SED-ML
Simulation Experiment Description Language

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● SED-ML
  - Some technical details
  - Main structure
● Examples, examples, examples
● Outstanding issues
● Jlibsedml (Stuart)
SED-ML is...

- ... a community effort
- ... [hopefully] “MIASE-compliant” [in the future]
- ... an XML format (XML Schema)
- ... also available as a UML model

http://www.ebi.ac.uk/compneur-srv/sed-ml

- ... using XPath to address (XML) elements in the model

  Example: /model/component[@cmeta:id='MT']
Model Class

- References to models used during simulation experiment
- Changes before simulation

Simulation Class

- Definition of simulation type, method and duration ...
Task Class
- Combination of a simulation and a model

DataGenerator Class
- Definition of variables to be used in the output

Output Class
- Output type
- Link to DataGenerators
SED-ML can be used to define many experiments.

- Simulation experiment encoding model perturbations, simulation settings, output
- Experiments using more than one model `listOfModels`
- Experiments using models from different formalisms, e.g. simulations using an SBML model and a CellML model
- Experiments on one model, but using different simulation methods `listOfSimulations`
- Sequential Experiments
  Steady state analysis for an SBML model, using the parameter values for simulation of a CellML model
- What more could you think of?
SED-ML : Examples
1. Take the Repressilator model
   <model id="modell" name="Repressilator" type="SBML"
   source="urn:miriam:biomodels.db:BIOMD0000000012" />

2. Run a time course with a deterministic simulator (LSODA)
   <uniformTimeCourse id="simulation1"
   algorithm="KiSAO:0000088" initialTime="0"
   outputStartTime="0" outputEndTime="1000"
   numberOfPoints="1000" />

3. Simulate the model with the defined simulation settings
   <task id="task1" modelReference="modell"
   simulationReference="simulation1"/>
4. Plot the protein numbers of over time
<dataGenerator id="LaCI" name="LaCI repressor">
<variable id="v4" taskReference="task2" target="/sbml/model/listOfSpecies/species[@id='PX']" />
</dataGenerator>

<plot2D id="plot1" name="protein numbers">
<listOfCurves>
<curve xDataReference="time" yDataReference="LaCI" />
[...]
</listOfCurves>
</plot2D>
1. Take the Repressilator model
   <model id="model2" name="Repressilator" type="SBML" source="model1" />

2. Change the relevant parameter (alpha)
   <listOfChanges>
   <changeAttribute
   target="/sbml/model/listOfParameters/
   parameter[@id='alpha']" newvalue="9" />
   </listOfChanges>
3. Run a time course with a deterministic simulator (LSODA)
   <uniformTimeCourse id="simulation1"
   algorithm="KiSAO:0000088" initialTime="0"
   outputStartTime="0" outputEndTime="1000"
   numberOfPoints="1000" />

4. Simulate the model with the defined simulation settings
   <task id="task1" modelReference="model2"
   simulationReference="simulation1"/>
5. Plot the protein numbers over time

```xml
<dataGenerator id="LaCI" name="LaCI repressor">
  <variable id="v4" taskReference="task2" target="/sbml/model/listOfSpecies/species[@id='PX']"/>

<plot2D id="plot1" name="protein numbers">
  <listOfCurves>
    <curve xDataReference="time" yDataReference="LaCI"/>
    [...]
  </listOfCurves>
</plot2D>
```
1. Take the (Leloup,99) model
   <model id="modell" name="Circadian Oscillations"
type="SBML" source="urn:miriam:biomodels.db:
BIOMD0000000021" />

2. Run a time course with a deterministic simulator (LSODE)
   <uniformTimeCourse id="simulation1"
algorithm="Kisao:0000071" numberOfPoints="1000" />

3. Simulate the model with the defined simulation settings
   <task id="task1" modelReference="modell"
simulationReference="simulation1"/>
4. Plot the tim mRNA concentration over time

```
<variable id="v1" taskReference="task1"
target="/sbml/model/listOfSpecies/
species[@id='Mt']" />

<plot2D>
<listOfCurves>
<curve xDataReference="time"
yDataReference="tim1" />
</listOfCurves>
<plot2D>
```
1. Take the (Leloup,99) model
   <model id="model1" name="Circadian Oscillations" type="CellML" source="http://www.cellml.org/models/leloup_gonze_goldbeter_1999_version02" />

2. Change the parameters in the model according to the paper
   <changeAttribute target="/model/component[@cmeta:id='MP']/variable[@name='vsP']/@initial_value" newValue="1"/>

3. Run a time course with a deterministic simulator (LSODE)
   <uniformTimeCourse id="simulation1" algorithm="KiSAO:0000071" numberOfPoints="1000" />
4. Simulate the model with the simulation settings

   `<task id="task1" modelReference="model1" simulationReference="simulation1"/>

5. Plot the tim mRNA concentration over time

   `<variable id="v1" taskReference="task1" target="/model/component[@cmeta:id='MT']"/>

   `<plot2D>
   `<listOfCurves>
   `<curve xDataReference="time" yDataReference="tim1"/>

   ![Plot of tim mRNA concentration over time](image.png)
SED-ML files for both experiments are similar except element addressing (XPath)

```xml
<model id="model1" name="Circadian Oscillations" type="SBML" source="urn:miriam:biomodels.db:BIOMD0000000021" />
[..]
<variable id="v1" taskReference="task1" target="/sbml/model/listOfSpecies/species[@id='Mt']" />
<plot2D> <listOfCurves>
<curve xDataReference="time" yDataReference="tim1" />
</listOfCurves> <plot2D>

<model id="model1" name="Circadian Oscillations" type="CellML" source="http://www.cellml.org/models/leloup_gonze_goldbeter_1999_version02" />
[..]
<variable id="v1" taskReference="task1" target="/model/component[@cmeta:id='MT']" />
<plot2D> <listOfCurves>
<curve xDataReference="time" yDataReference="tim1" />
</listOfCurves> <plot2D>
```
Simulating the SBML (Leloup,99) in COPASI with oscillating behaviour and chaotic behaviour (changed parameters $V_mT/V_dT$); comparing both curves in one plot (Gnumeric Spreadsheet)
http://miase.svn.sourceforge.net/viewvc/miase/sed-ml/examples/
• Support more simulation types
  - Supported: Uniform Time Course, AnySimulation
  - Desired: Parameter Scans, Optimisations …
  
  *Which ones would you like to encode?*

• Should we also consider to link to experiment results? And if yes, in what way?
  - Options: SBRML or link to tabular data or data files

• Technical issues
  - Xpath, Prototype implementations, Library development
  - Jlibsedml
Richard Adams (JlibSED-ML)
Frank Bergman (roadrunner)
Mike Hucka
Fedor Kolpakov (BioUML)
Nicolas Le Novère
Ion Moraru (Virtual Cell)
Sven Sahle (COPASI)
Henning Schmidt (SB Toolbox)

“What do you mean, ‘intractable’?”

http://www.ebi.ac.uk/compneur-srv/sed-ml/
miase-discuss@lists.sourceforge.net