Obtaining and Simulating the Example Models

model files obtained must be the Physiome Model Repository (http://models.physiomeproject.org). There are several ways to do this, from a simple download and local use of files to distributed source control of the model code across the internet. More details of Physiome Model Repository and examples of workflow can found http://models.physiomeproject.org/docs.

The simplest way to obtain the model files is to download a .zip file that contains them. Each of the Signalling and Core Domains example 'workspaces' in the Physiome Model Repository contains such a .zip file.

To download the Signalling Example .zip file, navigate to the Signalling Example workspace at http://models.physiomeproject.org/workspace/2c4. A list of model and documentation files will be presented, similar to Figure S1-1.

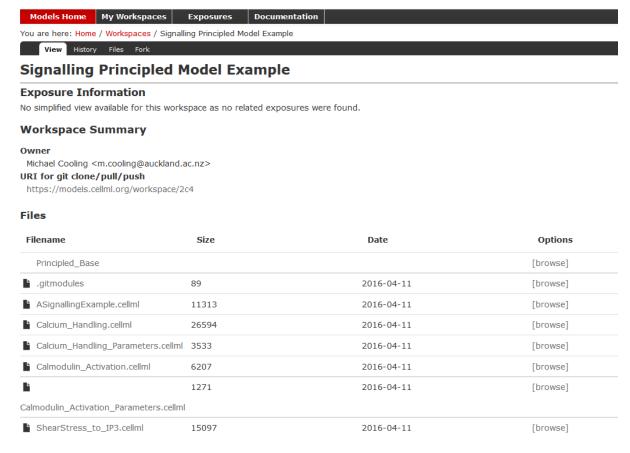


Figure S1-1: Listing of files in the Signalling Example's workspace

Find the file 'ASignallingExample_CompleteModel.zip' and use the '[browse]' link on the right-hand side to request a copy via a subsequent 'Download' button.

A similar process can be followed to obtain and simulate the Core Domains example. The corresponding workspace can be found at http://models.physiomeproject.org/workspace/2c5. The name of the file to obtain is 'ACoreDomainsExample_CompleteModel.zip'.

When unzipped, the contents of these files can be loaded into one's favourite CellML simulation environment. For a list of tools for CellML simulation, please see http://www.cellml.org/tools/. The recommended tool for this work is 'OpenCOR', which can be found at http://www.opencor.ws/. For the Signalling and Core Domains Examples, the corresponding top-level CellML model files to load are 'ASignallingExample.cellml' and 'ACoreDomainsExample.cellml', respectively.

For those desiring to start modifying or creating CellML modules or models, we recommend the tutorials and primers listed at http://www.cellml.org/getting-started.