

Systems Biology Toolbox 2

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Improved SBML Support

- Still only L2V1 and below
 - L2V2/3 will very soon be added

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- Features supported since Okinawa
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 - **Delayed events**
 - **Algebraic rules**
 - **Fast reactions**

Improved SBML Support

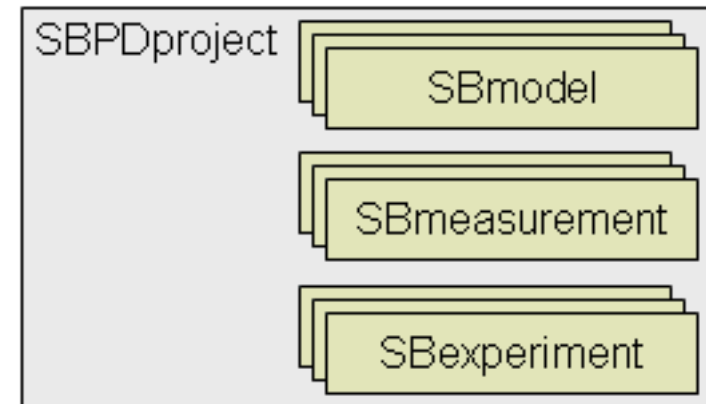
- Still only L2V1 and below
 - L2V2/3 will very soon be added
- Features supported since Okinawa
 - **Delays**
 - **Delayed events**
 - **Algebraic rules**
 - **Fast reactions**
- Known issues
 - Csymbol time at export
 - Csymbol delay at import and export
 - Fixed as soon as new SBML Toolbox available

SED-ML Support

- Import and export of SED-ML descriptions
 - **SBPDproject** => Sed-ML
 - Sed-ML => **SBPDproject**
 - **Parameter and initial condition changes only at the moment**

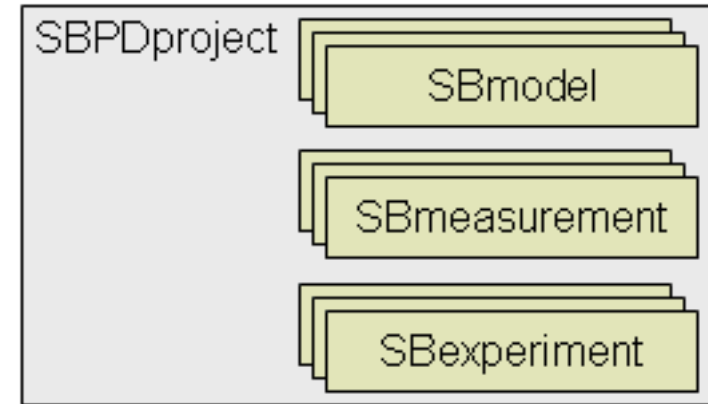
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 - Sed-ML => **SBPDproject**
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 - **Measurement data**
 - Experiment descriptions



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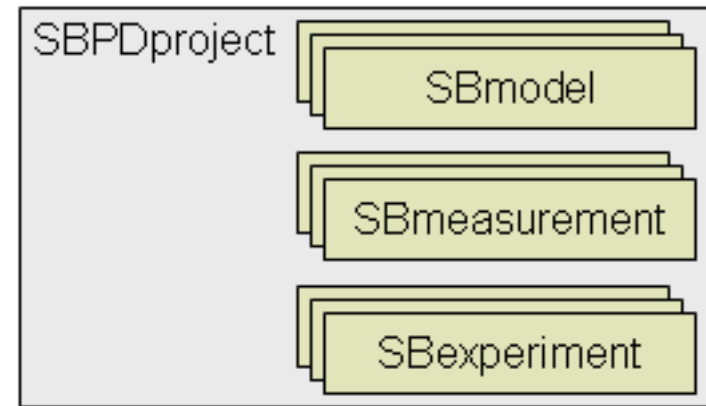


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- **Measurement data**
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- Parameter estimation, etc., can directly be run on projects

```

<sedML version="1.0" xmlns="http://www.miase.org/">
<listOfDataGenerators />
<listOfModels>
  <model id="model1" name="Inhibition_of_HIV_proteinase" type="SBML" source="http://www.sbi.uni-
    rostock.de/~ab358/sedml/Inhibition_of_HIV_proteinase.xml"></model>
  <model id="exp1_I_0" name="Inhibitor_Concentration_0nM" type="SBML" modelReference="model1">
    <listOfChanges>
      <changeAttribute target="/sbml/model/listOfSpecies/species[@id='I']/@initialConcentration"
        newValue="0">
      </changeAttribute>
    </listOfChanges>
    <listOfMeasurements>
      <measurement source="http://www.sbi.uni-rostock.de/~ab358/sedml/exp1
        measurement1.csv" />
    </listOfMeasurements>
  </model>
  <model id="exp2_I_15" name="Inhibitor_Concentration_1.5nM" type="SBML" modelReference="model1">
    <listOfChanges>
      <changeAttribute target="/sbml/model/listOfSpecies/species[@id='I']/@initialConcentration"
        newValue="1.5*1e-3">
      </changeAttribute>
    </listOfChanges>
    <listOfMeasurements>
      <measurement source="http://www.sbi.uni-rostock.de/~ab358/sedml/exp2measurement1.csv" />
    </listOfMeasurements>
  </model>
</listOfModels>
<listOfOutputs />
<listOfSimulations />
<listOfTasks />
<name>ex2 - Inhibition of HIV proteinase</name>
<notes> Ex2 - Parameter Identification Benchmark Project </notes>
</sedML>

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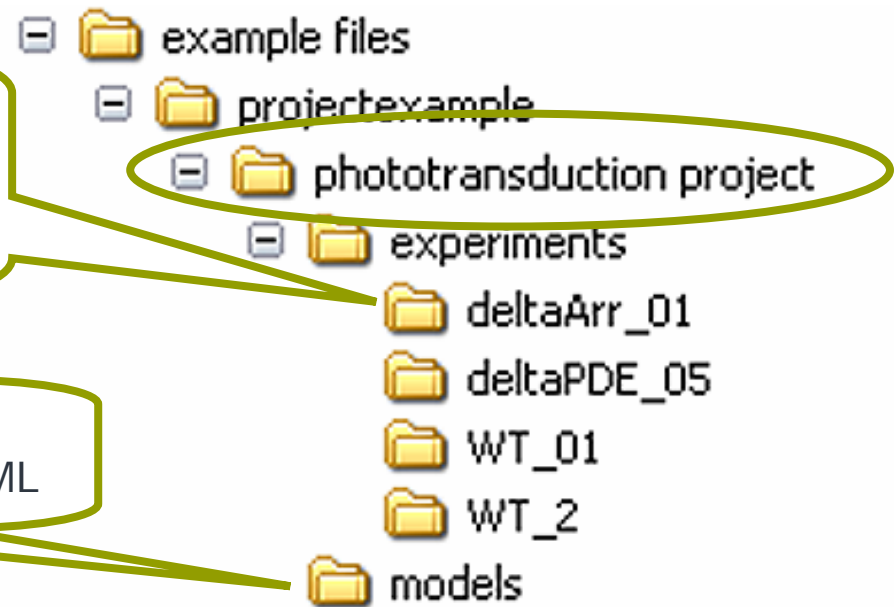
```
</sedML>
```

file:///...



Representation of SBPDprojects

- Folder structure, containing
 - Models
 - Experiments
 - Measurements



Experiment folders containing **experiment description file** and corresponding **measurement data**

Folder containing **model(s)** TEXT (ODE and/or BC) and/or SBML

SBPDprojects „One Click Parameter Estimation“

The screenshot displays the SBPDgui software interface with the following components:

- Menu Bar:** File, Model, Experiment, Estimation, Other, Debug, Desktop, Window, Help
- Select Model:** Project_example_model
- Select Experiments:** WT_0point1_stimulation, WT_2_stimulation, deltaARR_0point1_stimulation, deltaPDE_0point5_stimulation
- Select Estimation Settings:** 1: default
- Select Experiment Weights:** 1,1,1,1
- Global Parameters Table:**

Parameter	0	Low	1000	High
'kRGact'	0		1000	
'kIGact'	0		1000	
'k2Gact'	0		1000	
'kGactPDEact'	0		1000	
'kRArr1'	0		1000	
'kRArr2'	0		1000	
'kGr1'	0		1000	
'kGr2'	0		1000	
'kG'	0		1000	
'magStim'	0		2000	
'durStim'	0		100	
- Local (experiment dependent) Parameters:** (Empty table)
- States (always experiment dependent) Table:**

'Arr'	0	5000
'G'	0	3e+006
'Gact'	0	100
'GactPDEact'	0	100
'Gr'	0	100
'PDE'	0	100000
'R'	0	500000
'Ract'	0	100
- Optimizer Options:**
 - simplexSB: Nelder-Mead...
 - 1: use averages from fir... (1: max values)
 - 0: no timescaling (2: iteration and final)
- Run Estimation** (Green button)
- Residual Analysis** (Button)
- Run Fitanalysis** (Green button)
- Analysis Tools:** Boxplot, Clustering, Correlation, Pairwise Correlation, Histogram, Significant Correlation
- Estimation Settings Notes (First row: Name):** default, Default estimation setting.
- Control Buttons:** Update Estimation Settings, Save New Estimation Settings, Reset Project
- Simulation Controls:** Plot Measurements, Simulate single Experiment (20 Te), Compare Measurements, Manual Tuning, Identifiability Analysis

SBPDprojects „One Click Parameter Estimation“

The screenshot displays the SBPDgui software interface. The main window is titled "Figures - SBPDgui" and contains several panels for configuring parameter estimation. A large red watermark is overlaid diagonally across the center of the image, reading "That's why measurement references in SED-ML".

Select Model: Project_example_model

Select Experiments: WT_Opoint1_stimulation, WT_2_stimulation, deltaARR_Opoint1_stimulation, deltaPDE_Opoint5_stimulation

Select Estimation Settings: 1: default

Select Experiment Weights: 1,1,1,1

Global Parameters:

Parameter	0	Low	1000	High
'kRGact'	0	1000		
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'kRArr2'	0	1000		
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'kG'	0	1000		
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Local (experiment dependent) Parameters:

States (always experiment dependent):

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'R'	0	500000
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Estimation Settings: simplexSB: Nelder-Mead...
1: use averages from...
0: no timescaling...
1: ... values
2: iteration and final

Buttons: Run Estimation, Residual Analysis, Run Fitanalysis, Boxplot, Clustering, Correlation, Pairwise Correlation, Histogram, Significant Correlation, Update Estimation Settings, Save New Estimation Settings, Reset Project.

Question: Algebraic Rules

- $d/dt(A) = \dots$
- $d/dt(B) = \dots$

- $0 = C + k_1 * A$

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- $0 = C + k_1 * A$

- **Determine C or k1 by the algebraic relation???**