

## Summary of example:

The input data file ("131117-C2\_short.dat") contains one trace obtained from a ca1 layer pyramidal cell by using current clamp.

The cell was excited by a short 500pA and by a long 10pA pulse injected into the soma, so you have to use the provided stimuli file (for this, select the "Custom Waveform" option from the dropdown menu on the stimuli layer and then load the file: "cell2\_stim.dat").

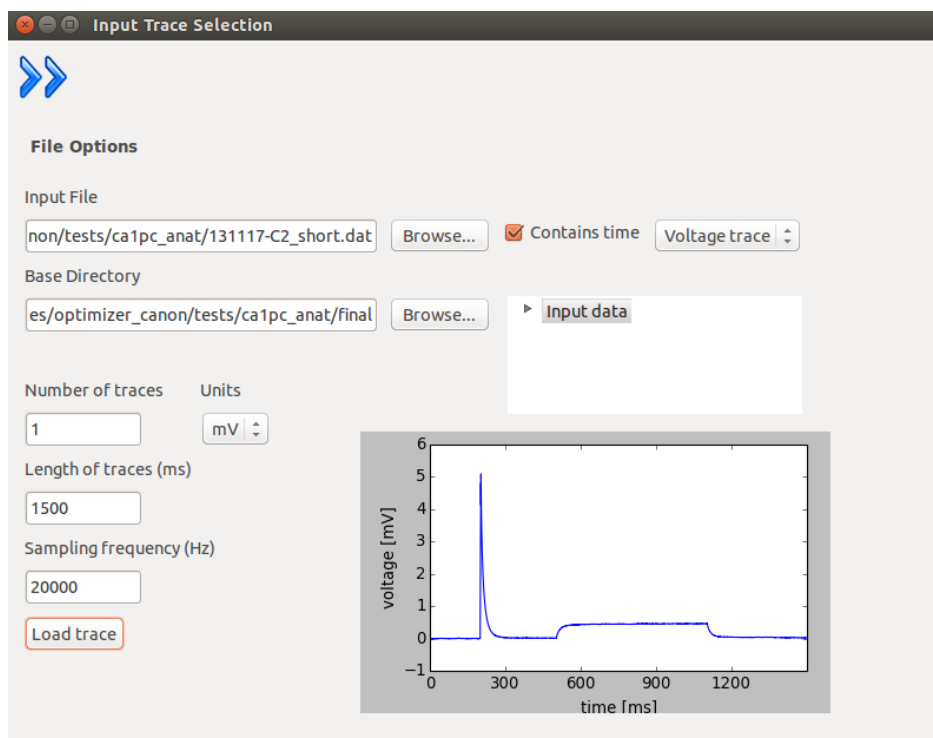
The data trace is 1500ms long and the sampling frequency was 20kHz.

The provided model is a passive one and it's based on a precise reconstruction, and we are interested in the  $cm$ ,  $R_a$ ,  $g_{pas}$  parameters.

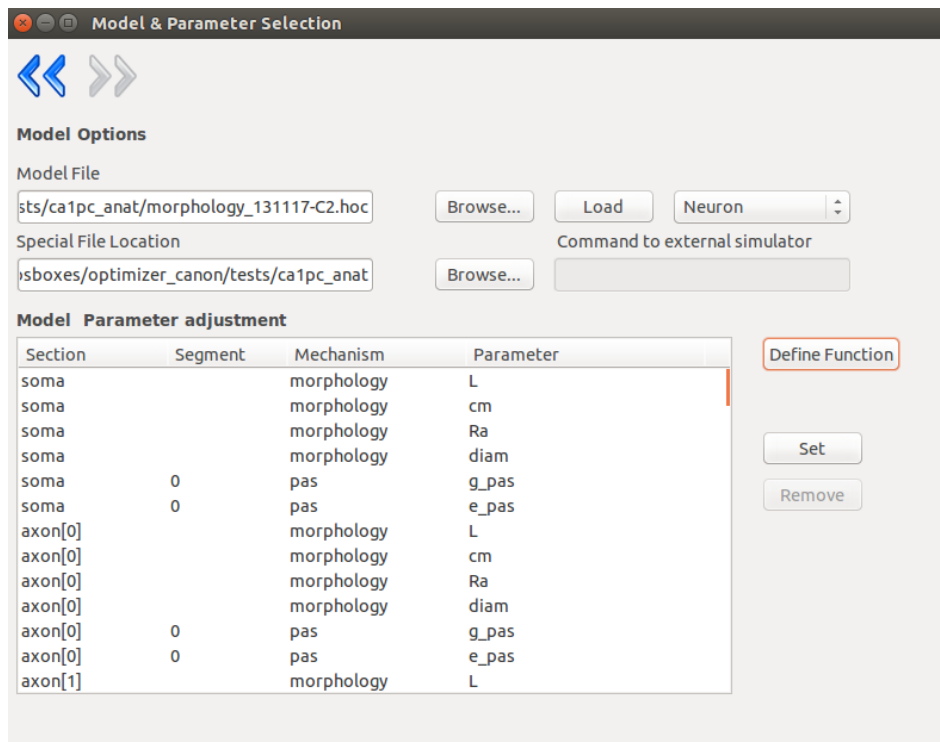
Because we had to set the  $e_{pas}$  parameter to 0 and we wanted to optimize the previous parameters in every section, we created a function to do this for us (see "udeffun\_pyr\_3param.txt"), you can load this on the model selection layer.

## Step-by-step instructions to run the example from the Optimizer GUI:

Run „python optimizer.py -g” to start the GUI

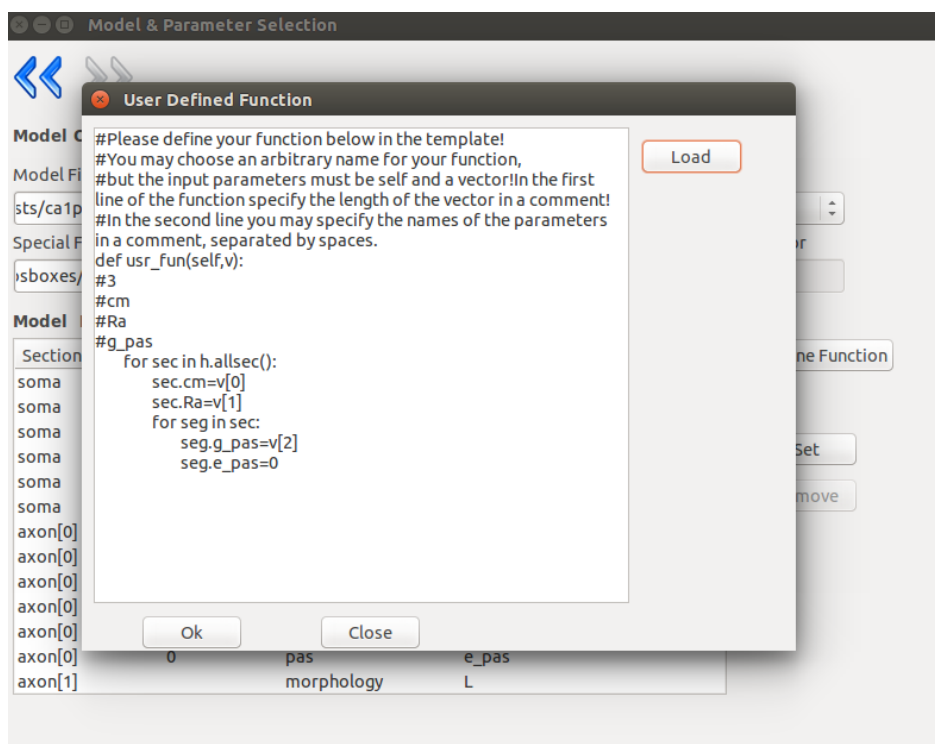


At 'Input File' load the target data, at 'Base Directory' choose the directory where you want to save the results. Fill out all the cells and press 'Load trace'. Go on by pressing the blue arrow.

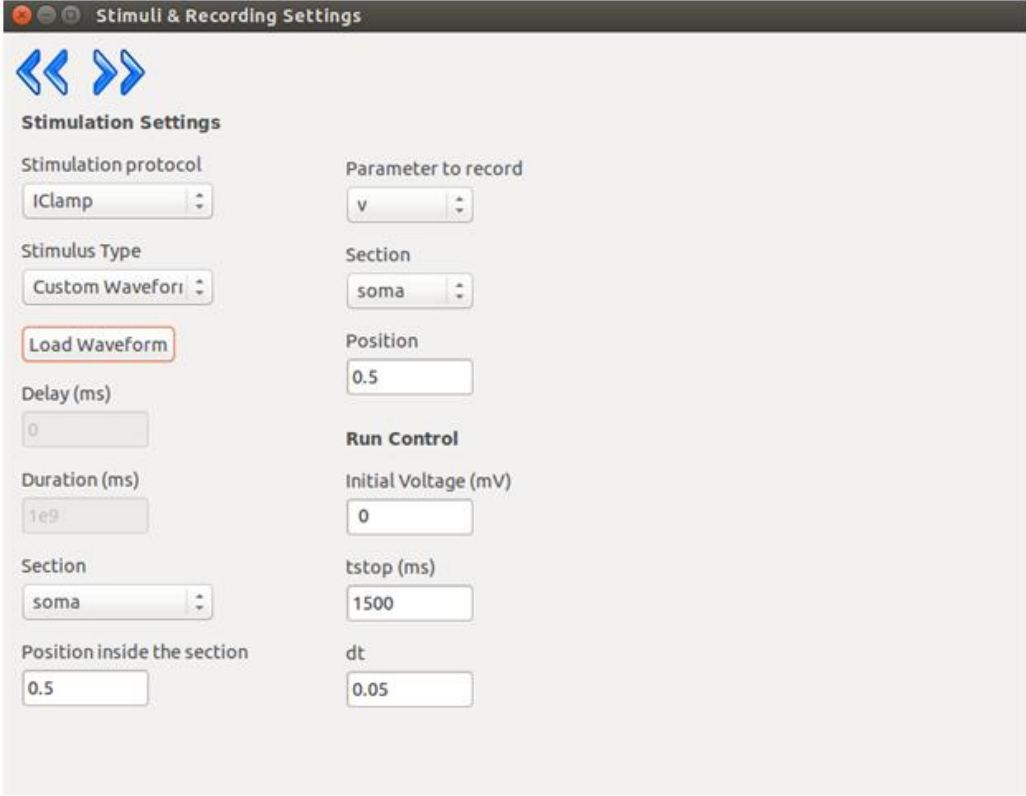


Browse to the model file and load the model.

Press the 'Define Function' button to load the user defined function:



Press 'Ok', then go on by pressing the right arrow.



**Stimuli & Recording Settings**

Stimulation protocol: IClamp

Parameter to record: v

Stimulus Type: Custom Waveform

Section: soma

Position: 0.5

Delay (ms): 0

Duration (ms): 1e9

Section: soma

Position inside the section: 0.5

Run Control

Initial Voltage (mV): 0

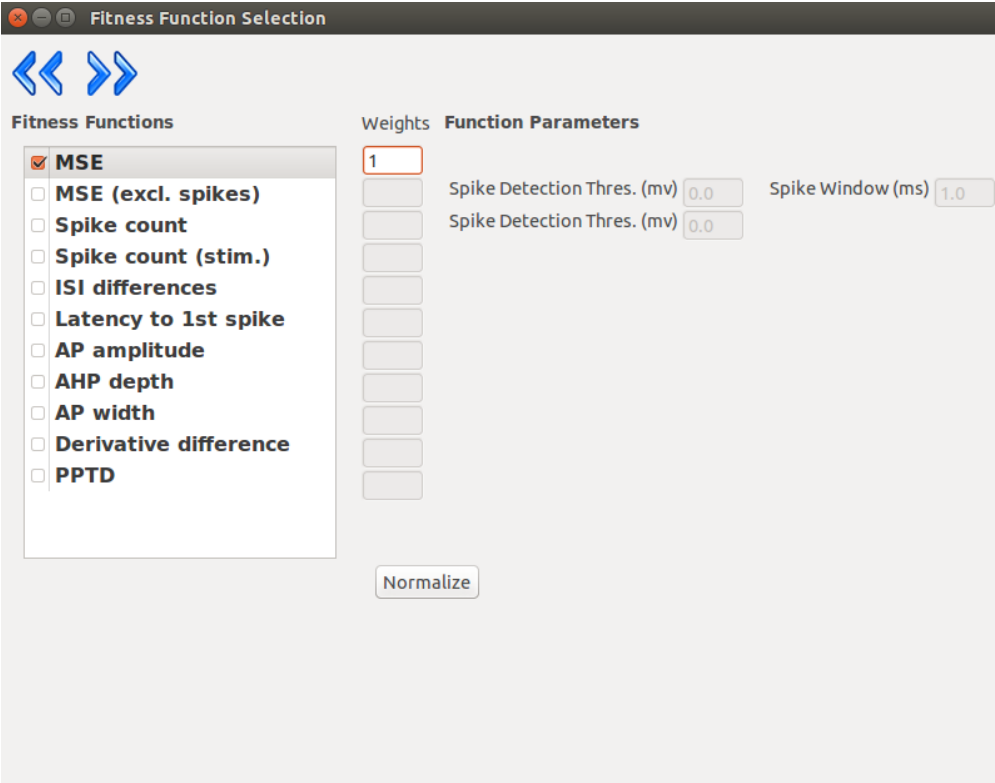
tstop (ms): 1500

dt: 0.05

Load Waveform

Choose 'Custom Waveform' as 'Stimulus Type', then press 'Load Waveform' to load the file: cell2\_stim.dat

Go on by pressing the right arrow.



**Fitness Function Selection**

**Fitness Functions**

- ☒ MSE
- ☐ MSE (excl. spikes)
- ☐ Spike count
- ☐ Spike count (stim.)
- ☐ ISI differences
- ☐ Latency to 1st spike
- ☐ AP amplitude
- ☐ AHP depth
- ☐ AP width
- ☐ Derivative difference
- ☐ PPTD

**Weights**

1

**Function Parameters**

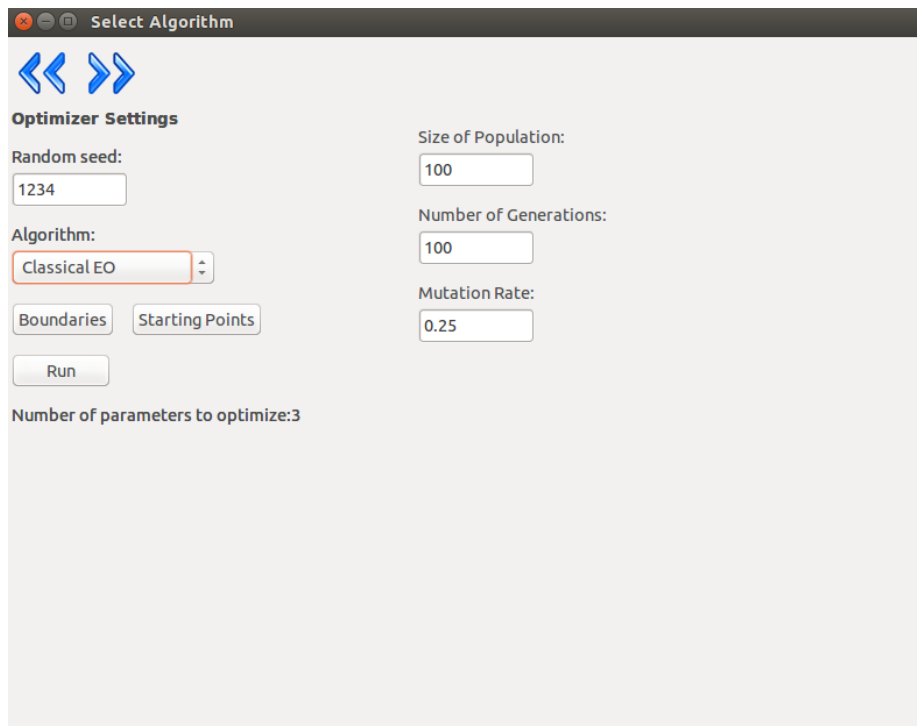
Spike Detection Thres. (mv): 0.0

Spike Detection Thres. (mv): 0.0

Spike Window (ms): 1.0

Normalize

Choose fitness function(s), and define their weights.



The 'Select Algorithm' window features a title bar with standard window controls. Below the title bar are two blue double-headed arrows. The 'Optimizer Settings' section includes a 'Random seed' text box with the value '1234', an 'Algorithm' dropdown menu currently set to 'Classical EO', and two buttons labeled 'Boundaries' and 'Starting Points'. To the right, there are three more text boxes: 'Size of Population' (100), 'Number of Generations' (100), and 'Mutation Rate' (0.25). A 'Run' button is located below the 'Boundaries' and 'Starting Points' buttons. At the bottom, it states 'Number of parameters to optimize:3'.

Select Algorithm

Optimizer Settings

Random seed: 1234

Algorithm: Classical EO

Boundaries Starting Points

Run

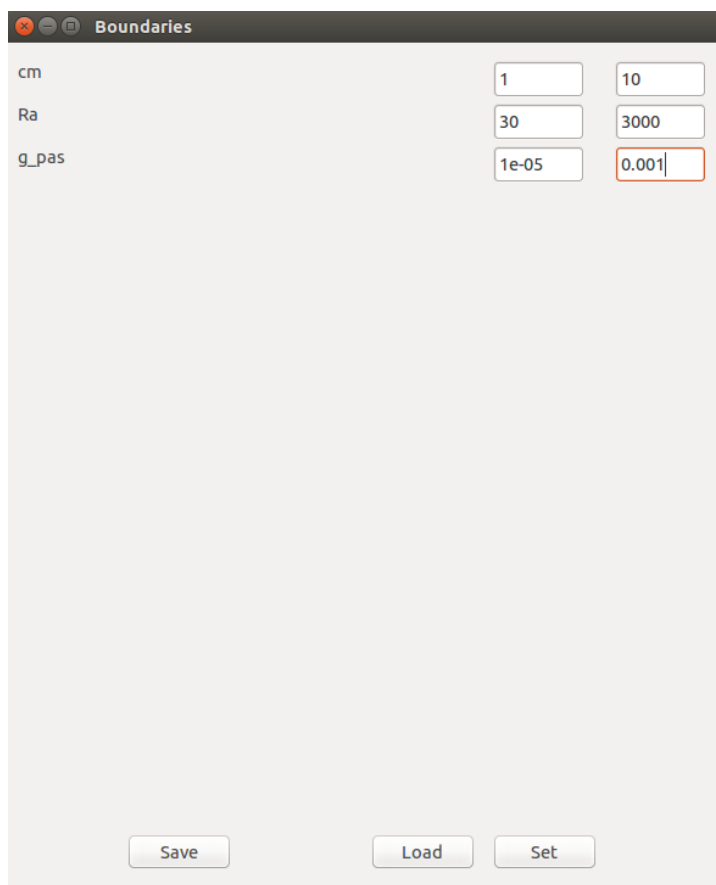
Size of Population: 100

Number of Generations: 100

Mutation Rate: 0.25

Number of parameters to optimize:3

Select an algorithm, and press the 'Boundaries' button to define the boundaries of the parameters to be optimized:



The 'Boundaries' window has a title bar with window controls. It displays three parameters on the left: 'cm', 'Ra', and 'g\_pas'. Each parameter has two corresponding text boxes for its boundaries. For 'cm', the values are 1 and 10. For 'Ra', the values are 30 and 3000. For 'g\_pas', the values are 1e-05 and 0.001. At the bottom, there are three buttons: 'Save', 'Load', and 'Set'.

Boundaries

cm 1 10

Ra 30 3000

g\_pas 1e-05 0.001

Save Load Set

Press 'Set'.

Start the optimization pressing the 'Run' button.