

Summary of example:

The data file has one trace, which is 1000 ms long and the sampling frequency was 40kHz.

The data file also contains the time and was obtained from the corresponding model by using an IClamp (connected to the middle (0.5) of the soma) with the following parameters:

stim.del=200

stim.dur=500

stim.amp=0.2

The following model parameters were set (the others are default):

gnabar_hh=0.1

gkbar_hh=0.03

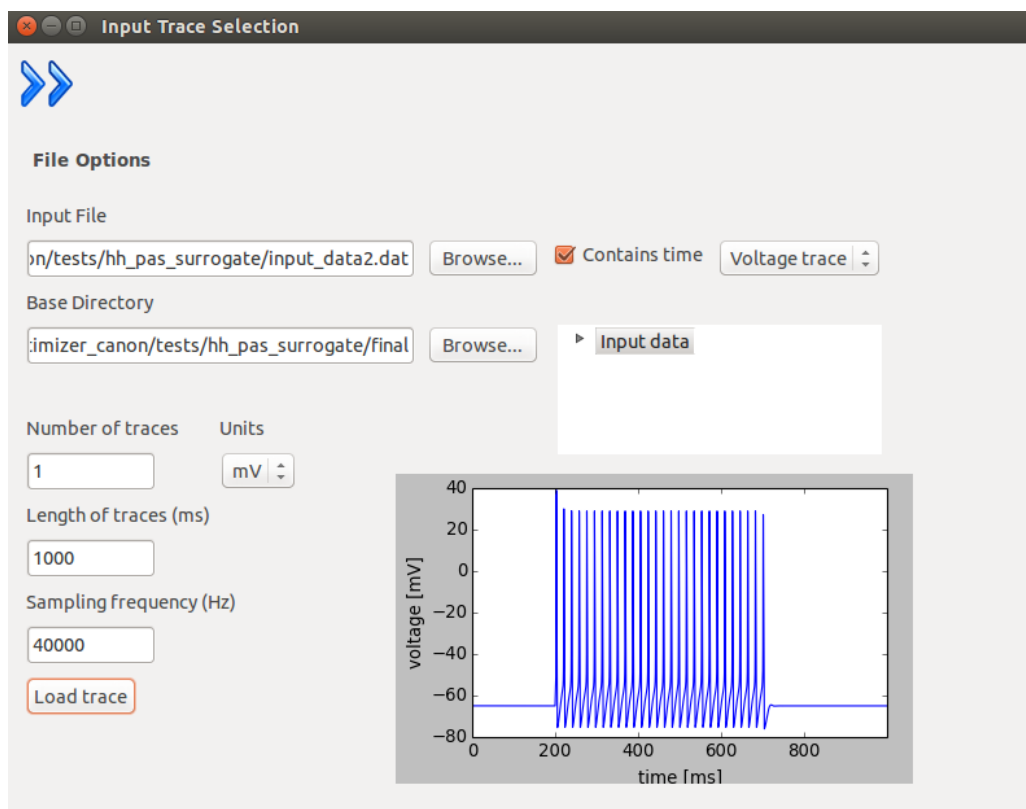
gl_hh=0.0001

input file: "input_data2.dat"

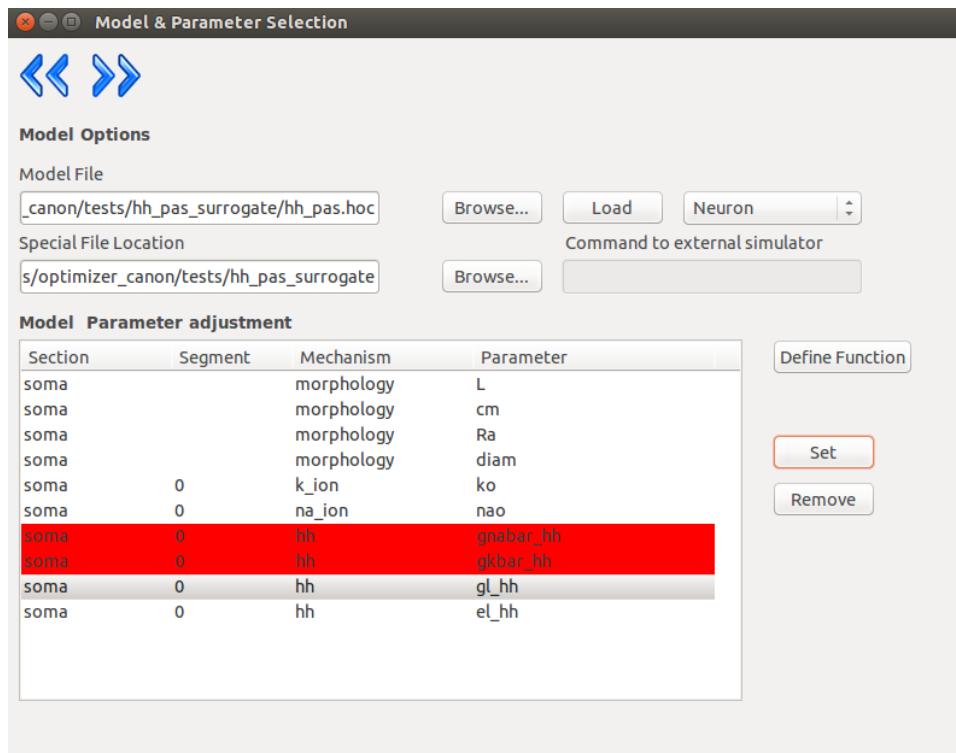
model: hh_pas.hoc

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

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

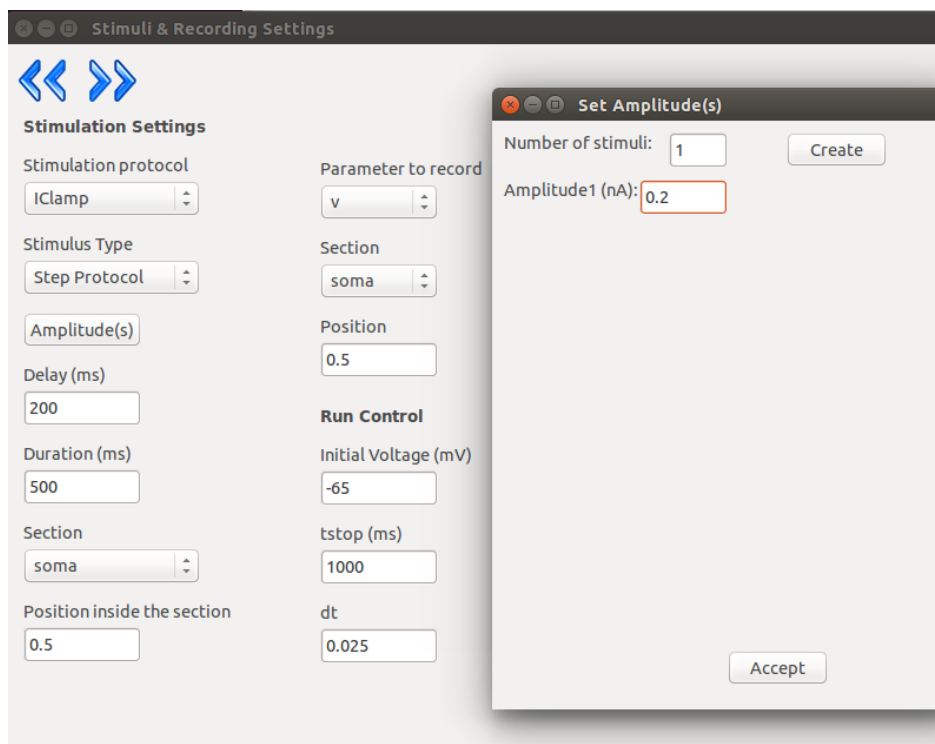


At 'Input File' load the target data, at 'Base Directory' choose the directory where you want to save the results. Fill out all the cells and press 'Load trace'. Go on by pressing the blue arrow.

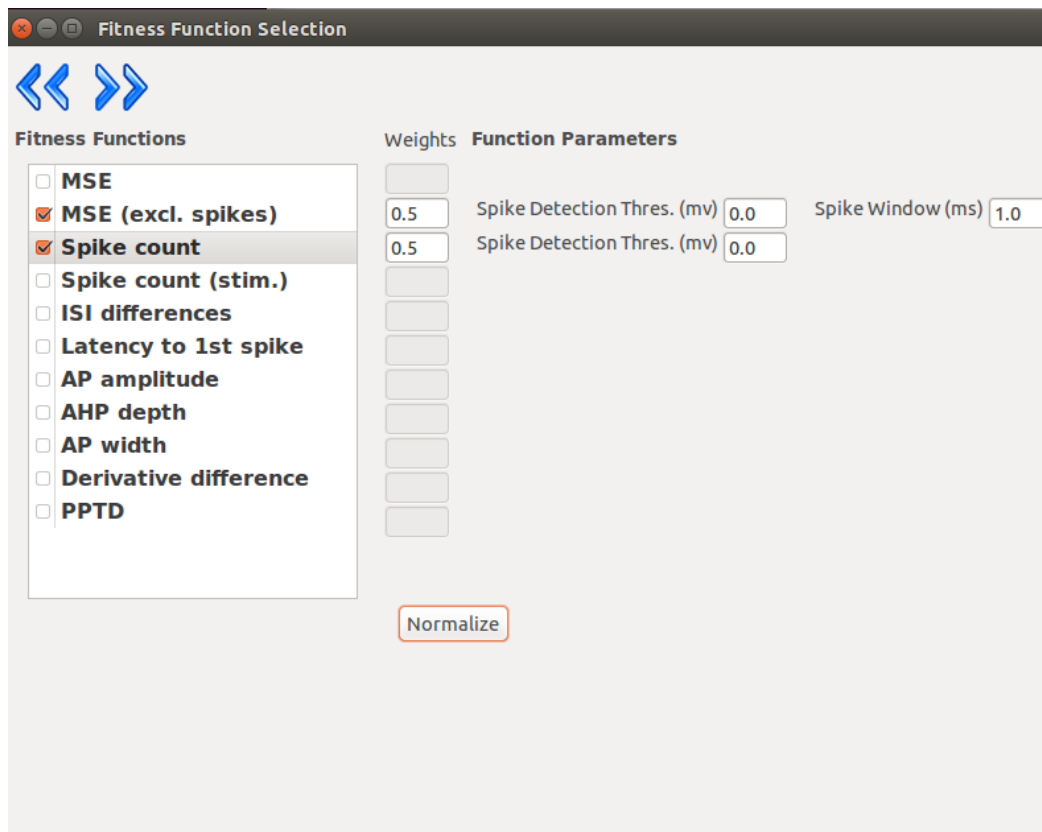


Browse to the model file and load the model. To select a parameter click first on the parameter, then press 'Set'. Repeat it to select a new parameter.

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.

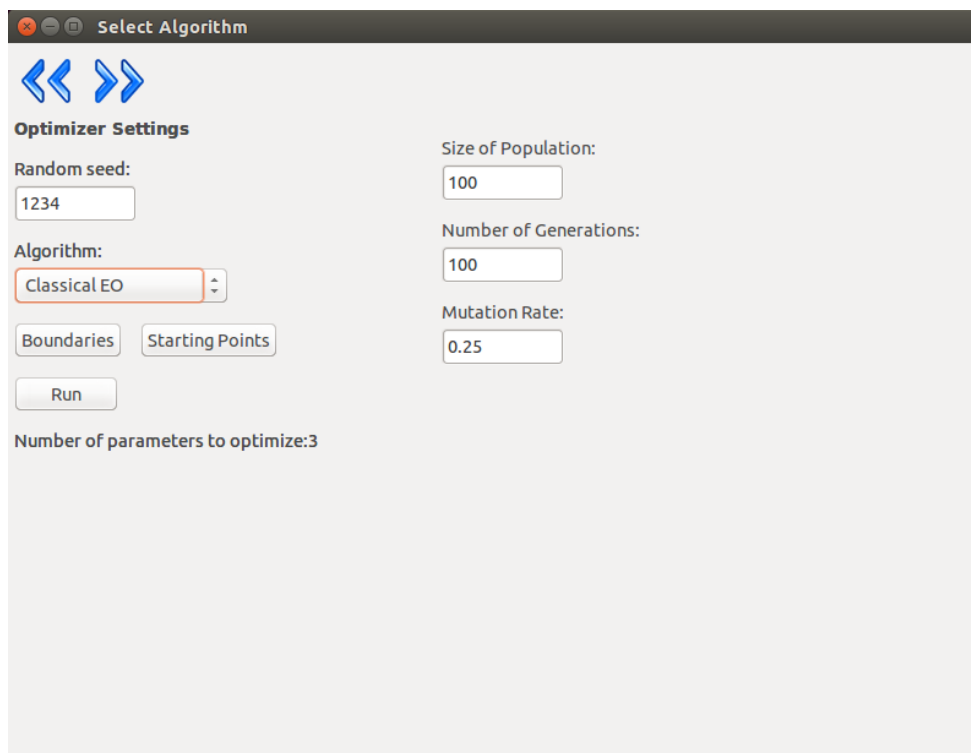


Fitness Function Selection

Navigation: << >>

Fitness Functions	Weights	Function Parameters
<input type="checkbox"/> MSE	<input type="text"/>	
<input checked="" type="checkbox"/> MSE (excl. spikes)	0.5	Spike Detection Thres. (mv) <input type="text" value="0.0"/> Spike Window (ms) <input type="text" value="1.0"/>
<input checked="" type="checkbox"/> Spike count	0.5	Spike Detection Thres. (mv) <input type="text" value="0.0"/>
<input type="checkbox"/> Spike count (stim.)	<input type="text"/>	
<input type="checkbox"/> ISI differences	<input type="text"/>	
<input type="checkbox"/> Latency to 1st spike	<input type="text"/>	
<input type="checkbox"/> AP amplitude	<input type="text"/>	
<input type="checkbox"/> AHP depth	<input type="text"/>	
<input type="checkbox"/> AP width	<input type="text"/>	
<input type="checkbox"/> Derivative difference	<input type="text"/>	
<input type="checkbox"/> PPTD	<input type="text"/>	

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



Select Algorithm

Navigation: << >>

Optimizer Settings

Random seed:

Algorithm:

Size of Population:

Number of Generations:

Mutation Rate:

Number of parameters to optimize: 3

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

×

▢

Boundaries

soma 0 gnabar_hh	<input type="text" value="0.01"/>	<input type="text" value="1"/>
soma 0 gkbar_hh	<input type="text" value="0.01"/>	<input type="text" value="1"/>
soma 0 gl_hh	<input type="text" value="1e-05"/>	<input type="text" value="0.001"/>

Save

Load

Set

Press 'Set'.

Start the optimization pressing the 'Run' button.