

Cardiac Physiome, 17-19th Oct 2013

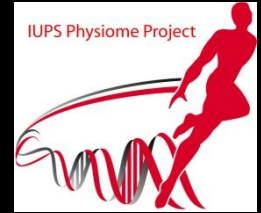
***The Physiome Project
and the
Virtual Physiological Human***

**Peter Hunter
Auckland University, New Zealand**

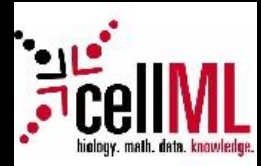


History of Physiome Project

1997 IUPS Physiome Committee



1998 CellML, FieldML



1999 Systems Biology Markup Language



2003 IMAG (NIH, NSF, FDA, NASA, DOE, DOD, ..)



2006 STEP: Strategy for European Physiome



2008 VPH Network of Excellence

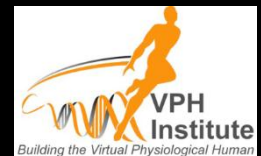
2009 Drug Disease Model Resources (DDMoRe)



2010 German Virtual Liver Network



2011 VPH Institute



Physiome colleagues



Marco Viceconti

Denis Noble

Yoshi Kurachi

Ilias Iakovidis



Jim Bassingthwaite



Andrew McCulloch



Dan Beard



Nic Smith



Stig Omholt



Adriano Henney

VPH Institute

The screenshot shows the VPH Institute website homepage. At the top left is the logo with the tagline "Building the Virtual Physiological Human". To the right are social media icons for Twitter, LinkedIn, Google+, and YouTube. A left sidebar contains a navigation menu with items: > ABOUT, > MEMBERSHIP, > GOVERNANCE, > DISCIPULUS, > VIDEOS, > DOCUMENTS, and > NATIONAL NETWORKS. Below the menu is a "HIGHLIGHT" section with a date "06/06/2013" and the title "EUROPEAN PARLIAMENT EVENT TO MARK 2 YEAR ANNIVERSARY OF THE VPH INSTITUTE". The main content area features a carousel of three 3D heart models: a wireframe with a color gradient, a solid color model, and a grayscale anatomical model. Below the carousel is a "WELCOME TO THE VPH INSTITUTE" banner with a "READ MORE" button. At the bottom, a "NEWS" section features a date "10/07/2013" and the text "Watch the DISCIPULS interviews on YouTube".



www.vph-institute.org

Virtual Liver Network

Objective:

- To create a multi-scale dynamic mathematical model that represents, rather than fully replicates human liver physiology, morphology and function
- A model that has a specific focus on application to address the needs of the patient and clinicians.

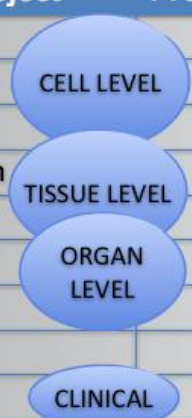


Steatosis
 HGF induced regeneration
 LPS induced inflammation
 LIAM: Liver Image Analysis-based Modelling



- 9 Workpackages
- 69 Principal Investigators
- 44 Projects
- >200 contributing Scientists
- 36 Independent Institutions
- Mix of academics & industry

Work Package Subject	Projects
Cellular Metabolism	3
Cellular Signalling	5
Cross Linking	6
Cell-Cell Communication	9
Liver Lobule	6
Whole Organ	4
Integrated Model	4
Data Management	3
Clinical Translation	4



A Vision and Strategy for the VPH in 2010 and beyond

Peter Hunter^{1,2}, Peter V. Coveney³, Bernard de Bono⁴, Vanessa Diaz⁵, John Fenner⁶,
Alejandro F. Frangi⁷, Peter Harris⁸, Rod Hose⁶, Peter Kohl², Pat Lawford⁶, Keith McCormack⁹,
Miriam Mendes³, Stig Omholt¹⁰, Alfio Quarteroni¹¹, John Skår¹², Jesper Tegner¹³, S. Randall Thomas¹⁴,
Ioannis Tollis¹⁵, Ioannis Tsamardinos¹⁵, Johannes HGM van Beek¹⁶ and Marco Viceconti¹⁷

¹ Auckland Bioengineering Institute (ABI), University of Auckland, New Zealand

² Department of Physiology Anatomy & Genetics, University of Oxford, UK

³ Centre for Computational Science, University College London, UK

⁴ European Bioinformatics Institute, European Molecular Biology Laboratory, Cambridge, UK

A vision and strategy for the virtual physiological human: 2012 update

Peter Hunter, Tara Chapman, Peter V. Coveney, Bernard de Bono, Vanessa Diaz, John Fenner, Alejandro F. Frangi, Peter Harris, Rod Hose, Peter Kohl, Pat Lawford, Keith McCormack, Miriam Mendes, Stig Omholt, Alfio Quarteroni, Nour Shublaq, John Skår, Karl Stroetmann, Jesper Tegner, S. Randall Thomas, Ioannis Tollis, Ioannis Tsamardinos, Johannes H. G. M. van Beek and Marco Viceconti

Interface Focus 2013 **3**, 20130004, published 21 February 2013

www.vph-noe.eu/images/vph_vision_2011_23dec2010.pdf

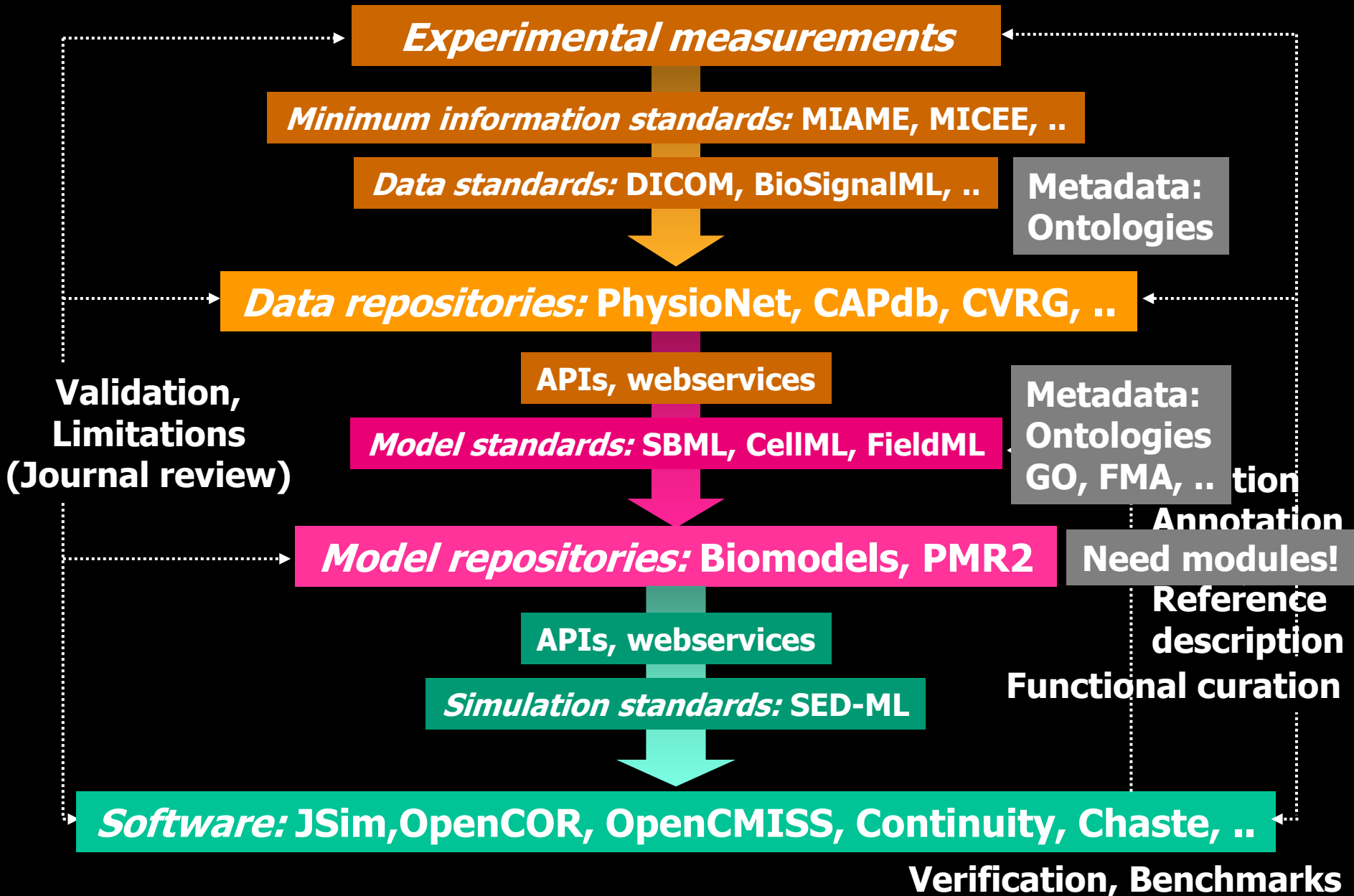


**To cope with the multi-physics,
multi-scale, complexity of human biology
we must create **reproducible models**
with **modular** approaches
based upon **data and modeling standards****

A multi-scale bioengineering approach needs:

- **Biophysically based models at every level**
 - as much as possible (there's always a black box!)
- **Adoption of model and data standards**
 - SBML, CellML, FieldML for models
- **Automated assembly of multi-scale models**
 - molecule to organ(ism)
- **Automated model reduction**
 - otherwise too expensive

Standards for models, data & software



Note on model publishing

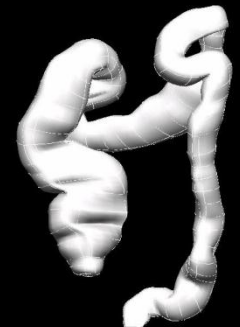
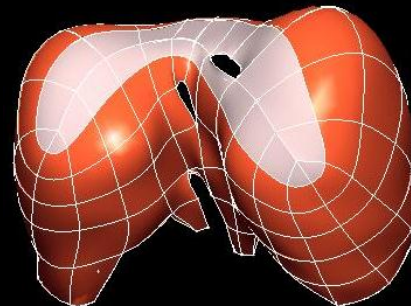
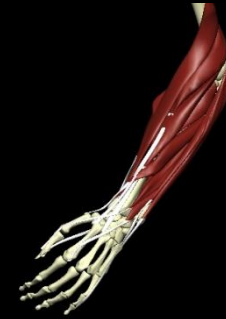
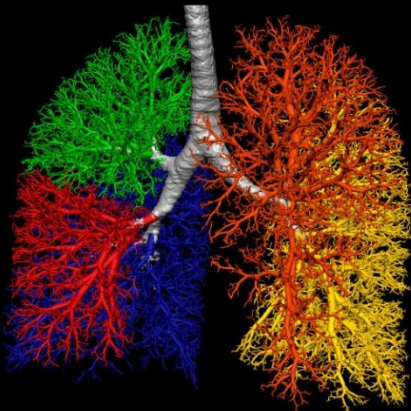
Biophysical Journal

“To assure public access to computational models, authors are strongly encouraged to deposit their models in the CellML Model Repository models.cellml.org/cellml or Biomodels Database www.ebi.ac.uk/biomodels-main/”

Similarly for many other journals.

Organ system Physiome Projects

Cardiovascular system
Respiratory system
Musculo-skeletal system
Digestive system
Skin (integument)
Urinary system
Lymphoid system
Female reproductive system
Special sense organs
Central nervous system
Endocrine system
Male reproductive system



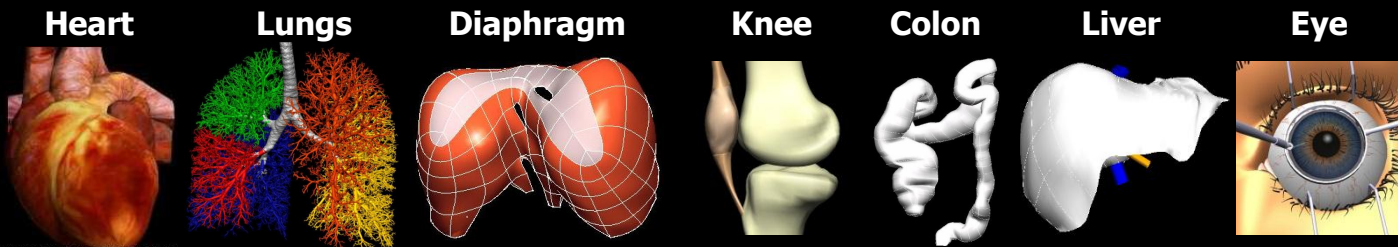
The challenge: organs to proteins

Environment

Organism

Organ system

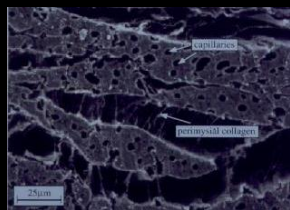
Organ



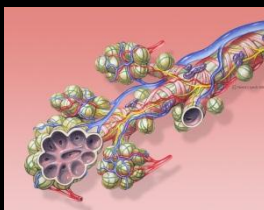
↑ x 1million ↓ 20 generations

Tissue

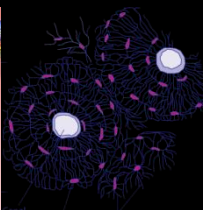
Cardiac sheets



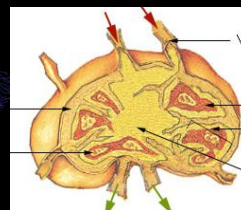
Acinus



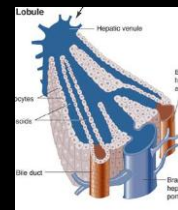
Osteon



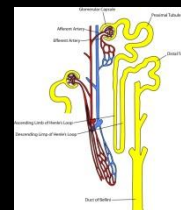
Lymph node



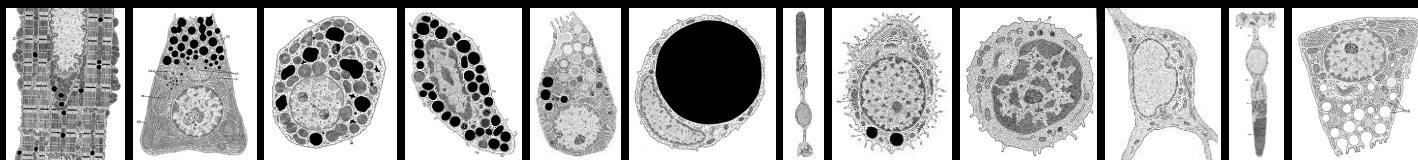
Liver lobule



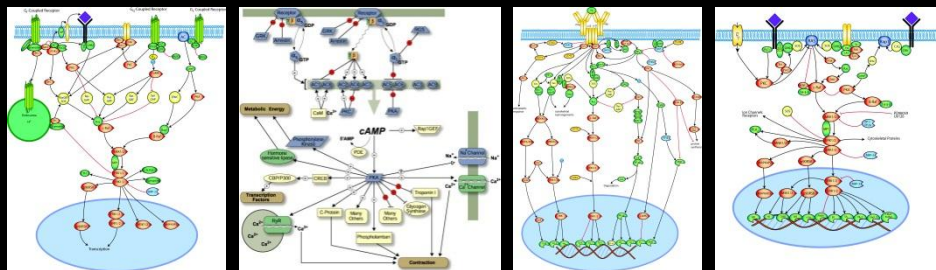
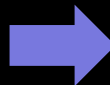
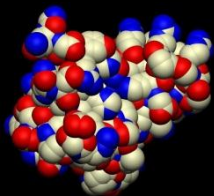
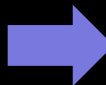
Nephron



Cell



Network
Protein
Gene
Atom



Physiome model repository (PMR)



Tommy Yu

Key features

- Version controlled storage of models
 - They are encapsulated as **Workspaces**.
- Content management system (CMS) for presentation of models.
 - The set of presentation views is known as **Exposures**.
- Provides services to store, access and interact with models.
- Links with external **web-services** to provide semantic reasoning against model metadata across models.

PMR for anatomical models - FieldML



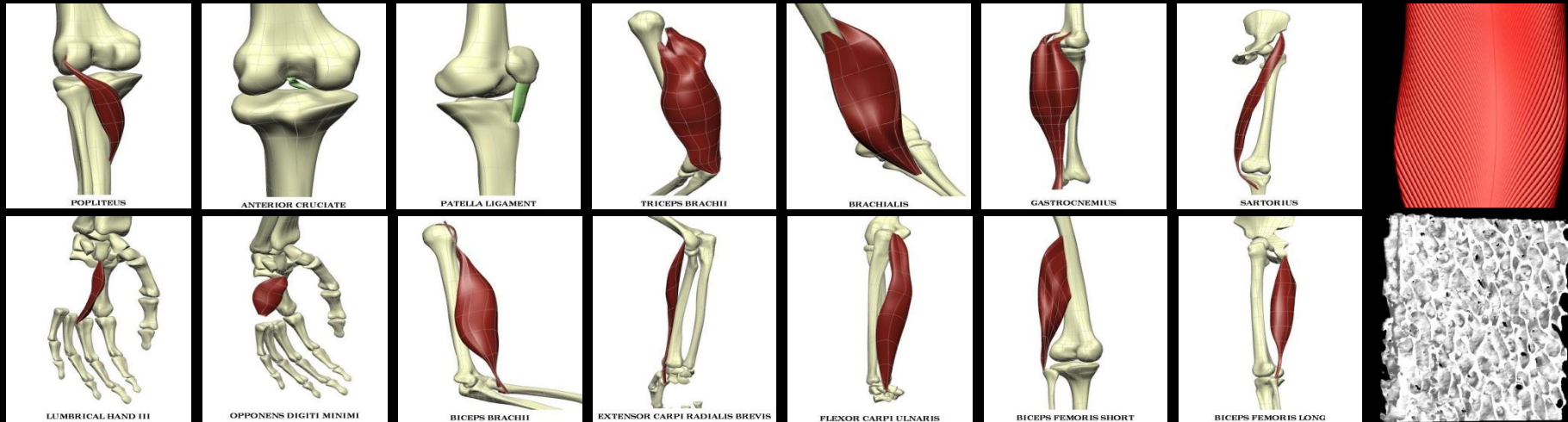
Thor Besier



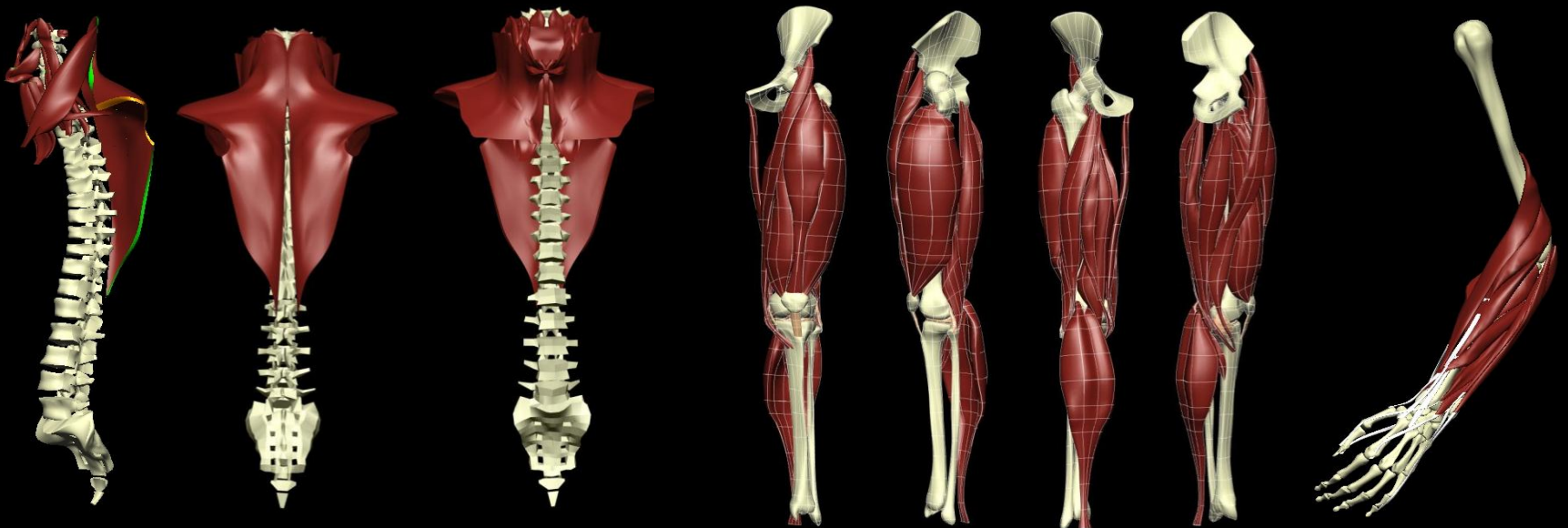
Hugh Sorby

Musculo-skeletal system

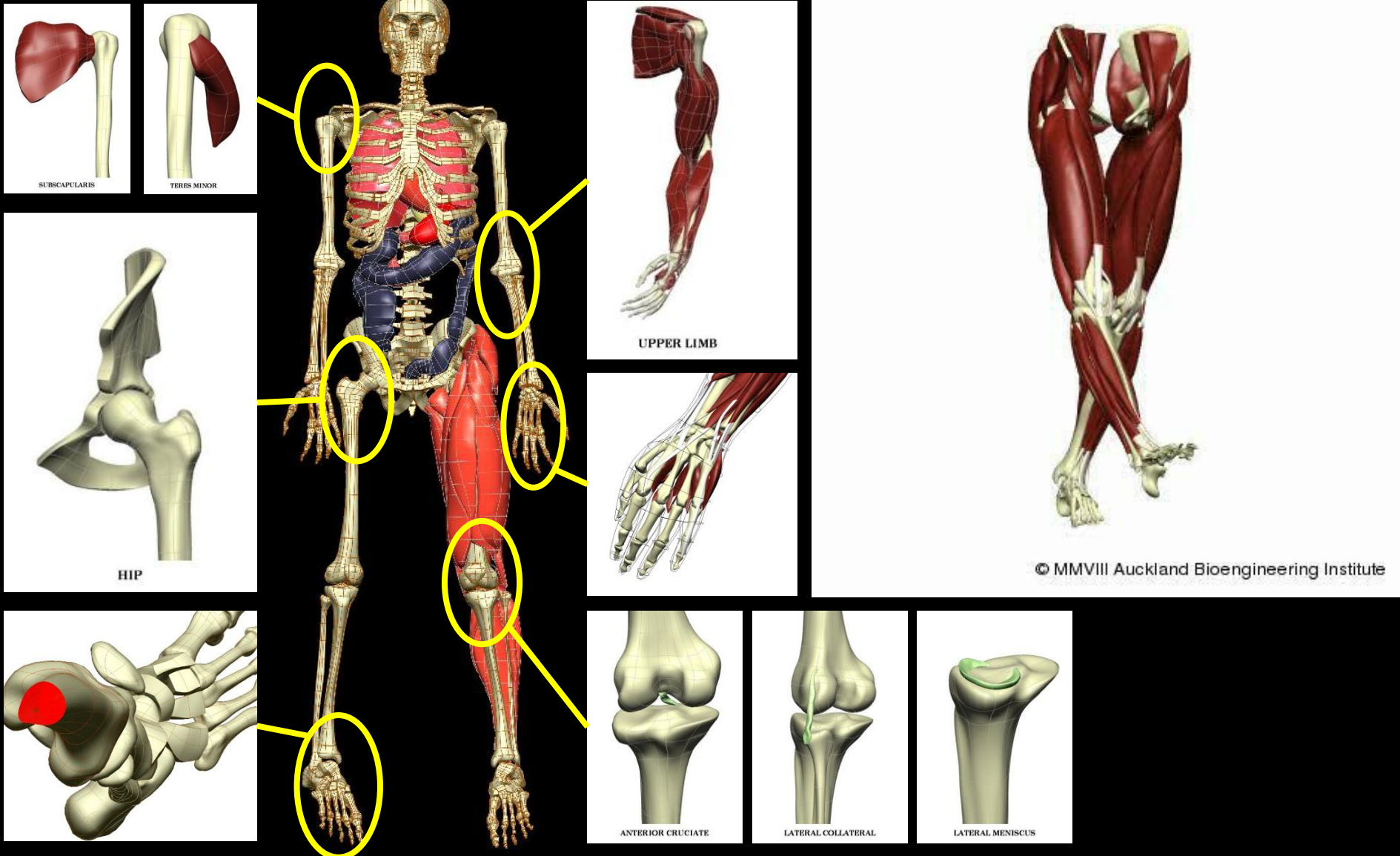
Web-accessible database of generic models (+ tissue structure):



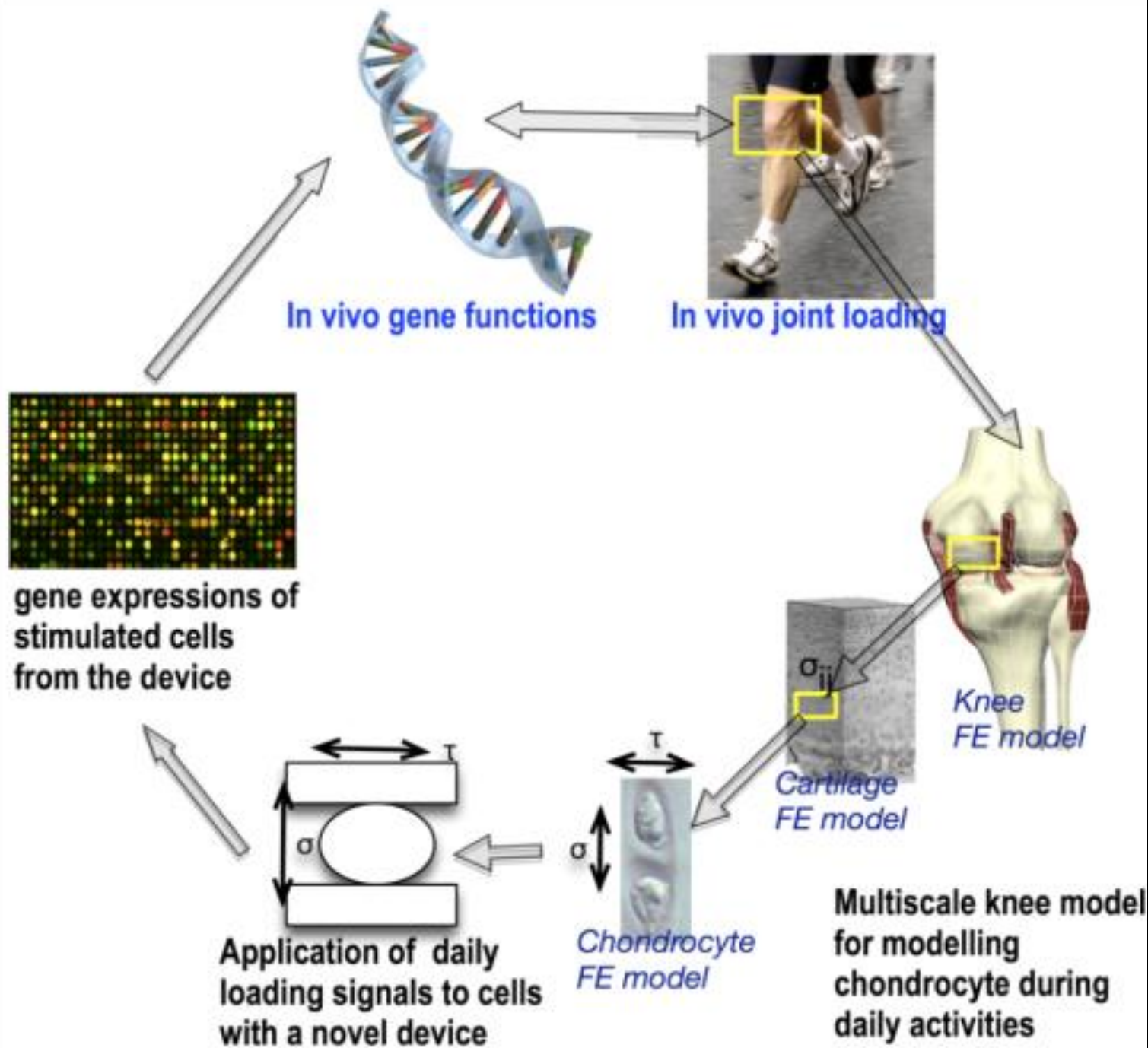
Load generic models into the anatomical component under study:



Generic models of the joints



Shim VB, Hunter PJ, Pivonka P, Fernandez JW. A multiscale framework based on the physiome markup languages for exploring the initiation of osteoarthritis at the bone-cartilage interface. *IEEE Trans Biomed Eng.* 58(12):3532-6, 2011





Population atlases



Alistair Young

www.cardiacatlas.org

Brett Cowan



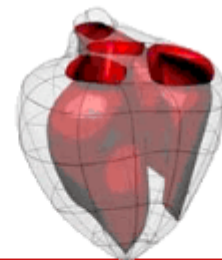
Welcome! ▾

Search... 🔍

Home About Resources Research News

The Cardiac Atlas Project

The Cardiac Atlas Project seeks to establish a structural and functional atlas of the heart. This project is dedicated to combine cardiac modeling and biophysical analysis methods with a structural database for the comprehensive mapping of heart structure and function.



The Cardia Atlas Project is presenting in the [STACOM-CESC'10 workshop @](#)



News

Ethics Essays posted

🕒 5/19/10 1:29 AM

We've posted essays about ethics of data ownership and value on our website. The essays are written by Sarah Anderson as part of her student project in Philosophy at the University of Auckland. They

CAP XML Model Format

🕒 3/8/10 4:13 AM

The Cardiac Atlas Project has released a DTD and XML Schema defining the structure of a model annotation and associated files e.g. CMGUI, exnode, files, contours. The XML Model definition is available

[About CAP](#)

[Resources](#)

[Policy Statements](#)

PMR for cell models - CellML



(www.cellml.org)



- Home
- About CellML
- Getting started
- Tools
- Models
- Specifications
- Community

You are here: [Home](#) Log in

The CellML project

The CellML language is an open standard based on the XML markup language. CellML is being developed by the Auckland Bioengineering Institute at the University of Auckland and affiliated research groups.

The purpose of CellML is to store and exchange computer-based mathematical models. CellML allows scientists to share models even if they are using different modelling tools. It also enables them to reuse components from one model in another, thus accelerating model development. [Read more...](#)

About CellML

Find out about the CellML language; what it can be used for, its history, and future directions.

Tools and API

The CellML community is committed to providing freely available tools for creating, editing, and using CellML models.

Specifications

Read the CellML specifications - core language and a variety of metadata specifications are available.

Getting started

New to CellML? This section collates information about CellML and tutorials that will help get you up and running with CellML.

Model repository

The model repository is a resource where modelers can collaborate with each other to build and share models with the rest of the world.

Community

CellML is built around open source science and software. The cellml.org website is a community hub for all things CellML.

CellML workshop 2010

The 2010 CellML workshop was held at The University of Auckland from Wednesday 24th - Friday 26th February. The meeting was a huge success and we'd like to thank all the participants - both present and virtually present!



Photo by Tommy Yu

News

- CellML API 1.8 and OpenCell 0.8 Released Oct 06, 2010
- EMBC 2010 VPH tools workshop Sep 02, 2010
- Physiome Model Repository 2 v0.3 Released Jul 01, 2010
- Improved quality of the models in the CellML model repository thanks to the curation team Jun 29, 2010

[More...](#)

Funding agencies

Thanks to our [funding partners](#): VPH NoE, aneurIST, euHeart, Foundation for Research, Science and Technology, Maurice Wilkins Centre for Molecular Biodiscovery, New Zealand Institute of Mathematics and its Applications, Wellcome Trust.

Featured articles

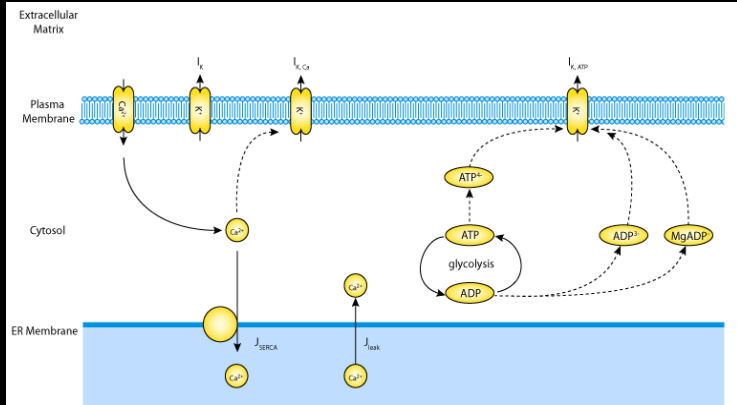
- CellML scope
- CellML publications listing
- OpenCell basic model building tutorial
- Frequently Asked Questions
- Modelling Tools: PCEnv, COR & OpenCell
- CellML Workshop 2009 report

[More...](#)

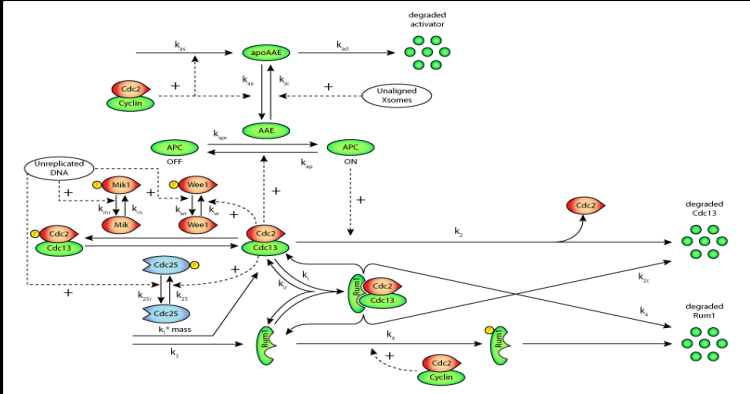


Cellar AA, Lloyd CM, Nielsen PF, Halstead MDB, Bullivant DP, Nickerson DP, Hunter PJ. An overview of CellML 1.1, a biological model description language. *SIMULATION: Transactions of the Society for Modeling and Simulation*, 79(12):740-747, 2003

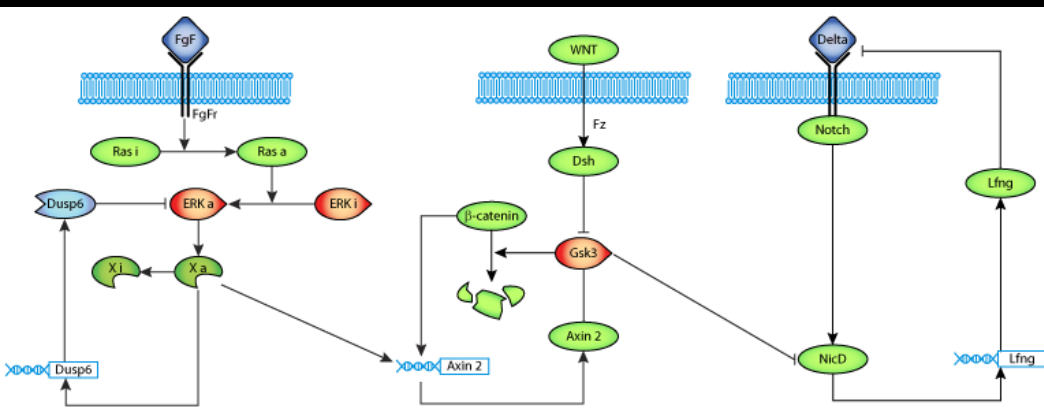
Calcium dynamics (63 models)



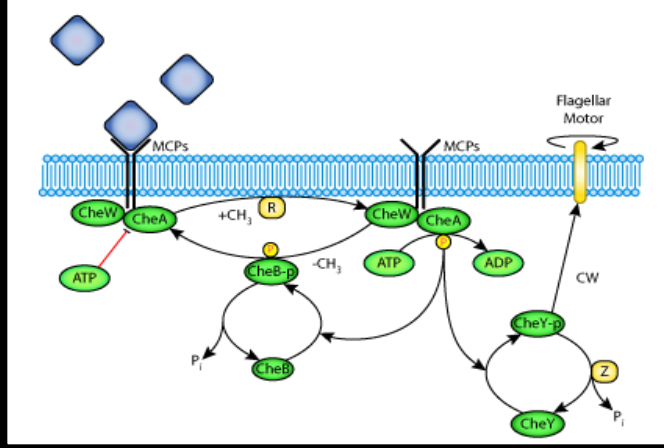
Cell cycle (25 models)



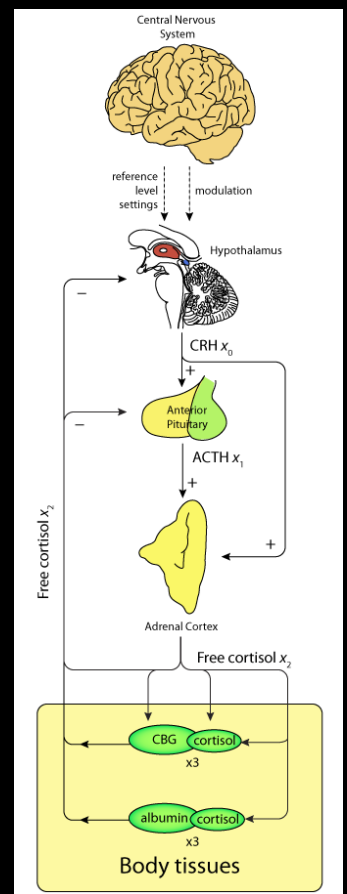
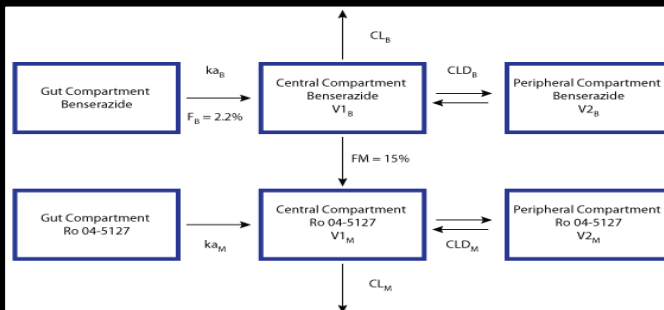
Circadian rhythms (9 models)



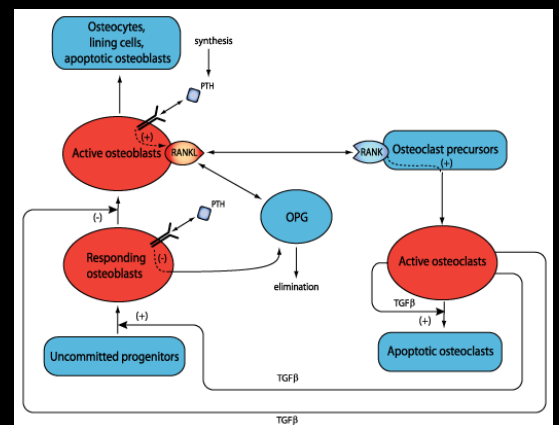
Cell migration (2 models)



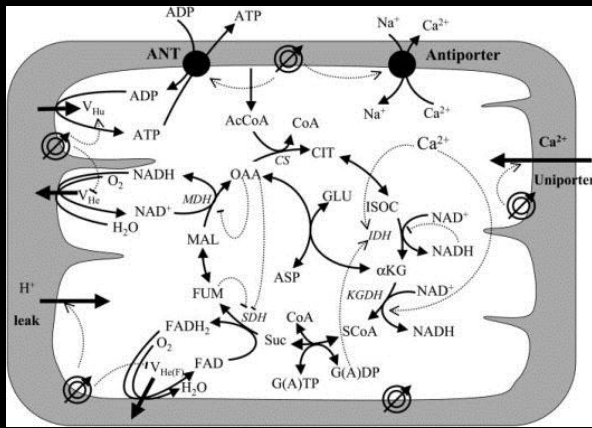
PKPD models (7 models)



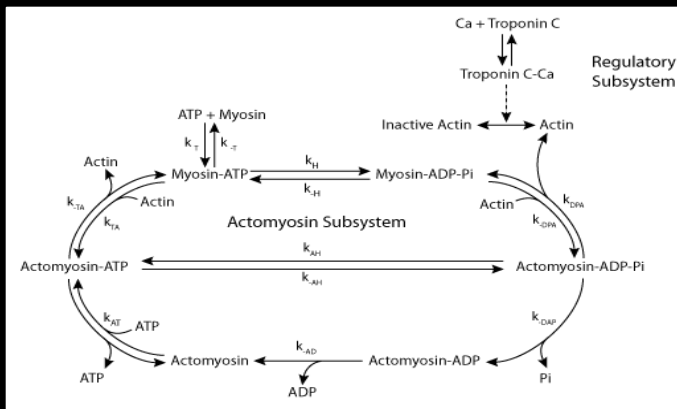
Endocrine system (29)



Metabolism (35 models)

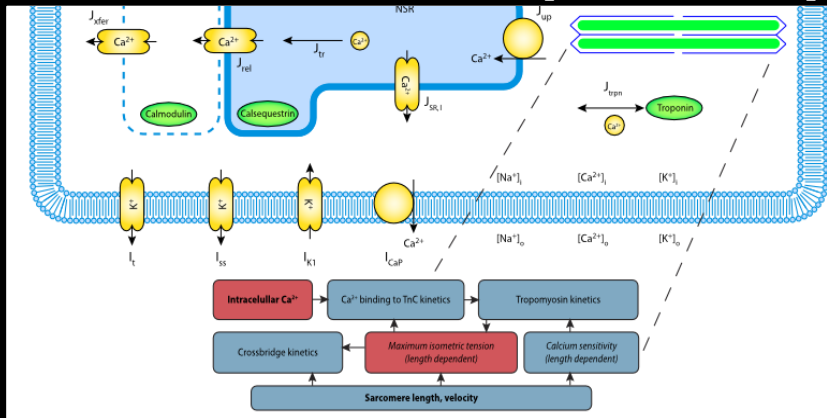


Myofilament mechanics (15)

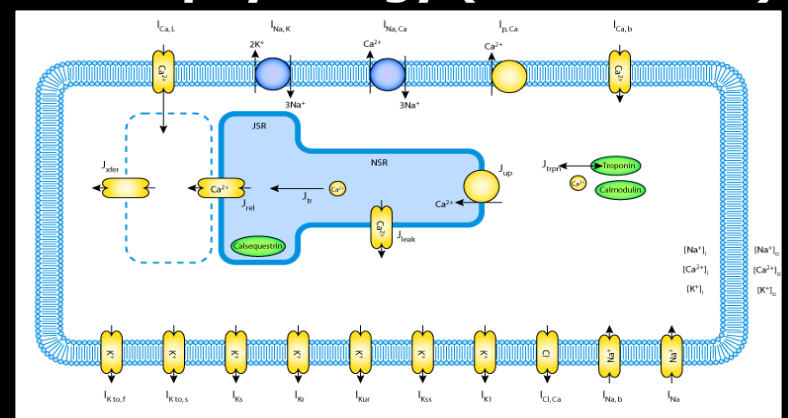


Material constitutive laws

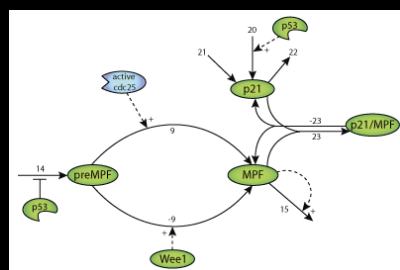
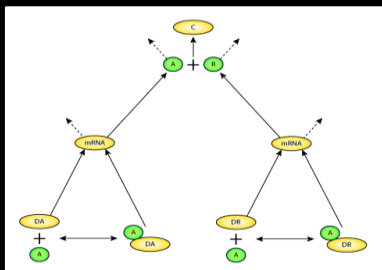
Excitation-contraction (15 models)



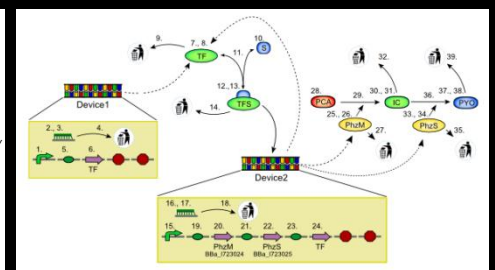
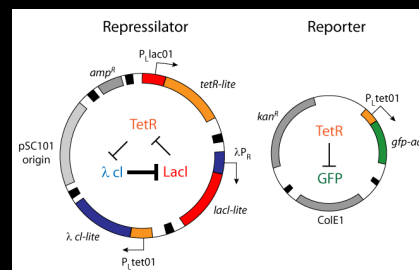
Electrophysiology (117 models)



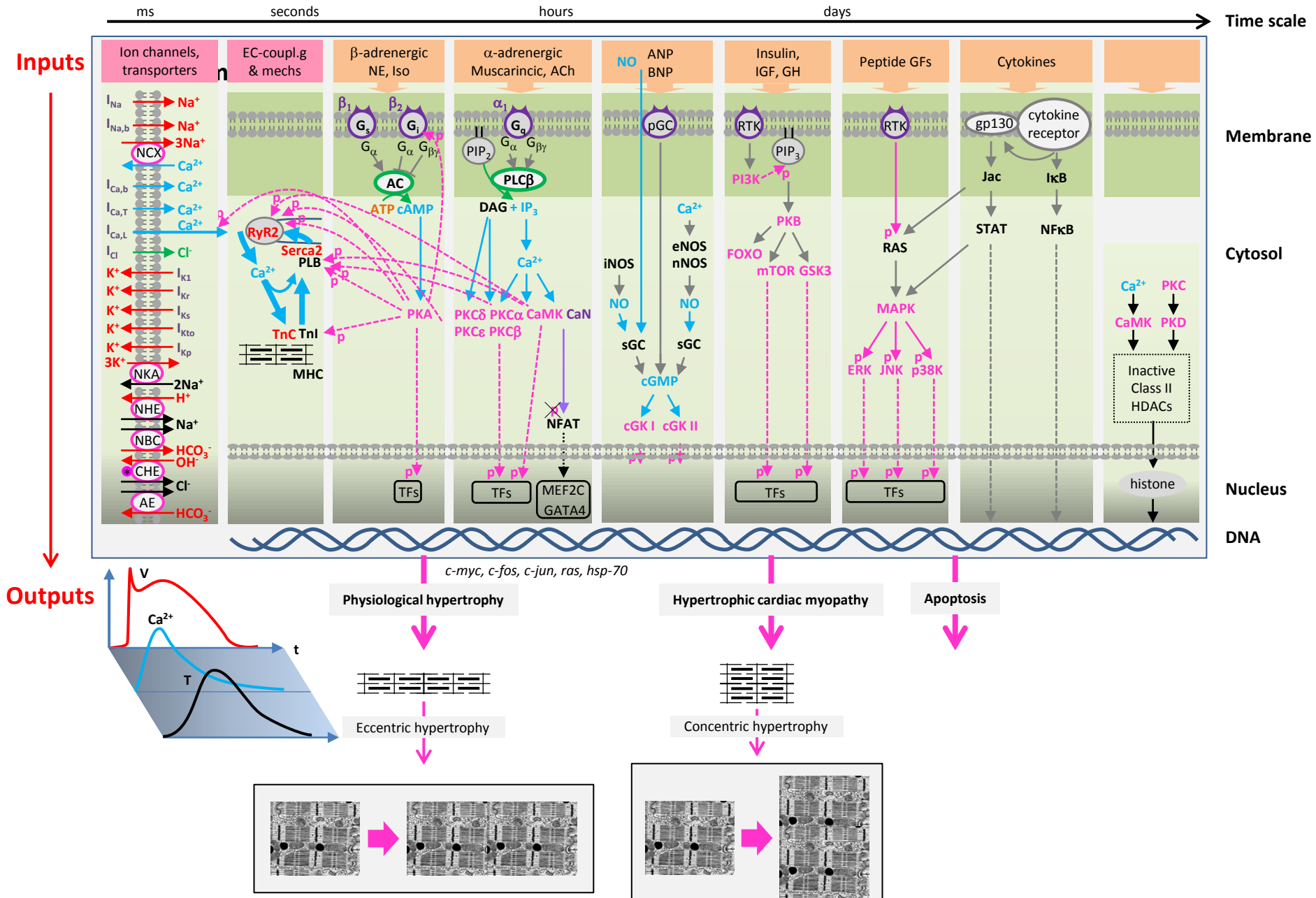
Gene regulation DNA repair (3)



Synthetic biology (5 models)

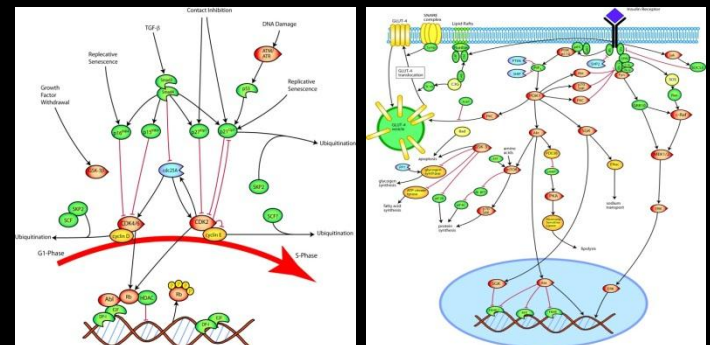
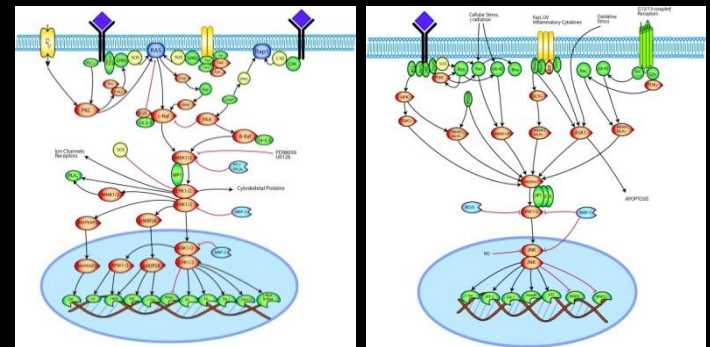
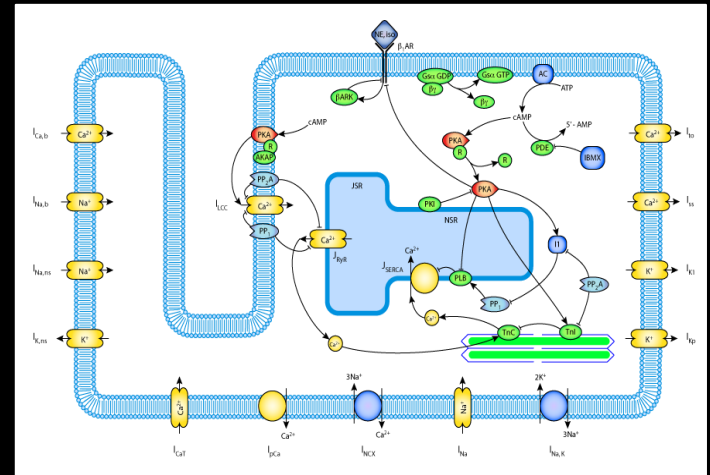


CellML signalling modules for the cardiac myocyte

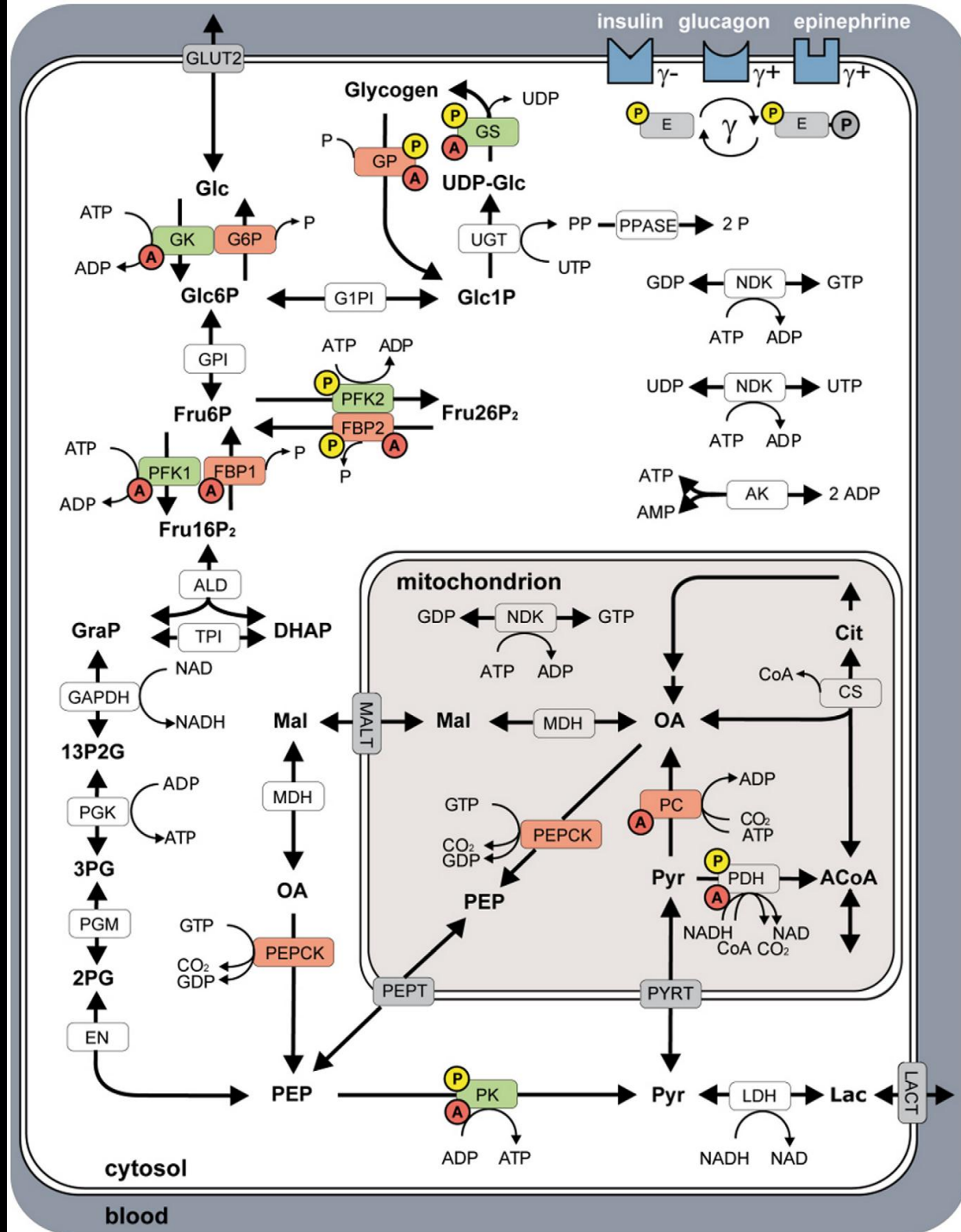


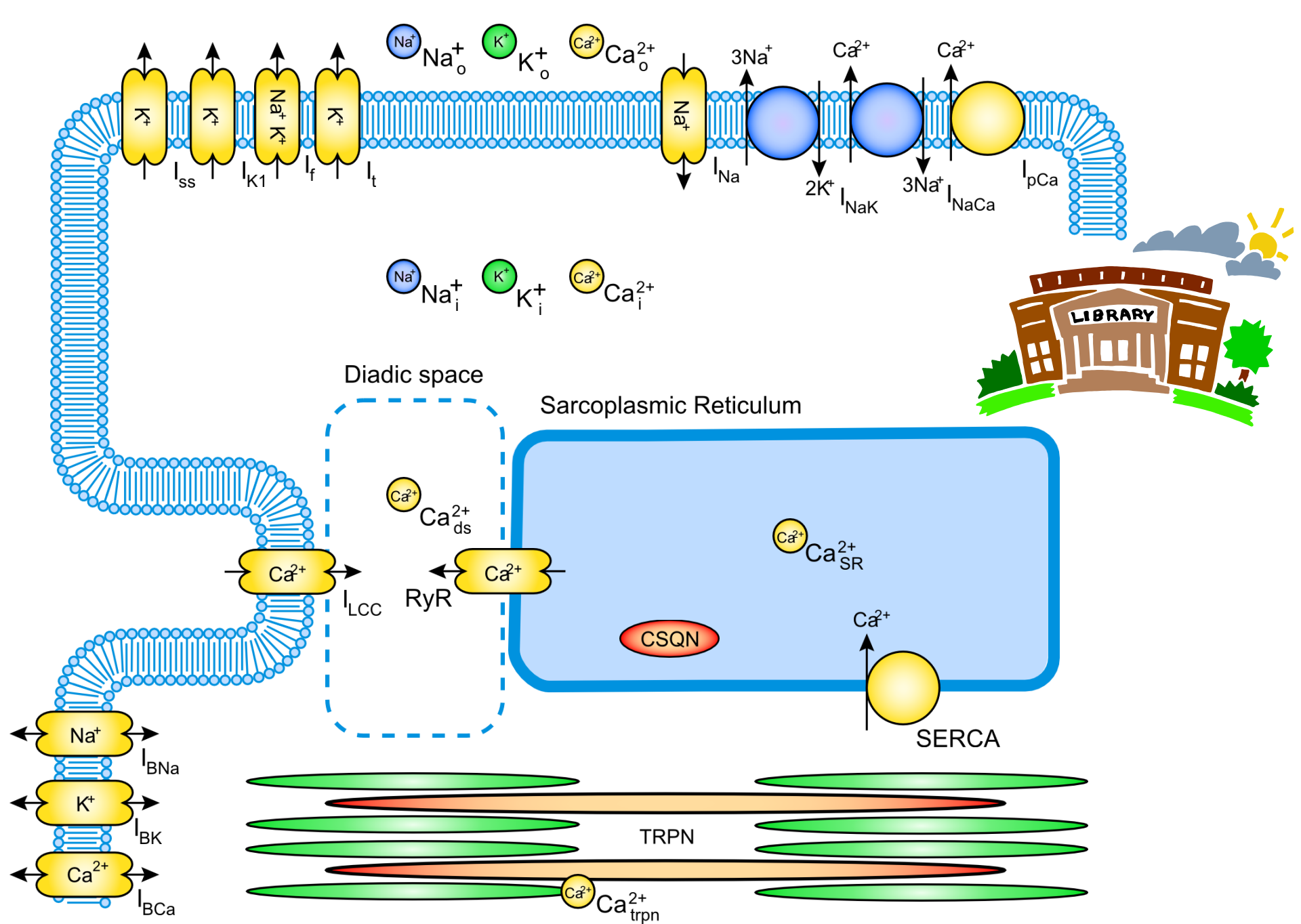
Signaling

1. cAMP signalling
2. Calcium signalling - via cADP-ribose signalling
3. NAADP signalling
4. Voltage operated channels (VOCs)
5. Receptor operated channels (ROCs)
6. IP₃-Ca²⁺ signalling (via PLC-PIP₂)
7. DAG-PKC signalling (via PLC-PIP₂)
8. PI4-5P₂ signalling
9. Inositol polyphosphate signalling
10. PI3-Kinase signalling
11. NO-cGMP signalling
12. Redox signalling
13. MAP-Kinase signalling
14. NF-kB signalling
15. Phospholipase D (PLD) signalling
16. Sphingomyelin signalling
17. JAK-STAT signalling
18. Smad signalling
19. Wnt signalling
20. Hedgehog signalling
21. Notch signalling
22. ER stress signalling
23. AMP signalling



- Glucose transporter (GLUT2)
- Glucokinase (GK)
- Glucose-6 phosphatase (G6Pase)
- Glucose-6-phosphate isomerase (GPI)
- Glucose-1-phosphate 1,6-phosphomutase (G16PI)
- UTP: Glucose-1-phosphate uridylyltransferase (UGT)
- Pyrophosphate phosphohydrolase (PPase)
- Glycogen synthase (GS)
- Glycogen phosphorylase (GP)
- Nucleosid diphosphate kinase (NDK)
- Adenylate kinase (AK)
- Phosphofructo kinase 2 (PFK2)
- Fructo-2,6-bisphosphatase (FBP2)
- Phosphofructo kinase (PFK1)
- Fructose-1,6-bisphosphatase (FBP1)
- Aldolase (ALD)
- Triosephosphate isomerase (TPI)
- D-Glyceraldehyde-3-phosphate: NAD⁺ oxidoreductase (GAPDH)
- Phosphoglycerate kinase (PGK)
- 3-Phosphoglycerate mutase (PGM)
- Enolase (EN)
- Pyruvate kinase (PK)
- Phosphoenolpyruvate carboxykinase (PEPCK)
- Pyruvate carboxylase (PC)
- Lactate dehydrogenase (LDH)
- Lactate transporter (LACT)
- Pyruvate transporter (PYRT)
- PEP transporter (PEPT)
- Pyruvate dehydrogenase (PDH)
- Citrate synthase (CS)
- Nucleosid diphosphate kinase (NDK)
- Oxalacetate flux (OAAflx)
- Acetyl-CoA flux (ACOAFlx)
- Citrate flux (CITflx)





www.cellml.org/tools

→ OpenCOR www.opencor.ws

The screenshot displays the OpenCOR software interface. The main window shows a simulation of a cardiac cell model. The left sidebar contains a list of 558 CellML models and a file browser. The central area features a parameter table and a plot of membrane potential over time. The parameter table lists various properties and their values, including leakage current, membrane properties, potassium channel properties, and sodium channel properties. The plot shows a series of action potentials. The bottom right corner of the interface displays a mathematical equation for the sodium current, i_{Na} .

Property	Value	Unit
leakage_current		
<input type="checkbox"/> E_L	-60	millivolt
<input type="checkbox"/> g_L	0.075	milliS_per_cm2
<input type="checkbox"/> i_{Leak}	-1.31415378072...	microA_per...
membrane		
<input type="checkbox"/> C_m	12	microF_per_c...
<input checked="" type="checkbox"/> V	-77.5220504097...	millivolt
<input type="checkbox"/> V'	0.047732503025...	millivolt
potassium_channel		
<input type="checkbox"/> g_{K1}	0.953440746043...	milliS_per_cm2
<input type="checkbox"/> g_{K2}	0.071583314496...	milliS_per_cm2
<input type="checkbox"/> i_K	23.040439161651	microA_per...
potassium_channel_n_gate		
<input type="checkbox"/> α_n	0.000187516151...	per_milliseco...
<input type="checkbox"/> β_n	0.001711162237...	per_milliseco...
<input type="checkbox"/> n	0.494205573988...	dimensionless
<input type="checkbox"/> n'	-	-
sodium_channel		
<input type="checkbox"/> E_{Na}	4	millivolt
<input type="checkbox"/> g_{Na}	0	milliS_per_cm2
<input type="checkbox"/> $g_{Na...}$	4	milliS_per_cm2
<input checked="" type="checkbox"/> i_{Na}	-	-
sodium_channel		
<input type="checkbox"/> α_n	0	per_milliseco...
<input type="checkbox"/> β_n	0	per_milliseco...

$$i_{Na} = \frac{g_{Na} \cdot m^3 \cdot h \cdot Na_o \cdot \frac{F^2}{R \cdot T} \cdot \left(e^{(V - E_{Na}) \cdot \frac{F}{R \cdot T}} - 1 \right)}{e^{V \cdot \frac{F}{R \cdot T}} - 1} \cdot V$$

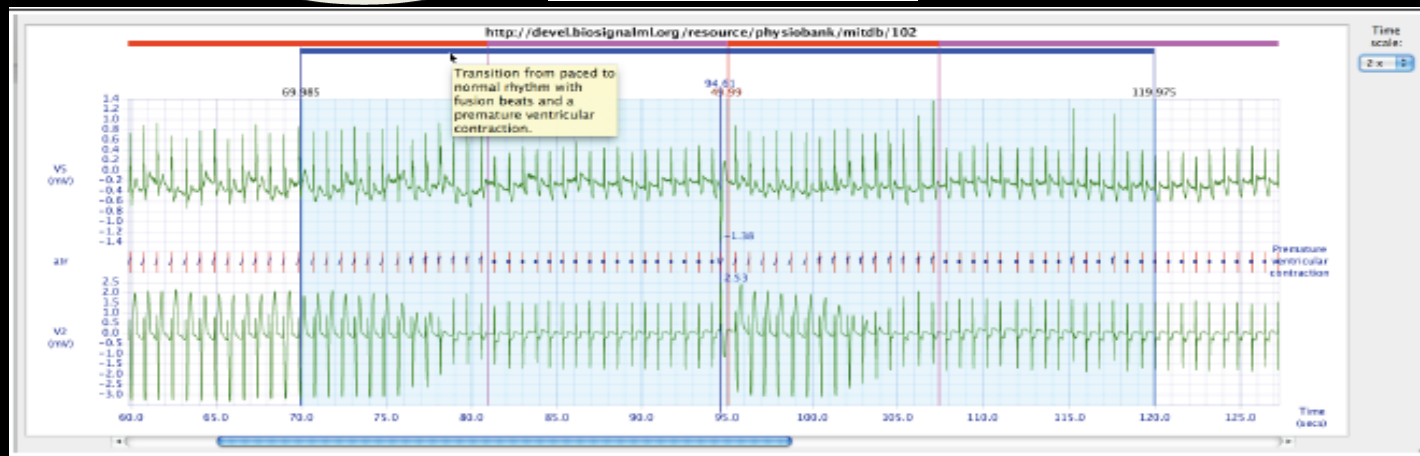
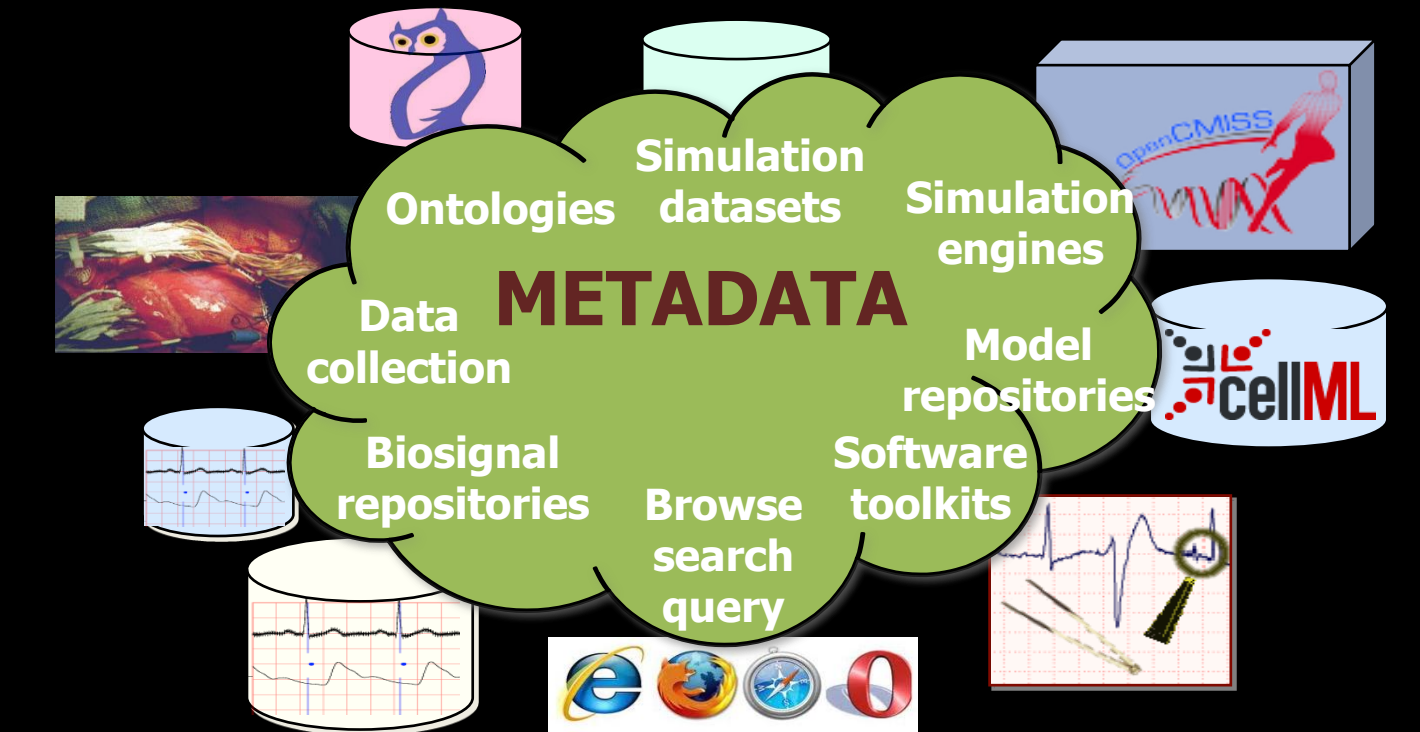

Alan Garry Run OpenCOR

6 month roadmap for OpenCOR

- CellML authoring. This will use the MathML renderer.
- Support for SED-ML (<http://sed-ml.org>) using Frank Bergmann's API: <https://github.com/fbergmann/libSEDML>
- Incorporate BioSignalML API
- CellML annotation using composites
- Drag & drop model building

Data standards

www.BioSignalML.org



Semantic annotation of models

The screenshot shows a software interface with a tree view of components. The tree is organized as follows:

- Units
 - Components
 - environment
 - membrane
 - calcium_concentration
 - calcium_fluxes
 - calcium_buffering
 - ryanodine_receptors
 - L_type_calcium_current
 - calcium_pump_current
 - sodium_calcium_exchange_current
 - calcium_background_current
 - sodium_concentration
 - fast_sodium_current
 - sodium_background_current
 - potassium_concentration
 - fast_transient_outward_potassium_current
 - slow_transient_outward_potassium_current
 - time_independent_potassium_current
 - slow_delayed_rectifier_potassium_current
 - ultra_rapidly_activating_delayed_rectifier_potassium_current
 - non_inactivating_steady_state_potassium_current
 - rapid_delayed_rectifier_potassium_current
 - sodium_potassium_pump_current
 - calcium_activated_chloride_current

At the bottom of the interface, there are two radio buttons for parameter settings:

- Ca_off_troponin_high_rateconstant
- Ca_off_troponin_low_rateconstant

The screenshot shows the KEGG database entry for compound C06421. The entry includes the following information:

- Entry: C06421 Compound
- Name: alpha-Cellobiose; 1-beta-D-Glucopyranosyl-4-alpha-D-glucopyranose
- Formula: C12H22O11
- Exact mass: 342.1162
- Mol weight: 342.2965
- Structure:
- Other DBs: PubChem: 8656, ChEBI: 28676, PDB-CCD: CBK, NIKKAJI: J2.129.875A

Ontologies:

ChEBI

- chemical IDs

GO

- cell component

CellType

- cells

FMA

- anatomy

OPB

- biophysics

Annotating CellML models

OpenCOR

- Authoring, curation
- Annotation
- Simulation



CellML Model

Metadata (semantics)

Author, publications, etc
Model annotations*

Maths (syntax)

$$\frac{dy}{dt} = f(x, \dots) \dots$$



PMR

Mercurial DVS
Imports, provenance

OWL knowledge base

Has all reference ontologies.

Chebi - **calcium**
OPB - **concentration**
GO (cell cpt) - **cytosol**
FMA, ...
+ units + **composites**



Ricordo

Reasoning
over OWL-KB



SemGen

Reasoning
over OWL-KB
→ OPB templates



Add new composite & **Reclassify**
i.e. '**calcium concentration in cytosol**' is indexed
so x_URI can be found in search

x is **calcium concentration in cytosol**
(a **property** associated with an **entity**)

SparQL queries



MIRIAM

Ricordo RDF Triple store

Stored as RDF triple (3 URIs, one being the **relation**):
x_URI is_a_computational cpt_for **composite_URI**

* www.cellml.org/specifications/metadata/mcdraft

Adding Annotations: SemGen



Max
Neal

File Annotate Extract Merge Encode Help

BIOMD0000000400.xml

Codewords (73)

Ca	P+X	F	●
Ca:time	P+	F	●
Cc	-	-	●
Compartment	P+X	F	●
Cp	-	-	●
Cpc	-	-	●
Gd	P+X	F	●
Gd:time	P+	F	●
Gt	P+X	F	●
Gt:time	P+	F	●
IP3	P+X	F	●
IP3:time	P+	F	●
J1	-	-	●
J10	-	-	●
J11	-	-	●

Sub-models (0)

+ -

Ca (M)

Chemical concentration of Ca in Compartment ✖

$Ca:time = Cpc * (J8 + J11) * (-1)$

Composite annotation

Chemical concentration (OPB) ✖

property_of

calcium(2+) (CHEBI) ✖

contained_in

Cytosol of cardiac myocyte (FMA) ✖

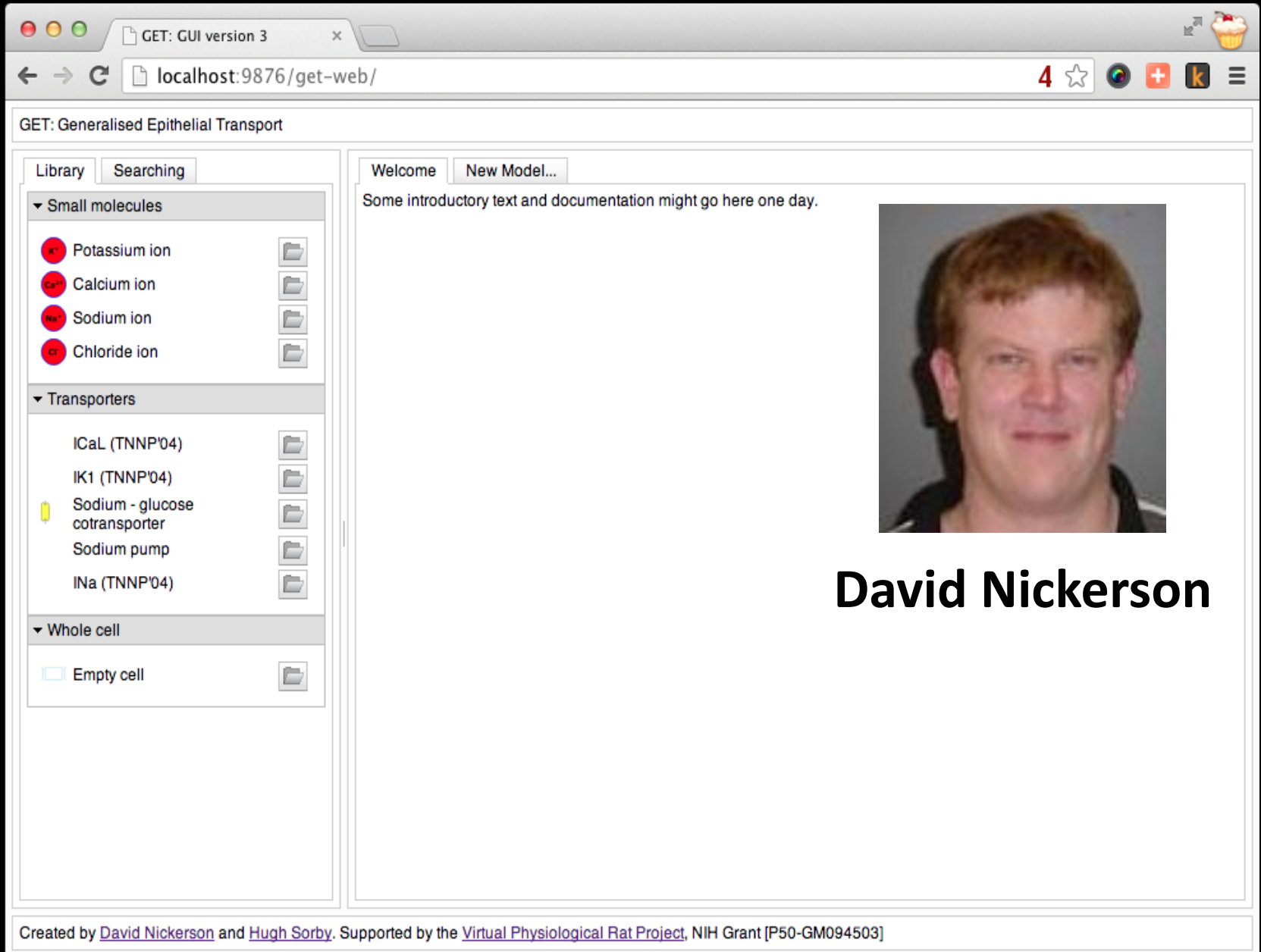
Add entity Add process

Singular annotation

Click to add annotation ✖

```
<?xml version="1.0" ?>
<rdf:Bag>
  <rdf:li rdf:resource="http://identifiers.org/uniprot/Q9Z1B3"/>
</rdf:Bag>
</bqbiol:isVersionOf>
</rdf:Description>
</rdf:RDF>
</annotation>
</species>
<species id="Pg" initialConcentration="0" name="Pg" metaid="_118916" sboterm="SBO:0000296" compartment="Compartment">
  <annotation>
    <rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:bqmodel="http://biomodels.net/model-qualifiers/">
      <rdf:Description rdf:about="#_118916">
        <bqbiol:hasPart>
          <rdf:Bag>
            <rdf:li rdf:resource="http://identifiers.org/obo.chebi/CHEBI:15996"/>
            <rdf:li rdf:resource="http://identifiers.org/uniprot/Q9Z1B3"/>
            <rdf:li rdf:resource="http://identifiers.org/uniprot/P27600"/>
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
</rdf:RDF>
</species>
<species id="Ca" initialConcentration="0.1" name="Ca" metaid="_118896" sboterm="SBO:0000247" compartment="Compartment">
```

Drag & drop model building







The screenshot shows a web browser window with the address bar displaying 'localhost:9876/get-web/'. The page title is 'GET: Generalised Epithelial Transport'. The interface is divided into two main sections. On the left is a 'Library' panel with two tabs: 'Library' and 'Searching'. It contains three expandable categories: 'Small molecules', 'Transporters', and 'Whole cell'. Under 'Small molecules', there are four items: Potassium ion (K⁺), Calcium ion (Ca²⁺), Sodium ion (Na⁺), and Chloride ion (Cl⁻), each with a red circular icon and a folder icon. Under 'Transporters', there are five items: ICaL (TNNP'04), IK1 (TNNP'04), Sodium - glucose cotransporter (with a yellow pill icon), Sodium pump, and INa (TNNP'04), each with a folder icon. Under 'Whole cell', there is one item: Empty cell, with a folder icon. On the right is a 'Welcome' panel with two tabs: 'Welcome' and 'New Model...'. It contains the text 'Some introductory text and documentation might go here one day.' and a portrait photograph of a man with short brown hair. Below the photograph is the name 'David Nickerson' in a large, bold, black font. At the bottom of the browser window, a footer reads: 'Created by [David Nickerson](#) and [Hugh Sorby](#). Supported by the [Virtual Physiological Rat Project](#), NIH Grant [P50-GM094503]


GET: Generalised Epithelial Transport

Library Searching


Small molecules

-  Potassium ion
-  Calcium ion
-  Sodium ion
-  Chloride ion

Transporters

- ICaL (TNNP'04)
- IK1 (TNNP'04)
-  Sodium - glucose cotransporter
- Sodium pump
- INa (TNNP'04)

Whole cell

-  Empty cell

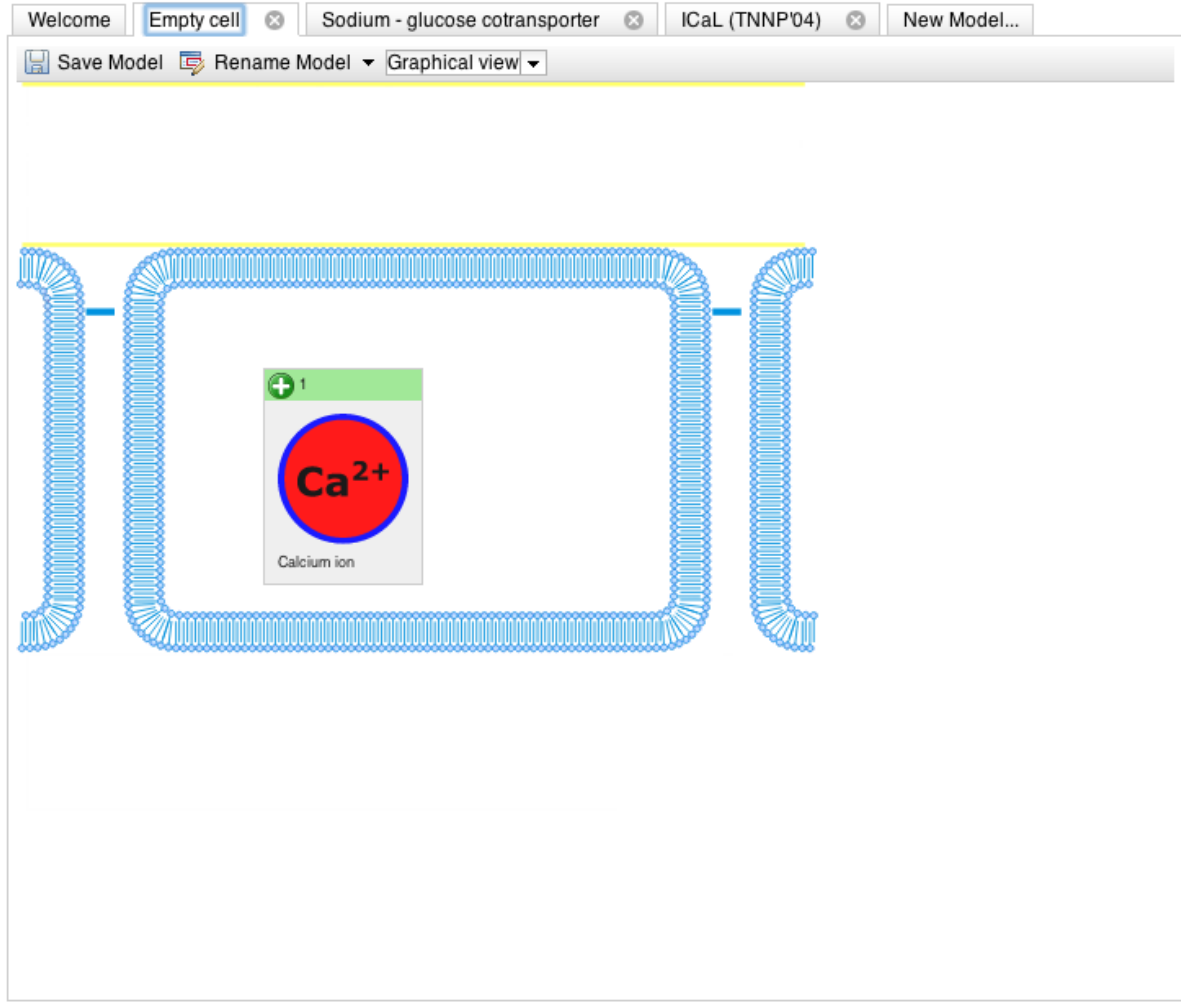
Welcome ICaL (TNNP'04) Empty cell Sodium - glucose cotransporter New Model...

Save Model Rename Model Graphical view



GET: Generalised Epithelial Transport





- Library Searching
- Small molecules
 - Potassium ion
 - Calcium ion
 - Sodium ion
 - Chloride ion
- Transporters
 - ICaL (TNNP'04)
 - IK1 (TNNP'04)
 - Sodium - glucose cotransporter
 - Sodium pump
 - INa (TNNP'04)
- Whole cell
 - Empty cell




GET: Generalised Epithelial Transport

Library Searching


Small molecules

-  Potassium ion
-  Calcium ion
-  Sodium ion
-  Chloride ion

Transporters

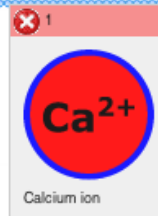
- ICaL (TNNP'04)
- IK1 (TNNP'04)
-  Sodium - glucose cotransporter
- Sodium pump
- INa (TNNP'04)

Whole cell

-  Empty cell

Welcome Empty cell Sodium - glucose cotransporter ICaL (TNNP'04) New Model...

Save Model Rename Model Graphical view







Ca²⁺
Calcium ion


GET: Generalised Epithelial Transport

Library Searching


Small molecules

-  Potassium ion
-  Calcium ion
-  Sodium ion
-  Chloride ion

Transporters

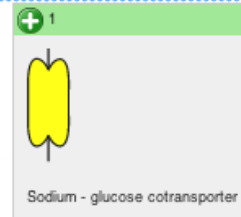
- ICaL (TNNP'04)
- IK1 (TNNP'04)
-  Sodium - glucose cotransporter
- Sodium pump
- INa (TNNP'04)

Whole cell

-  Empty cell

Welcome Empty cell Sodium - glucose cotransporter ICaL (TNNP'04) New Model...

Save Model Rename Model Graphical view



GET: Generalised Epithelial Transport

Library Searching

Small molecules

- K^+ Potassium ion
- Ca^{2+} Calcium ion
- Na^+ Sodium ion
- Cl^- Chloride ion

Transporters

- ICaL (TNNP'04)
- IK1 (TNNP'04)
- Sodium - glucose cotransporter
- Sodium pump
- INa (TNNP'04)

Whole cell

- Empty cell

Welcome ICaL (TNNP'04) Empty cell Sodium - glucose cotransporter New Model...

Save Model Rename Model Simulation view

Protocols

- Generic current-voltage
- Calcium clamp
- Voltage clamp

The top graph shows a current-voltage relationship. The x-axis represents voltage (mV) from 1 to 8, and the y-axis represents current (nA) from 1 to 4. The curve starts at (1, 1), rises linearly to (2, 2), remains constant at 2 nA until 3 mV, then rises linearly to (6, 4).

The bottom graph shows a similar current-voltage relationship. The x-axis represents voltage (mV) from 1 to 8, and the y-axis represents current (nA) from 1 to 7. The curve starts at (1, 1), rises linearly to (2, 2), remains constant at 2 nA until 3 mV, then rises linearly to (6, 5), remains constant at 5 nA until 7 mV, and finally rises linearly to (8, 7).

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www.vph-institute.org

