

Mesoscopic model of size dynamics

Hazan L, Ziv NE (2020) Activity dependent and independent determinants of synaptic size diversity. J Neuroscience (in press)

The model, written in C as a Win32 console application, is provided as two source files and two header files:

- Sim dynamics and FRAP.c
- rand.c
- standard.h
- rand.h

The latter 3 files are part of the cryptographic random number generator ISAAC (Indirection, Shift, Accumulate, Add, and Count)
<http://burtleburtle.net/bob/rand/isaacafa.html>)

Used here to generate streams of pseudorandom numbers

The code was compiled and run using Visual Studio 2017

To compile using Visual C++:

- 1) Create a new project (File-->New-->Project...)
- 2) Create a Visual C++, Empty Project
- 3) Add the four files to the project as Source Files and Header Files, respectively using the Solution Explorer
- 4) Compile and run

Two tab delimited text files are generated:

- 1) Synapse size trajectories for all synapses (rows) at all simulated time steps (columns). Synapse size is defined as the momentary # of molecules bound to the synapse's matrix
- 2) # of bound 'fluorescent' molecules for the 'photobleached' synapses (rows) at all simulated time steps (columns) starting at the photobleaching time step

All parameters and output file names are 'hardwired' into the code.

To modify these, edit the definitions at the top of the file "Sim dynamics and FRAP.c"

MATRIXDIM	Matrix dimension (matrix size will be MATRIXDIM x MATRIXDIM)
N_SYNAPSES	Number of synapses (matrices) that will be simulated
STEPS	Number of simulation steps to run
P_ON	Maximal On rate (scales with # of free molecules)
P_OFF	Maximal Off rate
ALPHA	Non-specific binding rate (scales with # of free molecules)
TOTAL_MOLECULES	Total amount of scaffold molecules in the 'cell'
FRAP_CYCLE	Simulation cycle at which 'photobleaching' will occur
FRAP_SYNAPSES	Number of synapses to photobleach
OUTPUTFILENAME	Full path to simulation output file
FRAPOUTPUTFILENAME	Full path to FRAP data output file