

# Developing the Virtual Physiological Human: tools, techniques, and best practices for data exchange, storage, and publication

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## The Virtual Physiological Human

The Virtual Physiological Human (VPH) initiative is a worldwide effort to develop next-generation computer technologies to integrate all information available for each patient, and generated computer models capable of predicting how the health of that patient will evolve under prescribed conditions [1-3]. An illustrative example of such a computational model is presented in Figure 1.

Achieving such a goal requires the participation of a very large and diverse community of scientists. Effective and efficient communication in a globally distributed network of collaborating scientists is essential to the success of this initiative.

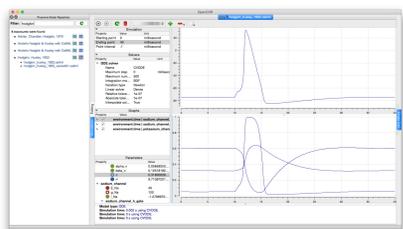
The IUPS Physiome Project, from which the VPH initiative grew, has been leading the way in developing standards for encoding models of computational physiology [4].

## Enabling technology: Standards

The Computational Modelling in BIology NETwork (COMBINE) initiative was established to coordinate community standards and formats for computational models [5,6]. The COMBINE core standards CellML and SED-ML are most relevant to this work, and the FieldML standard is being developed to replace the range of *ad-hoc* file formats currently used for sharing, archiving, and exchanging finite element models.

## Enabling technology: OpenCOR

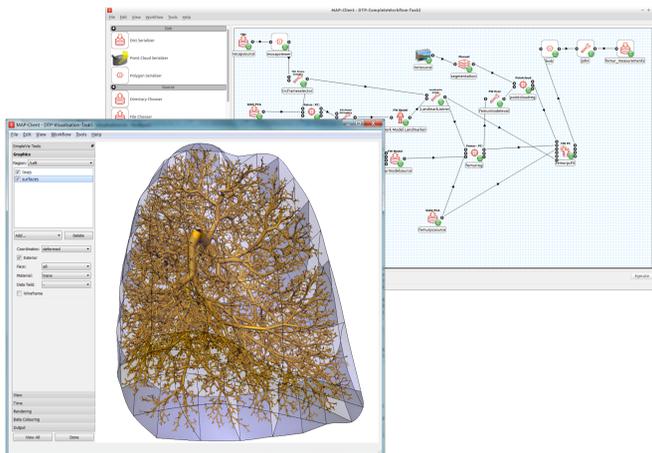
OpenCOR [9,10] is an open-source software tool for creating, editing, annotating, and simulating CellML models. As demonstrated in Figure 3, OpenCOR is able to find, open, and simulate models directly from PMR.



**Figure 3:** Screenshot of OpenCOR with the PMR browser showing the Hodgkin & Huxley model that has been opened and a simulation executed to display simulation results.

## Enabling technology: MAP Client

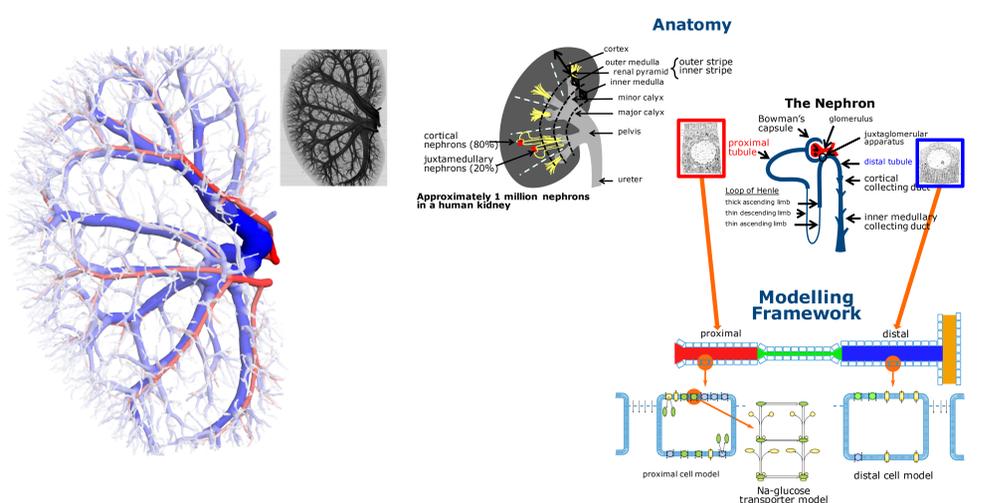
The Musculoskeletal Atlas Project (MAP) Client [11] integrates disparate software tools into a workflow of processing steps to achieve a specific objective in order to capture the workflows used by scientists in the generation and analysis of their data. See Figure 4 for an illustrative example. Capturing a complete description of the workflow and archiving that description in PMR ensures that a given study can not only be understood by another scientist, but can also be reproduced by that scientist.



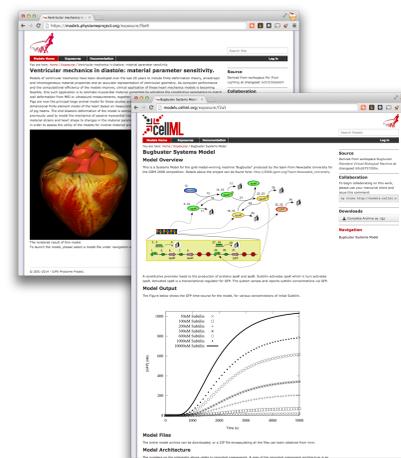
**Figure 4:** Screenshots of the MAP Client, showing an example workflow in the background and an example data visualisation result in the foreground.

## References

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**Figure 1:** Example of a multiscale modelling framework in the kidney. The left panel shows a computational model of the renal vasculature (blue veins, red arteries) extracted from micro-CT images (inset) of a rat kidney (based on data from [14]). The right panels show an illustration of the renal anatomy and the nephron, consisting of different cell types, details that can then be represented in the modelling framework.



**Figure 2:** Screenshots of two different types of models in PMR.

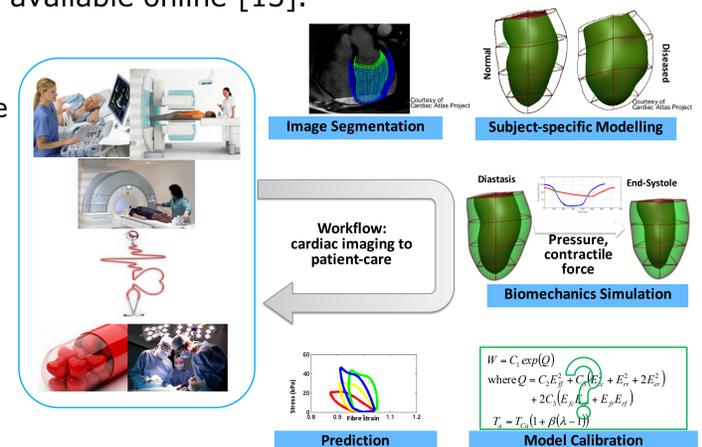
## Enabling technology: PMR

The Physiome Model Repository (PMR) [7,8] is a free and open repository used by the Physiome Project and VPH members. Key features of PMR are configurable access controls, provenance management, version tracking, and comprehensive web service API. Specific types of data, such as CellML or FieldML models, stored in PMR can be specially rendered for presentation on the web – as shown in Figure 2.

## Instructing the next generation of scientists

The MedTech CoRE [12] is a new centre for research excellence in New Zealand. Exemplifying the best practices developed in our work toward a virtual physiological human, we are developing a computational physiology module to introduce new doctoral students entering the CoRE to fundamental concepts in the application of engineering and mathematical sciences to the study of physiology. The module uses the tools and technologies described here to lead the students through several “typical” clinical workflows which involve computational physiology. Figure 5 illustrates a cardiac example of this. A virtual machine containing all the required software for this module is available on request and the documentation is all freely available online [13].

**Figure 5:** Illustrative example computational physiology of the heart workflow. Starting with clinical imaging and ending with a clinically relevant prediction of cardiac functions. This example is courtesy of Martyn Nash and Vicky Wang, Auckland Bioengineering Institute.



## Acknowledgements