



<https://cellml.org>

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**AUCKLAND
BIOENGINEERING INSTITUTE**

THE UNIVERSITY OF AUCKLAND
NEW ZEALAND

Te Whare Wānanga o Tāmaki Makaurau



<https://cellml.org/>



- Modular framework for encoding mathematical models:
 - focus on encoding models consisting of differential algebraic equations using MathML
 - math is the primary data, biological context, provenance, etc., provided through annotations using RDF
- All quantities require physical units ensuring unambiguous conversion of numerical values where required
- CellML models able to define hierarchies of modules to enable mathematical abstraction
- Hierarchical modules able to be imported from external CellML models enabling reuse

- Current version: 1.1
- Latest version: 2.0 (draft)

libCellML

- <https://github.com/cellml/libcellml>
- CellML 2.0 only
- replacement of the CellML API
- aims to become an easy to use library that will be useful to developers of CellML applications
- well documented and tested

Current state

- “full” data model for CellML 2.0
- C++ implementation, Python bindings available
- validation
- working on code generation

Physiome Model Repository



- <https://models.physiomeproject.org>
- free and open repository supporting versioned model reuse, archiving, collaboration...

The image displays two overlapping screenshots of the Physiome Model Repository website. The top screenshot shows a model page for "Ventricular mechanics in diastole: material parameter sensitivity". It includes a 3D model of a heart and a graph showing pressure vs. time. The bottom screenshot shows a model page for "Bugbuster Systems Model". It includes a flowchart diagram and a graph showing pressure vs. time.

Key resources

https://models.physioemproject.org/prote

Models Home

My Workspaces

Exposures

Documentation

David Nickerson

Mode

You are here: [Home](#) / [Exposures](#) / [SED-ML example](#) / [vanderpol.cellml](#)

View

Wizard

Exposure Root

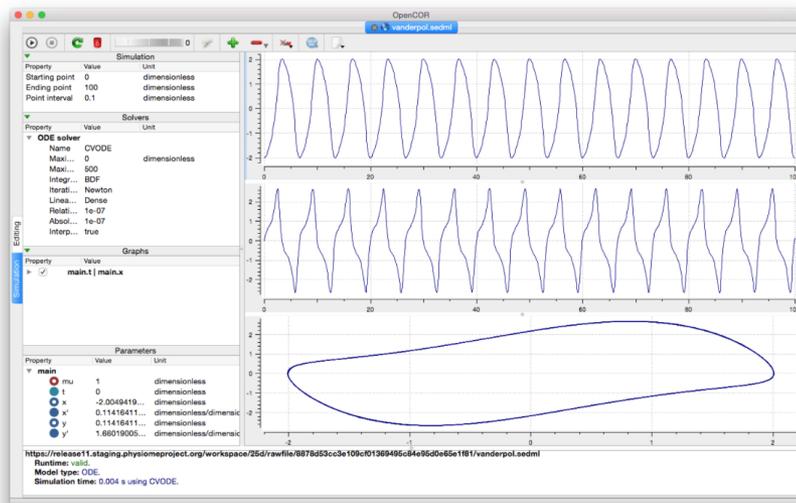
Sharing

Na⁺ vanderpol.cellml

Annot by [David Nickerson](#) — last modified Sep 27, 2017 09:19 AM — [History](#)

Description: Van der Pol oscillator

A kinetic model described in 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.



A screenshot illustrating the results when the associated SED-ML document is loaded into OpenCOR and the simulation executed.

This can be reproduced directly from the repository by choosing the **Launch with OpenCOR** link from the [Views Available](#).

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.physio
```

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

Tools

Compare...

CombineArchive Web

License

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Models Home

Expos

You are here: [Home](#) / [Protein M](#)

Protein Modules

25D

HH potassium ion channel r

25D

HH sodium ion channel mod

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 thiaz

Eskandari, Wright, Loo,

Kinetics of the Reverse Mod

Mackenzie, Loo, Panayoto

Biophysical Characteristics

Work

This wo
model a
models

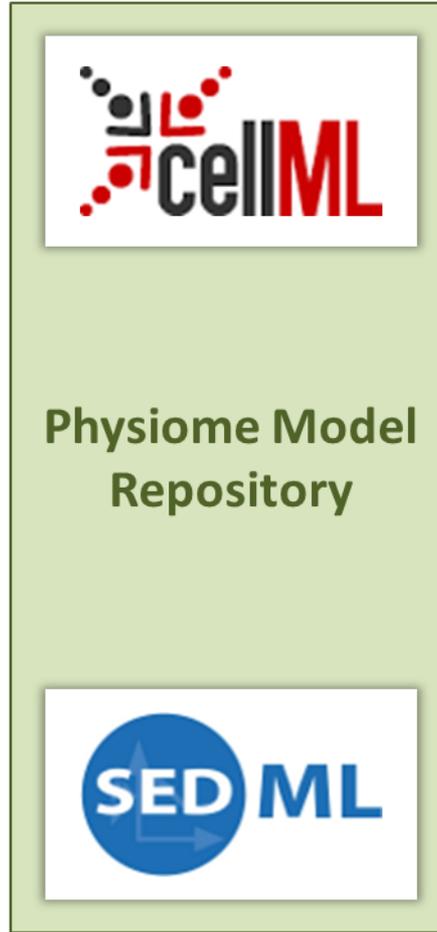
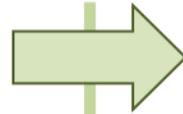
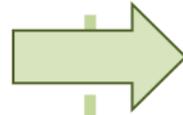
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CellML Annotation
CellML Text
Raw CellML
Raw SED-ML
Raw Text
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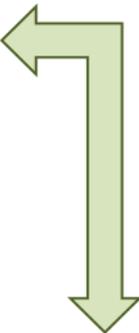
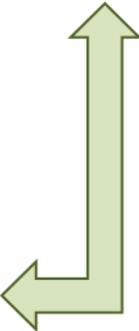
OpenCOR

- Modelling environment for organising, editing, simulating and analysing CellML files on Windows, Linux and macOS.
- Plugin-based application with both a command line (CLI) and a graphical user interface (GUI).
- Full CellML support and partial SED-ML support.
- Open source project (GPL v3.0 license).
- (Very) simple website: opencor.ws.
- On GitHub: github.com/opencor/opencor.
- Prerequisites: Git, CMake, C++ toolchain and Qt.
Optional: Ninja, cmake/ccache, NSIS (Windows) and PackageMaker (macOS).

Mathematical modelling → CellML and SED-ML → OpenCOR



OpenCMISS-Iron
OpenCMISS-Zinc



Publication

Software

OpenCOR

PMR window

PMR Workspaces window

OpenCOR

OpenCOR is a cross-platform modelling environment, which is aimed at organising, editing, simulating and analysing CellML files on Windows, Linux and macOS. It can be downloaded here.

Various information about OpenCOR and its use can be found in the following pages:

- How to get started?
- What is new?
- User interfaces
 - Command line interface (CLI)
 - Graphical user interface (GUI)
- Plugins
 - Data Store:
 - BioSignalMLDataStore
 - CSVDataStore
 - Editing:
 - CellML AnnotationView

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Web Browser

CellML Annotation
CellML Text
Raw CellML
Raw SED-ML
Raw Text

PMR

Filter: Noble 

Models Site

- DiFrancesco, Noble, 1985
- Earm, Noble, 1990
- Fink, Noble, Virag, Varro, Giles, 2008
- Garny, Kohl, Hunter, Boyett, Noble, 2003
- Hilgemann, Noble, 1987
- Hunter, McNaughton, Noble, 1975
- Iribe, Kohl, Noble, 2006
- McAllister, Noble, Tsien, 1975
- Noble 1962 model for Physiome article
- ▼ Noble, 1962
 - noble_1962.cellml
 - noble_1962.sedml
- Noble, DiFrancesco, Denyer, 1989
- Noble, Noble, 1984
- Noble, Noble, 2001
- Noble, Noble, Bett, Earm, Ho, So, 1991
- Noble, Varghese, Kohl, Noble, 1998
- Noble, Varghese, Kohl, Noble, 1998
- Roux, Noble, Noble, Marhl, 2006
- Sakmann, Spindler, Bryant, Linz, Noble, 2000
- Stewart, Aslanidi, Noble, Noble, Boyett, Zhang, 2009
- Ten Tusscher, Noble, Noble, Panfilov, 2004
- The Noble (1962) cell model
- The Noble (1962) cell model

[Models Home](#)[My Workspaces](#)[Exposures](#)[Documentation](#)

Alan Garry ▾

You are here: [Home](#)**Info** Welcome! You are now logged in.

A client application is awaiting your approval

OpenCOR is requesting access to the following resources using your credentials:

Full workspace access

Access and create workspaces.

Searching

Search and return listing of private objects belonging to the user.

Temporary Credentials for Workspace Access

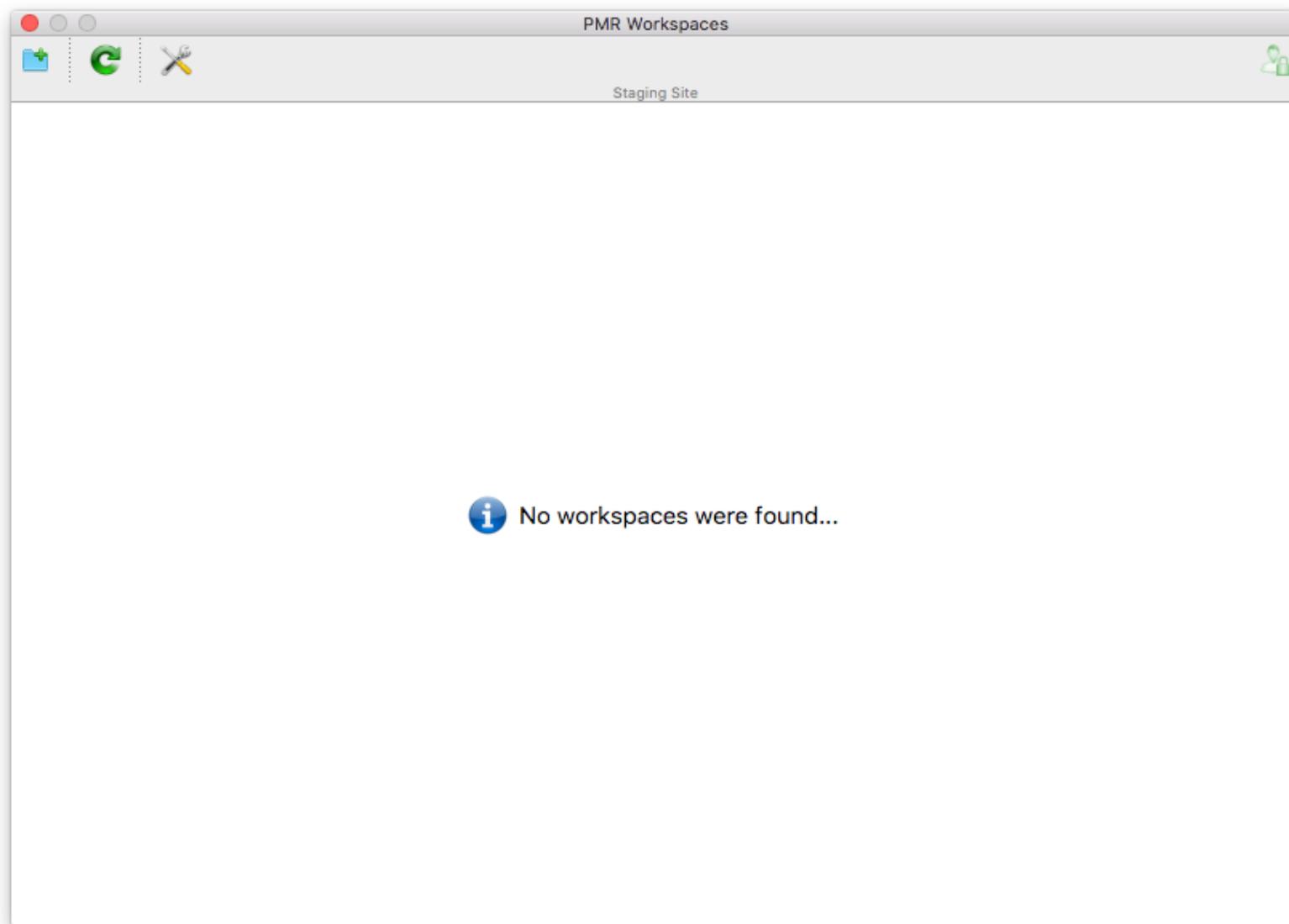
Allow the client to generate temporary access credentials to your workspaces, to be used by applications that are not compatible with OAuth, such as Mercurial.

View collections

Get a listing of objects within collections.

[Details](#)

Please note that you should only grant access if and only if you trust this application with your data that are within the scope as outlined above. Otherwise please deny access.



PMR

Filter: Noble 

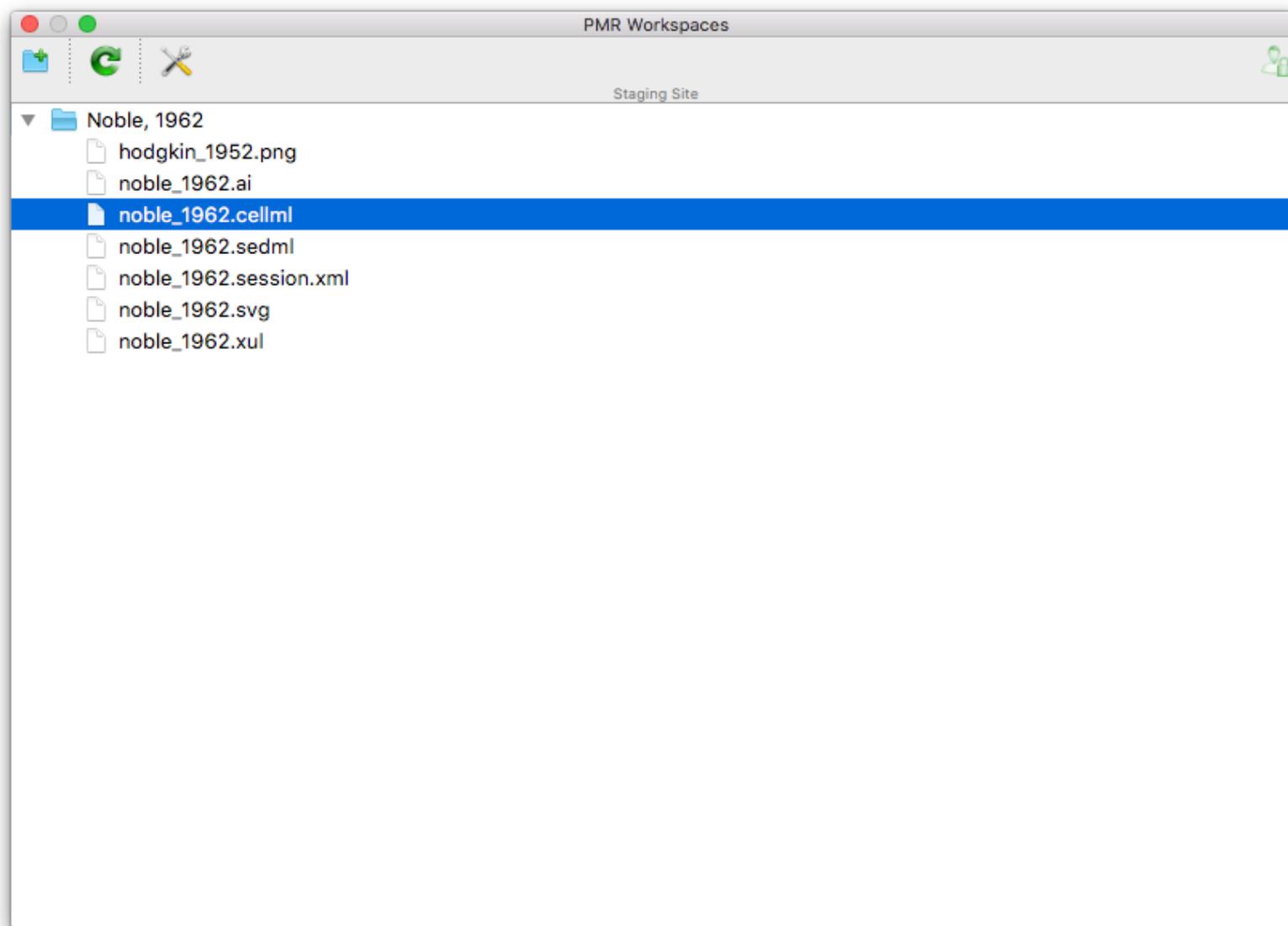
Staging Site

- DiFrancesco, Noble, 1985
- Earm, Noble, 1990
- Fink, Noble, Virag, Varro, Giles, 2008
- Garny, Kohl, Hunter, Boyett, Noble, 2003
- Hilgemann, Noble, 1987
- Hunter, McNaughton, Noble, 1975
- Iribe, Kohl, Noble, 2006
- McAllister, Noble, Tsien, 1975
- Noble 1962 model for Physiome article
- ▼ Noble, 1962**
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- Roux, Noble, Noble, Marhl, 2006
- Sakmann, Spindler, Bryant, Linz, Noble, 2000
- Stewart, Aslanidi, Noble, Noble, Boyett, Zhang, 2009
- Ten Tusscher, Noble, Noble, Panfilov, 2004
- The Noble (1962) cell model
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 View In PMR

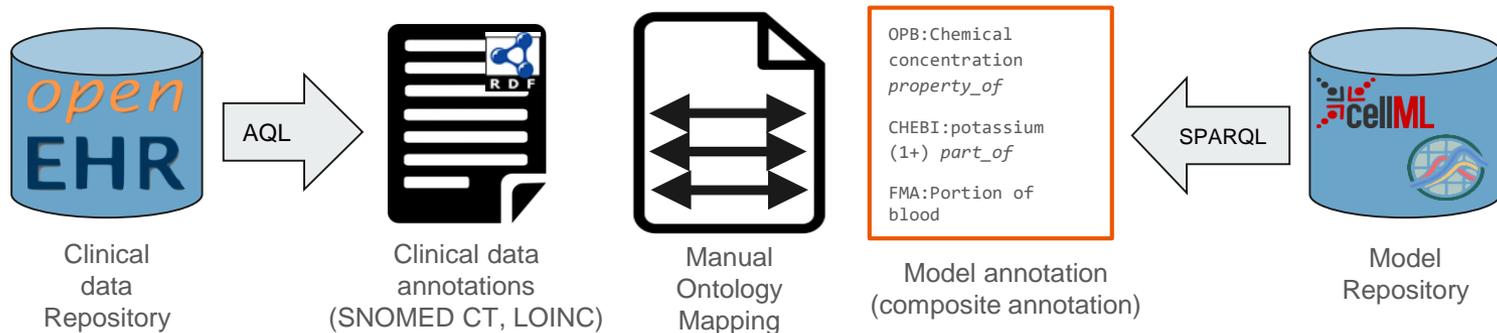
 Copy URL

 Make Local Copy...



Annotation harmonization

- Common approaches for annotation
- Speak the “same” language
 - cross-repository discovery
 - cross-standard reuse and merging
 - common software tools
- COMBINE archive?
- Linking between models and health data



COMBINE goals

- Annotation, annotation, annotation...
 - Wednesday late afternoon to get started
 - Friday early afternoon to wrap up
- Encoding and Exchanging Medical Data in Standards
 - Thursday early afternoon

- No specific breakout
 - data, experiment, workflow annotation
 - reproducibility centre (Ion's talk Friday morning)
 - *Physiome* journal