

## Summary of example:

The data trace was obtained from a biophysically accurate reconstruction of a CA1 layer pyramidal cell, by stimulating the somatic section with a 200 pA current stimuli. The experiment lasted for 1000 ms and the stimuli started at 200 ms and lasted for 600 ms (ended at 800 ms). The sampling frequency was 5kHz.

WARNING: the data is given in V not in mV

The model was created by clusterizing the branches of the detailed model into 6 compartments, the parameter values of the channels were obtained by averaging the values in the detailed model.

The somatic parameters are the subjects of optimization.

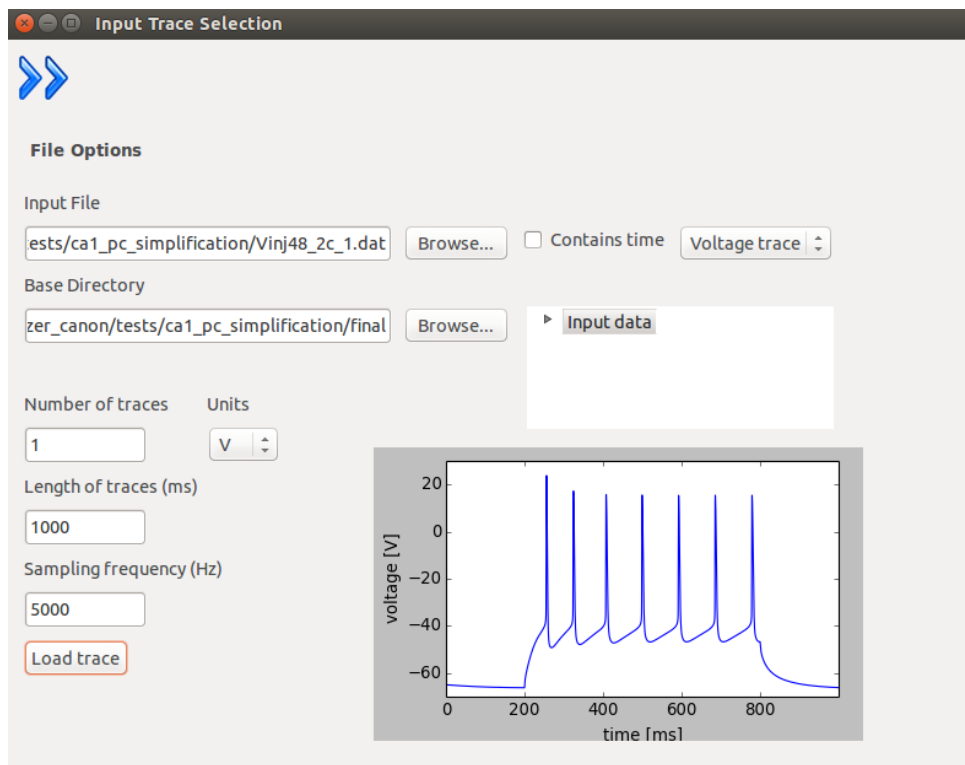
The additional mechanisms required by the model are in the mod\_files folder. You must run the `nrnivmodl` command to obtain the necessary files (you should select the folder containing the files obtained by `nrnivmodl` as the special folder in the program)

input file: Vinj48\_2c\_1.dat

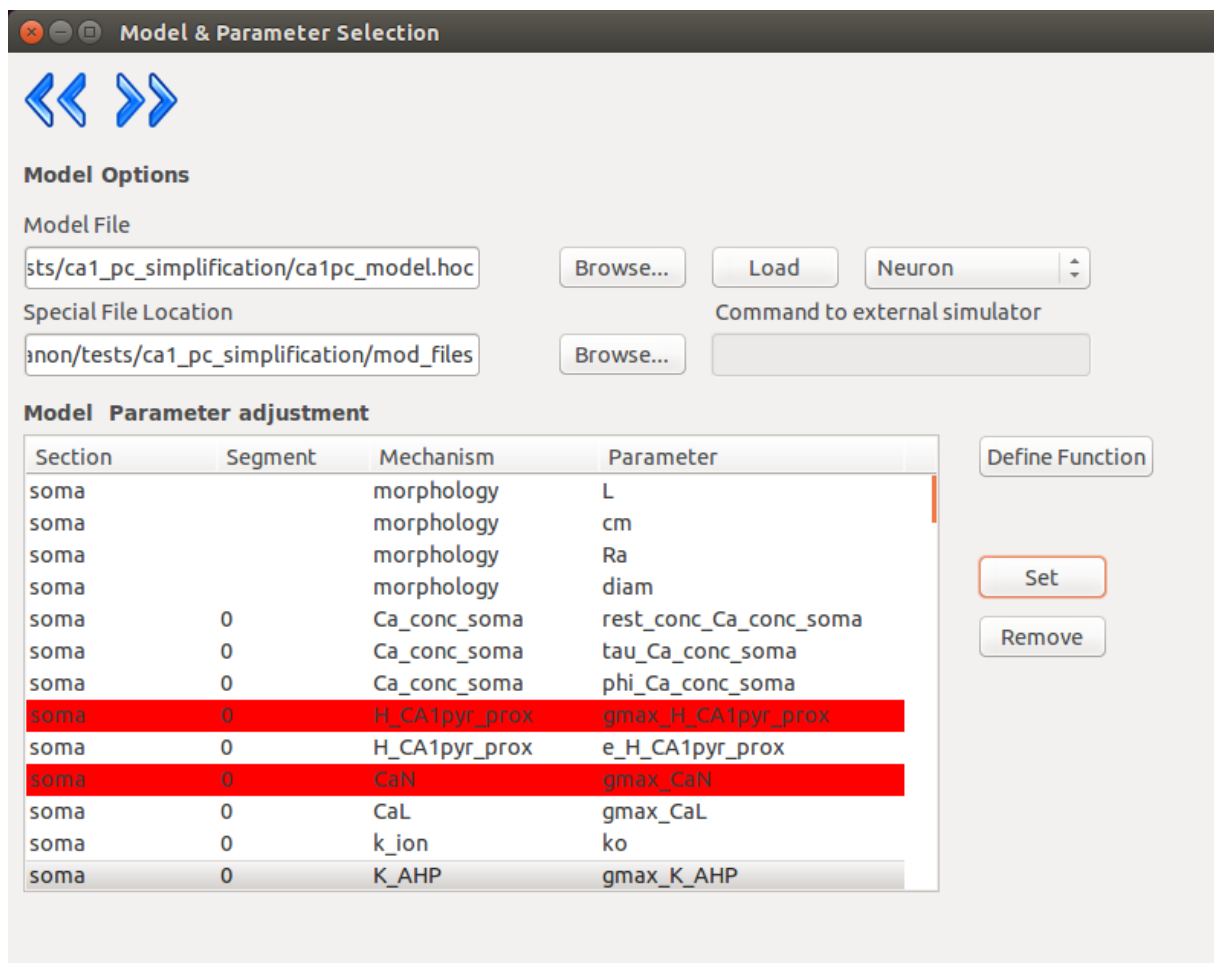
model: ca1pc\_model.hoc

## 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 to the directory containing the mod files, then load the model. To select a parameter click first on the parameter, then press 'Set'. Repeat it to select a new parameter.

Select the following parameters:

soma 0 H\_CA1pyr\_prox gmax\_H\_CA1pyr\_prox

soma 0 CaN gmax\_CaN

soma 0 CaL gmax\_CaL

soma 0 K\_AHP gmax\_K\_AHP

soma 0 K\_C\_1D gmax\_K\_C\_1D

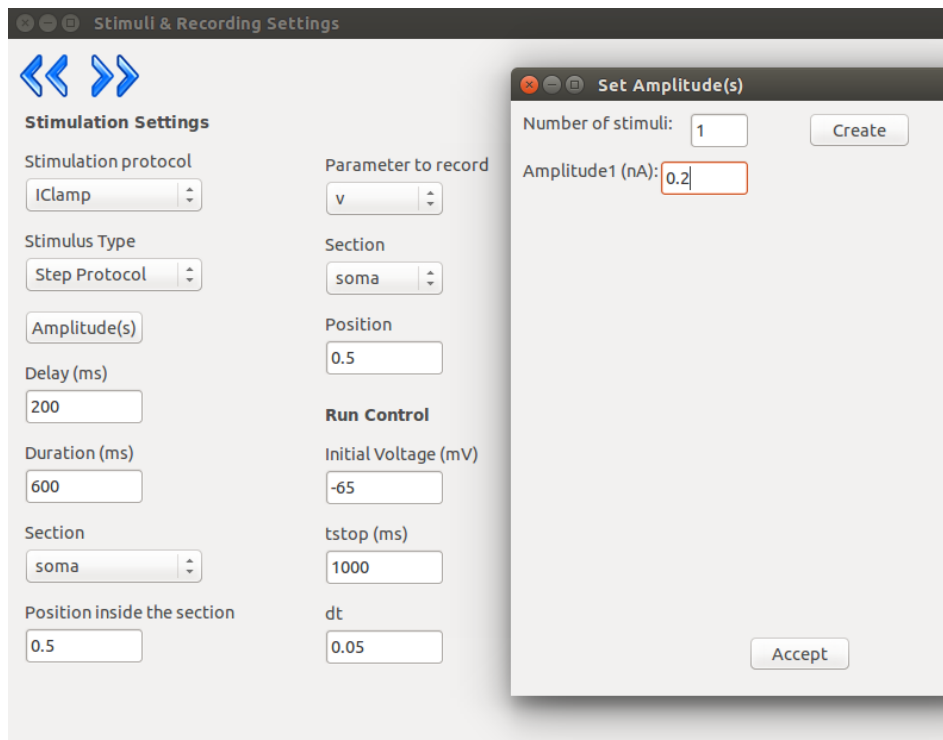
soma 0 K\_M gmax\_K\_M

soma 0 K\_A\_prox gmax\_K\_A\_prox

soma 0 K\_DR gmax\_K\_DR

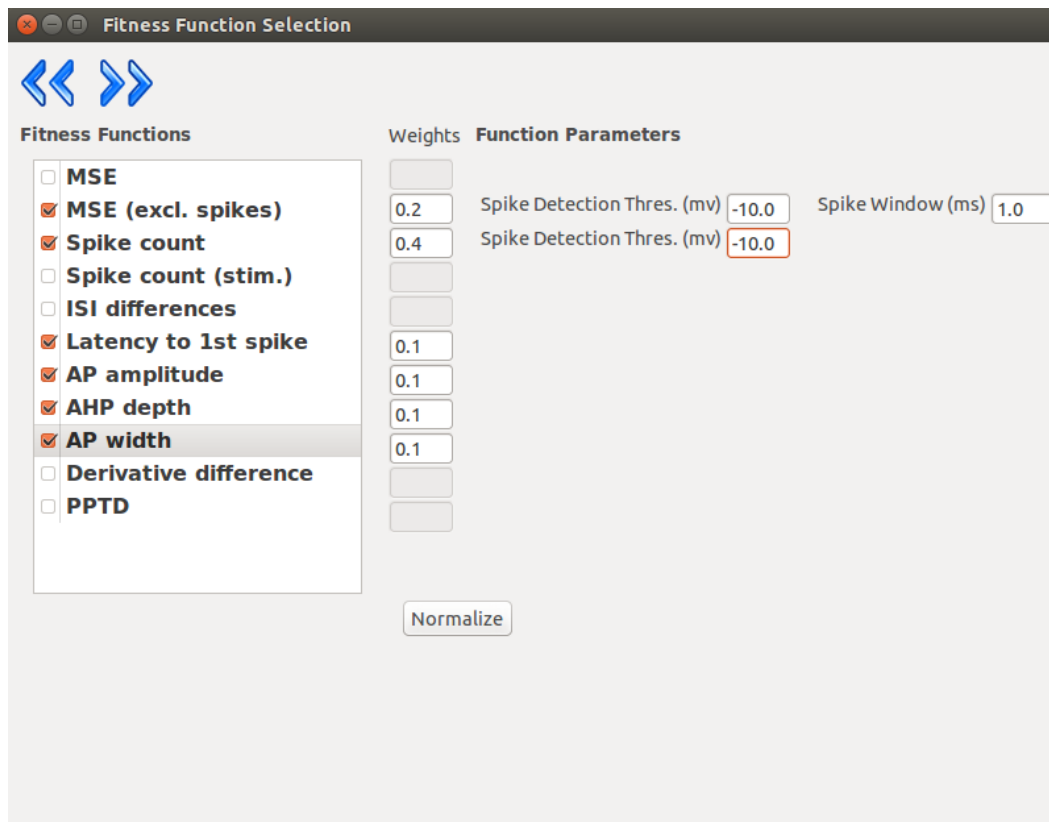
soma 0 Na\_soma gmax\_Na\_soma

Go on by pressing the right arrow.

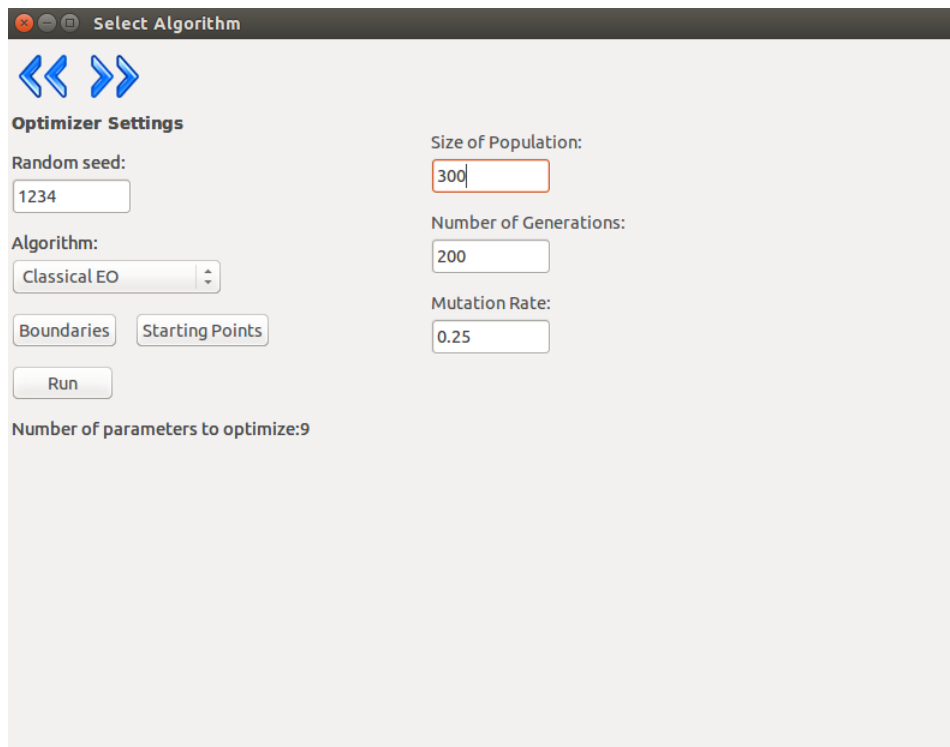


Fill in all the cells. Press 'Amplitude(s)' to open the 'Set Amplitude(s)' window.

Go on by pressing the right arrow



Choose fitness function(s), and define their weights. Go on by pressing the right arrow.



**Select Algorithm**

Optimizers Settings

Random seed: 1234

Algorithm: Classical EO

Boundaries Starting Points

Run

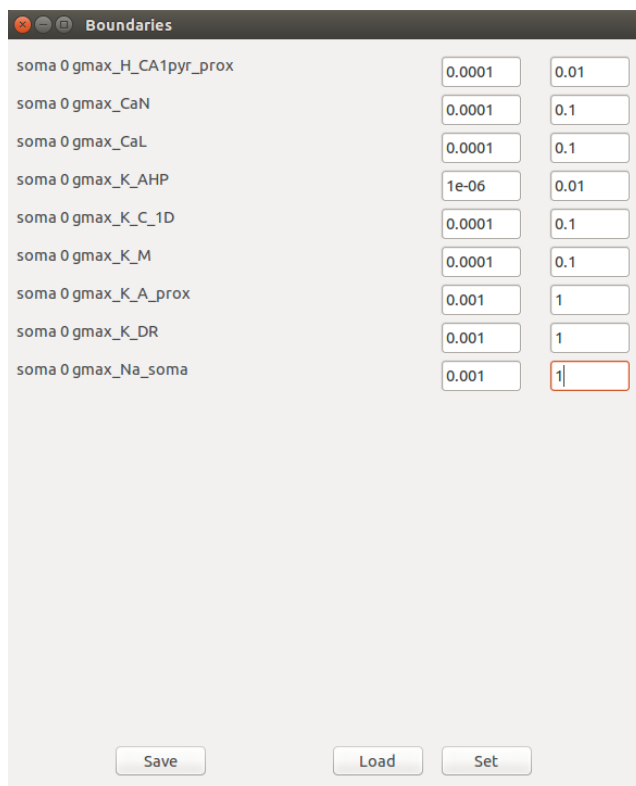
Size of Population: 300

Number of Generations: 200

Mutation Rate: 0.25

Number of parameters to optimize:9

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



**Boundaries**

soma 0 gmax_H_CA1pyr_prox	0.0001	0.01
soma 0 gmax_CaN	0.0001	0.1
soma 0 gmax_CaL	0.0001	0.1
soma 0 gmax_K_AHP	1e-06	0.01
soma 0 gmax_K_C_1D	0.0001	0.1
soma 0 gmax_K_M	0.0001	0.1
soma 0 gmax_K_A_prox	0.001	1
soma 0 gmax_K_DR	0.001	1
soma 0 gmax_Na_soma	0.001	1

Save Load Set

Press 'Set'.

Start the optimization pressing the 'Run' button. Boundaries can also be loaded from a file.