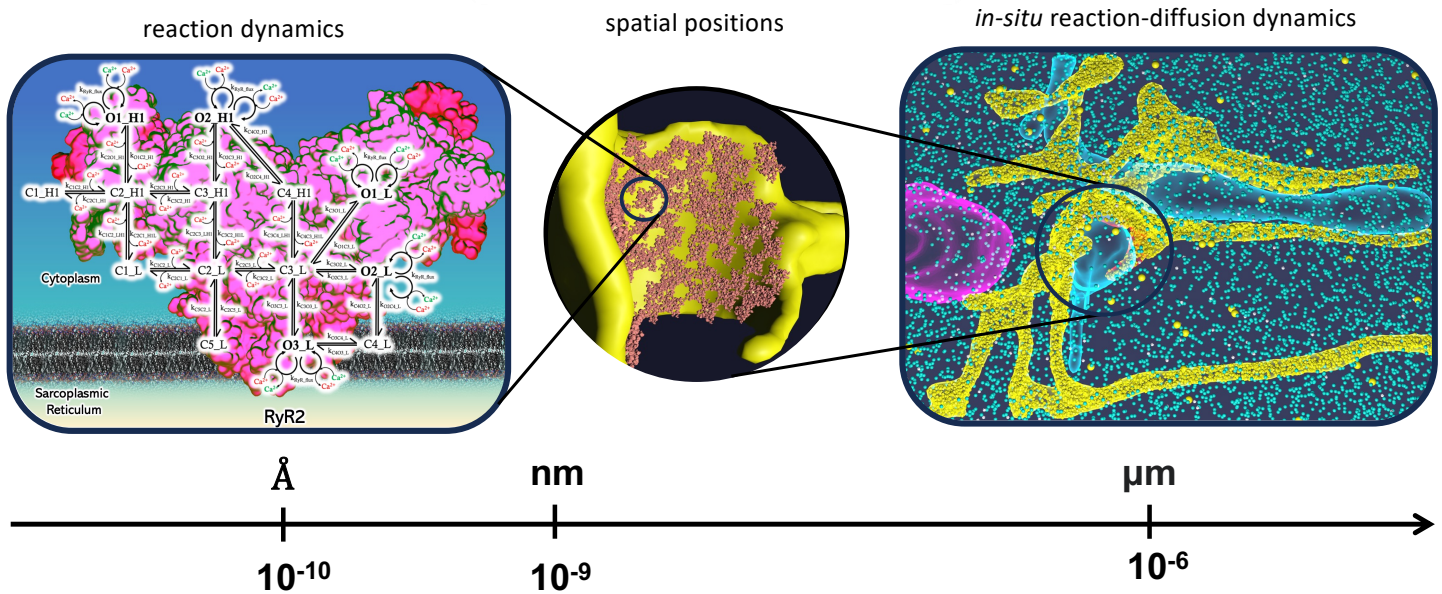


# Calcium Release Unit

## MCell System Tutorial



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## Installing the software

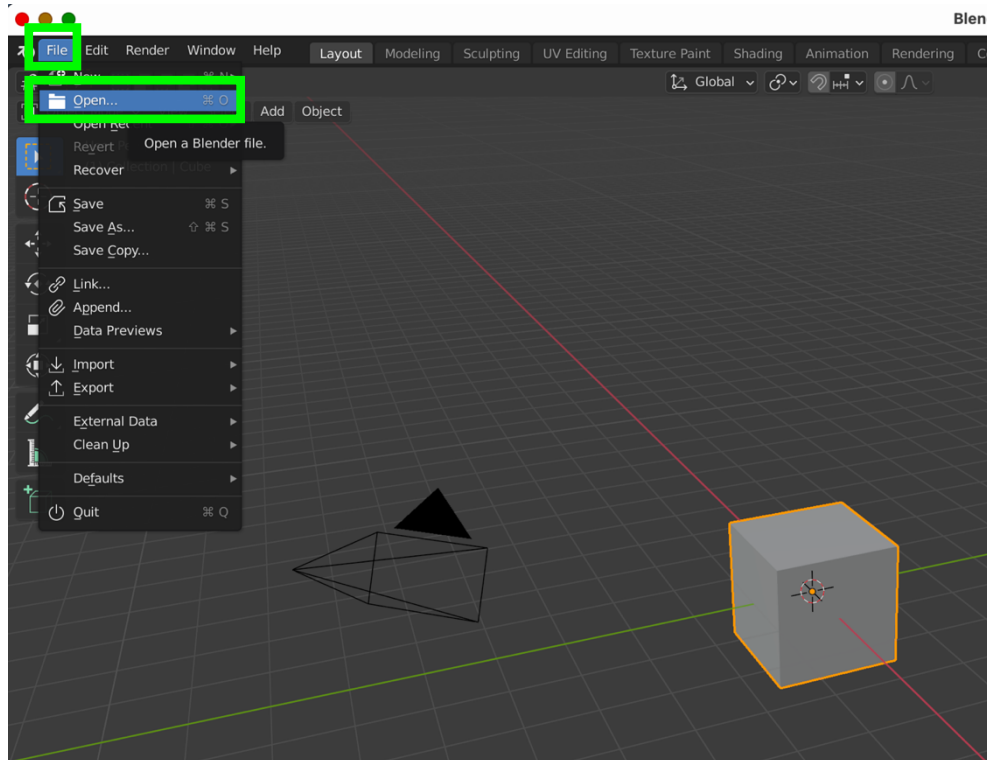
Navigate to the Calcium Release Unit (CRU) model github site

<https://github.com/sophiahirakis/CRU>

For those unfamiliar with blender, we recommend a series of youtube tutorials to help you navigate through the blender user interface which can be found here:

[https://www.youtube.com/playlist?list=PLa1F2ddGya\\_-UvuAqHAksYnB0qL9yWDO6](https://www.youtube.com/playlist?list=PLa1F2ddGya_-UvuAqHAksYnB0qL9yWDO6)

Install the software for your appropriate operating system, with the install files located in the software/ directory. After the successful installation of CellBlender/MCell, start-up Blender and navigate on the top right to File > Open

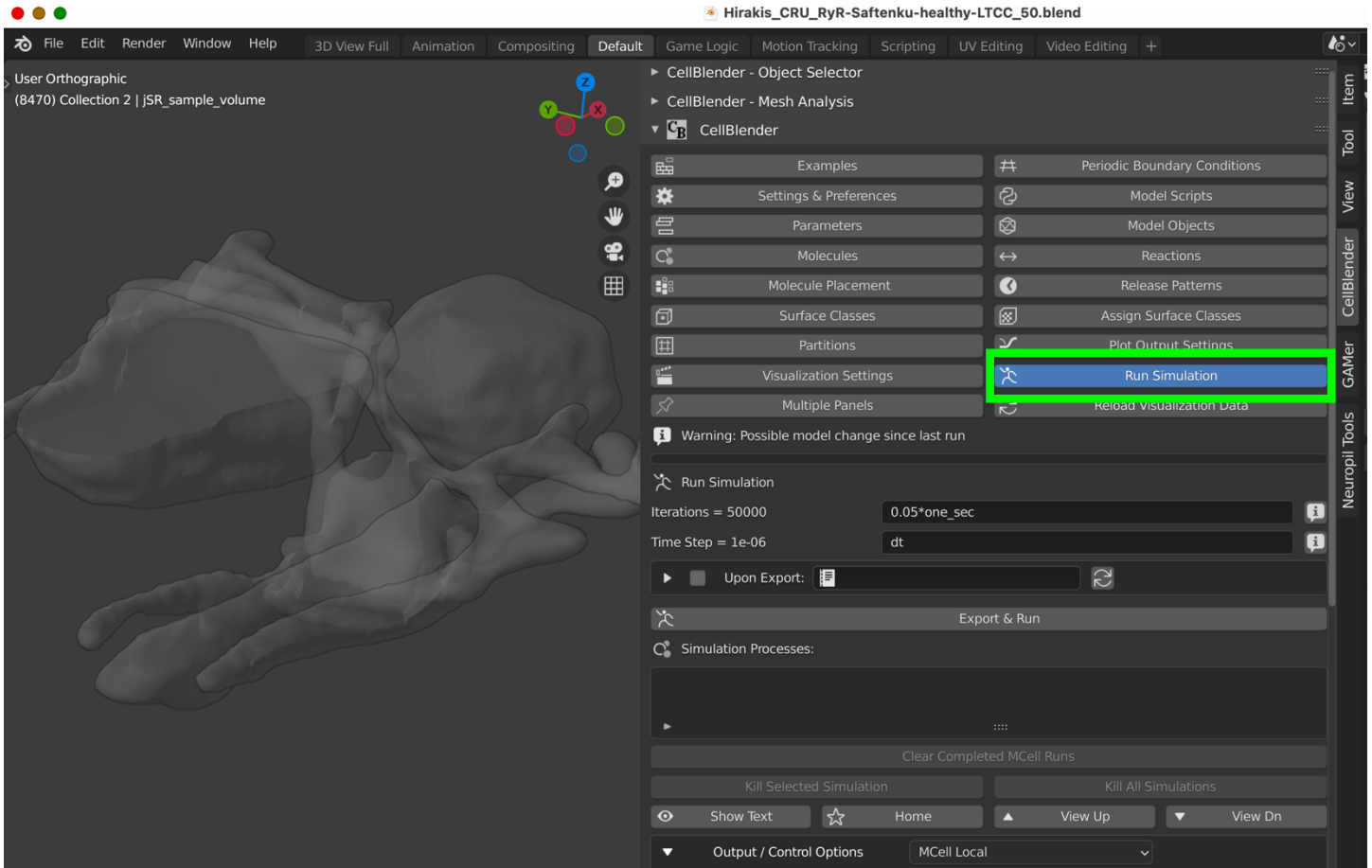


Download the provided .blend file and load into your blender environment.

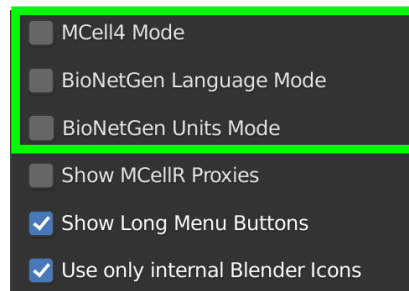
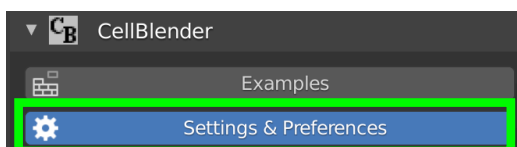
## Using CellBlender with MCell3 Mode

Upon opening the model, you may see several toolbars open. Toggle the left toolbar off by hitting the “t” key on your keyboard. Toggle the right toolbar off by hitting the “n” key on your keyboard. This can be undone by hitting the respective keys to turn the toolbars on and off as desired.

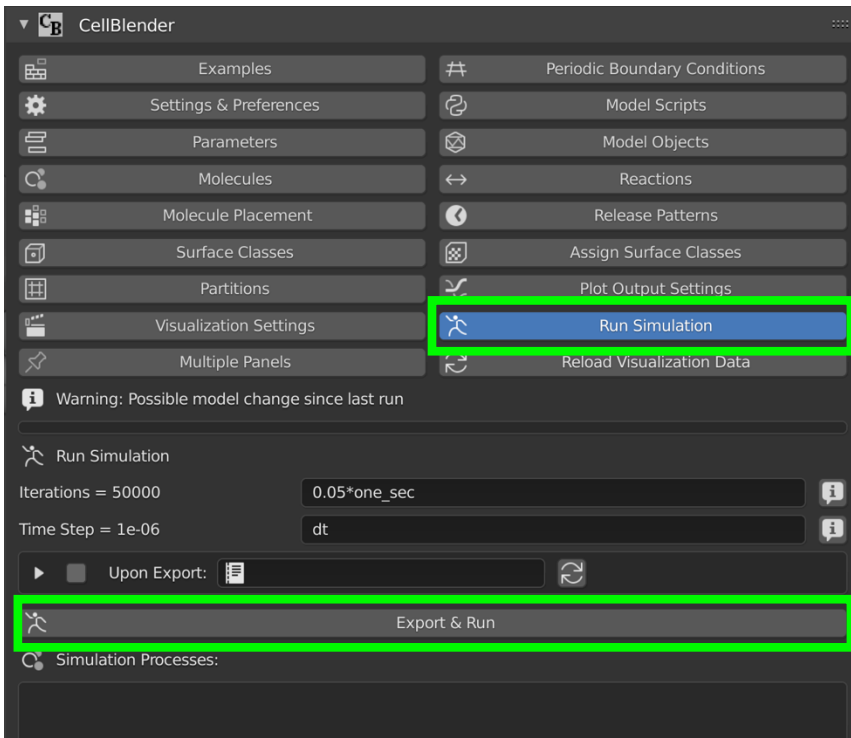
Open the right panel using the “n” keyboard key, navigate to the CellBlender tool.



To run the model with MCell3 settings, it is essential to adjust the settings of the model. Navigate to the **Settings & Preferences** tab and **turn off MCell4 mode** as well as **BioNetGen Language and Units modes**



## Running a simulation



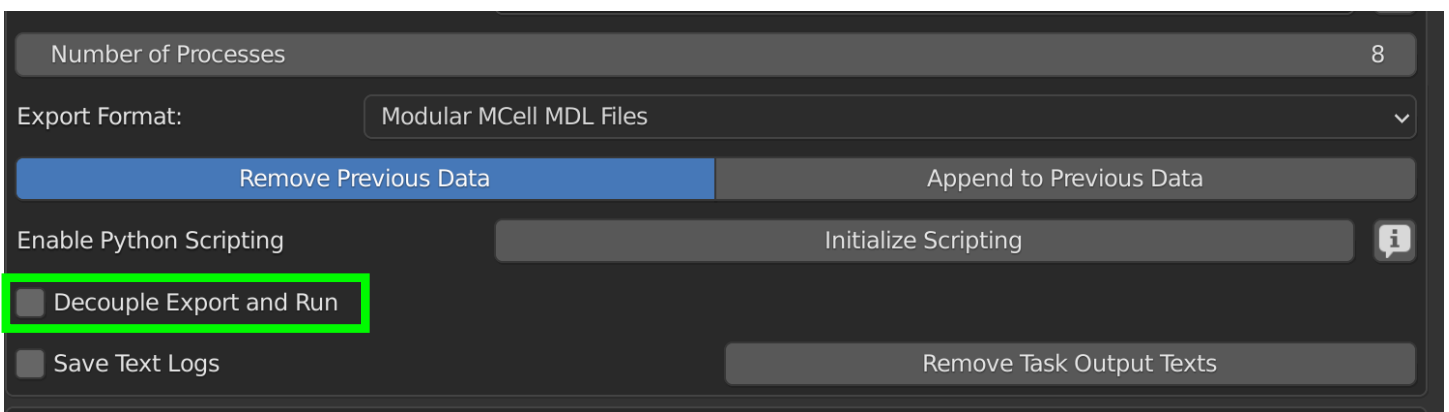
To run the simulation with the system, as is, navigate to the **Run Simulation** tab.

Ensure the **Action\_Potential** folder is in the same directory as your \*.blend file

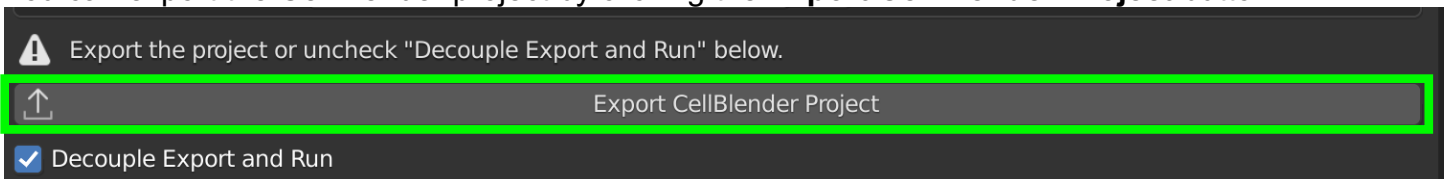
Ensure you **Save** your system to a .blend file prior to running any simulations.

Click **Export and Run** to run the MCell simulation in the local graphic user interface.

To inspect the files prior to running the simulation, you can choose to **Decouple Export and Run** by scrolling down in the **Run Simulation** tab. The files will be exported to a directory that is named according to your blend file name with a “\_files” suffix. For example:  
YourBlendFileName\_files

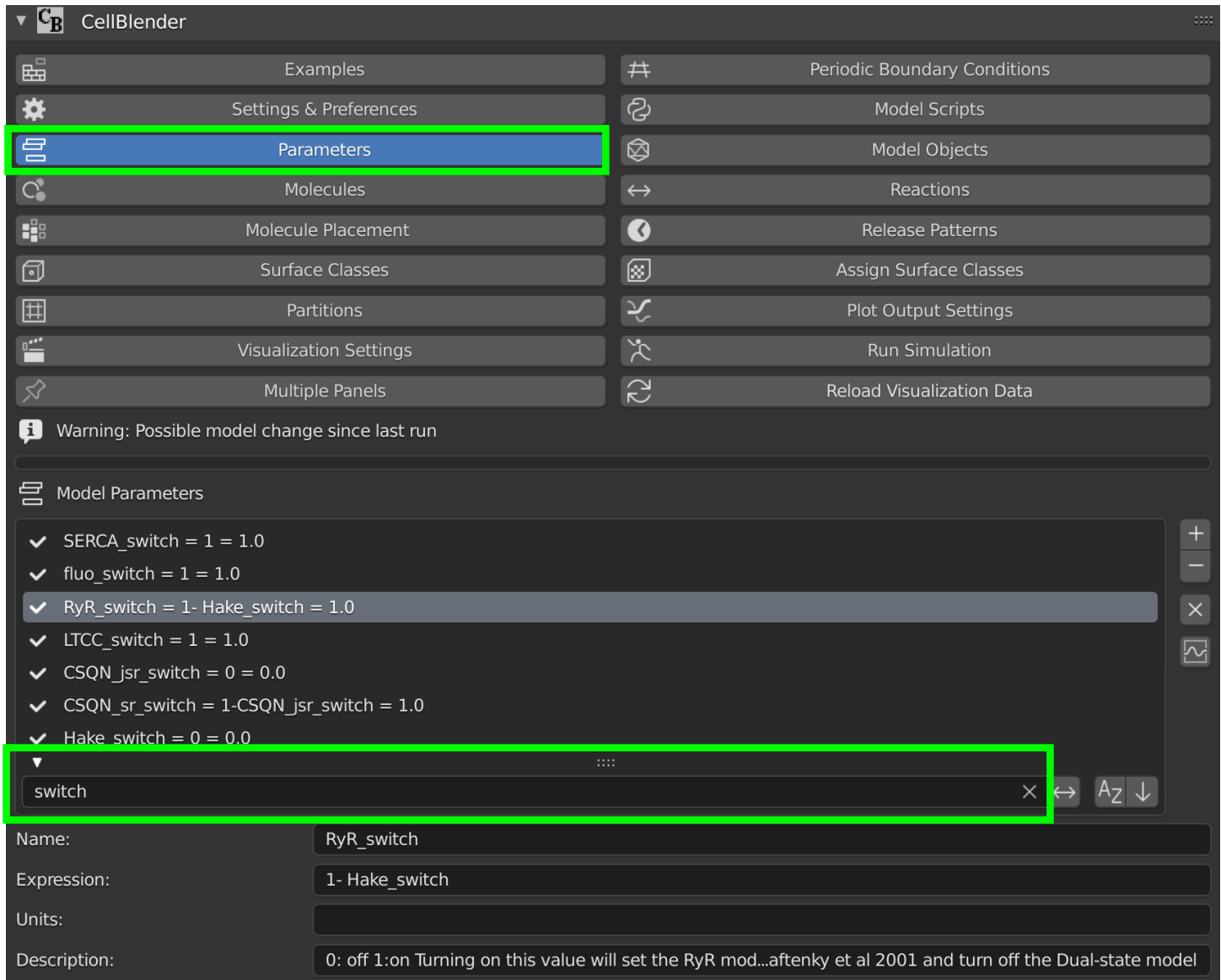


You can export the CellBlender project by clicking the **Export CellBlender Project** button.



## Switches and Modes

There are several switches and modes programmed into the model that allow you to globally modulate settings in the model. You can find these various modes in the Parameters tab and search “switch” or “mode.”



CellBlender

Examples

Settings & Preferences

**Parameters**

Molecules

Molecule Placement

Surface Classes

Partitions

Visualization Settings

Multiple Panels

Periodic Boundary Conditions

Model Scripts

Model Objects

Reactions

Release Patterns

Assign Surface Classes

Plot Output Settings

Run Simulation

Reload Visualization Data

Warning: Possible model change since last run

Model Parameters

- ✓ SERCA\_switch = 1 = 1.0
- ✓ fluo\_switch = 1 = 1.0
- ✓ RyR\_switch = 1- Hake\_switch = 1.0
- ✓ LTCC\_switch = 1 = 1.0
- ✓ CSQN\_jsr\_switch = 0 = 0.0
- ✓ CSQN\_sr\_switch = 1-CSQN\_jsr\_switch = 1.0
- ✓ Hake\_switch = 0 = 0.0

switch

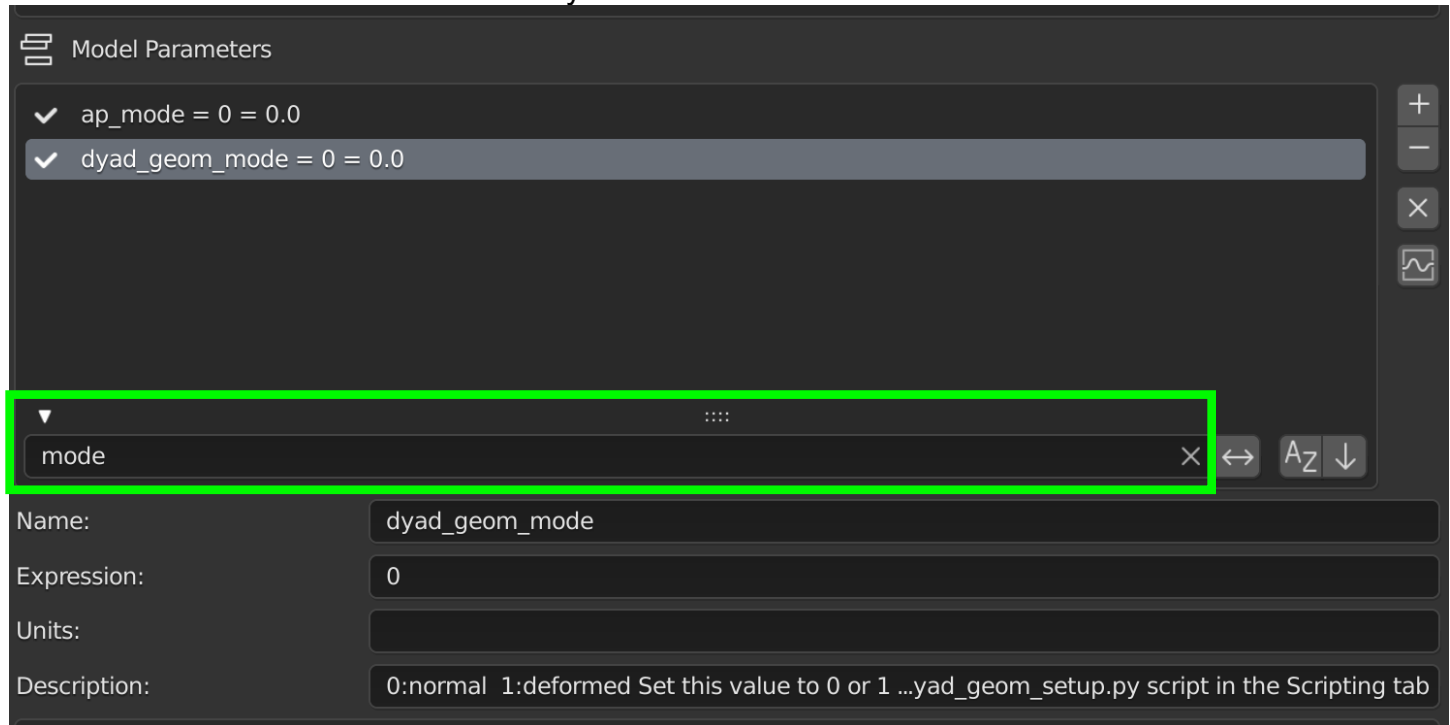
Name: RyR\_switch

Expression: 1- Hake\_switch

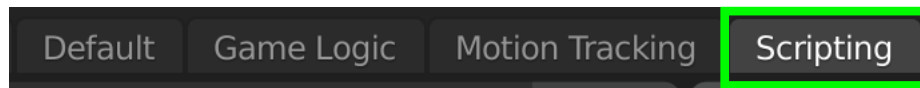
Units:

Description: 0: off 1:on Turning on this value will set the RyR mod...afternky et al 2001 and turn off the Dual-state model

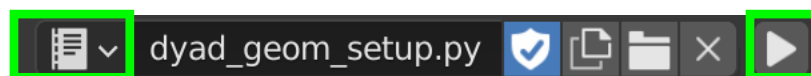
Very importantly, some mode parameters are connected to scripts, such as the `ap_mode` which alters the action potential from healthy to diseased to no\_AP modes; and the `dyad_geom_mode` parameter which sets the T-Tubule to either healthy or deformed.



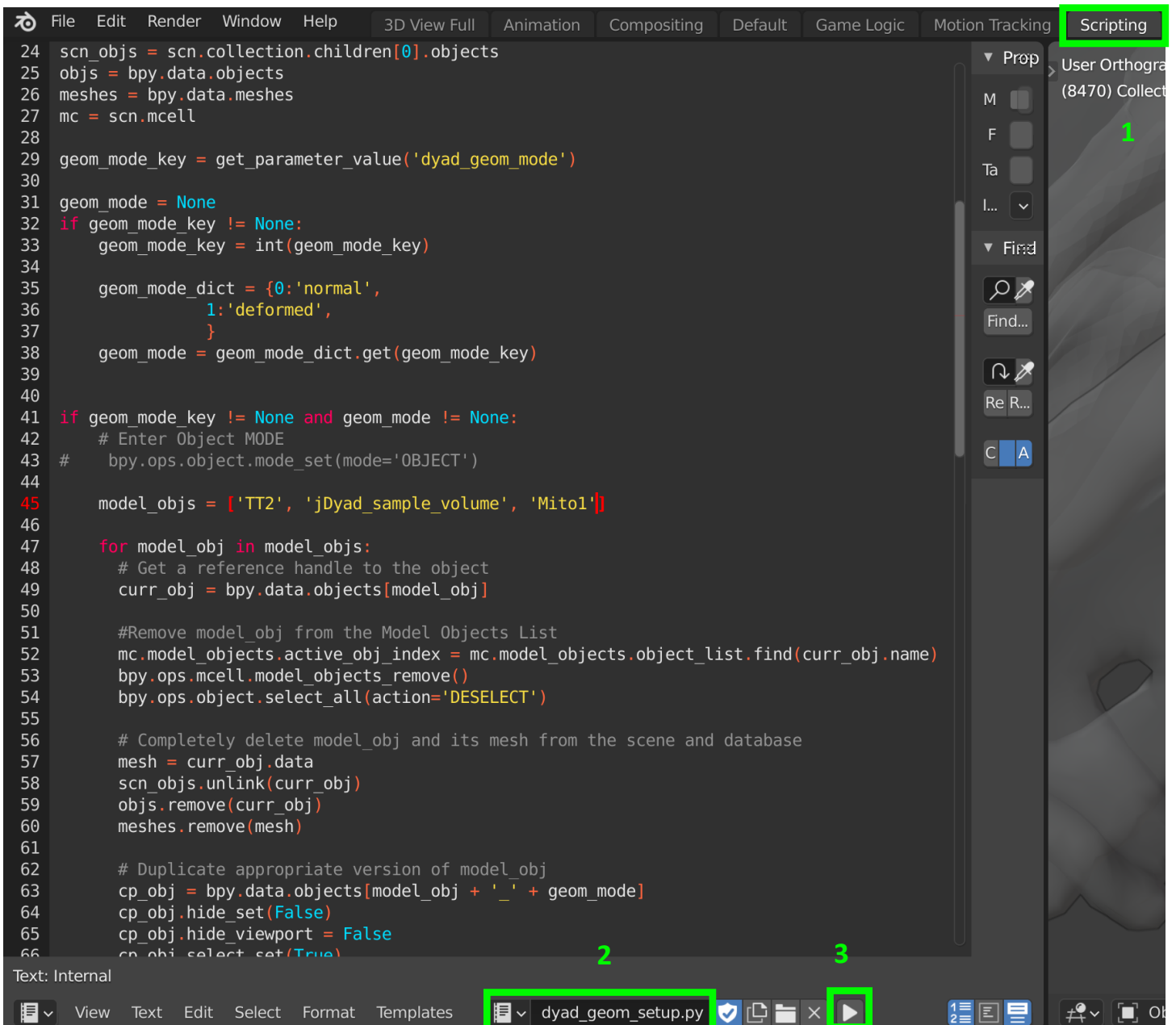
In the case of altering the T-Tubule geometry, this must be done manually by navigating to the scripting tab, at the top of the Blender window.



Once in the scripting tab, you can search for the appropriate script by clicking the drop-down menu and running the script by clicking the play button.



The rest of the scripts are run by the CellBlender system internally prior to the exporting of the system and running of the simulation.



## Visualizing the simulation output in Blender

To visualize the simulation output in Blender, navigate to the **Visualization Settings** tab. You can manually select the visualization directory by selecting **Manually Select Viz Directory** or clicking the **Read Viz Data** button.

