

Modularity in CellML

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Background

- **Mathematical models of cellular physiology are rapidly increasing in biophysical detail:**
 - electrophysiology and mechanics;
 - + calcium dynamics;
 - + mitochondrial energetics;
 - + signalling cascades;
 - + ...
- **Models routinely now consist of large systems of differential & algebraic equations and many parameters.**
- **Modelling studies typically require multiple models, each with many parameterizations.**

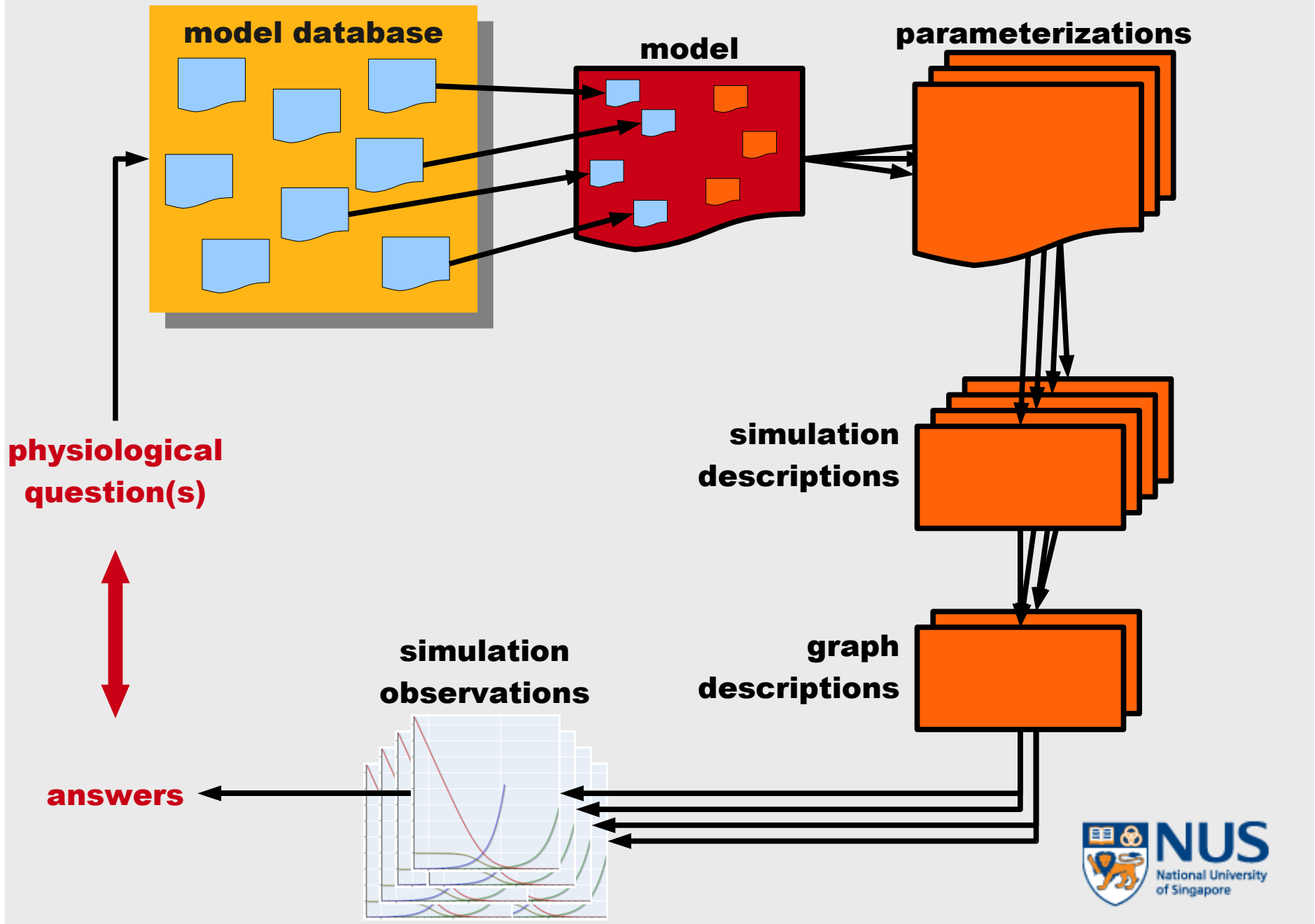
The Problem

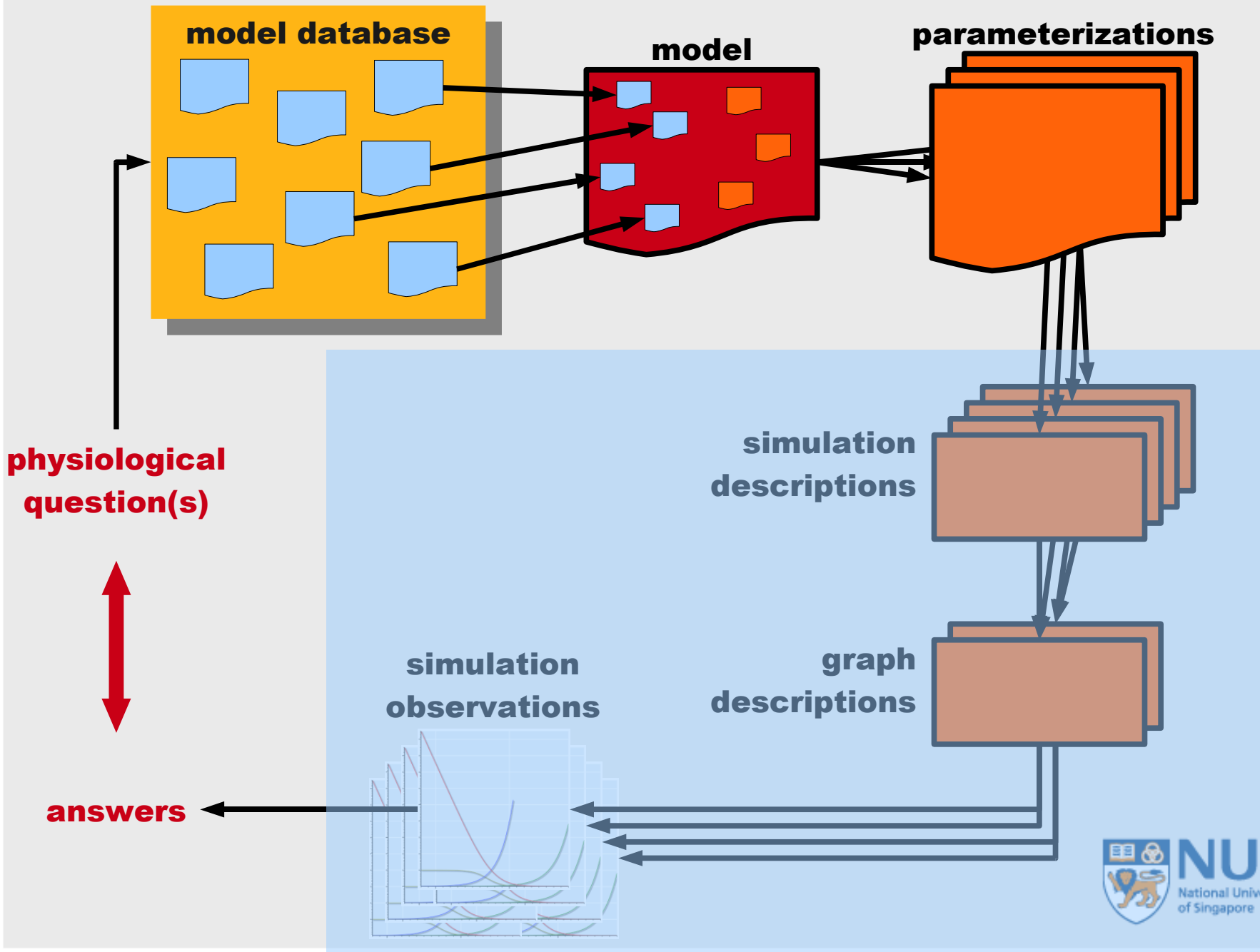
- **How do model authors:**
 - describe such complex models?
 - share them with colleagues and the scientific community?
 - reuse bits and pieces of existing models?
 - publish them?
- **Several (almost) independent sub-problems:**
 - the mathematical model(s);
 - parameterizations of the mathematical model(s);
 - instantiation of the models as specific and reproducible computational simulations;
 - extraction of specific “simulation observations” from simulation datasets.
- **Machine vs human interpretation and interaction.**

Our solution

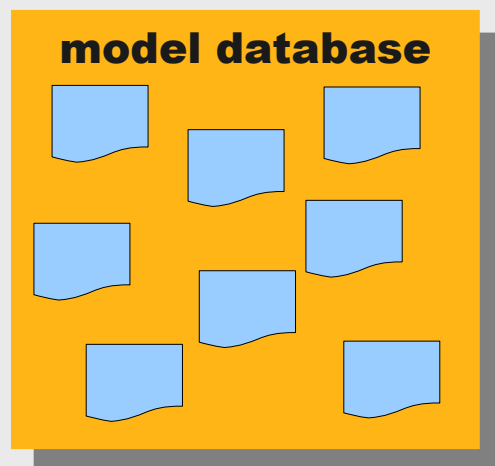
- Annotated CellML models....

<http://www.cellml.org>





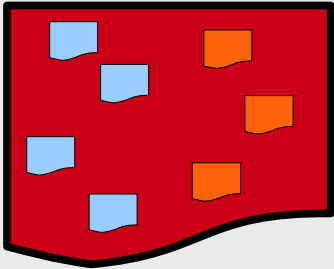
Model repositories



- Freely available & online model repositories.
- Contain models described in standard formats.
- Curated to various levels of “correctness”.
- **Examples:**
 - <http://www.cellml.org/models/>
 - <http://www.biomodels.net/biomodels/>

New models and model components

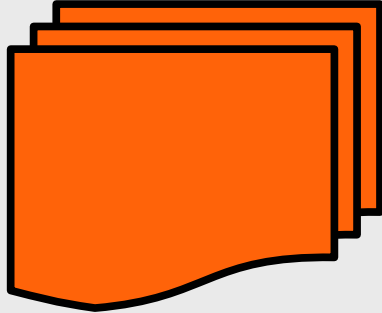
model



- **Answering novel questions generally requires the development of new models in combination with existing models:**
 - reparameterizing existing models;
 - combining existing models;
 - altering the dynamics of certain components of the model;
 - extending models to include new behaviour.

Model parameterization

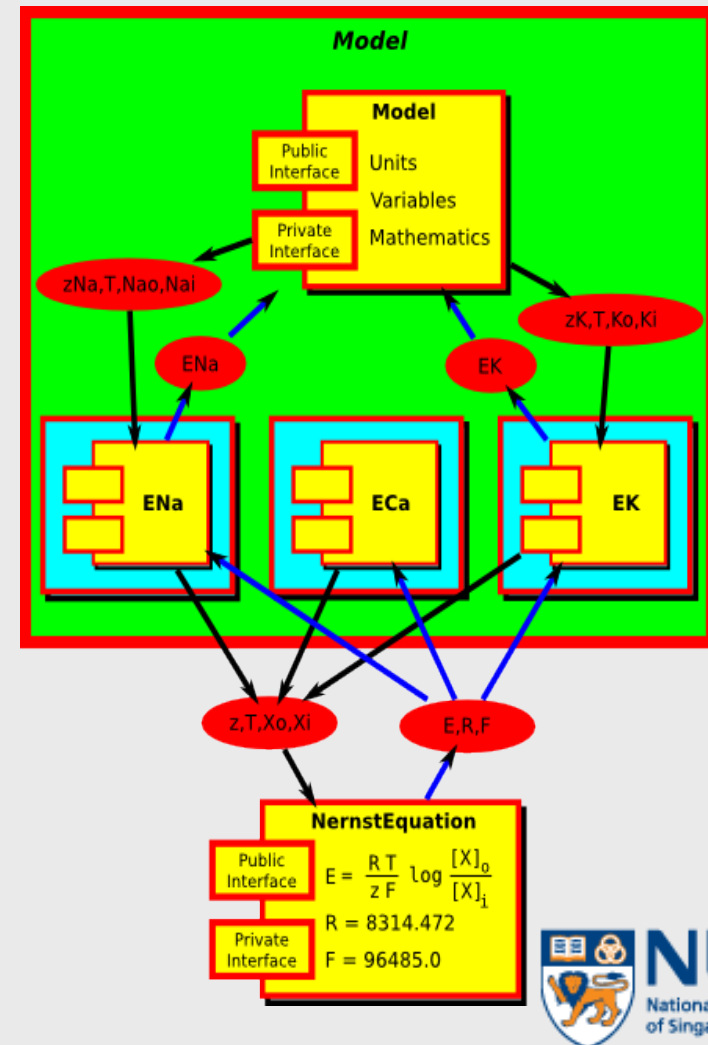
parameterizations

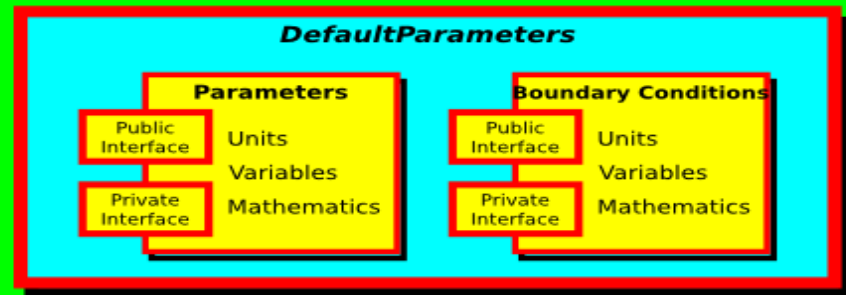
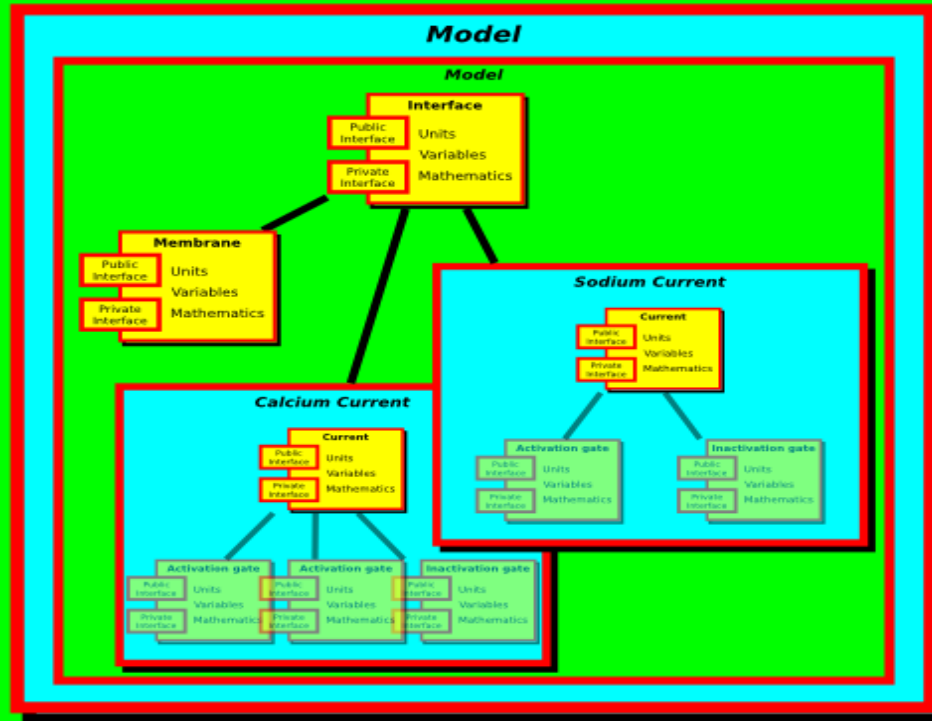
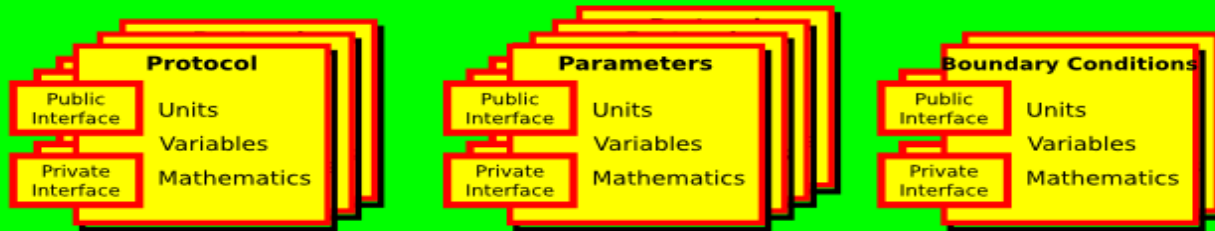


- Each mathematical model may be parameterized for many different scenarios.
- Specializing generic mathematical model for specific purpose.

Mechanics of Modularity in CellML

- **CellML 1.1:**
 - import element;
 - use of variables in setting `initial_value` attribute.





Mechanics of Modularity in CellML


- **CellML 1.2 (?)**:
 - variable typing, sets:
 - avoid current necessity to recompose model hierarchies to expose species rate variables;
 - simply add new fluxes to the set of all fluxes for that species.

Enhancing Modularity in CellML

- **Model repository (PMR2):**
 - model workspaces;
 - DVCS;
 - curation and authorship;
 - programatic access.
- **Tool support:**
 - C++ API exists and generally works, why aren't people using it?
- **Model component curation:**
 - what does it mean to use a model component outside its original model?
 - annotation? licensing? PMR2...

Enhancing Modularity in CellML

- Guidelines on the use of CellML 1.1 to ensure we all create models suitable for re-use by the community wherever possible...




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Modelling with CellML 1.1

Best Practice (???)

- Components should only contain one equation.
- A component with math in it should define no `initial_value` attributes with a numerical value.
- As a mathematical model is assembled, all components should be encapsulated by a sensible interface component.
- All variables should be exposed via the encapsulating interface component.



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References

- Nickerson & Buist (2008): Prog Biophys Mol Biol. 98(1):38–51; doi: 10.1016/j.pbiomolbio.2008.05.006
- <http://www.cellml.org/publications>

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