Cerebellum Simulator: 2019

This is a readme file to facilitate use of the enclosed cerebellum simulation. The simulation is written for Visual Basic and therefore runs only on Windows (Windows 7 or higher). This simulation was developed over 27 years, starting in 1992 with code written in C. It was ported to visual basic 6 in 2001. The files here are from the version used for the data and figures of the MLI paper (Halverson et al.).

Source code:

The source code can be viewed from the visual basic IDE or with any text viewer/editor. Most of the source code related to the simulation itself (as opposed to graphics and the GUI) is found in the files ending with .bas.

cbm Main Module 6.bas: This contains the bulk of the code that implements the training trials and time bins during execution.

The code specific to each type of cell is contained in a separate .bas file. These hold the parameters and define variables and arrays related to that cell type. These include:

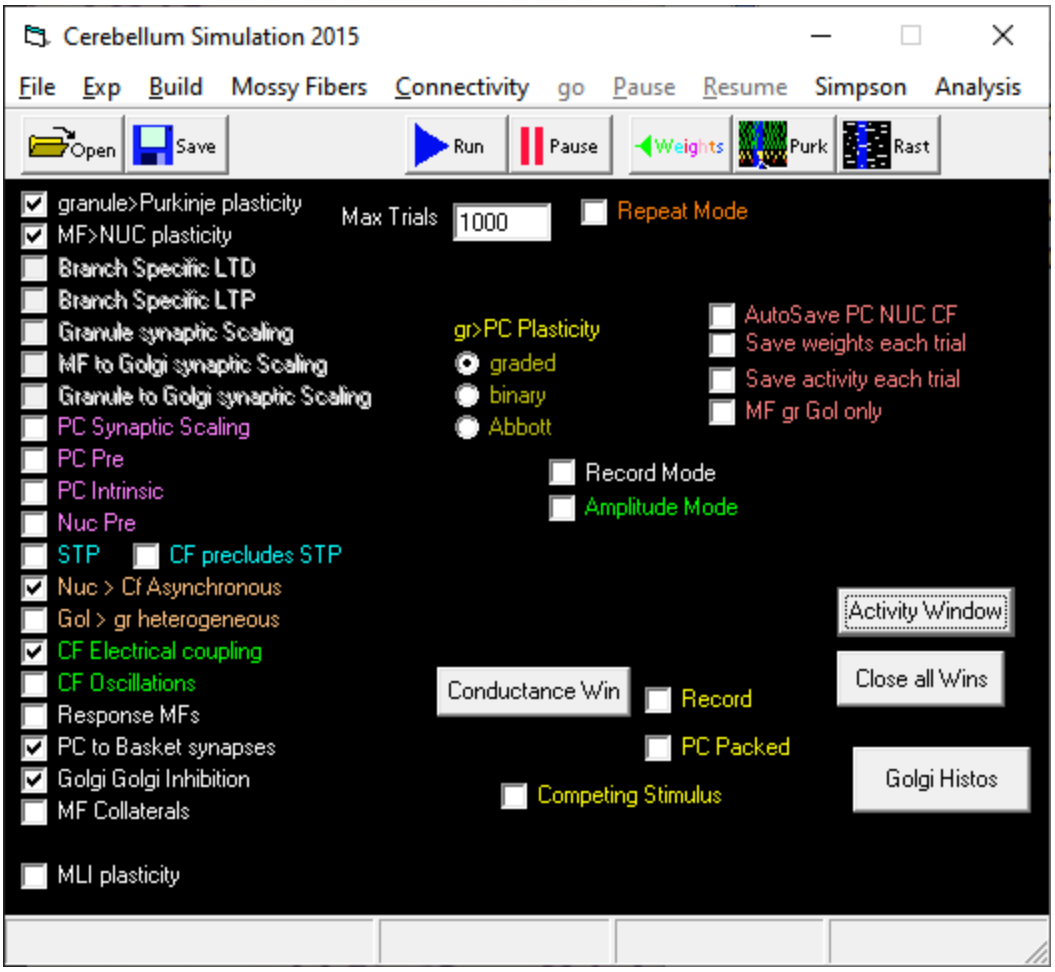
MossyFibers.bas
granule 6.bas
Golgi_cells7.bas
BasketCells.bas
StellateCells.bas
Purkinje_cells6.bas
UBC 6.bas (disabled for the simulations presented in the paper)
Nucleus_cells 6.bas
Climbing_fibers 6.bas

There are files that contain important supporting defines and functions:

SynGenesis7.bas (Contains the function that uses specified rules to wire the entire network)
Connectivity_defines.bas (constants and variables related to wiring the network)
Diagnostic_variables.bas (contains many of the support variables for graphics and saving data)
Histograms.bas (Variables and defines used to store PSTHs)
Plasticity_variables 6.bas (constants and defines for plasticity at gr>PC and MF>DCN synapses

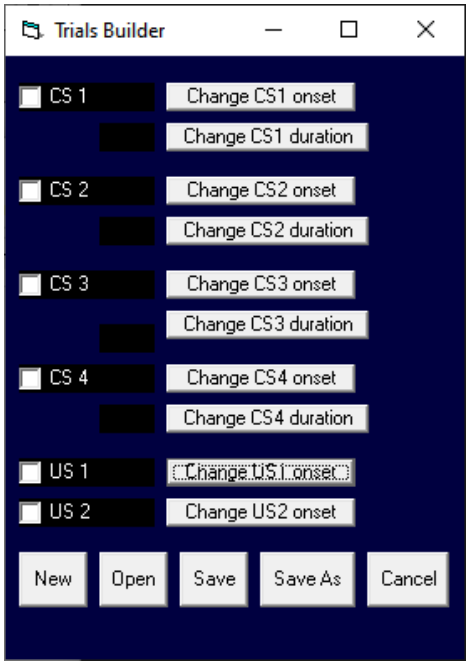
Quick start:

To run the simulation, launch one of the cbm2019X.exe files. This will display a small GUI window that can be used to set up sims, launch/pause them, as well as to control a variety of graphics that are available.



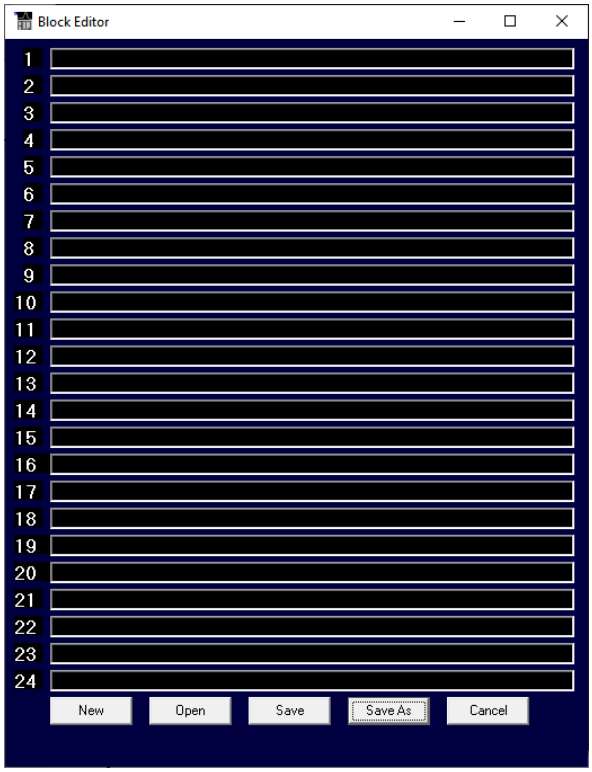
Steps to run the simulations.

1) Set up a training experiment. This involves building training trial(s), building blocks (which are lists of trials), building sessions (which are lists of blocks) and building experiments (which are lists of sessions). Each of these lists must contain at least one member. The total number of trials in the entire experiment cannot exceed 1000.
    a. Building a sample trial: On the menu bar select Build and “Build Trial” in the pulldown menu. This will open the following window:

b. 

c. To get started select CS 1 and US 1.
    i. Click the Change CS1 onset button and type 200
    ii. Click the Change CS1 duration button and type 750
    iii. Click the Change US1 onset button and type 700
    iv. Click the save button and name it “Delay500Paired”
    v. This will create the following file “Delay500Paired.trl”

d. Close the Trials Builder Window and open the Blocks builder.



e. Double click the text box to the right of 1, and a file chooser window will appear. Select the just-created Delay500Paired.trl file. Eight more identical trials can be included by clicking the numeral below the last trial on the list. This adds the same trial to the next box. Once 9 trials are indicated, Click save and call the file "Delay500Paired" which will create a Delay500Paired.blc file.
f. Close this file and now open the sessions builder. Follow the same steps to make a session with 10-12 of the just-created block files. Save this as Delay500 (which creates Delay500.ses file).
g. One more time, open the experiment builder and add at least one instance of the just-created session file, but no more than 9 of them as this would exceed the 1000 trials limit. Save this file as Delay500 to create the Delay500.exp file that will be used to run the simulation.

2) Now to run a simulation requires either Building a New simulation or opening a previously-saved file. As this will be your first simulation, now select File from the menu bar and select "Build New Simulation". Click the Build button at the top as the default simulation is what you will want.
3) Now select "exp" from the main menu bar and select the Delay500 experiment file you just created. After this another file chooser will appear, this is asking for the root filename that will be used for all of the data files generated during the run. Here, just type test01 or something of the sort.
4) Click Run in the tool bar to start the simulation, and Pause to pause it.

Visualization:

PC activity: By default, the PC activity window is open. It shows real-time activity of the Purkinje cells, cerebellar nucleus (output) cells and the climbing fibers. Each sweep is 5000 time bins, or five simulated seconds. For each sweep, the time when the CS is presented is indicated by the light blue rectangle. Along the very bottom of this window there is a white trace. This is the predicted eyelid response given the activity of the cerebellar nucleus neurons.

Rasters: Click the Rast button in the tool bar to show a large raster window. The default mode of this window is to show real-time raster activity for granule cells 1-1000. Again, the CS is indicated by the light blue rectangle each sweep. There are many modes with this window. Use the cell type pulldown menu to select a cell type other than granule cells (Basket cells here are the PC MLIs, whereas the Stellate cells are the non-PC MLIs). Click mode in the menu bar to change the nature of the display. The most useful option here is the bottom one, "cumulative activity during CS only". Here the non-CS times are the same real-time rasters. During the CS period the coding is a gray scale PSTH where white means highest activity.

Recreating experiments from paper:

Various options on the main GUI will allow you to turn on and off various features to recreate the simulations used for the paper. These are:

1) MF collaterals. This options makes the indicated percentage of the mossy fiber inputs into DCN collaterals that fire spike for spike with one of the DCN output neurons. This was used in the paper to see whether MLI activity that is highly correlated on a trial by trial basis with the eyelid CRs can be explained by these inputs (it can't).
2) MLI plasticity. Here, the granule to PC-MLI synapses undergo climbing fiber controlled plasticity. This too was used to test whether this plasticity could explain the high correlation between PC-MLI activity and the eyelid CRs (the correlation is equally high with or without this plasticity).
3) PC to Basket synapses. This can be used to turn off the PC to MLI synapses that are the subject of the paper. All correlations between PC MLI activity and eyelid responses disappears without this connection.
4) There are many other options, most relate to previously published work from this lab.
5) Click the Record check box to tell the simulation to save PSTHs for the run (this will slow down the simulation considerably, but can be used for offline analyses of each cell type's activity.