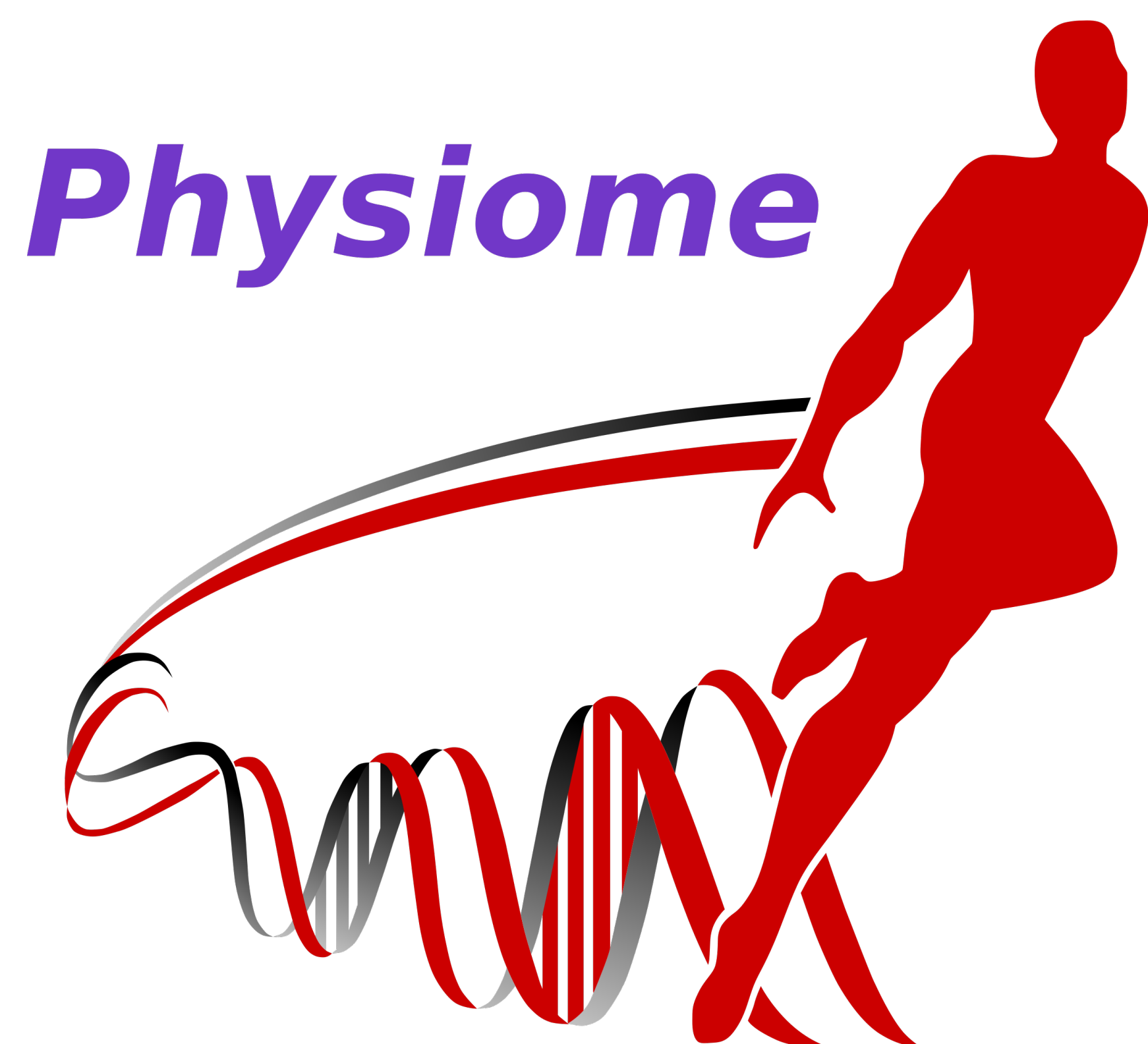




Introducing the *Physiome* Journal: Improving Reproducibility, Reuse, and Discovery of Computational Models

David Nickerson (about.me/david.nickerson) & Peter Hunter

Auckland Bioengineering Institute, University of Auckland, New Zealand



<https://journal.physiomeproject.org>

Physiome publishes reproducible and reusable mathematical models of physiological processes where the experimental details and model validation have been published or accepted for publication in a recognised 'primary' peer-reviewed journal.

Physiome is open access with a low Author Processing Charge. Where possible, models can be displayed (in mathematical form and in various programming languages) and run directly from the journal website with freely available open source software.

The Physiome Project

The International Union for Physiological Sciences (IUPS) launched the Physiome Project at the IUPS World Congress in St Petersburg in 1997 in order to bring quantitative bioengineering approaches to the study of anatomy and physiology. The major focus of the project has been the creation of standards, tools and databases for reproducible and reusable mathematical models of physiological processes (www.physiomeproject.org).

Note that we currently define the following, but aim for community consensus on these definitions – feedback more than welcome.

- A model simulation is **repeatable** when re-running it produces a consistent result.
- A model is **reproducible** when its outputs can be reproduced by a machine from an unambiguous statement of the model equations, together with specified values of the model parameters, initial conditions and boundary conditions. Markup languages such as [CellML](#), [SBML](#), [NeuroML](#) and [FieldML](#) are designed to encode a model in unambiguous form. The markup language [SED-ML](#) is designed to specify the simulation protocol for running the model with specified inputs and outputs.
- A model is **reusable** when it can be used as an independent model or as a module within another model. This requires that the appropriate use of the model is well documented and that its limitations are clear, and that the model is semantically annotated to provide the biological and biophysical meaning of all of its variables and components. One of the goals of the Physiome Project is to encourage modular approaches to modelling to facilitate the reuse of well documented and validated modules.
- A model is **discoverable** when it has been annotated with metadata that describe the purpose and use of the model sufficiently to allow the model to be retrieved via a webservice.
- A model is **validated** when its predictions under specified conditions match experimental observations.

The *Physiome* journal publishes models that are reproducible, reusable and discoverable. It is the role of the companion primary journal to ensure that the model has been validated. Evaluating reproducibility for large scale simulation experiments is an area of active research – feedback welcome.

Submission types

Original submission: author initiated submissions directly associated with a primary experimental or modelling paper that has been accepted by a peer-reviewed physiology, bioengineering, or biophysics journal.

Retrospective: similar in most regards to an original submission, but is associated with an historical primary article which has been deemed to provide substantial value to the physiological modelling community in making a reusable, reproducible, and discoverable version of the study available.

Reviews: the *Physiome* editorial board may solicit review submissions that document a range of published models in a given area.

Letters: an original submission that provides new insights about, or refinement of, a model that is already published on the Physiome site.

Standards

The use of appropriate standards is essential to ensuring computational models are reproducible, reusable, and discoverable. Standards do not yet exist to guarantee that all computational models submitted to *Physiome* can be encoded in a suitable standard. Part of the evaluation of the submission involves checking that where suitable standards exist that they are used. The *Physiome* curators are able to help authors encode their submissions when required. When determining suitable standards, we follow the Computational Modeling in Biology Network ([COMBINE](#)) standards.

Published *Physiome* articles are distributed as [COMBINE archives](#), distributable bundles containing all required resources to reproduce the published simulations.

Acknowledgements

We thank the members of the *Physiome* Management Board: Professors Denis Noble, Walter Boron, Andrew McCulloch, and Stig Omholt.

David Nickerson also acknowledges funding from the Aotearoa Foundation.

