

Summary of example:

The data trace was obtained from a morphologically and biophysically detailed model of a hippocampal CA1 pyramidal cell, by stimulating the somatic section with a 200 pA step current stimulus. 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 clustering the branches of the detailed model based on their voltage responses. The resulting clusters defined the six compartments of the simplified model. The densities of the channels in each dendritic section were obtained by averaging the density values in the corresponding branches of the detailed model. The somatic channel density parameters are the subjects of the optimization.

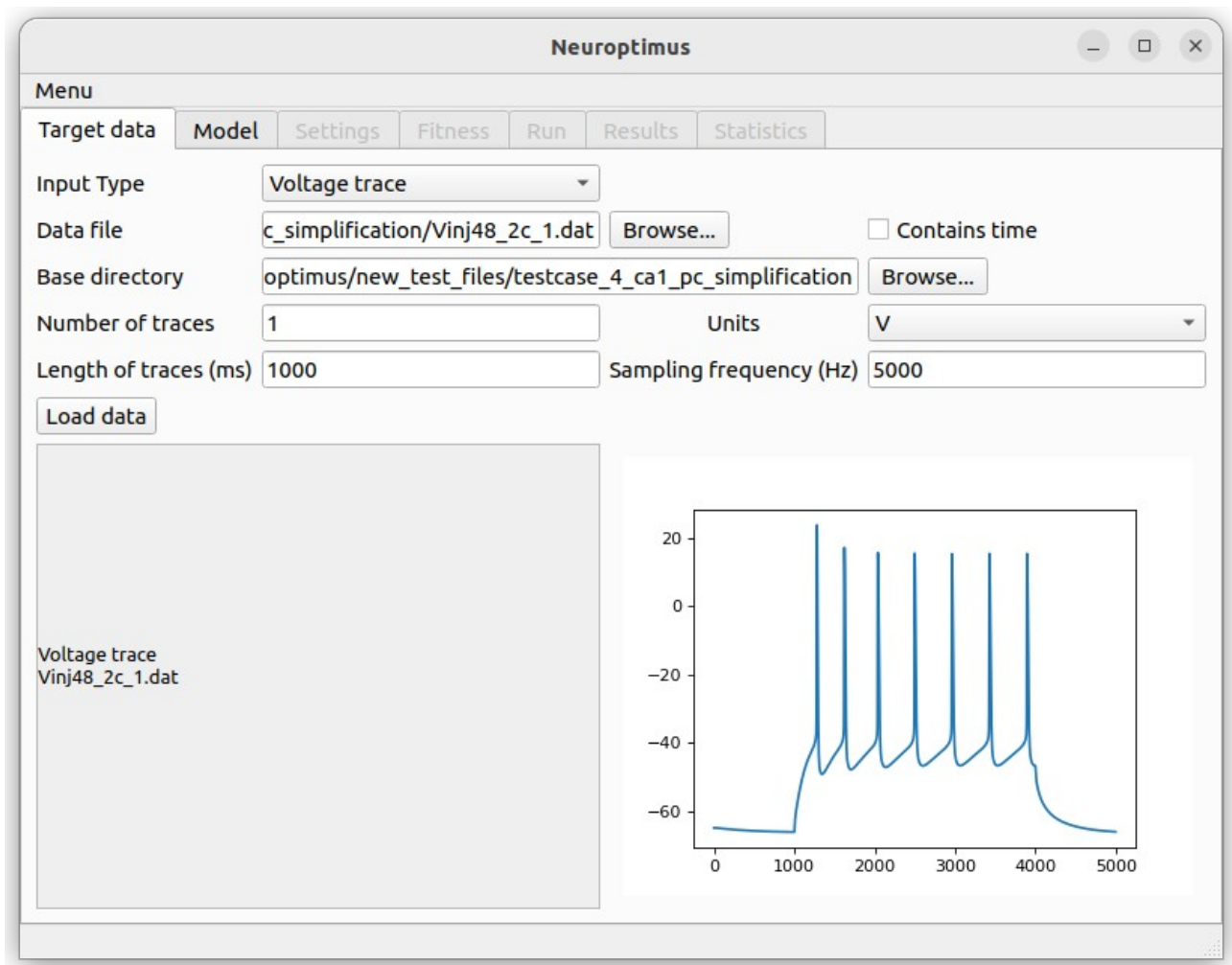
The additional mechanisms required by the model are in the mod_files folder. You must run the 'nrnivmodl' command (which is installed with NEURON) to make the mechanisms available to the simulator.

input file: Vinj48_2c_1.dat

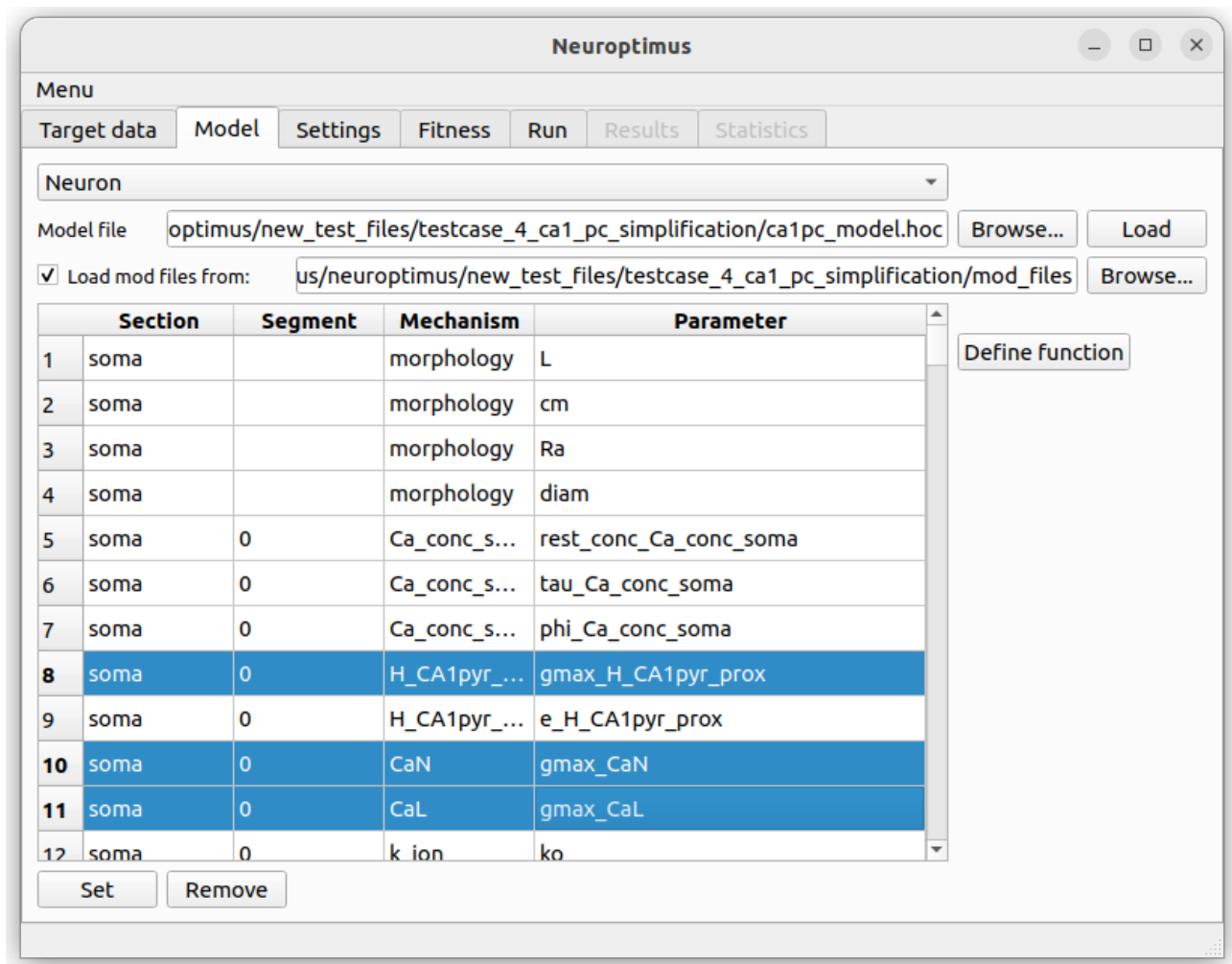
model: ca1pc_model.hoc

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

Run „python3 neuroptimus.py -g” to start the GUI



At 'DataFile' 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 data'. Go on by pressing the Model Tab.



Browse to the model file and load the model.

Check the “Load model files from” box and browse for the mod files directory (you should select the folder where the x86_64 directory and files were created by the nrvmodl), then load the model.

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

Press 'Set'. Go on by pressing the Settings Tab

Neuroptimus

Menu

Target data

Model

Settings

Fitness

Run

Results

Statistics

Stimulation protocol

IClamp

Stimulus Type

Step Protocol

Amplitude(s)

Stimulation Time Settings

Delay (ms)

200

Duration (ms)

600

Stimulus Position Configuration

Section

soma

Position inside section

0.5

Recording Settings

Parameter to record

v

Section

soma

Position inside section

0.5

Simulation Settings

Initial voltage (mV)

-65

tstop (ms)

1000.0

Time step

0.05

Fill in all the cells. Press 'Amplitude(s)' to open a new window. and set the amplitude of the stimulus.

Stimuli Window

Number of stimuli:

1

Create

Amplitude (nA)

1	0.2
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Accept

Neuroptimus

Menu

Target dataModelSettingsFitnessRunResultsStatistics

Normalize

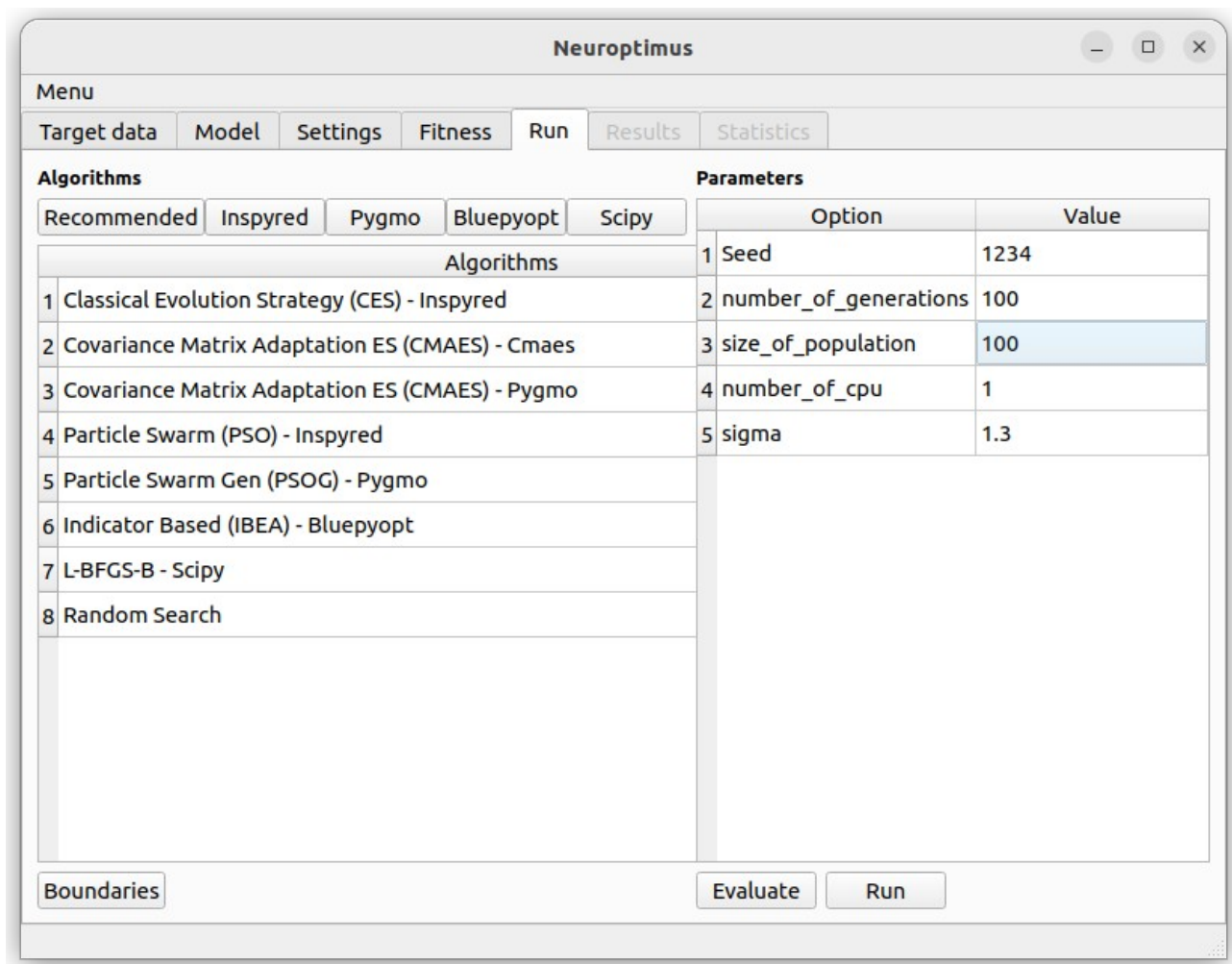
	Fitness functions	Weights
1	MSE	0
2	MSE (excl. spikes)	0.2
3	Spike count	0.4
4	Spike count (stim.)	0
5	ISI differences	0
6	Latency to 1st spike	0.1
7	AP amplitude	0.1
8	AHP depth	0.1
9	AP width	0.1
10	Derivative difference	0

Spike Detection Parameters
Spike detection tresh. (mV)

Spike window (ms)

Go on by pressing the Fitness Tab.

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

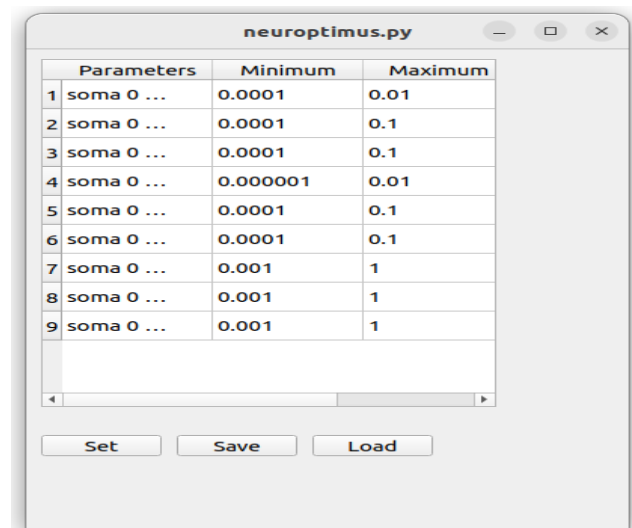


Select an algorithm, and set its parameters.

Press the 'Boundaries' button to define the boundaries of the parameters to be optimized:

Press 'Set'.

Boundaries can also be loaded from a file.



Start the optimization pressing the 'Run' button.