The function of this converter is to convert SBML files to the StochKit2 model definition format [Window lite version].

Installation

There is no installation required. You can directly use bin\sbml2stochkit.exe to convert a SBML format model file.

Converting an SBML model to StochKit2 format

The converter is an executable called “sbml2stochkit” that takes at most two arguments: the input path to the sbml file and the output path to the StochKit2 model file. For example, if I have a file called “mySBMLmodel.xml” and I want to convert it to StochKit model format with the name “myStochKitModel.xml”, (on the command line from the tools/SBMLconverter folder):

.\bin\sbml2stochkit mySBMLmodel.xml myStochKitModel.xml

If the output file name is not given, the default name is "<input file name without .xml>.stochkit.xml". So if you call:

.\bin\sbml2stochkit mySBMLmodel.xml

it creates an output file named “mySBMLmodel.stochkit.xml” in the same directory as the file “mySBMLmodel.xml”.

If no argument is given, i.e. you call

.\bin\sbml2stochkit

the executable will return a message says

Please input the SBML file name:

You can input the filename right now. After you hit enter, the executable will ask you if you want to input the output file name,

Do you want to input the output file name (y or n):

If you type “y” or “yes”, you can input the output file after the message,

Type in the file name:

If you choose “n” or ”no”, the executable will generate the output file with the default name.

The converter executes the sbml format verification when it reads the data file, so you may receive error or warning messages if the data file does not follow the sbml format perfectly. However, most errors and warnings are not critical,and the converter generates an output file even though error or warning messages appear. The verification messages are written in a log file, which is in the same directry as the generated .xml file and the name of the log file is “ <outputfilename>.log”. When the SBML format data file does not have all the information required by StochKit2, the converter also provides warnings to help you locate the missing parts.

Currently StochKit does not support the following features of SBML.

Multiple compartments
Function definition
SBML format event

Constraint
Initial assignment
Rule
Boundary condition for a species
Unit definition
Parameters with the same name
Modifier

Explanations of the warnings

- **No model name is provided.**
  In the data file, the component <model /> does not have the attribute “name”.
- **Number of reactions is zero.**
  The data file includes no reaction in <listOfReactions /> tag or the tag has no element.
- **Number of species is zero.**
  The data file includes no species in <listOfSpecies /> tag or the tag has no element.
- **The i th global parameter missed its id.**
  In the data file, the i th parameter in the global parameter list <listOfParameters/> does not have the attribute “id” (or “name” for SBML Level 1).
- **The value of the i th global parameter 'PARAMETER NAME' is not set.**
  In the data file, the i th parameter 'PARAMETER NAME' in the global parameter list <listOfParameters/> does not have the attribute “value”.
- **Reaction i missed its id.**
  In the data file, the i th reation in the reaction list <listOfReactions/> dosen’t have the attribute “id” (or “name” for Level 1).
- **The i th reaction 'REACTION NAME' does not have kineticLaw.**
  In the data file, the i th reaction ‘REACTION NAME’ in the reaction list <listOfReactions/> does not have the component “kineticLaw”.
- **The j th reactant in the i th reaction 'REACTION NAME' missed its id.**
  In the data file, the j th reactant in the reactant list <listOfReactants/> of the i th reaction 'REACTION NAME' in the reaction list <listOfReactions/> does not have the attribute “species”.
- **The j th product in the i th reaction 'REACTION NAME' missed its id.**
  In the data file, the j th product in the product list <listOfProducts/> of the i th reaction 'REACTION NAME' in the reaction list <listOfReactions/> does not have the attribute “species”.
- **The j th parameter in the i th reaction 'REACTION NAME' missed its id.**
  In the data file, the j th parameter in the local parameter list <listOfParameters/> of i th reaction 'REACTION NAME' in the reaction list <listOfReactions/> dosen’t have the attribute “id” (or ‘name’ for Level 1).
- **The value of the j th parameter 'PARAMETER NAME' in the i th reaction 'REACTION NAME' is not set**.
  In the data file, the j th parameter in the local parameter list <listOfParameters/> of i th reaction 'REACTION NAME' in the reaction list <listOfReactions/> dosen’t have the attribute “value”.
- **The i th species in the species list missed its id.**
  In the data file, the i th species in the species list <listOfSpecies/> does not have the attribute “id” (or ‘name’ for Level 1).

- **Initial amount of the i th species 'SPECIES NAME' is negative.**
  In the data file, the attribute “initialAmount” of the i th species in the species list <listOfSpecies/> has a negative value.
- **The initial polulation of the i th species 'SPECIES NAME' is given in the form of initial concentration**.
  In the data file, the attribute “initialConcentration” of the i th species in the species list <listOfSpecies/> is given rather than the attribute “initialAmount”.
- **Initial concentration of the i th species 'SPECIES NAME' is negative.**
  In the data file, the attribute “initialConcentration” of the i th species in the species list <listOfSpecies/> has a negative value.
- **The units of the initial concentration of the i th species 'SPECIES NAME’ is not set.**
  In the data file, the i th species in the species list <listOfSpecies/> does not have the attribute “units”, which may be necessary when the population is given in the form of concentrition.
- **Initial amount and initial concentration of the i th species 'SPECIES NAME’ are unknown.**
  In the data file, the i th species in the species list <listOfSpecies/> does not have the attributes “initialAmount” and “initialConcentration”.
- **'PARAMETER NAME' is an unrecognized parameter in reaction 'REACTION NAME'.**
  The 'PARAMETER NAME' is neither a global parameter,local parameter of 'REACTION NAME', nor a species name.
- **The propensity function of reaction 'REACTION NAME' is ‘ORIGINAL FORMULA’ : we changed it to the mass-action form rate*'SPECIES NAME’*('SPECIES NAME’-1)/2.**
  If a propensity function with the form rate*'REACTION NAME'*'REACTION NAME' is met, we assume the user want to have a second order mass action reaction and the converter will change the original propensity function to the corresponding mass action propensity function.