



Workshop Series Summer 2023

CAM BAM

Centre for Applied Mathematics  
in Bioscience and Medicine

June 16<sup>th</sup>, 2023

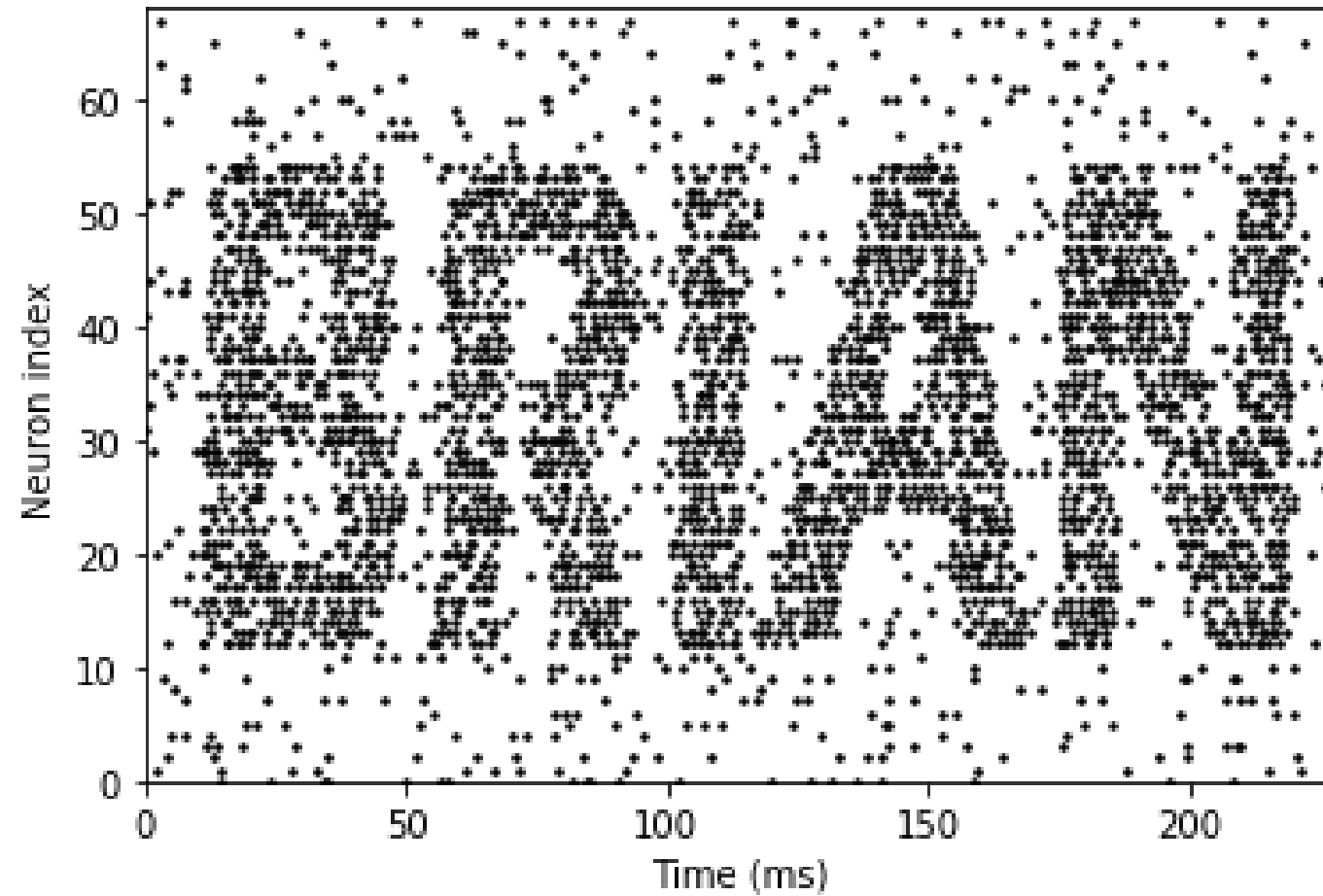
# **Exploring Single Neuron Excitability with Mathematical and Computational Models**

By Niklas Brake and Nils Koch

Lecture 3: Model Fitting and Brian2

# Part 3: Brian2

# BRIAN



<https://brian2.readthedocs.io>



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# Part 3: Brian2



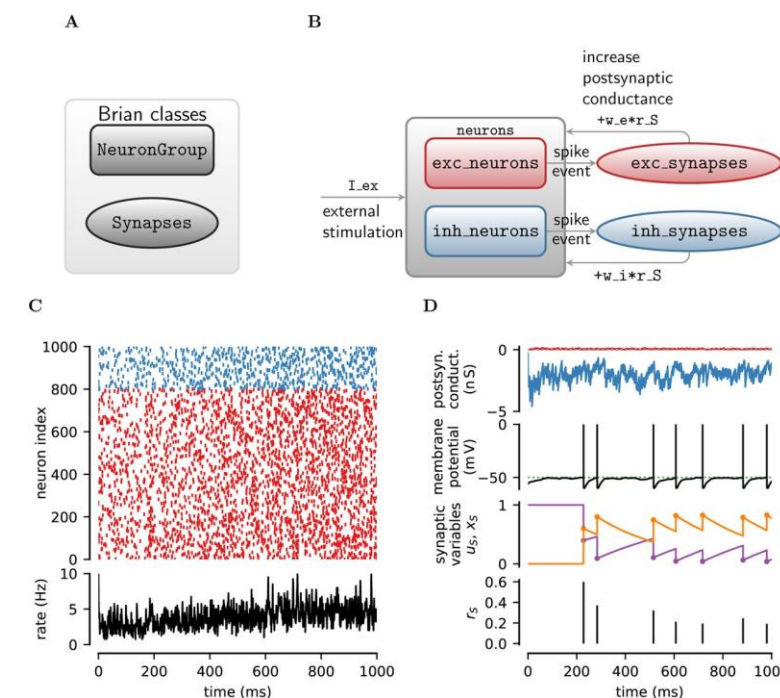
<https://briansimulator.org/>

<https://brian2.readthedocs.io>

## Brian2

Free, open-source Python simulator for spiking neural network

- Easy to use
  - Easy to understand syntax to define, run and plot neural models in just a few lines of code
- Flexible
  - Any model: write equations in standard mathematical notation and run
- Performance
  - Automatically converting your equations into low level C++ code, compiling and running
- Reliable
  - widely used: <https://briansimulator.org/papers-using-brian/>



Marcel Stimberg, Dan F. M. Goodman, Romain Brette, Maurizio De Pittà.  
Modeling neuron–glia interactions with the *Brian 2* simulator. bioRxiv 198366



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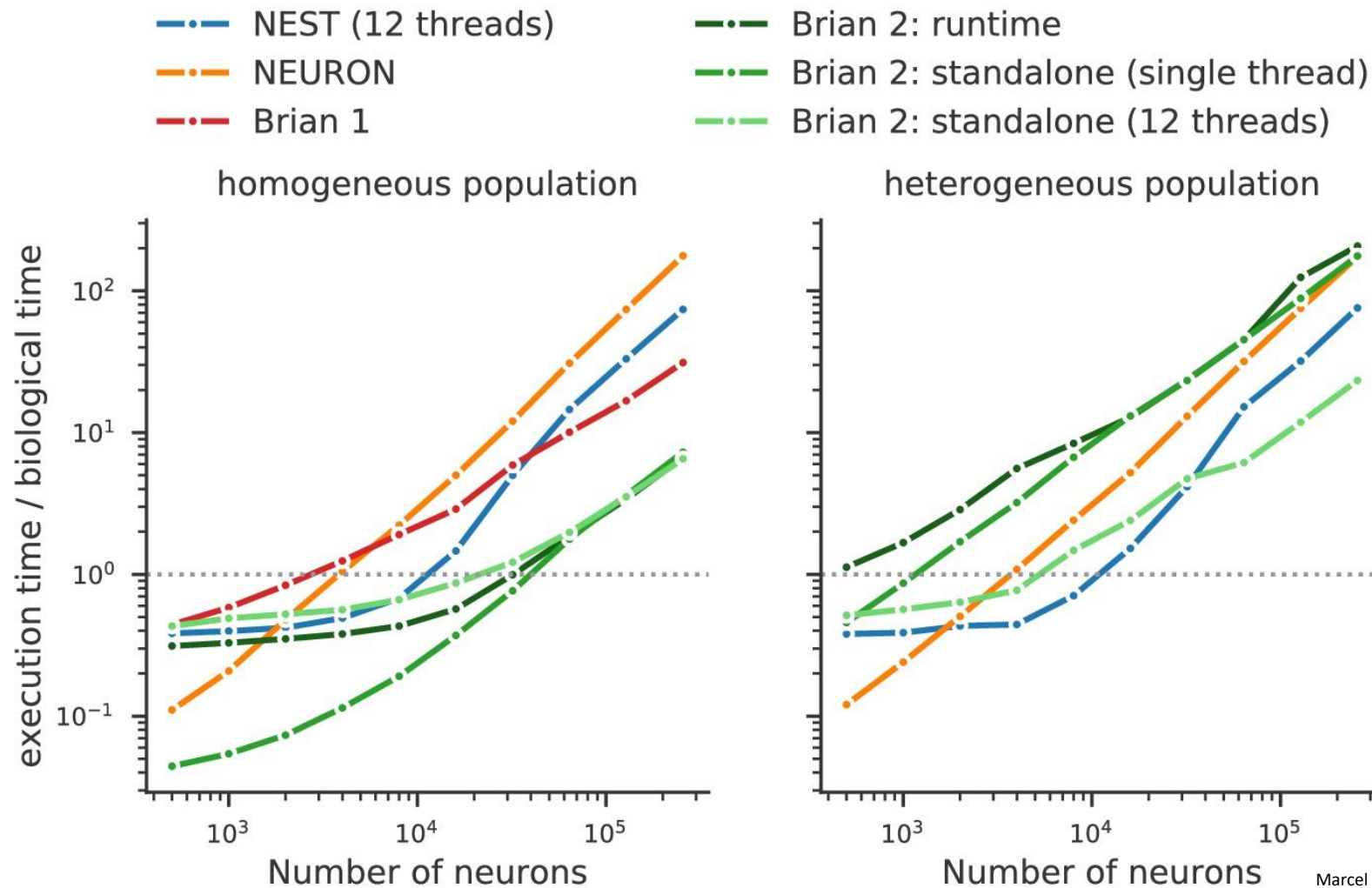
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# Part 3: Brian2



Marcel Stimberg, Romain Brette, Dan FM Goodman (2019) Brian 2, an intuitive and efficient neural simulator eLife 8:e47314

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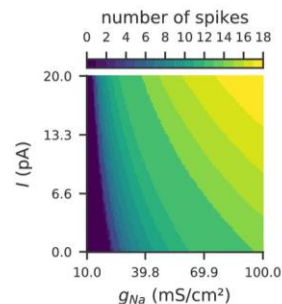
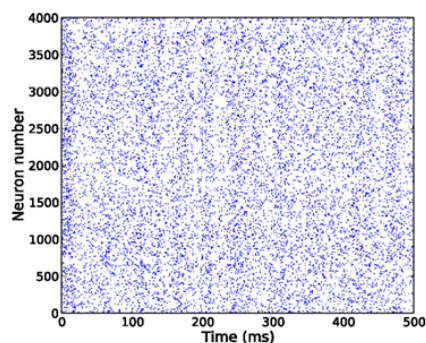
# Part 3: Brian2



```
from brian import *
eqs = '''
dV/dt = (g+g_i-(V+49*mV))/(20*ms) : volt
dge/dt = -ge/(5*ms) : volt
dgi/dt = -gi/(10*ms) : volt
'''

P = NeuronGroup(4000, model=eqs,
                threshold=-50*mV, reset=-60*mV)
Pe = P.subgroup(3200)
Pi = P.subgroup(800)
Ce = Connection(Pe, P, 'ge')
Ci = Connection(Pi, P, 'gi')
Ce.connect_random(Pe, P, p=0.02,
                  weight=1.62*mV)
Ci.connect_random(Pi, P, p=0.02,
                  weight=-9*mV)

M = SpikeMonitor(P)
P.V = -60*mV+10*mV*rand(len(P))
run(.5*second)
raster_plot(M)
show()
```



(b)

```
from brian2 import *
import brian2genn
set_device('genn')

# HH model with injected current
area = 20000*umetre**2; Cm = (1*ufarad*cm**2) * area;
gl = (5e-5*siemens*cm**2) * area; EI = -60*mV; EK = -90*mV; ENa = 50*mV;
g_kd = (30*msiemens*cm**2) * area; VT = -63*mV
eqs = Equations('''
dv/dt = (gl*(EI-v)- g_na*(m*m)*h*(v-ENa)- g_kd*(n*n*n*n)*(v-EK) + I)/Cm : volt
dm/dt = alpha_m*(1-m)-beta_m*m : 1
dn/dt = alpha_n*(1-n)-beta_n*n : 1
dh/dt = alpha_h*(1-h)-beta_h*h : 1
alpha_m = 0.32*(mV**1)*(13*mV-v+VT)/ (exp((13*mV-v+VT)/(4*mV))-1)/ms : Hz
beta_m = 0.28*(mV**1)*(v-VT-40*mV)/ (exp((v-VT-40*mV)/(5*mV))-1)/ms : Hz
alpha_h = 0.128*exp((17*mV-v+VT)/(18*mV))/ms : Hz
beta_h = 4./(1+exp((40*mV-v+VT)/(5*mV)))/ms : Hz
alpha_n = 0.032*(mV**1)*(15*mV-v+VT)/ (exp((15*mV-v+VT)/(5*mV))-1)/ms : Hz
beta_n = .5*exp((10*mV-v+VT)/(40*mV))/ms : Hz
I : amp (constant)
g_na : siemens (constant)
''')

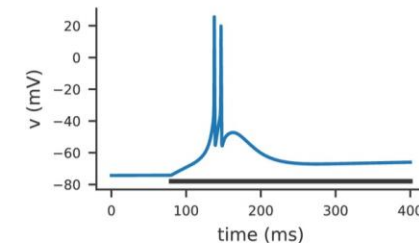
# Explore 300 * 300 values
g_na_values, I_values = np.linspace(10, 100, num=300), np.linspace(0, 20, num=300)
neuron = NeuronGroup(len(g_na_values)*len(I_values), eqs, method='exponential_euler',
                    threshold='v>-20*mV', refractory='v>-20*mV')

neuron.v = EI
spike_mon = SpikeMonitor(neuron)
all_g_na_values, all_I_values = np.meshgrid(g_na_values, I_values)
all_g_na_values, all_I_values = all_g_na_values.flat[:], all_I_values.flat[:]
neuron.g_na, neuron.I = all_g_na_values*msiemens*cm**2 * area, all_I_values*pA

run(1*second)
```

Simulation time

Brian 2 (single thread)	109.8s
Brian 2 (12 threads)	11.8s
Brian2Genn (GPU)	2.4s



(b)

```
# Constants
EI = -76.5*mV; ENa = 50*mV; EK = -100*mV
# ...
eqs = Equations('''
Im = gl*(EI-v) - I_Na - I_K - I_T : amp/meter**2
I_inj : amp (point current)
''')

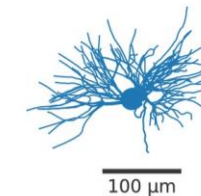
# HH-type currents for spike initiation
g_Na : siemens/meter**2
I_Na = g_Na * m**3 * h * (v-ENa) : amp/meter**2
v2 = v - VT : volt # shifted membrane potential (Traub convention)
dm/dt = (0.32*(mV**1)*(13.*mV-v2)/
        (exp((13.*mV-v2)/(4.*mV))-1.)*(1-m)-0.28*(mV**1)*(v2-40.*mV)/
        (exp((v2-40.*mV)/(5.*mV))-1.)*m) / ms * tadj_HH : 1
# ...
''')

# Load morphology from SWC file
morpho = Morphology.from_file('tc200.CNG.swc')
neuron = SpatialNeuron(morpho, eqs, Cm=0.88*uF/cm**2, Ri=173*ohm*cm,
                      method='exponential_euler')

# Only the soma has Na/K channels
neuron.main.g_Na = 100*msiemens/cm**2
neuron.main.g_K = 100*msiemens/cm**2
neuron.P_Ca = 1.7e-5/cm/second

# Distal dendrites
neuron.P_Ca['(distance + length/2) > 11*um'] = 8.5e-5/cm/second
neuron.v = -74*mV
neuron.m_T = 'm_T_inf'
neuron.h_T = 'h_T_inf'

mon = StateMonitor(neuron, ['v'], record=morpho[0]) # Record at soma
```



Goodman, Dan & Brette, Romain. (2008). Brian: A Simulator for Spiking Neural Networks in Python. Frontiers in neuroinformatics. 2. 5. 10.3389/neuro.11.005.2008.

Marcel Stimberg, Romain Brette, Dan FM Goodman (2019) Brian 2, an intuitive and efficient neural simulator eLife 8:e47314

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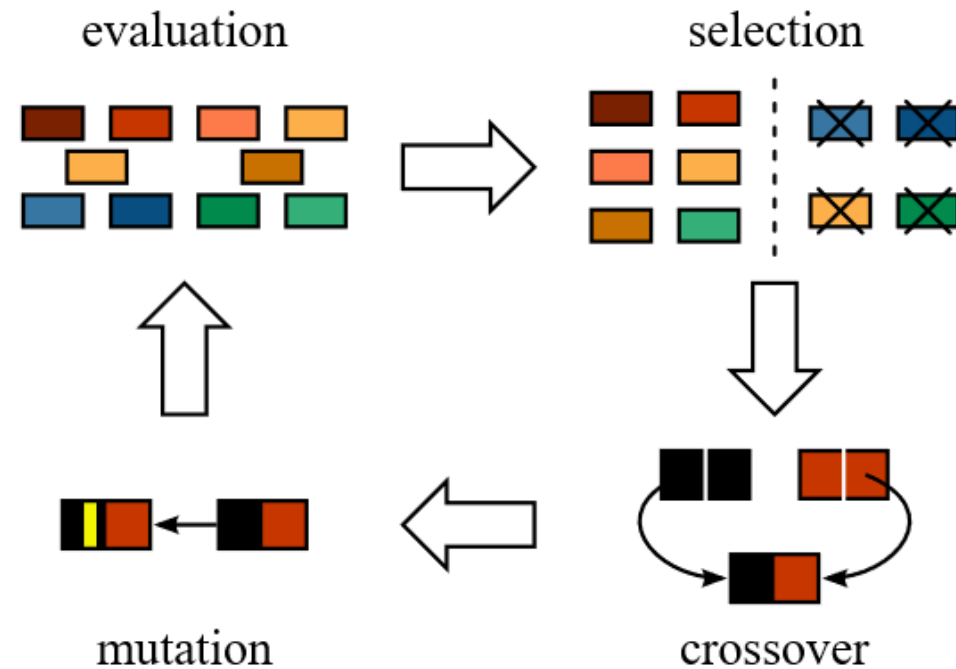
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- Many different optimization algorithms and packages
  - PyGAD



<https://www.electricalibrary.com/en/2018/04/13/what-is-genetic-algorithm/>

**Break: 15:00 – 15:15**



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