

MOEA_EH is the multi objective evolutionary algorithm used to arrive at the models published in:

Hay E, Hill S, Schürmann F, Markram H, Segev I (2011) Models of Neocortical Layer 5b Pyramidal Cells Capturing a Wide Range of Dendritic and Perisomatic Active Properties. PLoS Comput Biol 7(7): e1002107. doi:10.1371/journal.pcbi.1002107

The code is a derivative of the algorithm written by Shaul Druckmann (see Druckmann et al., 2007), and similarly tailored towards the particular goals and needs, rather than being fully generic. Therefore, in most cases I advise modellers to write their own version of the algorithm or use a more generic code than this one.

Basic usage

1. Main executable file: MOEA_parallel_ga.hoc

2. Configuration files:

fit_config.hoc

- Morphology file and path
- Population size
- Number of iterations (MaxGeneration)
- Random seed (BaseSeed)
- Mutation and crossover probabilities

Folder “ConfigFiles”

- Channels used and distribution functions
- Free parameters and their search ranges
- Features and objectives
- Stimuli

Note – I’ve supplied two example configuration folders.

config1 contains the configuration files constraining BAC firing, and config2 contains the configuration files constraining step current firing (corresponding to figures 1 and 2 in Hay et al., 2011, respectively).

Note – for distribution functions format, refer to the function “distribute_channels” in the cell template “GAccl.hoc”, which is in folder “celltypes”.

0 – linear, 1 – sigmoid, 2 - exponential, 3 – step function.

3. GAccl.hoc (in folder celltypes)

The cell template used by the algorithm.

Fixed parameters are written into the “hardcode_biophys” function.

4. Folder “ga_results_seed_1234”

Where the optimization results are stored, every few iterations.

- Clean_population_file.txt - the parameters of the population
- Clean_error_file.txt – the objectives errors of the population
- The order of objectives or parameters is as in the corresponding configuration files