

CellML Specification 1.1

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9 Importing Models

9.1 Introduction

The modular structure of CellML seen so far can be taken up one level to make it easier to build a model on previously published models. Often in systems biology, molecular behaviour is researched, modelled, and described in steps. One (group of) scientist(s) will model the flux of ions across a cell membrane, for instance, limiting their study to certain variables. Others will build on the first's work, expanding the focus of the study, and so on. To reflect a realistic method of model building, a CellML modeller may choose to use the import features described below.

9.2 Basic Structure

9.2.1 Definition of imported models

To be able to reuse a model, the model must first be imported into the current model. The `<cellml:import-model>` element is used to locate the model that will be imported. The CellML import feature makes use of the W3C hyperlink standard, [XLink](http://www.w3.org/TR/2001/REC-xlink-20010627/)¹, to identify the link between the current model and the model being imported. Each `<cellml:import-model>` element must have an `xlink:title` attribute and an `xlink:href` attribute. The `xlink` and `cellml` namespace prefixes are used throughout this section to indicate that the elements are in the XLink and CellML namespaces, respectively. The value of the `xlink:title` attribute is a CellML identifier which must be unique amongst all `<cellml:import-model>` elements within the current model. It *need not* be equal to the value of the `cellml:name` attribute of the root `<cellml:model>` element of the imported model. The `xlink:href` attribute has a value equal to the Uniform Resource Identifier that identifies the location of the imported cell model. Throughout the current CellML model, the value of the `xlink:title` attribute will be used to point to the model identified by the value of the `xlink:href` attribute. A model may import any number of valid CellML models.

9.2.2 Referencing units from an imported model

Units from an imported model may be called in the current model by use of the `cellml:units_model` attribute. Any `cellml:units` attribute may be clarified by tagging a `cellml:units_model` attribute to the same element the `cellml:units` attribute qualifies. If the `cellml:units_model` attribute is present, the units referenced by the `cellml:units` attribute must be a globally defined units in the model referenced by the `cellml:cellmlunits_model` attribute.

9.2.3 Mapping variables between models

Variables can be mapped between models in much the same way as mapping variables between components in a model. Variables must still be mapped through components, and connections can be made between two models' components by using the `cellml:model_1` and `cellml:model_2` attribute qualifiers on a `<cellml:map_components>` element. If the `cellml:model_1` attribute is present, the model referenced must contain the component referenced by the `cellml:component_1` attribute on the same

¹<http://www.w3.org/TR/2001/REC-xlink-20010627/>

element. Similarly, the model referenced by the `cellml:model_2` attribute, if present, must contain the component referenced by the `cellml:component_2` attribute on the same element.

9.3 Examples

Figure 17 shows the use of the `<cellml:import_model>` element to import a CellML model located at

`http://www.example.com/units.xml` that contains two units definitions: one with the name of `microF` and another named `microA_per_microF`. The imported model is aliased to the name `units_dictionary` so that when a `cellml:units_model` attribute calls the alias, a processor knows in which document to look for the corresponding units.

When a connection is made between the `membrane` component and another imported model, the `cellml:model_1` attribute is tagged to the `<cellml:map_components>` element to indicate that the component referenced by the `cellml:component_1` attribute can be found in the model aliased to the name `sodium_current_component`. In this example, the model containing the `membrane` component, `cellml:component_2`, is the current model; therefore, no `cellml:model_2` attribute is necessary.

```

<model
  xmlns="http://www.cellml.org/cellml/1.1#"
  xmlns:xlink="http://www.w3.org/1999/xlink">
  <import_model
    xlink:href="http://www.example.com/units.xml"
    xlink:title="units_dictionary" />
  <import_model
    xlink:href="http://www.example.com/sodium_current_component.xml"
    xlink:title="sodium_current_component" />

  <component name="membrane">
    <variable name="Cm" units="microF" units_model="units_dictionary" />
    <variable
      name="I_st" units="microA_per_microF" units_model="units_dictionary" />
    ...
  </component>

  <connection>
    <map_components
      component_1="sodium_current" component_2="membrane"
      model_1="sodium_current_component" />
    <map_variables variable_1="V" variable_2="V" />
    <map_variables variable_1="constant_T" variable_2="T" />
  </connection>
</model>

```

FIGURE 17: The `<cellml:import_model>` identifies the URI of the file being imported and gives the model a name by which it will be referred in the current model. See text for more details.

9.4 Rules for CellML Documents

9.4.1 The `<import_model>` element

1. Allowed use of the `<import_model>` element

- A `<cellml:import_model>` element must contain only the following elements:
 - `<RDF>` elements in the RDF namespace.
- Each `<cellml:import_model>` element must define an `xlink:title` attribute and an `xlink:href` attribute.
[In this and subsequent rules, the `cellml` and `xlink` prefixes are used to indicate that elements and attributes are in the CellML and XLink namespaces, respectively.]

2. Proper use of the `<cellml:import_model>` element

- A model must not import a model that directly or indirectly imports itself.
[The model tree must be acyclic.]

3. Allowed values of the `xlink:title` attribute

- The value of the `xlink:title` attribute must be a valid CellML identifier as discussed in [Section 2.2.1](#)².
- The value of the `xlink:title` attribute must be unique across all `<cellml:import_model>` elements contained in the parent `<cellml:model>` element.

4. Allowed values of the `xlink:href` attribute

- The value of the `xlink:href` attribute must be a valid [Uniform Resource Identifier](#)³.

9.5 Rules for Processor Behaviour

9.5.1 Treatment of imported models

CellML processing software must include the imported models in the current model. Values of every `name` attribute in the imported models must be qualified with the value of the `xlink:title` attribute associated with the imported model.

E-mail questions, criticism, submissions or info to info@cellml.org
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²http://www.cellml.org/public/specification/20021106/cellml_specification.html#sec_fundamentals_identifiers

³<http://www.ietf.org/rfc/rfc2396.txt>