Visualisation of CellML Models

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CellML

- CellML is an implementation-independent simulation modelling language.

- It is mainly used for understanding the dynamics of complex biological processes.

A reaction modelled in CellML; L + R →RI

```xml
<model name="complex_formation" cmeta:id="complex_formation"
    xmlns="http://www.cellml.org/cellml/1.0#"
    xmlns:cellml="http://www.cellml.org/cellml/1.0#"
    xmlns:cmeta="http://www.cellml.org/metadata/1.0#"
    xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
    xmlns:dc="http://www.purl.org/dc/elements/1-1#"
    xmlns:biopaxbinding="http://www.sarala.bioeng.auckland.ac.nz/cellmlbiopaxbindin
  <units name="micromolar">
    <unit units="mole" prefix="micro"/>
    <unit units="litre" exponent="-1"/>
  </units>
  <units name="flux">
    <unit units="micromolar"/>
    <unit units="second" exponent="-1"/>
  </units>
  <units name="second_order_rate_constant">
    <unit units="micromolar" exponent="-1"/>
    <unit units="second" exponent="-1"/>
  </units>
  <component name="environment">
    <variable name="time" units="second" public_interface="out"/>
  </component>
  <component name="L">
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    <variable name="J_L" units="flux" public_interface="in"/>
    <variable name="time" units="second" public_interface="in"/>
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      <apply>
        <eq/>
        <apply>
          <diff/>
          <bvar>
            <ci>time</ci>
          </bvar>
          <ci>L</ci>
        </apply>
        <ci>J_L</ci>
      </apply>
    </math>
  </component>
  <component name="R">
    <variable name="R" units="micromolar" initial_value="1" public_interface="out"/>
    <variable name="J_R" units="flux" public_interface="in"/>
    <variable name="time" units="second" public_interface="in"/>
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        <eq/>
        <apply>
          <diff/>
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            <ci>time</ci>
          </bvar>
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        </apply>
        <ci>J_R</ci>
      </apply>
    </math>
  </component>

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    <variable name="time" units="second" public_interface="in"/>
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          <bvar>
            <ci>time</ci>
          </bvar>
          <ci>RI_complex</ci>
        </apply>
        <ci>J_RI</ci>
      </apply>
    </math>
  </component>
  <component name="reaction">
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    <variable name="J_RI" units="flux" public_interface="out"/>
    <variable name="J" units="flux"/>
    <variable name="L" units="micromolar" public_interface="in"/>
    <variable name="R" units="micromolar" public_interface="in"/>
    <variable name="RI_complex" units="micromolar" public_interface="in"/>
    <variable name="time" units="second" public_interface="in"/>
    <variable name="k1" units="second_order_rate_constant" public_interface="in"/>
    <math xmlns="http://www.w3.org/1998/Math/MathML">
      <apply>
        <eq/>
        <ci>J</ci>
        <apply>
          <times/>
          <ci>k1</ci>
          <ci>L</ci>
          <ci>R</ci>
        </apply>
      </apply>
      <apply>
        <eq/>
        <ci>J_L</ci>
        <apply>
          <times/>
          <ci>J</ci>
          <apply>
            <minus/>
            <cn cellml:units="dimensionless">1</cn>
          </apply>
        </apply>
      </apply>
      <apply>
        <eq/>
        <ci>J_R</ci>
        <apply>
          <times/>
          <ci>J</ci>

<apply>
          <minus/>
          <cn cellml:units="dimensionless">1</cn>
        </apply>
      </apply>
    </apply>
    <apply>
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      <ci>J_RI</ci>
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        <times/>
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        <cn cellml:units="dimensionless">1</cn>
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    </apply>
  </math>
</component>
<component name="rate_constant">
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</component>
<connection>
    <map_components component_1="L" component_2="reaction"/>
    <map_variables variable_1="L" variable_2="L"/>
    <map_variables variable_1="J_L" variable_2="J_L"/>
</connection>
<connection>
    <map_components component_1="L" component_2="environment"/>
    <map_variables variable_1="time" variable_2="time"/>
</connection>
<connection>
    <map_components component_1="R" component_2="reaction"/>
    <map_variables variable_1="R" variable_2="R"/>
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    <map_components component_1="R" component_2="environment"/>
    <map_variables variable_1="time" variable_2="time"/>
</connection>
<connection>
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    <map_variables variable_1="RI_complex" variable_2="RI_complex"/>
    <map_variables variable_1="J_RI" variable_2="J_RI"/>
</connection>
<connection>
    <map_components component_1="RI_complex" component_2="environment"/>
    <map_variables variable_1="time" variable_2="time"/>
</connection>
<connection>
    <map_components component_1="reaction" component_2="rate_constant"/>
    <map_variables variable_1="k1" variable_2="k1"/>
</connection>
<connection>
    <map_components component_1="reaction" component_2="environment"/>
    <map_variables variable_1="time" variable_2="time"/>
</connection>
</model>
```
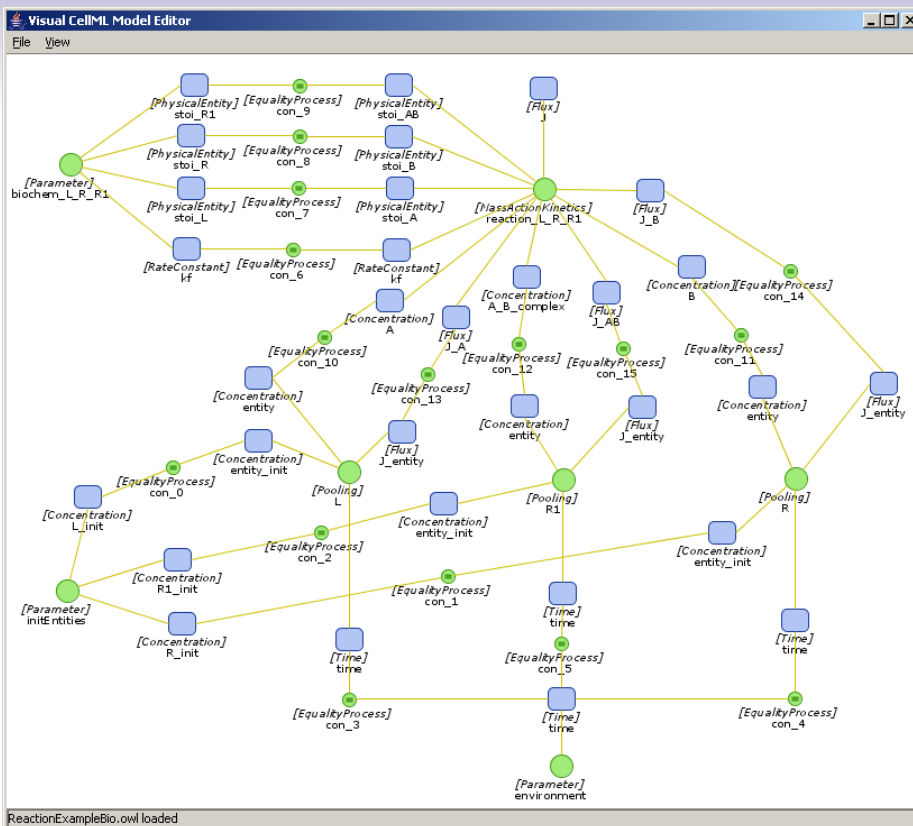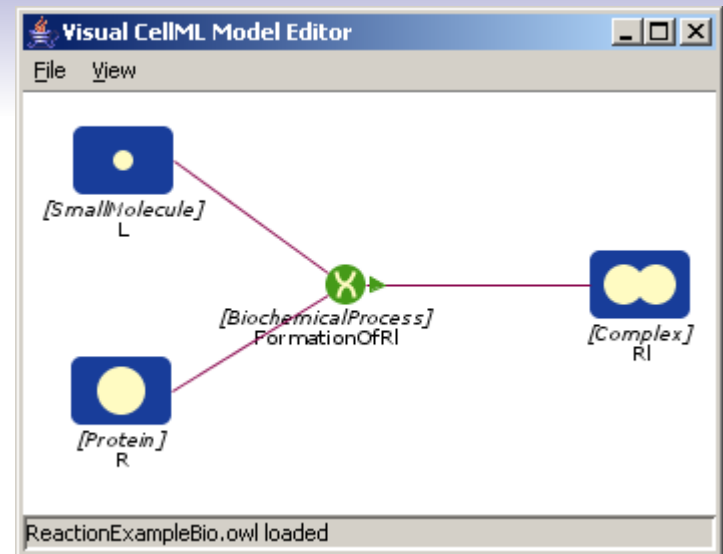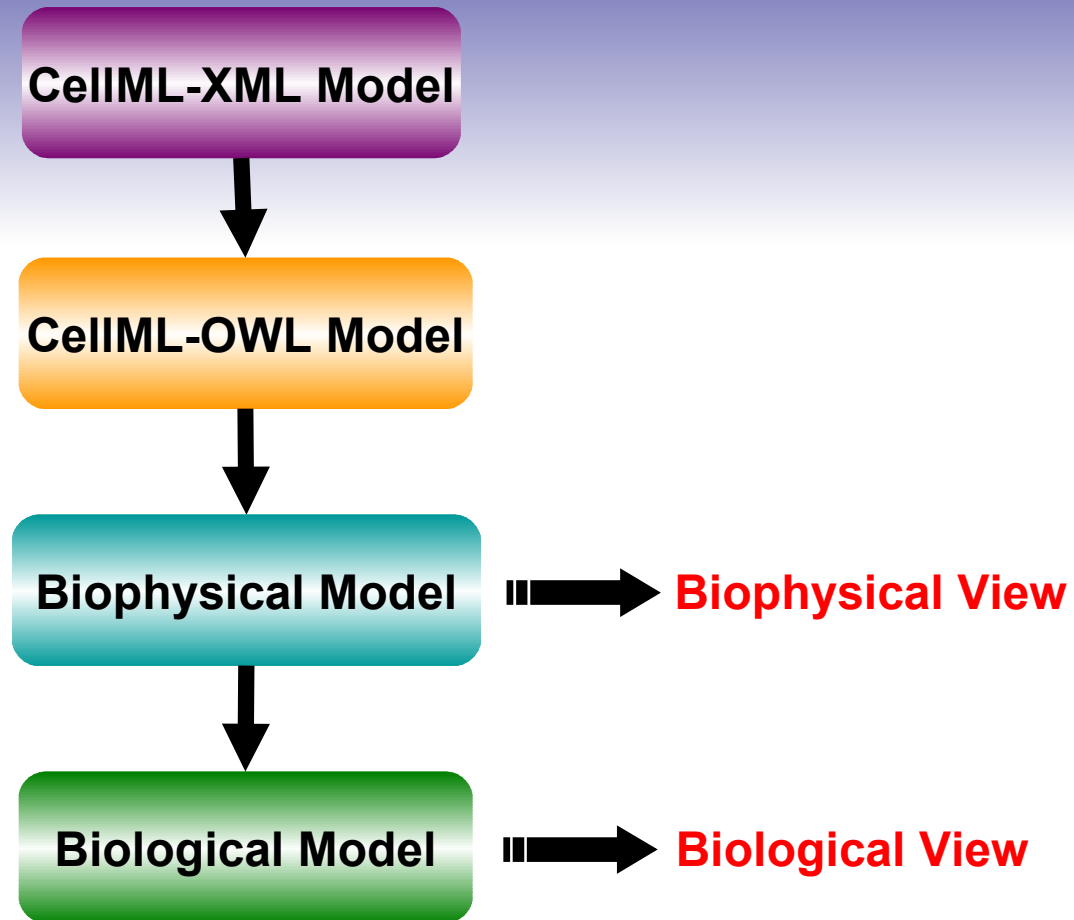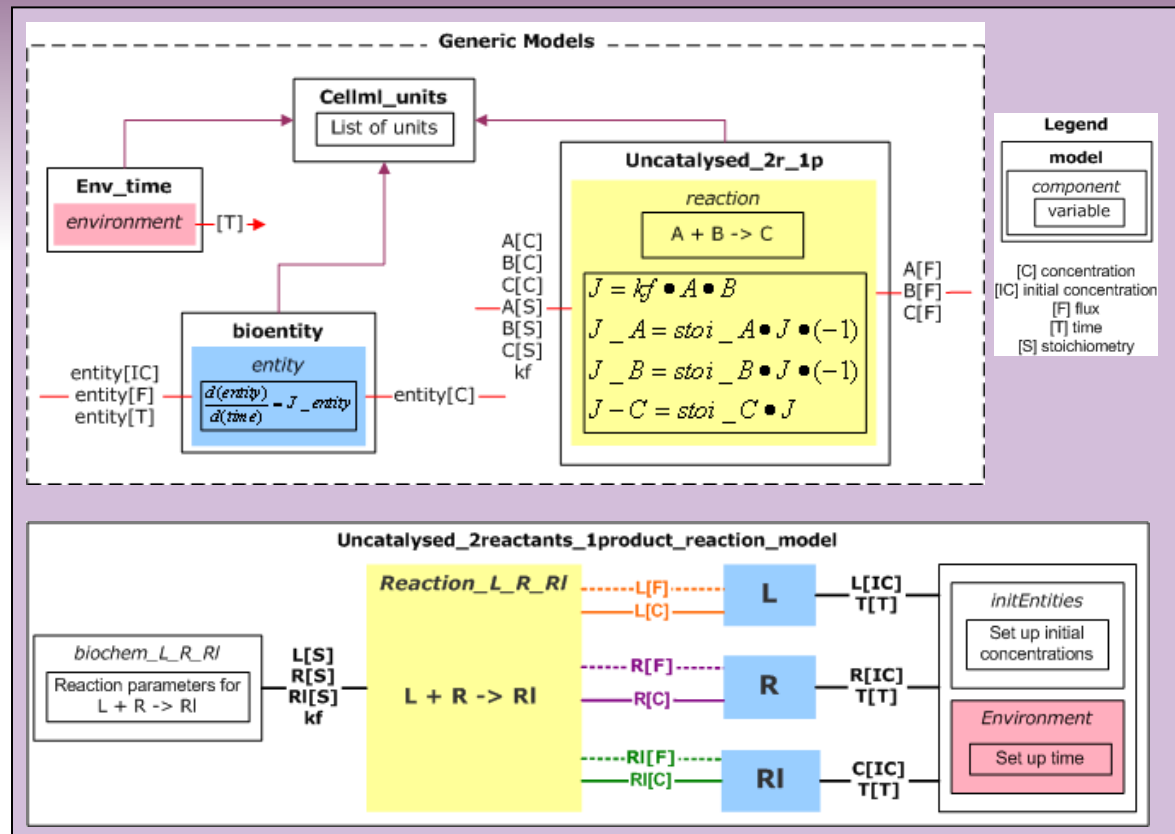
Providing Visual Support

CellML Structure
(Biophysical View)

Underlying Biology
(Biological View)

Workflow

Modularising CellML Models

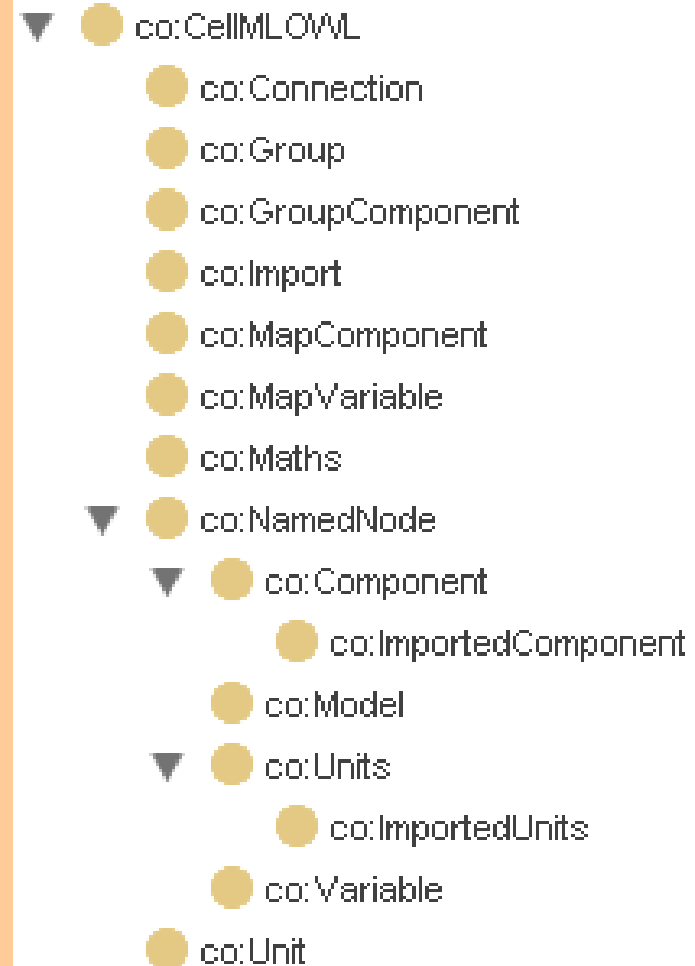# Generation of CellML-OWL

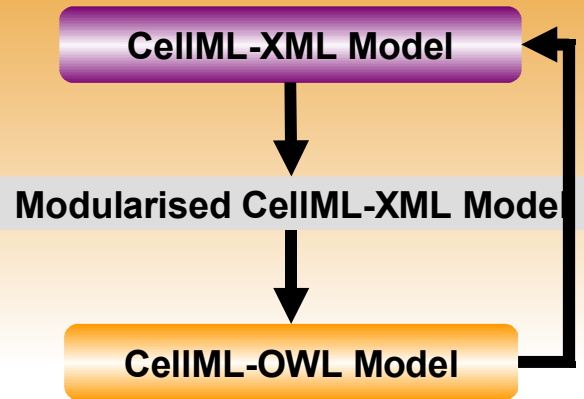**CellML-XML Model**

↓

Modularised CellML-XML Model

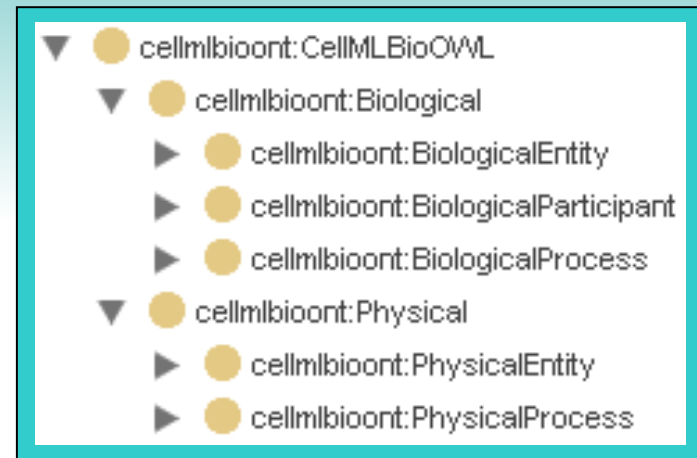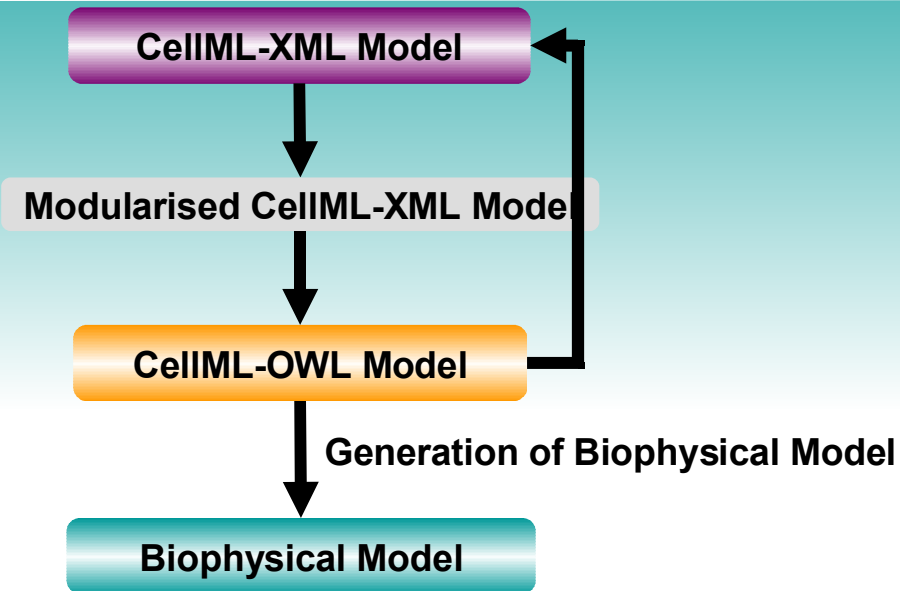↓ **Generation of CellML-OWL**
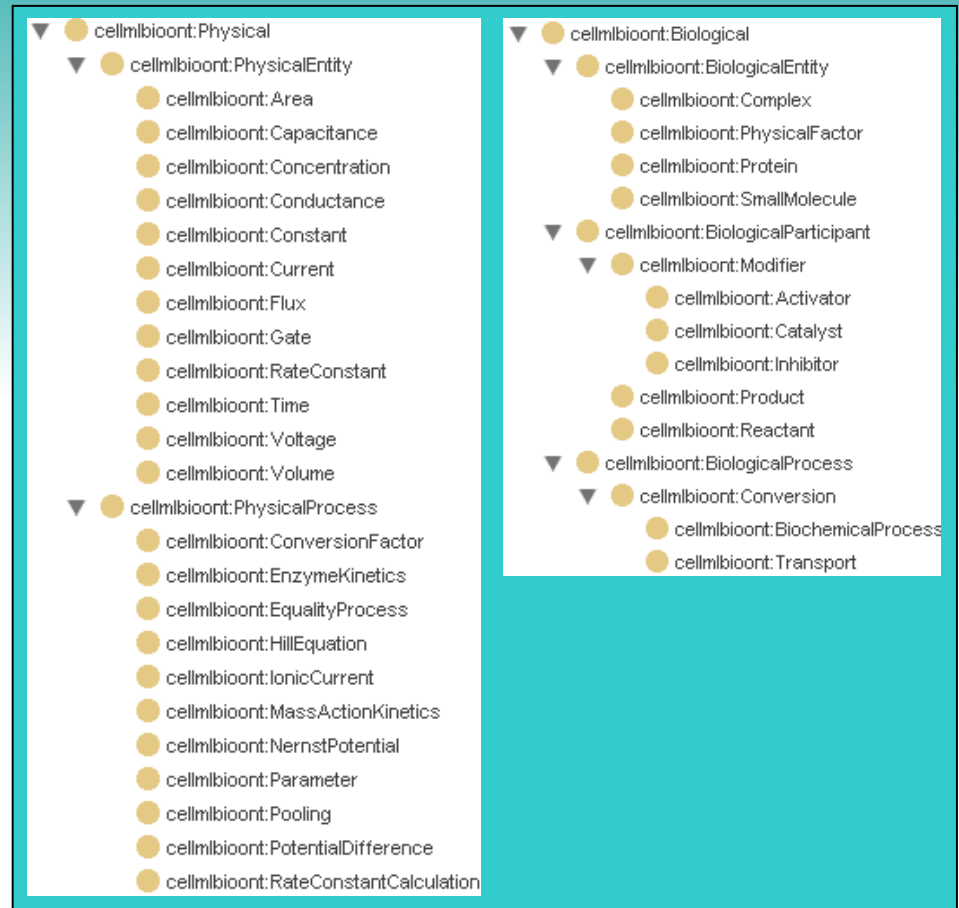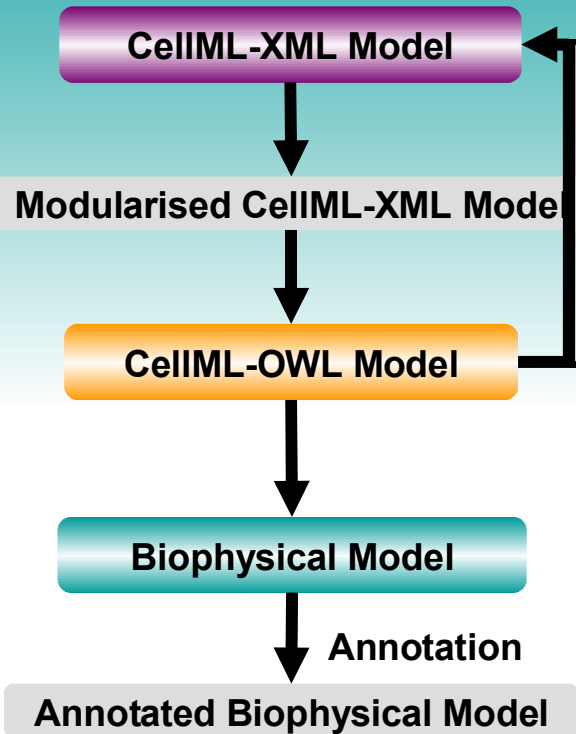
CellML-OWL Model

Linking CellML-XML & CellML-OWL

```
┌──────────────────────┐
│   CellML-XML Model    │◄─────┐
└──────────────────────┘       │
          │                     │
          ▼                     │
┌──────────────────────┐       │
│ Modularised CellML-XML Model  │
└──────────────────────┘       │
          │                     │
          ▼                     │
┌──────────────────────┐       │
│   CellML-OWL Model    │──────┘
└──────────────────────┘
```

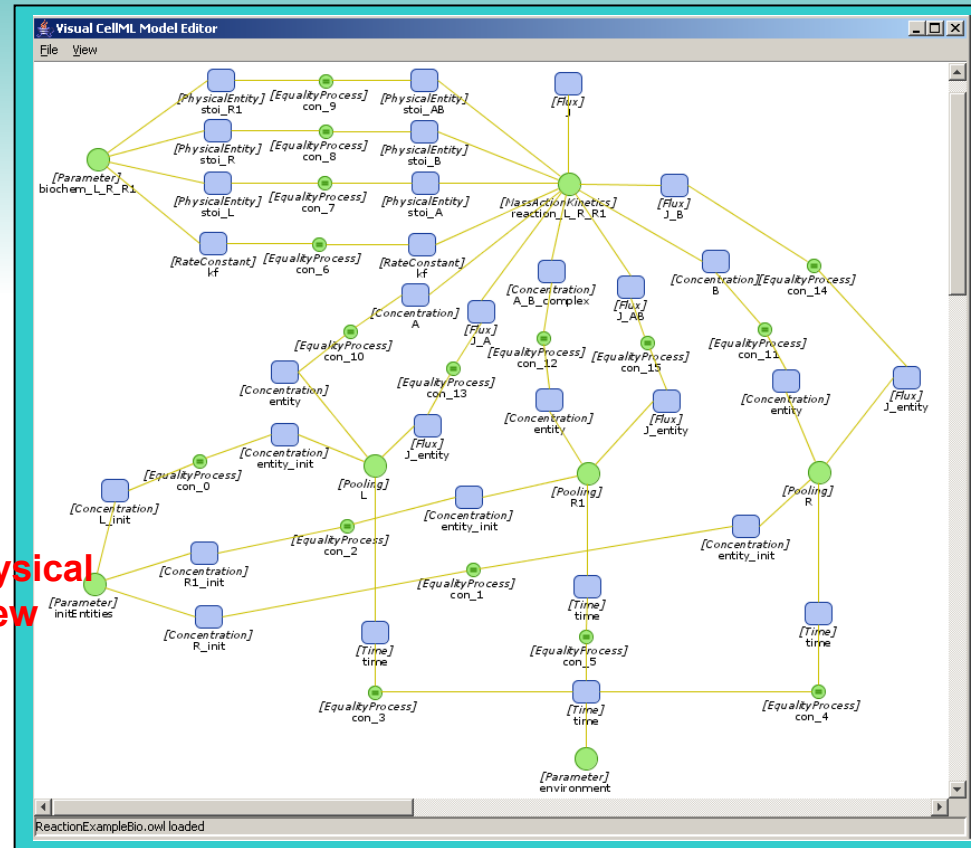**Linking CellML-XML**
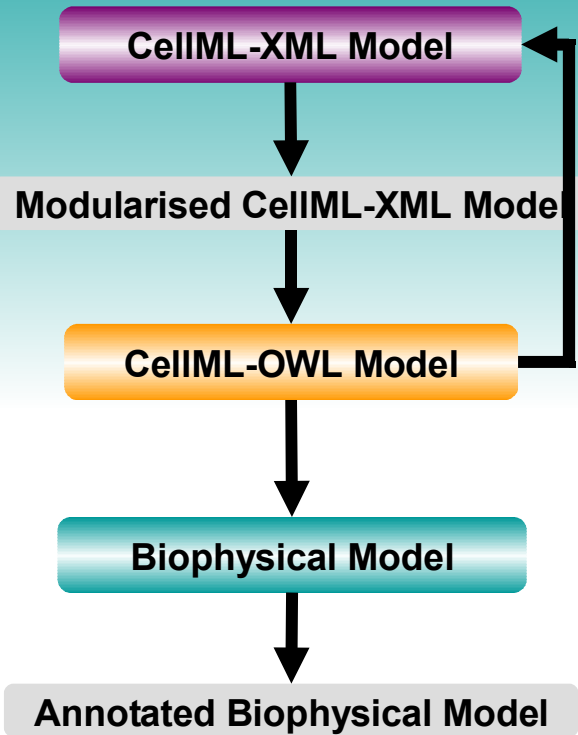**& CellML-OWL**
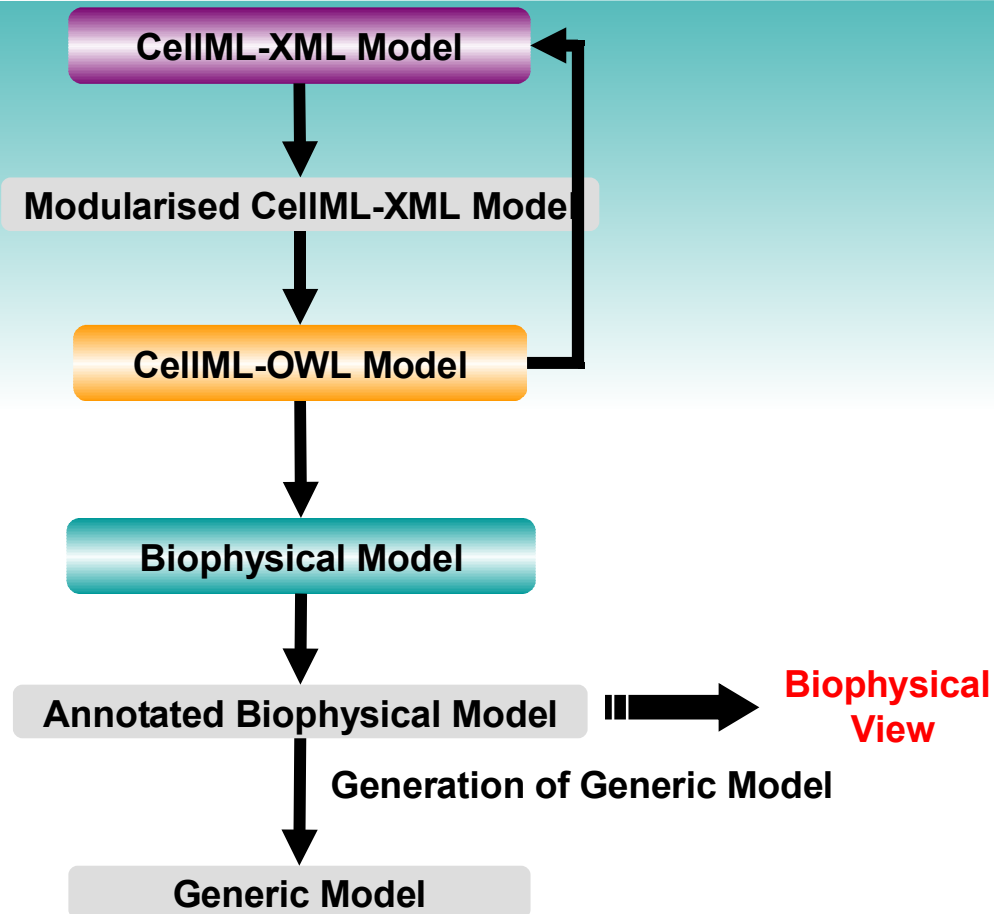
Generation of Biophysical Model
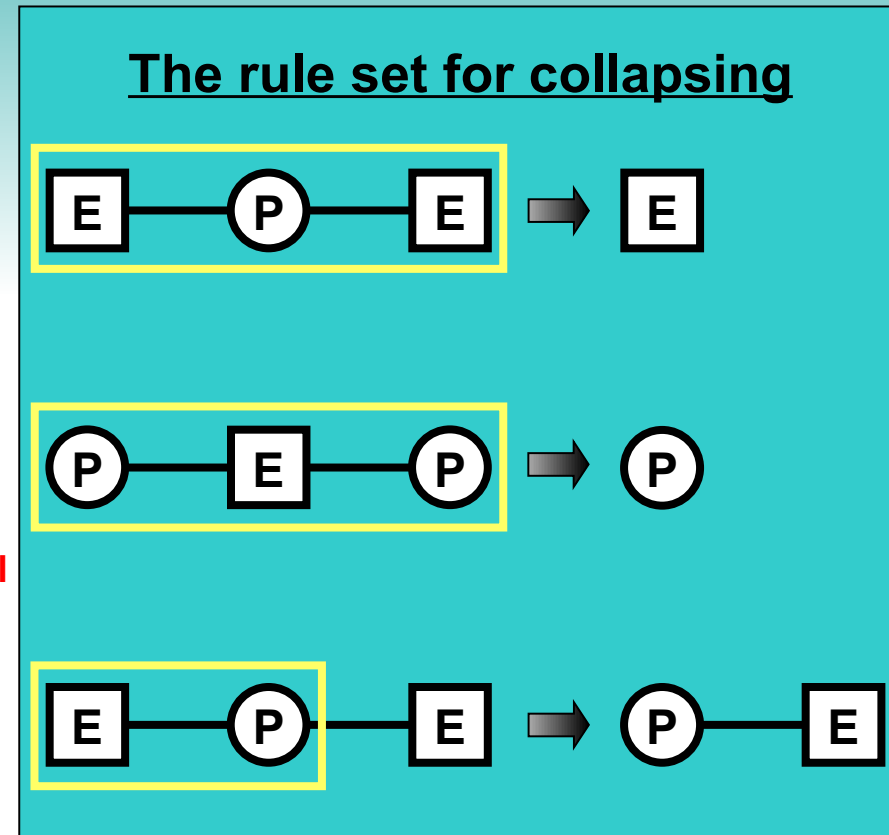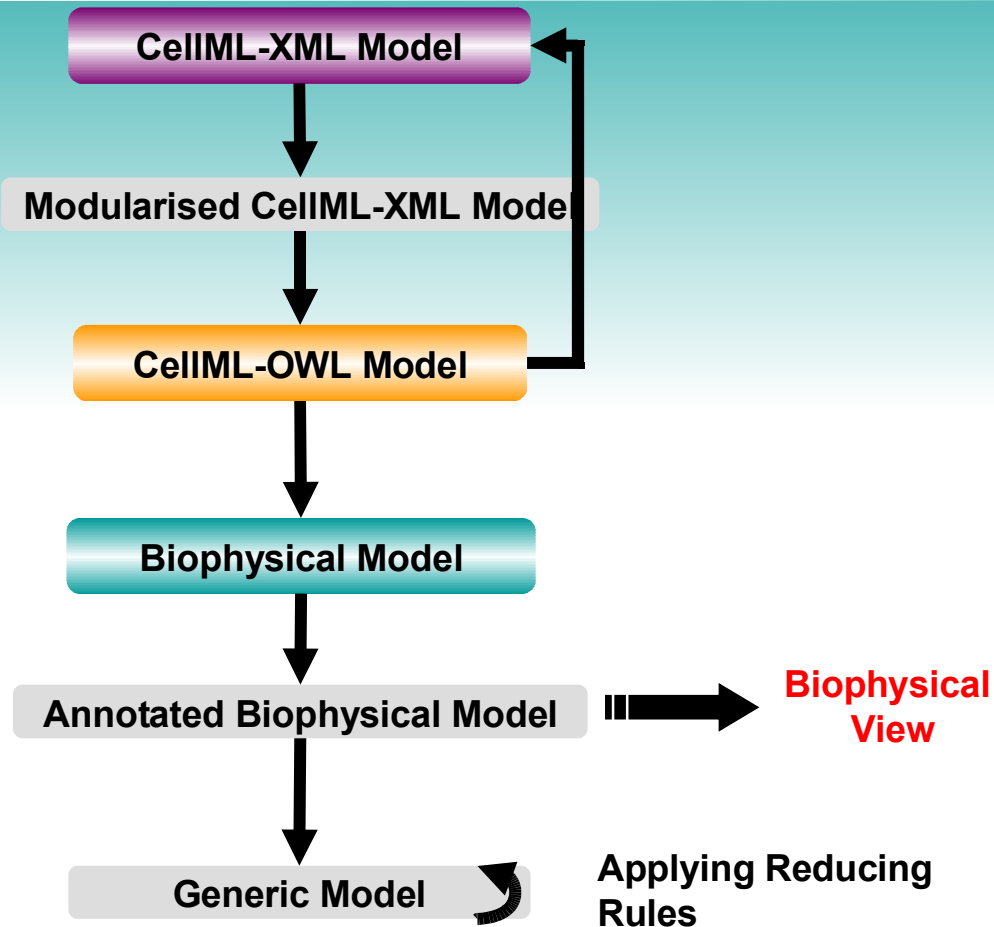
Annotating Biophysical Models

Biophysical View

CellML-XML Model
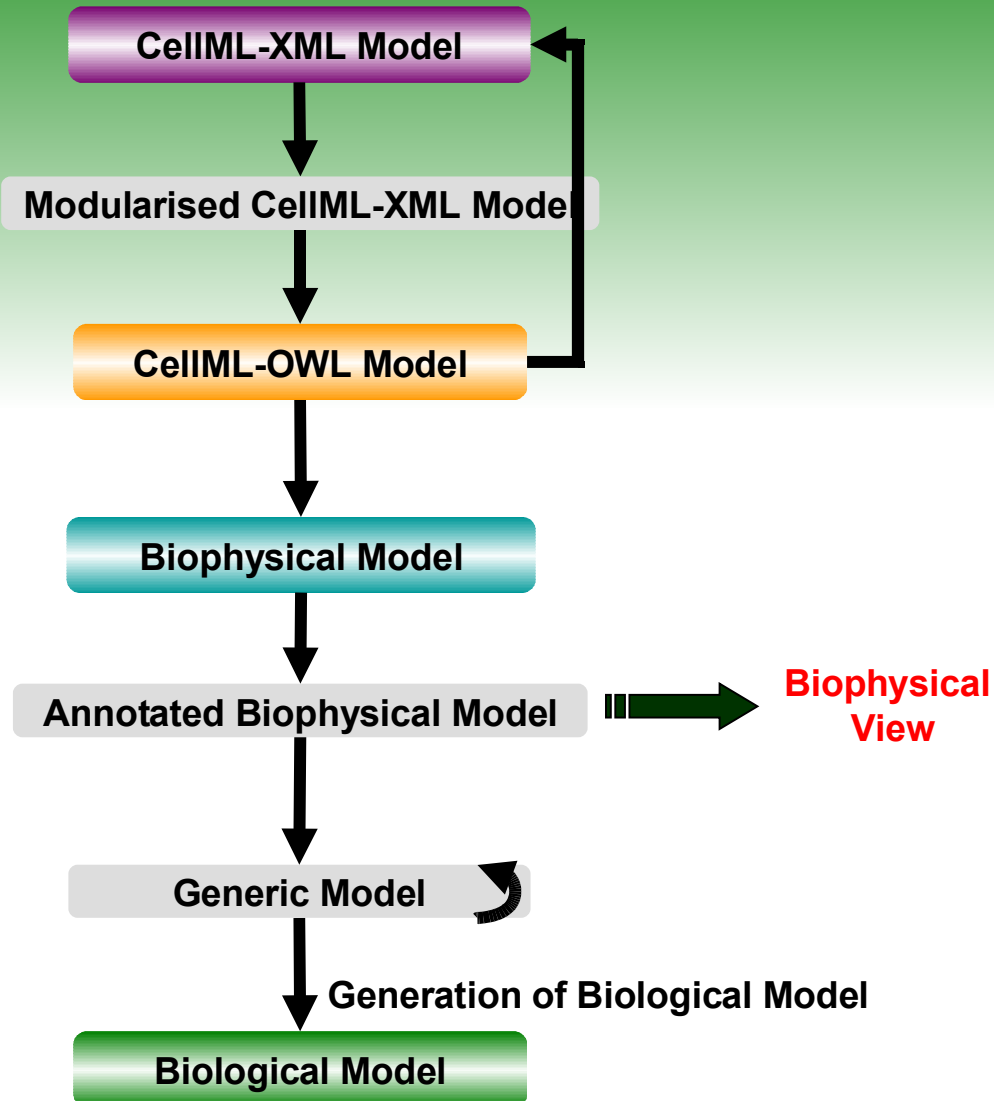
Modularised CellML-XML Model

CellML-OWL Model

Biophysical Model

Annotated Biophysical Model

Linking to glyphs

```
▼ ● visualtemp:VisualTemplate
   ● visualtemp:Interaction
   ▼ ● visualtemp:Entity
      ▼ ● visualtemp:BiologicalEntity
         ● visualtemp:Compartment
         ● visualtemp:Complex
         ● visualtemp:DNA
         ● visualtemp:Protein
         ● visualtemp:RNA
         ▶ ● visualtemp:SmallMolecule
      ● visualtemp:PhysicalEntity
   ▼ ● visualtemp:Process
      ● visualtemp:BiologicalProcess
      ● visualtemp:PhysicalProcess
```

Biophysical View

Generation of Generic Model

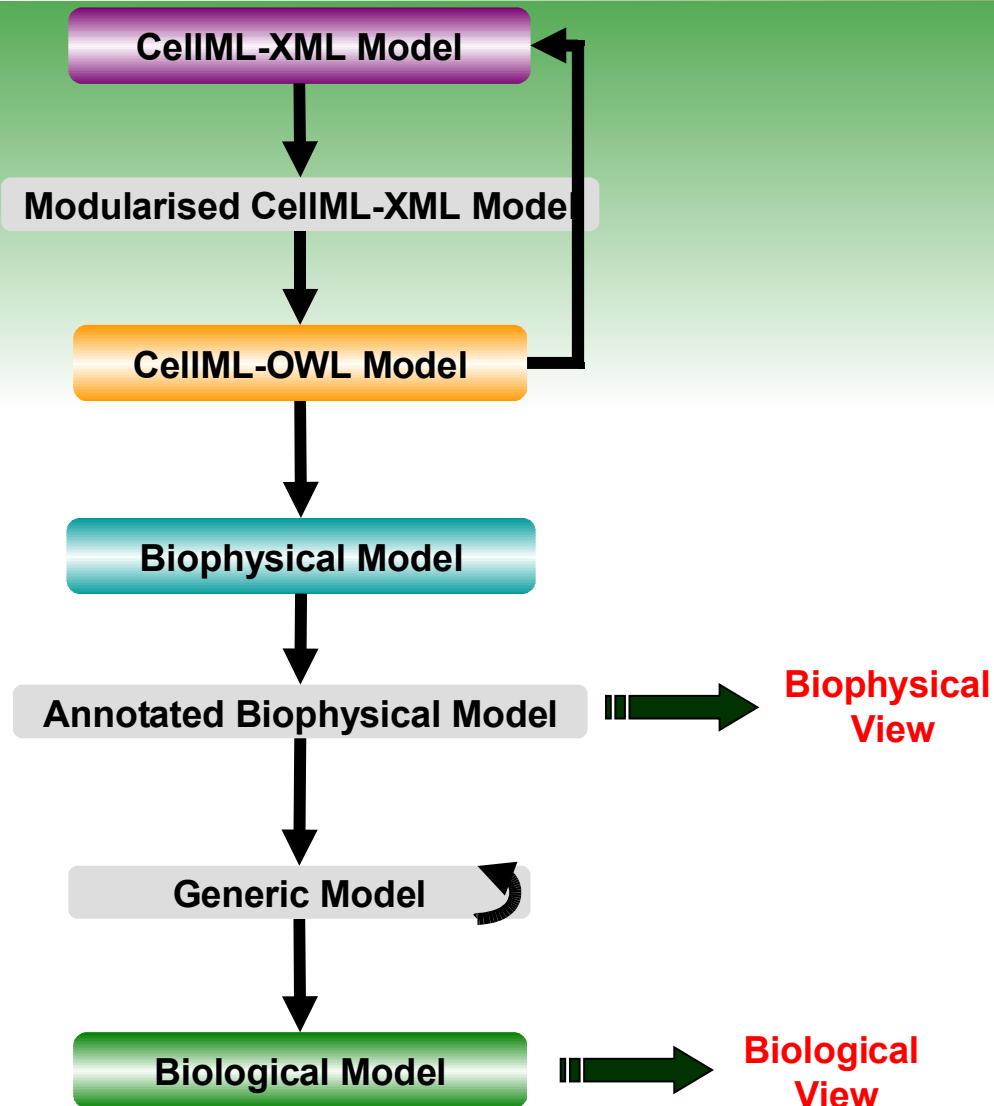# Applying Reducing Rules

CellML-XML Model

Modularised CellML-XML Model

CellML-OWL Model

Biophysical Model

Annotated Biophysical Model → **Biophysical View**

Generic Model

Applying Reducing Rules

The rule set for collapsing

E — P — E ⇒ E

P — E — P ⇒ P

E — P — E ⇒ P — E
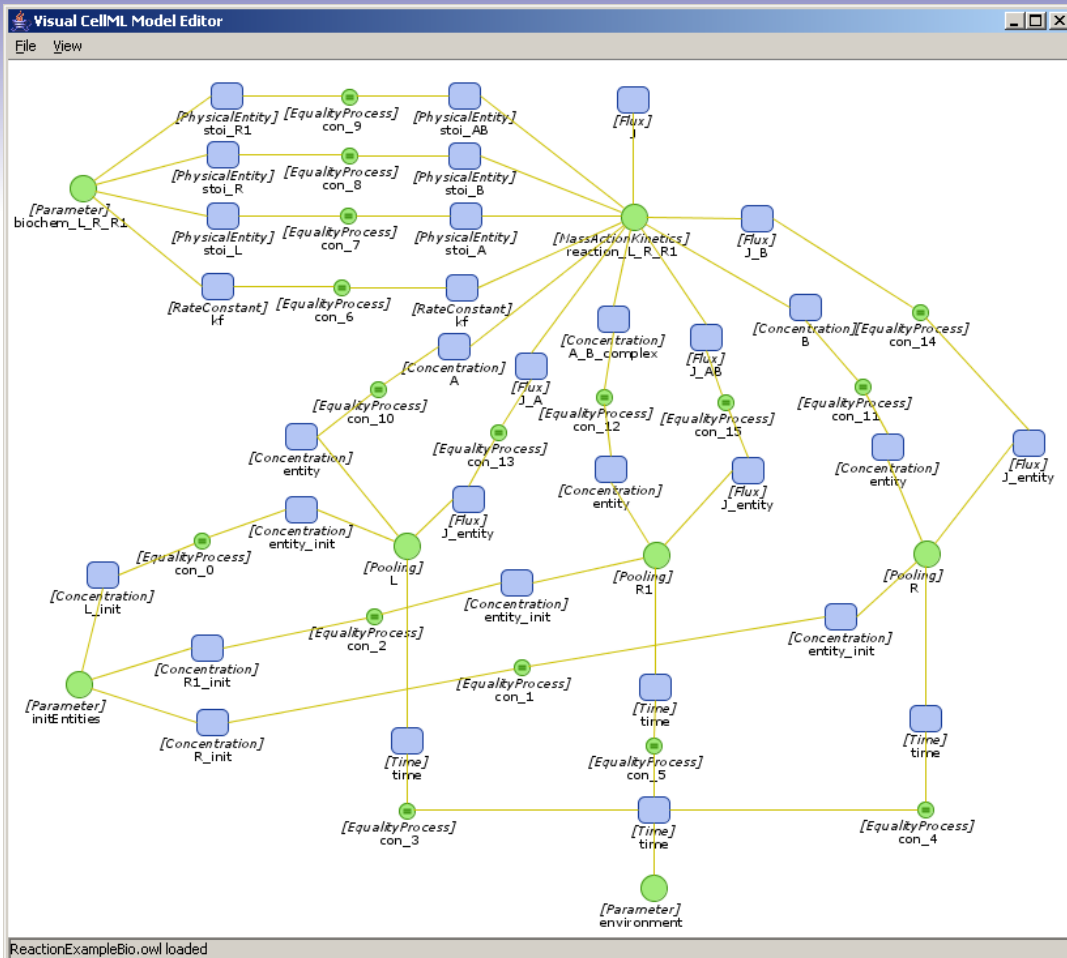
Generation of Biological Model
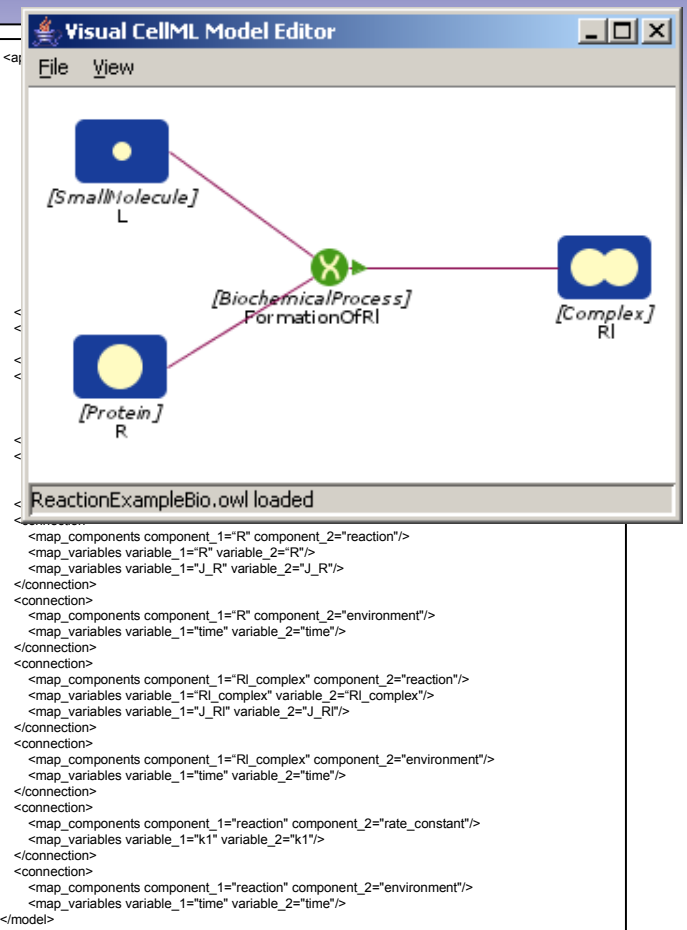
Biological View

Conclusion

Biophysical View **CellML Structure** **Biological View**

Future work

- Enhancing the tool to support automated layout of the diagrams.

- Enhancing the ontologies to support reasoning.

Thank You