

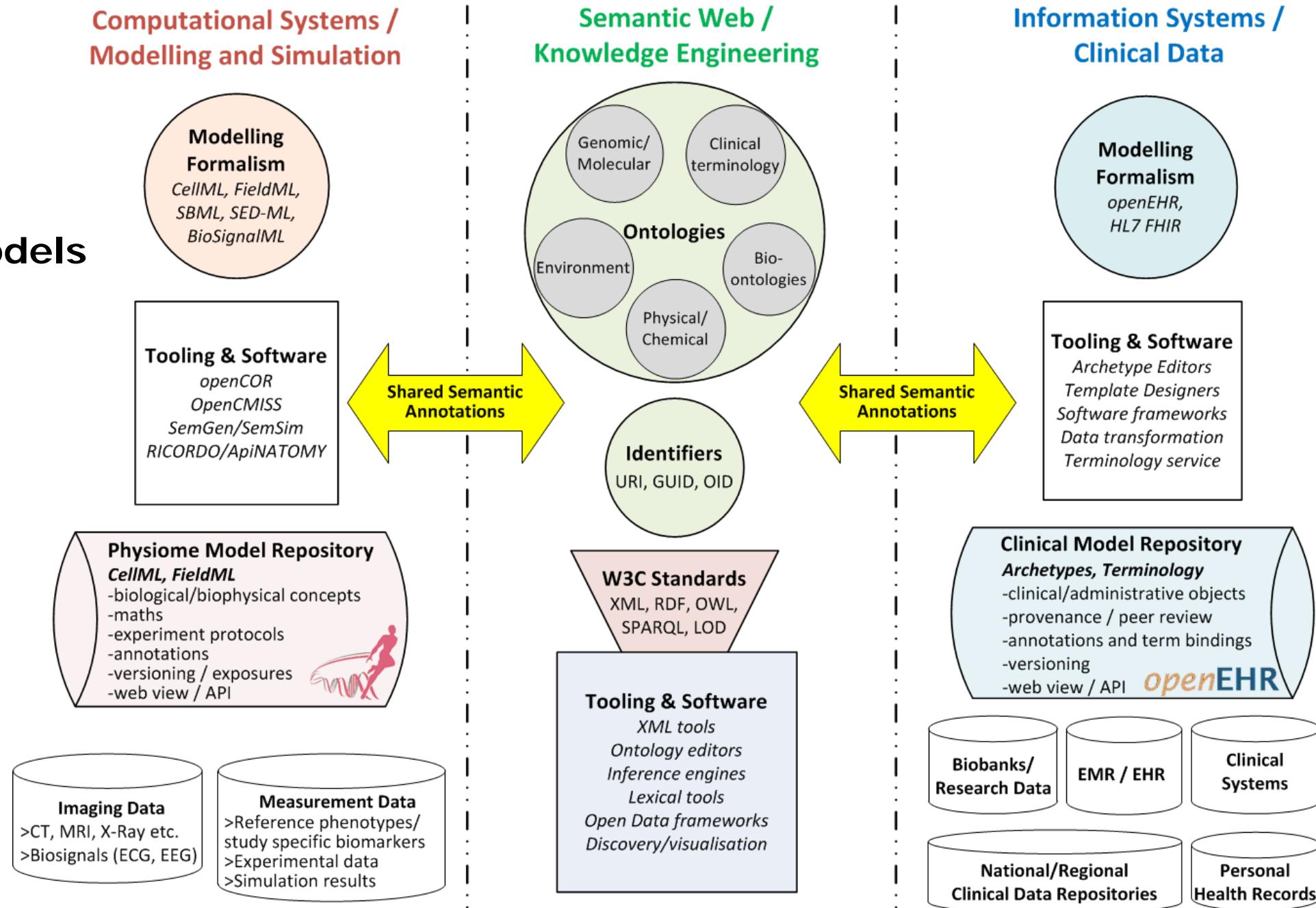
Model semantics for discovery, composition, and personalisation

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Tommy Yu, Peter Hunter



**AUCKLAND
BIOENGINEERING
INSTITUTE**

Big Picture: Linking Computational Models to Data

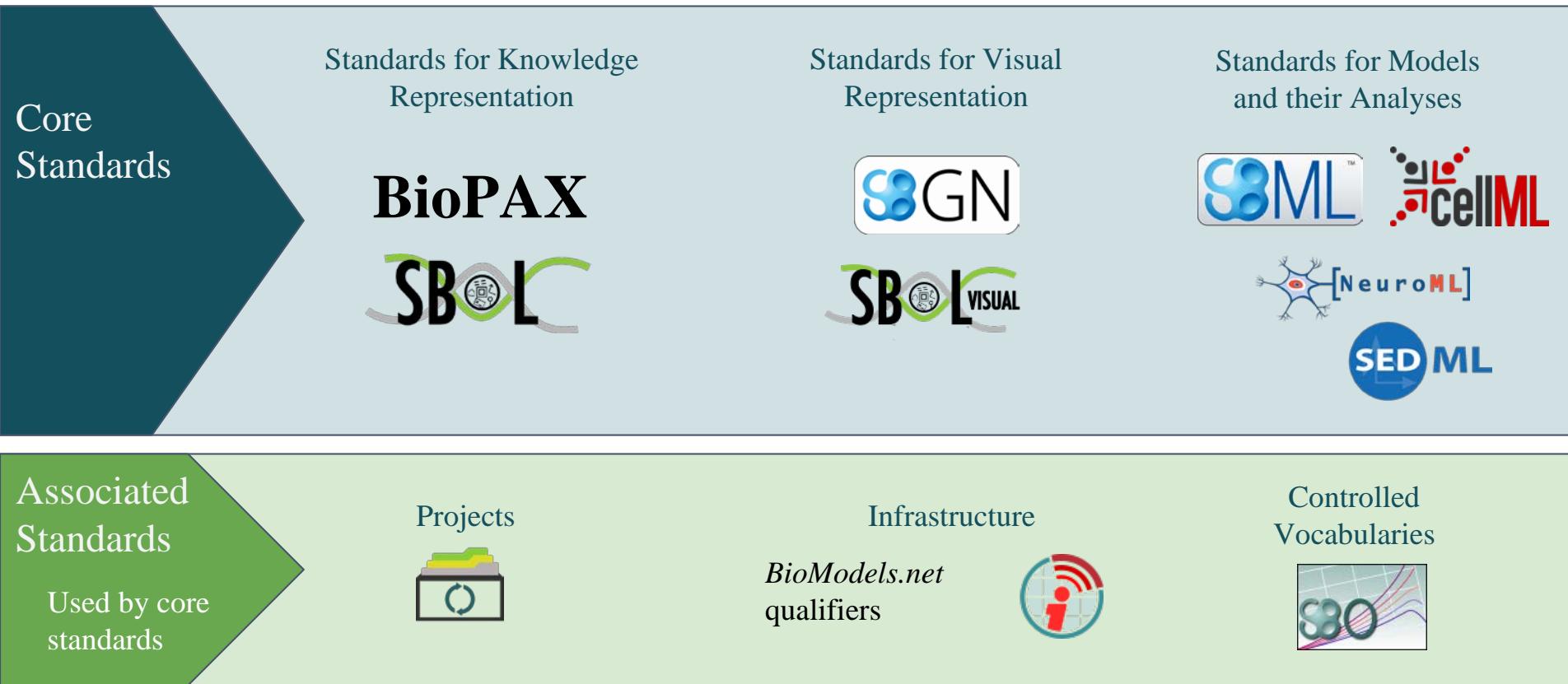


Standards

- Sharing, archiving, reuse, reproducibility



- Bond graph-based modelling frameworks
 - going beyond the math, capture the physics
 - essential for cross-domain modelling



<http://co.mbine.org/>

Meeting in Boston this October: http://co.mbine.org/events/COMBINE_2018
(travel grants available for US-based students!)

Collaboration & comprehension

- Modularity and reuse
- Versioning, provenance, capturing key decisions
- Describing the model
- Common approaches for annotation – speak the “same” language
 - cross-repository discovery
 - cross-standard reuse and merging
 - common software tools
- Discovering relevant information

Physiome Model Repository (PMR)

<https://models.physiomeproject.org>

<https://models.physiomeproject.org/proteins>

Models Home My Workspaces Exposures Documentation David Nickerson ▾

You are here: Home / Exposures / SED-ML example / vanderpol.cellml

Mode View Wizard Exposure Root Sharing

You are 1

Na+ vanderpol.cellml

Annot by David Nickerson — last modified Sep 27, 2017 09:19 AM — History

Describe Van der Pol oscillator

A kinetic model of the Van der Pol oscillator is used in the *Create and run a simple CellML model: editing and simulation* section of the tutorial. The simulation experiment for this model described in the tutorial can be obtained by loading the corresponding SED-ML document into OpenCOR and executing the simulation. The results of which are shown below. A rendering of the mathematical model itself is available here.

Protein Modules

- 25D HH potassium ion channel model
- 25D HH sodium ion channel model
- 28F A kinetic model of Na+/H+
- 290 A kinetic model of Cl-/HCO3
- 293 A kinetic model of V-type H
- 294 A kinetic model of Na+/K+
- 295 A kinetic model of Na+/HCO3

Chang, Fujita, 1999

A kinetic model of the thiazolidine kinase inhibitor Loo, Eskandari, Wright, Loo, Kinetics of the Reverse Model Mackenzie, Loo, Panayotou, Biophysical Characteristics of

Locate

Proximal Apical Epithelial

Work This work model a models

- NHI
- NHI
- NHI
- NHI
- NHI
- NHI

OpenCOR vanderpol.sedml

Simulation

Property	Value	Unit
Starting point	0	dimensionless
Ending point	100	dimensionless
Point interval	0.1	dimensionless

Solvers

Property	Value	Unit
ODE solver	CVODE	dimensionless
Max... Max... Max... Integ... Iterat... Newton Lines... Relati... Absolu... Interp...	0 500 BDF 1e-07 1e-07 true	dimensionless

Graphs

Editing main.t | main.x

Parameters

Property	Value	Unit
main.mu	1	dimensionless
main.t	0	dimensionless
main.x	-0.0049419...	dimensionless
main.x'	0.11416411...	dimensionless/dimensionless
main.y	0.11416411...	dimensionless
main.y'	1.66019005...	dimensionless/dimensionless

Source

Derived from workspace SED-ML example at changeset 5257320c5ba4.

Collaboration

To begin collaborating on this work, please use your git client and issue this command:

```
git clone https://models.physiomeproject.org/vanderpol.cellml
```

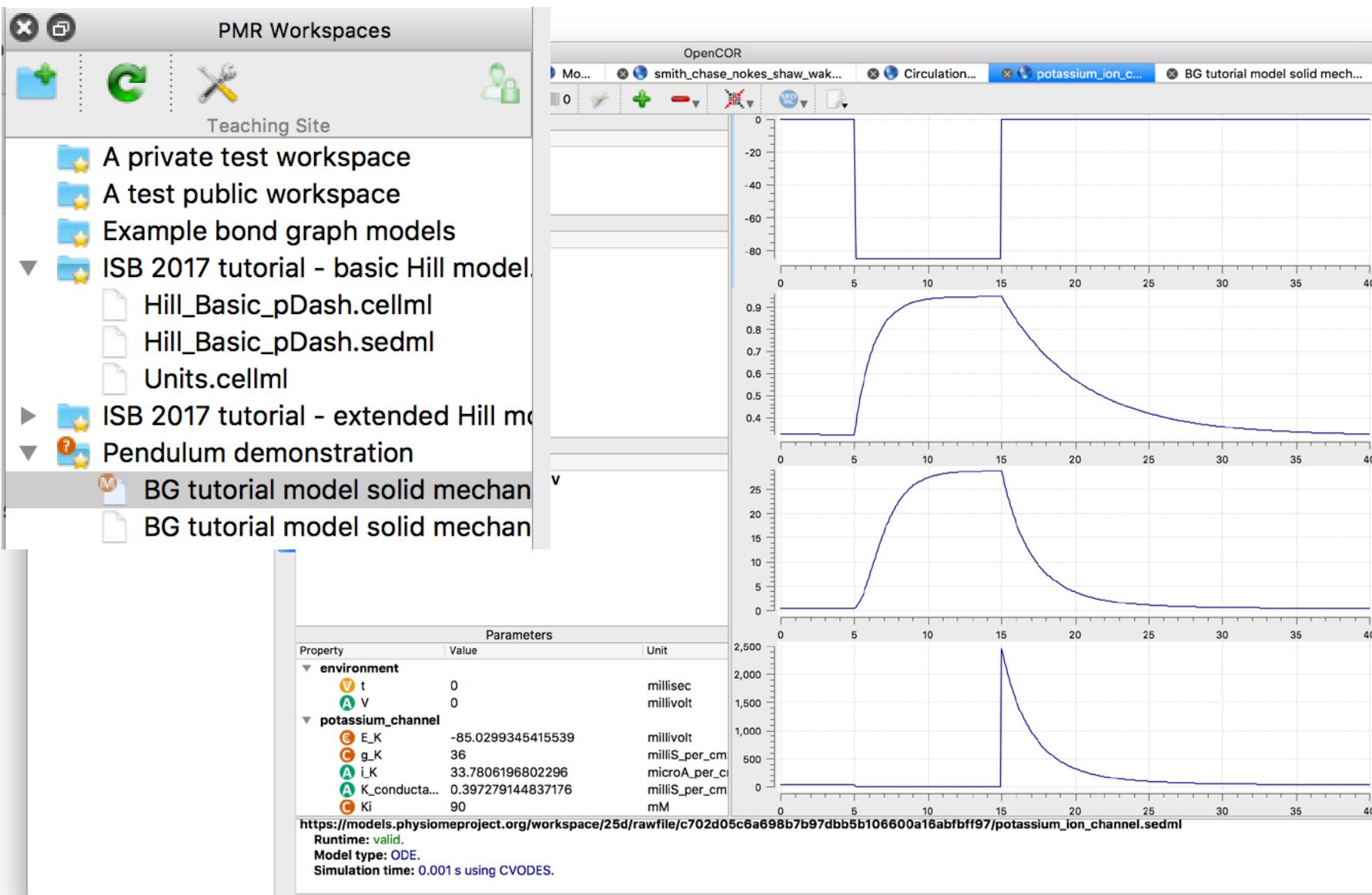
Downloads

- Download This File
- Complete Archive as .tgz
- COMBINE Archive

Views Available

- Documentation
- Model Metadata
- Model Curation
- Mathematics
- Generated Code
- Cite this model
- Source View
- Launch with OpenCOR

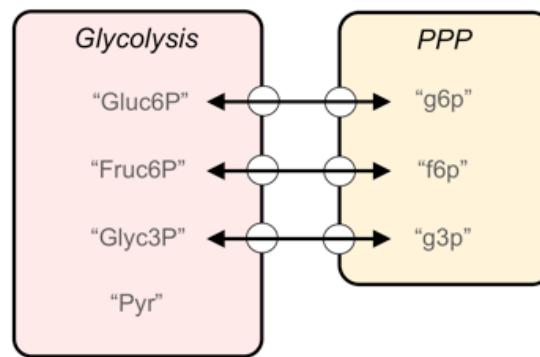
A blue arrow points from the 'Downloads' section to the 'COMBINE Archive' link.



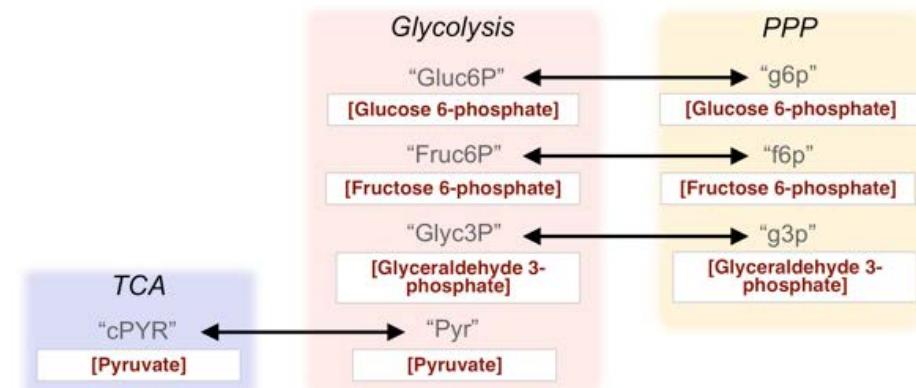
Semantic annotation

From Neal ML *et al.* PLoS Comp Bio, 2014.

A



B



Epithelial Model Platform

Home Model Discovery Load Models

flux of sodium

 View Add to Model

Model_entity

 mackenzie_1996#NBC_current mackenzie_1996#phenomenon mackenzie_1996#ion_concentration mackenzie_1996#rate_constants mackenzie_1996#ion_concentration mackenzie_1996#rate_constants weinstein_1995#NHE3_J_NH4 weinstein_1995#Concentrations weinstein_1995#NHE3_C_ext weinstein_1995#Concentrations weinstein_1995#NHE3_C_int

Epithelial Model Platform

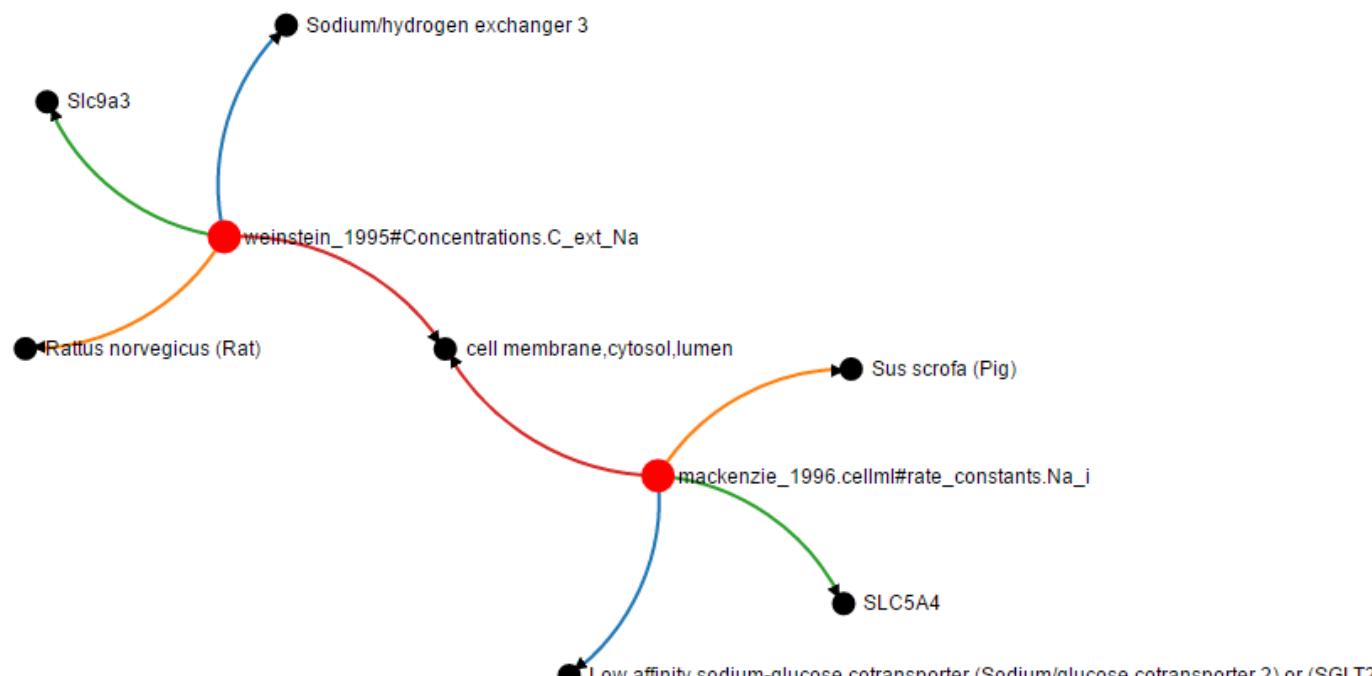
Home Model Discovery Load Models Documentation

Protein

Species

Gene

Compartment



Apical Membrane

Basolateral Membrane

Luminal Compartment

Cytosol Compartment

Interstitial Fluid

Paracellular Pathway

 $J_{\text{mc}}_{\text{Na}} J_{\text{mc}}_{\text{Cl}}$ $J_{\text{mc}}_{\text{K}} J_{\text{mc}}_{\text{Cl}}$ $G_{\text{mc}}_{\text{Na}}$ channel G_{mc}_{K} channel $G_{\text{mc}}_{\text{Cl}}$ channel $J_{\text{sc}}_{\text{Na}} J_{\text{sc}}_{\text{K}}$ $G_{\text{sc}}_{\text{Cl}}$ channel G_{sc}_{K} channel $G_{\text{ms}}_{\text{Na}}$ diffusive channel $G_{\text{ms}}_{\text{Cl}}$ diffusive channel G_{ms}_{K} diffusive channel

Simulation experiments

- Annotate simulation experiments
 - common similarity tools
 - discover suitable protocols to test models
 - “continuous integration”
 - automated model validation?
- Cardiac Electrophysiology Web Lab

Available experiments

Show: [Moderated experiments](#) [All public experiments](#)

This matrix shows the latest versions (visible to you) of the models and protocols in our database, with the corresponding experiments.

Note that you can compare models' behaviours under a particular protocol by viewing the protocol (click on a column heading), selecting the 'Compare models' button, and comparing the experiments using models of interest. The converse comparison (one model, many protocols) is available via viewing a model.

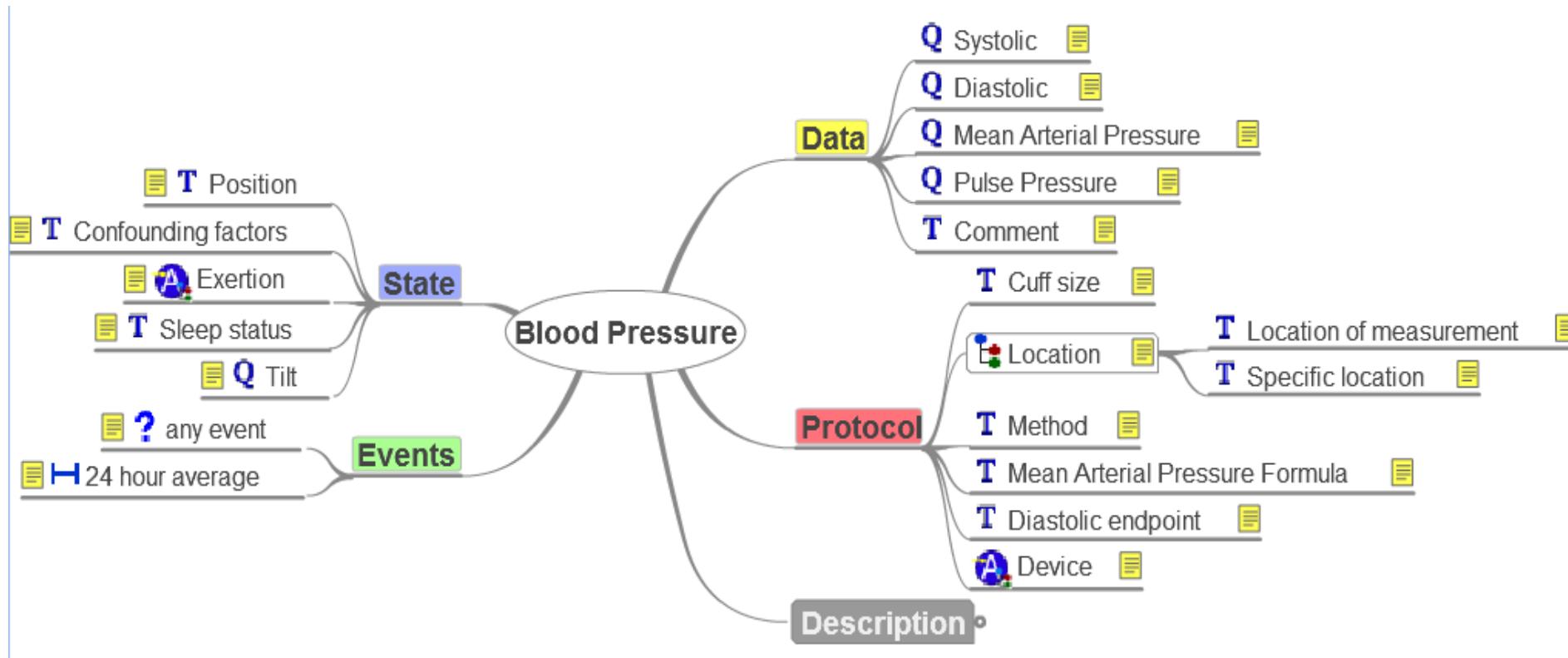
Alternatively, enable 'comparison mode' to allow selecting arbitrary experiments from this matrix view to compare. Click on a column or row heading to select the entire column or row.

Comparison mode: [Enable](#)



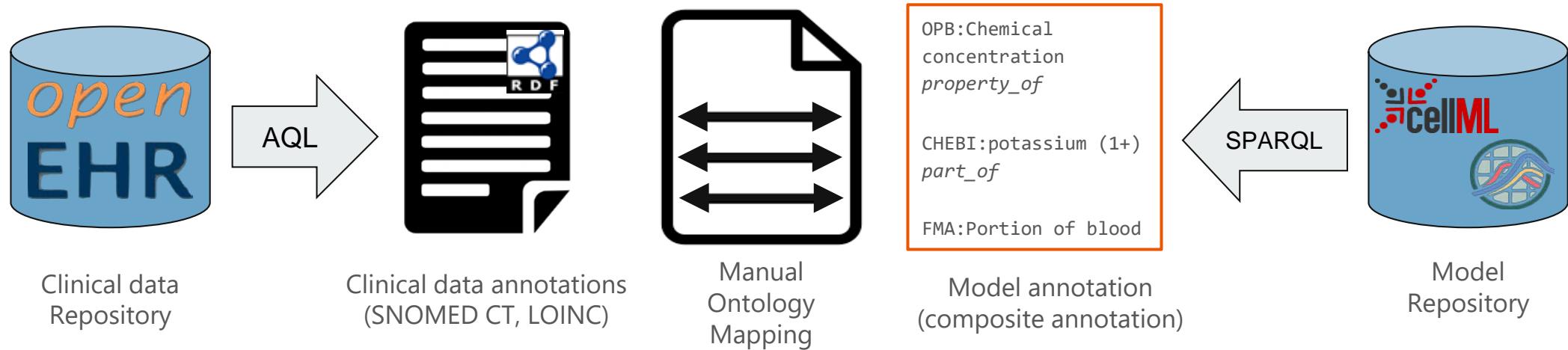
<https://travis.cs.ox.ac.uk/FunctionalCuration/db>

Clinical data annotations



mindmap representation of openEHR Archetype

Clinical data annotations



Result: Experimental & Simulation Data Integration

Extended prototype cardiac electrophysiology web lab to link to experimental data described in an openEHR database.



Acknowledgements



Koray Atalag



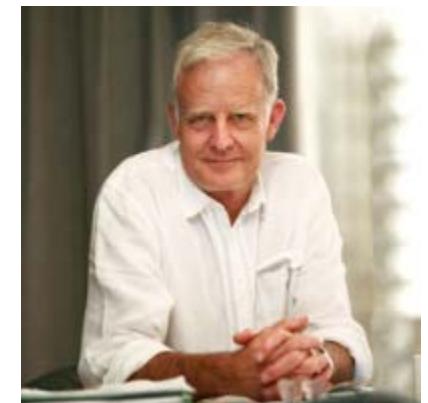
Reza Kalbasi



Dewan Sarwar



Tommy Yu



Peter Hunter

- Cardiac electrophysiology web lab team
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 - Centre for Reproducible Biomedical Modeling
 - <http://reproduciblebiomodels.org/>
- Aotearoa Foundation