use: Validation of Model.		
o	pyVipr			Widget for visualization in jupyter notebook
X, 1	libRoadRunner	Simulation tool, import & simulation successful		Very bad documentation
o	CompuCell3d	Simulation tool		Intended Use as GUI
o	LibSBMLSi	Simulation tool	Couldn’t find installer	Depends on

	m		file Download libSBMLSim Installer for Windows (libsbmlsim-1.4.0-win{32,64}.exe)	libsbml, C code
o	MASSpy	Simulation tool	Failed to install	pip install masspy pip install biosimulators-masspy Intended use with Cobrapy, relies on libroadrunner
o	SBMLToolbox	Simulation tool		For matlab, octave
	deSolve, ODE solver	Simulation tool		Check which packages can spit out system of ODEs
x	biosimulators-libsbmlsim 0.0.3			Depends on libsbmlsim, libsbml
x	bioconductor		https://pythonhosted.org/rpy2-bioconductor-extensions/introduction.html#installing-bioconductor-packages	Intended use with R
	Bionetgen			

0 Github private repository

1. Plot same as Matlab
2. Difference between matlab results & python results would be great

Virtual-pip (alternative to conda?)