Brian Documentation

Release 1.0.0

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CONTENTS

The manual for Brian is not yet entirely complete, we are working on filling in the gaps signposted 'TODO'. See also the automatically generated API documentation and the reference sheet. You can also download a PDF version of the documentation here.

CHAPTER

ONE

Introduction

Brian is a clock driven simulator for spiking neural networks, written in the Python programming language.

The simulator is written almost entirely in Python. The idea is that it can be used at various levels of abstraction without the steep learning curve of software like Neuron, where you have to learn their own programming language to extend their models. As a language, Python is well suited to this task because it is easy to learn, well known and supported, and allows a great deal of flexibility in usage and in designing interfaces and abstraction mechanisms. As an interpreted language, and therefore slower than say C++, Python is not the obvious choice for writing a computationally demanding scientific application. However, the SciPy module for Python provides very efficient linear algebra routines, which means that vectorised code can be very fast.

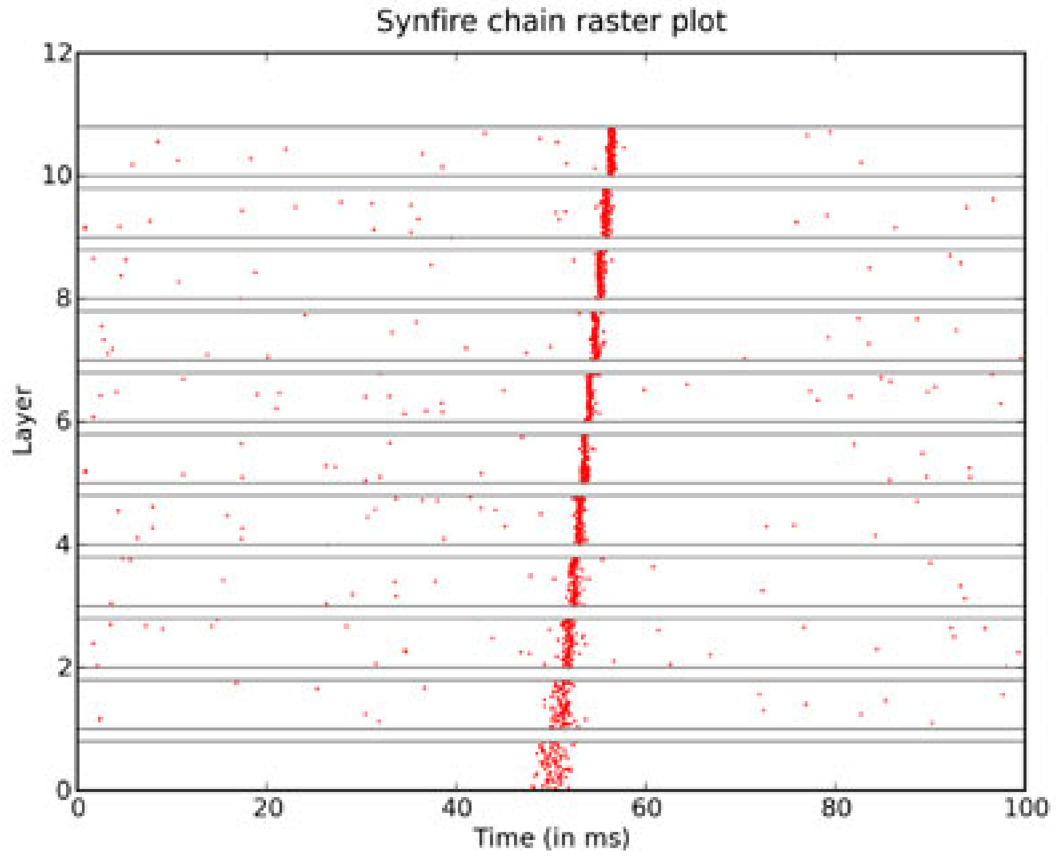
Here's what the Python web site has to say about themselves:

> Python is an easy to learn, powerful programming language. It has efficient high-level data structures and a simple but effective approach to object-oriented programming. Python's elegant syntax and dynamic typing, together with its interpreted nature, make it an ideal language for scripting and rapid application development in many areas on most platforms.
>
> The Python interpreter and the extensive standard library are freely available in source or binary form for all major platforms from the Python Web site, http://www.python.org/, and may be freely distributed. The same site also contains distributions of and pointers to many free third party Python modules, programs and tools, and additional documentation.

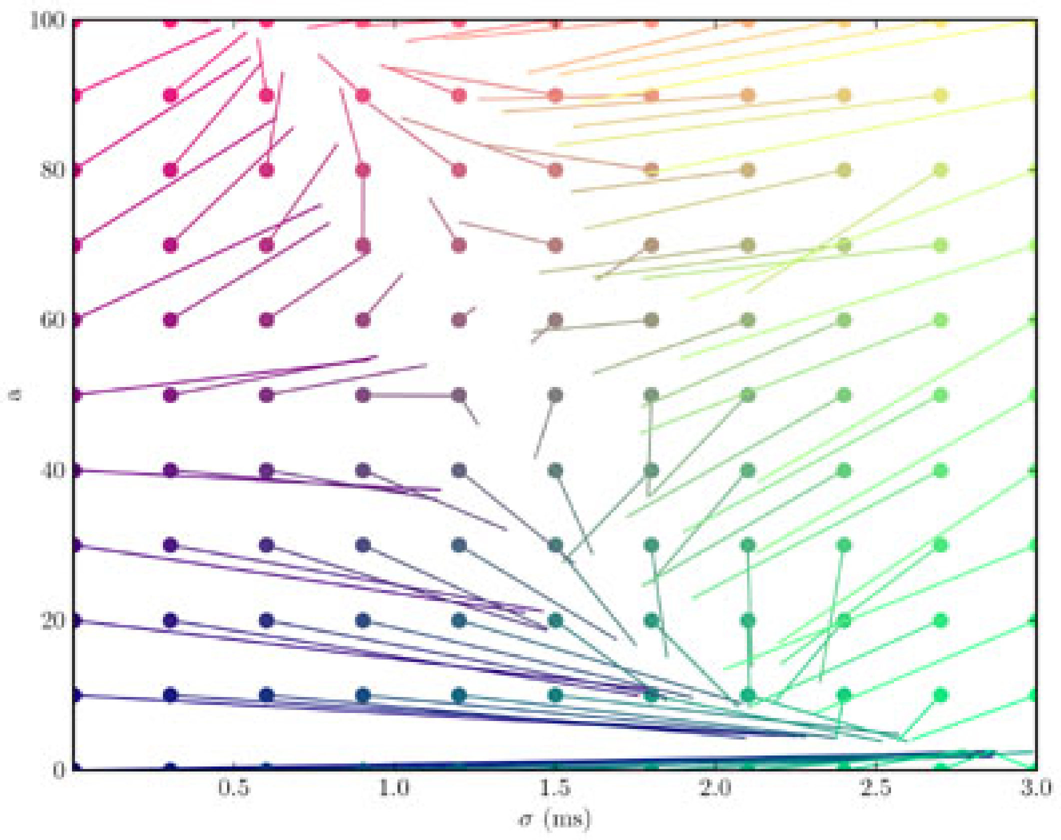
As an example of the ease of use and clarity of programs written in Brian, the following script defines and runs a randomly connected network of 4000 integrate and fire neurons with exponential currents:

```
from brian import *
eqs='''
dv/dt = (ge+gi-(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)
P.v=-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, 0.02,weight=1.62*mV)
Ci.connect_random(Pi, P, 0.02,weight=-9*mV)
M=SpikeMonitor(P,True)
run(1*second)
raster_plot(M)
show()
```

As an example of the output of Brian, the following two images reproduce figures from Diesmann et al. 1999 on synfire chains. The first is a raster plot of a synfire chain showing the stabilisation of the chain.



The simulation of 1000 neurons in 10 layers, each all-to-all connected to the next, using integrate and fire neurons with synaptic noise for 100ms of simulated time took 1 second to run with a timestep of 0.1ms on a 2.4GHz Intel Xeon dual-core processor. The next image is of the state space, figure 3:



The figure computed 50 averages for each of 121 starting points over 100ms at a timestep of 0.1ms and took 201s to run on the same processor as above.

CHAPTER

TWO

Installation

If you already have a copy of Python 2.5 or 2.6, try the Quick installation below, otherwise take a look at Manual installation.

2.1 Quick installation

The easiest way to install Brian if you already have a version of Python 2.5 or 2.6 including the `easy_install` script is to simply run the following in a shell:

```
easy_install brian
```

This will download and install Brian and all its required packages (NumPy, SciPy, etc.).

2.2 Manual installation

Installing Brian requires the following components:

1. Python version 2.5 or 2.6.
2. NumPy and Scipy packages for Python: an efficient scientific library.
3. PyLab package for Python: a plotting library similar to Matlab (see the detailed installation instructions).
4. SymPy package for Python: a library for symbolic mathematics (not mandatory yet for Brian).
5. Brian itself (don't forget to download the extras.zip file, which includes examples, tutorials, and a complete copy of the documentation). Download the latest release: file ending `.win32.exe` for Windows, filenames ending `.tar.gz` or `.zip` for other operating systems. Brian is also a Python package and can be installed as explained below.

Fortunately, Python packages are very quick and easy to install, so the whole process shouldn't take very long.

We also recommend using the following for writing programs in Python (see details below):

1. Eclipse IDE with PyDev
2. IPython shell

Finally, if you want to use the (optional) automatic C++ code generation features of Brian, you should have the `gcc` compiler installed (on Cygwin if you are running on Windows).

Mac users: the Scipy Superpack for Intel OS X includes recent versions of Numpy, Scipy, Pylab and IPython.

2.2.1 Installing Python packages

On Windows, Python packages (including Brian) are generally installed simply by running an .exe file. On other operating systems, you can download the source release (typically a compressed archive .tar.gz or .zip that you need to unzip) and then install the package by typing the following in your shell:

```
python setup.py install
```

2.2.2 Installing Eclipse

Eclipse is an Integrated Development Environment (IDE) for any programming language. PyDev is a plugin for Eclipse with features specifically for Python development. The combination of these two is excellent for Python development (it's what we use for writing Brian).

To install Eclipse, go to their web page and download any of the base language IDEs. It doesn't matter which one, but Python is not one of the base languages so you have to choose an alternative language. Probably the most useful is the C++ one or the Java one. The C++ one can be downloaded here.

Having downloaded and installed Eclipse, you should download and install the PyDev plugin from their web site. The best way to do this is directly from within the Eclipse IDE. Follow the instructions on the PyDev manual page.

2.2.3 Installing IPython

IPython is an interactive shell for Python. It has features for SciPy and PyLab built in, so it is a good choice for scientific work. Download from their page. If you are using Windows, you will also need to download PyReadline from the same page.

2.2.4 C++ compilers

The default for Brian is to use the `gcc` compiler which will be installed already on most unix or linux distributions. If you are using Windows, you can install cygwin (make sure to include the `gcc` package). Alternatively, some but not all versions of Microsoft Visual C++ should be compatible, but this is untested so far. See the documentation for the SciPy Weave package for more information on this.

2.3 Testing

You can test whether Brian has installed properly by running Python and typing the following two lines:

```
from brian import *
run_all_tests()
```

A series of tests should run and return 'ok' for each one. If not, and all of the packages other than Brian work OK, please let us know.

CHAPTER

THREE

Getting started

3.1 Tutorials

These tutorials cover some basic topics in writing Brian scripts in Python. The complete source code for the tutorials is available in the tutorials folder in the extras package.

3.1.1 Tutorials for Python and Scipy

Python

The first thing to do in learning how to use Brian is to have a basic grasp of the Python programming language. There are lots of good tutorials already out there. The best one is probably the official Python tutorial. There is also a course for biologists at the Pasteur Institute: Introduction to programming using Python.

NumPy, SciPy and Pylab

Unfortunately, the quality of the documentation and tutorials for SciPy lags a long way behind the quality of the package itself. For the moment, the first place to look is the SciPy getting started page, and then the complete documentation page. To start using Brian, you do not need to understand much about how NumPy and SciPy work, although understanding how their array structures work will be useful for more advanced uses of Brian.

The syntax of the Numpy and Pylab functions is very similar to Matlab. If you already know Matlab, you could read this tutorial: NumPy for Matlab users and this list of Matlab-Python translations (pdf version here). A tutorial is also available on the web site of Pylab.

3.1.2 Tutorial 1: Basic Concepts

In this tutorial, we introduce some of the basic concepts of a Brian simulation:

- Importing the Brian module into Python
- Using quantities with units
- Defining a neuron model by its differential equation
- Creating a group of neurons
- Running a network
- Looking at the output of the network

- Modifying the state variables of the network directly
- Defining the network structure by connecting neurons
- Doing a raster plot of the output
- Plotting the membrane potential of an individual neuron

The following Brian classes will be introduced:

- `Model`
- `NeuronGroup`
- `Connection`
- `SpikeMonitor`
- `StateMonitor`

We will build a Brian program that defines a randomly connected network of integrate and fire neurons and plot its output.

This tutorial assumes you know:

- The very basics of Python, the `import` keyword, variables, basic arithmetical expressions, calling functions, lists
- The simplest leaky integrate and fire neuron model

The best place to start learning Python is the official tutorial:

http://docs.python.org/tut/

Tutorial contents

Tutorial 1a: The simplest Brian program

Importing the Brian module

The first thing to do in any Brian program is to load Brian and the names of its functions and classes. The standard way to do this is to use the Python `from ... import *` statement.

```
from brian import *
```

Integrate and Fire model

The neuron model we will use in this tutorial is the simplest possible leaky integrate and fire neuron, defined by the differential equation:

tau dV/dt = -(V-El)

and with a threshold value Vt and reset value Vr.

Parameters

Brian has a system for defining physical quantities (quantities with a physical dimension such as time). The code below illustrates how to use this system, which (mostly) works just as you'd expect.

```
tau = 20*msecond        # membrane time constant
Vt  =-50*mvolt          # spike threshold
Vr  =-60*mvolt          # reset value
El  =-60*mvolt          # resting potential (same as the reset)
```

The built in standard units in Brian consist of all the fundamental SI units like second and metre, along with a selection of derived SI units such as volt, farad, coulomb. All names are lowercase following the SI standard. In addition, there are scaled versions of these units using the standard SI prefixes m=1/1000, K=1000, etc.

Neuron model and equations

The simplest way to define a neuron model in Brian is to write a list of the differential equations that define it. For the moment, we'll just give the simplest possible example, a single differential equation. You write it in the following form:

```
dx/dt = f(x) : unit
```

where `x` is the name of the variable, `f(x)` can be any valid Python expression, and `unit` is the physical units of the variable `x`. In our case we will write:

```
dV/dt = -(V-El)/tau : volt
```

to define the variable `V` with units `volt`.

To complete the specification of the model, we also define a threshold and reset value.

```
model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)
```

The statement creates a new object 'model' which is an instance of the Brian class `Model`, initialised with the values in the line above. In Python, you can call a function or initialise a class using keyword arguments as well as ordered arguments, so if I defined a function `f(x,y)` I could call it as `f(1,2)` or as `f(y=2,x=1)` and get the same effect. See the Python tutorial for more information on this.

Group of neurons

We create a group of 40 neurons with the model defined above.

```
G = NeuronGroup(N=40,model=model)
```

The `N` keyword gives the number of neurons in the group and the `model` keyword is used to pass the neuron model.

For the moment, we leave the networks in this group unconnected to each other, each evolves separately from the others.

Simulation

Finally, we run the simulation for 1 second of simulated time. By default, the simulator uses a timestep dt = 0.1 ms.

```
run(1*second)
```

And that's it! To see some of the output of this network, go to the next part of the tutorial.

Exercise

The units system of Brian is useful for ensuring that everything is consistent, and that you don't make hard to find mistakes in your code by using the wrong units. Try changing the units of one of the parameters and see what happens.

Solution

You should see an error message with a Python traceback (telling you which functions were being called when the error happened), ending in a line something like:

```
Brian.units.DimensionMismatchError: The differential equations
are not homogeneous!, dimensions were (m^2 kg s^-3 A^-1)
(m^2 kg s^-4 A^-1)
```

Tutorial 1b: Counting spikes

In the previous part of the tutorial we looked at the following:

- Importing the Brian module into Python
- Using quantities with units
- Defining a neuron model by its differential equation
- Creating a group of neurons
- Running a network

In this part, we move on to looking at the output of the network.

The first part of the code is the same.

```
from brian import *

tau = 20*msecond        # membrane time constant
Vt  =-50*mvolt          # spike threshold
Vr  =-60*mvolt          # reset value
El  =-60*mvolt          # resting potential (same as the reset)

model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)

G = NeuronGroup(N=40,model=model)
```

Counting spikes

Now we would like to have some idea of what this network is doing. In Brian, we use monitors to keep track of the behaviour of the network during the simulation. The simplest monitor of all is the `SpikeMonitor`, which just records the spikes from a given `NeuronGroup`.

```
M = SpikeMonitor(G)
```

Results

Now we run the simulation as before:

```
run(1*second)
```

And finally, we print out how many spikes there were:

```
print M.nspikes
```

So what's going on? Why are there 40 spikes? Well, the answer is that the initial value of the membrane potential for every neuron is 0 mV, which is above the threshold potential of -50 mV and so there is an initial spike at t=0 and then it resets to -60 mV and stays there, below the threshold potential. In the next part of this tutorial, we'll make sure there are some more spikes to see.

Tutorial 1c: Making some activity

In the previous part of the tutorial we found that each neuron was producing only one spike. In this part, we alter the model so that some more spikes will be generated. What we'll do is alter the resting potential `El` so that it is above threshold, this will ensure that some spikes are generated. The first few lines remain the same:

```
from brian import *

tau = 20*msecond         # membrane time constant
Vt  =-50*mvolt           # spike threshold
Vr  =-60*mvolt           # reset value
```

But we change the resting potential to -49 mV, just above the spike threshold:

```
El  =-49*mvolt           # resting potential (same as the reset)
```

And then continue as before:

```
model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)

G = NeuronGroup(N=40,model=model)

M = SpikeMonitor(G)
```

```
run(1*second)

print M.nspikes
```

Running this program gives the output `840`. That's because every neuron starts at the same initial value and proceeds deterministically, so that each neuron fires at exactly the same time, in total 21 times during the 1s of the run.

In the next part, we'll introduce a random element into the behaviour of the network.

Exercises

1. Try varying the parameters and seeing how the number of spikes generated varies.
2. Solve the differential equation by hand and compute a formula for the number of spikes generated. Compare this with the program output and thereby partially verify it. (Hint: each neuron starts at above the threshold and so fires a spike immediately.)

Solution

Solving the differential equation gives:

V = El + (Vr-El) exp (-t/tau)

Setting V=Vt at time t gives:

t = tau log((Vr-El) / (Vt-El))

If the simulator runs for time T, and fires a spike immediately at the beginning of the run it will then generate n spikes, where:

n = [T/t] + 1

If you have m neurons all doing the same thing, you get nm spikes. This calculation with the parameters above gives:

t = 48.0 ms n = 21 nm = 840

As predicted.

Tutorial 1d: Introducing randomness

In the previous part of the tutorial, all the neurons start at the same values and proceed deterministically, so they all spike at exactly the same times. In this part, we introduce some randomness by initialising all the membrane potentials to uniform random values between the reset and threshold values.

We start as before:

```
from brian import *

tau = 20*msecond        # membrane time constant
Vt  =-50*mvolt          # spike threshold
```

```
Vr   =-60*mvolt           # reset value
El   =-49*mvolt           # resting potential (same as the reset)

model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)

G = NeuronGroup(N=40,model=model)

M = SpikeMonitor(G)
```

But before we run the simulation, we set the values of the membrane potentials directly. The notation `G.V` refers to the array of values for the variable `V` in group `G`. In our case, this is an array of length 40. We set its values by generating an array of random numbers using Brian's `rand` function. The syntax is `rand(size)` generates an array of length `size` consisting of uniformly distributed random numbers in the interval 0, 1.

```
G.V=Vr+rand(40)*(Vt-Vr)
```

And now we run the simulation as before.

```
run(1*second)

print M.nspikes
```

But this time we get a varying number of spikes each time we run it, roughly between 800 and 850 spikes. In the next part of this tutorial, we introduce a bit more interest into this network by connecting the neurons together.

Tutorial 1e: Connecting neurons

In the previous parts of this tutorial, the neurons are still all unconnected. We add in connections here. The model we use is that when neuron i is connected to neuron j and neuron i fires a spike, then the membrane potential of neuron j is instantaneously increased by a value `psp`. We start as before:

```
from brian import *

tau = 20*msecond          # membrane time constant
Vt   =-50*mvolt           # spike threshold
Vr   =-60*mvolt           # reset value
El   =-49*mvolt           # resting potential (same as the reset)
```

Now we include a new parameter, the PSP size:

```
psp = 0.5*mvolt           # postsynaptic potential size
```

And continue as before:

```
model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)

G = NeuronGroup(N=40,model=model)
```

Connections

We now proceed to connect these neurons. Firstly, we declare that there is a connection from neurons in G to neurons in G. For the moment, this is just something that is necessary to do, the reason for doing it this way will become clear in the next tutorial.

```
C = Connection(G,G)
```

Now the interesting part, we make these neurons be randomly connected with probability 0.1 and weight psp. Each neuron i in G will be connected to each neuron j in G with probability 0.1. The weight of the connection is the amount that is added to the membrane potential of the target neuron when the source neuron fires a spike.

```
C.connect_random(G,G,0.1,weight=psp)
```

Now we continue as before:

```
M = SpikeMonitor(G)

G.V=Vr+rand(40)*(Vt-Vr)

run(1*second)

print M.nspikes
```

You can see that the number of spikes has jumped from around 800-850 to around 1000-1200. In the next part of the tutorial, we'll look at a way to plot the output of the network.

Exercise

Try varying the parameter psp and see what happens. How large can you make the number of spikes output by the network? Why?

Solution

The logically maximum number of firings is 400,000 = 40 * 1000 / 0.1, the number of neurons in the network * the time it runs for / the integration step size (you cannot have more than one spike per step).

In fact, the number of firings is bounded above by 200,000. The reason for this is that the network updates in the following way:

1. Integration step
2. Find neurons above threshold
3. Propagate spikes
4. Reset neurons which spiked

You can see then that if neuron i has spiked at time t, then it will not spike at time t+dt, even if it receives spikes from another neuron. Those spikes it receives will be added at step 3 at time t, then reset to Vr at step 4 of time t, then the thresholding function at time t+dt is applied at step 2, before it has received any subsequent inputs. So the most a neuron can spike is every other time step.

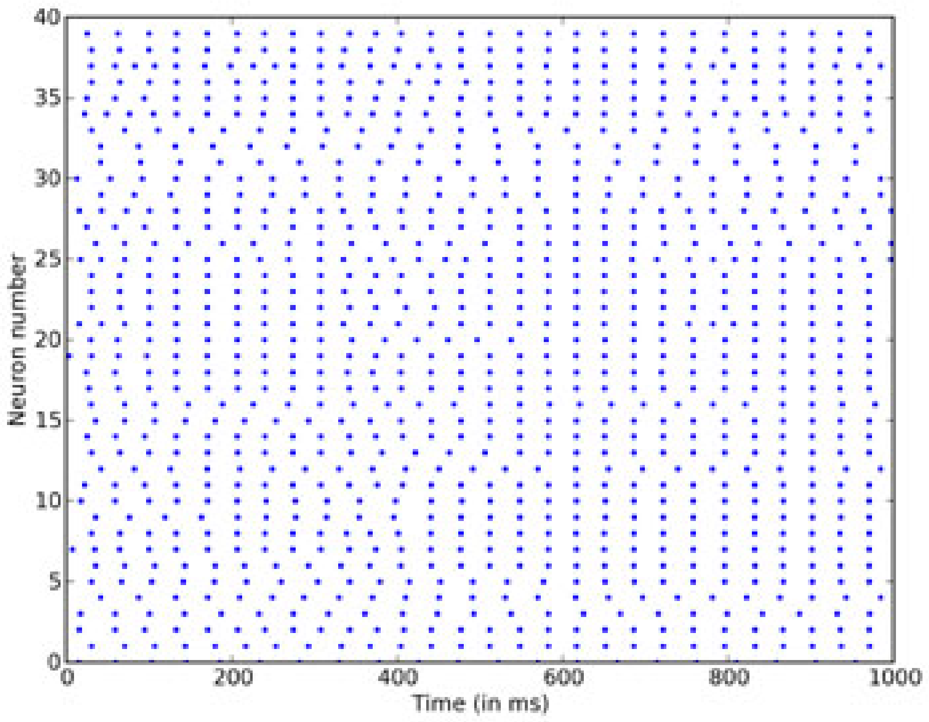
Tutorial 1f: Recording spikes

In the previous part of the tutorial, we defined a network with not entirely trivial behaviour, and printed the number of spikes. In this part, we'll record every spike that the network generates and display a raster plot of them. We start as before:

```
from brian import *

tau = 20*msecond        # membrane time constant
Vt  =-50*mvolt          # spike threshold
Vr  =-60*mvolt          # reset value
El  =-49*mvolt          # resting potential (same as the reset)
psp = 0.5*mvolt         # postsynaptic potential size

model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)

G = NeuronGroup(N=40,model=model)

C = Connection(G,G)
C.connect_random(G,G,0.1,weight=psp)

M = SpikeMonitor(G)

G.V=Vr+rand(40)*(Vt-Vr)

run(1*second)

print M.nspikes
```

Having run the network, we simply use the `raster_plot()` function provided by Brian. After creating plots, we have to use the `show()` function to display them. This function is from the PyLab module that Brian uses for its built in plotting routines.

```
raster_plot()
show()
```



As you can see, despite having introduced some randomness into our network, the output is very regular indeed. In the next part we introduce one more way to plot the output of a network.

Tutorial 1g: Recording membrane potentials

In the previous part of this tutorial, we plotted a raster plot of the firing times of the network. In this tutorial, we introduce a way to record the value of the membrane potential for a neuron during the simulation, and plot it. We continue as before:

```
from brian import *

tau = 20*msecond        # membrane time constant
Vt  =-50*mvolt          # spike threshold
Vr  =-60*mvolt          # reset value
El  =-49*mvolt          # resting potential (same as the reset)
psp = 0.5*mvolt         # postsynaptic potential size

model = Model(equation='dV/dt = -(V-El)/tau : volt',
              threshold=Vt,reset=Vr)

G = NeuronGroup(N=40,model=model)

C = Connection(G,G)
C.connect_random(G,G,0.1,weight=psp)
```

This time we won't record the spikes.

Recording states

Now we introduce a second type of monitor, the `StateMonitor`. The first argument is the group to monitor, and the second is the state variable to monitor. The keyword `record` can be an integer, list or the value `True`. If it is an integer `i`, the monitor will record the state of the variable for neuron `i`. If it's a list of integers, it will record the states for each neuron in the list. If it's set to `True` it will record for all the neurons in the group.

```
M = StateMonitor(G,'V',record=0)
```

And then we continue as before:

```
G.V=Vr+rand(40)*(Vt-Vr)
```

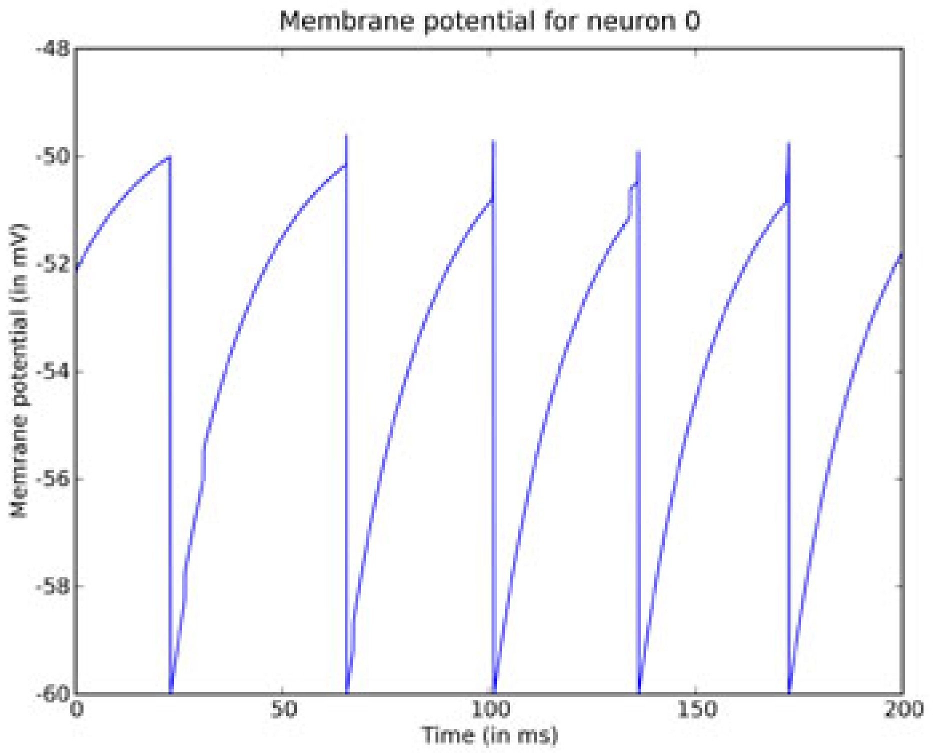
But this time we run it for a shorter time so we can look at the output in more detail:

```
run(200*msecond)
```

Having run the simulation, we plot the results using the `plot` command from PyLab which has the same syntax as the Matlab `plot`` command, i.e. `plot(xvals,yvals,...)`. The `StateMonitor` monitors the times at which it monitored a value in the array `M.times`, and the values in the array `M[0]`. The notation `M[i]` means the array of values of the monitored state variable for neuron `i`.

In the following lines, we scale the times so that they're measured in ms and the values so that they're measured in mV. We also label the plot using PyLab's `xlabel`, `ylabel` and `title` functions, which again mimic the Matlab equivalents.

```
plot(M.times/(1*msecond),M[0]/(1*mvolt))
xlabel('Time (in ms)')
ylabel('Memrane potential (in mV)')
title('Membrane potential for neuron 0')
show()
```



You can clearly see the leaky integration exponential decay toward the resting potential, as well as the jumps when a spike was received.

3.1.3 Tutorial 2: Connections

In this tutorial, we will cover in more detail the concept of the Connection in Brian.

This tutorial assumes you have followed *Tutorial 1: Basic Concepts*. It would also be useful to read the *Overview* section of the *Concepts* chapter of the main documentation.

Tutorial contents

Tutorial 2a: The concept of a Connection

The network

In this first part, we'll build a network consisting of three neurons. The first two neurons will be under direct control and have no equations defining them, they'll just produce spikes which will feed into the third neuron. This third neuron has two different state variables, called Va and Vb. The first two neurons will be connected to the third neuron, but a spike arriving at the third neuron will be treated differently according to whether it came from the first or second neuron (which you can consider as meaning that the first two neurons have different types of synapses on to the third neuron).

The program starts as follows.

```
from brian import *
```

```
tau_a =  1*ms
tau_b = 10*ms
Vt    = 10*mV
Vr    =  0*mV
```

Differential equations

This time, we will have multiple differential equations. We will use the `Equations` object, although you could equally pass the multi-line string defining the differential equations directly when initialising the `Model` object (see the next part of the tutorial for an example of this).

```
eqs = Equations('''
      dVa/dt = -Va/tau_a : volt
      dVb/dt = -Vb/tau_b : volt
      ''')
model = Model(equations=eqs,threshold=Vt,reset=Vr)
```

So far, we have defined a model neuron with two state variables, `Va` and `Vb`, which both decay exponentially towards 0, but with different time constants `tau_a` and `tau_b`. This is just so that you can see the difference between them more clearly in the plot later on.

SpikeGeneratorGroup

Now we introduce the `SpikeGeneratorGroup` class. This is a group of neurons without a model, which just produces spikes at the times that you specify. You create a group like this by writing:

```
G = SpikeGeneratorGroup(N,spiketimes)
```

where `N` is the number of neurons in the group, and `spiketimes` is a list of pairs `(i,t)` indicating that neuron `i` should fire at time `t`. In fact, `spiketimes` can be any 'iterable container' or 'generator', but we don't cover that here (see the detailed documentation for `SpikeGeneratorGroup`).

In our case, we want to create a group with two neurons, the first of which (neuron 0) fires at times 1 ms and 4 ms, and the second of which (neuron 1) fires at times 2 ms and 3 ms. The list of `spiketimes` then is:

```
spiketimes = [(0,1*ms), (0,4*ms),
              (1,2*ms), (1,3*ms)]
```

and we create the group as follows:

```
G1 = SpikeGeneratorGroup(2,spiketimes)
```

Now we create a second group, with one neuron, according to the model we defined earlier.

```
G2 = NeuronGroup(N=1,model=model)
```

Connections

In Brian, a Connection from one NeuronGroup to another is defined by writing:

```
C = Connection(G,H,state)
```

Here G is the source group, H is the target group, and state is the name of the target state variable. When a neuron i in G fires, Brian finds all the neurons j in H that i in G is connected to, and adds the amount C[i,j] to the specified state variable of neuron j in H. Here C[i,j] is the (i,j)th entry of the connection matrix of C (which is initially all zero).

To start with, we create two connections from the group of two directly controlled neurons to the group of one neuron with the differential equations. The first connection has the target state Va and the second has the target state Vb.

```
C1 = Connection(G1,G2,'Va')
C2 = Connection(G1,G2,'Vb')
```

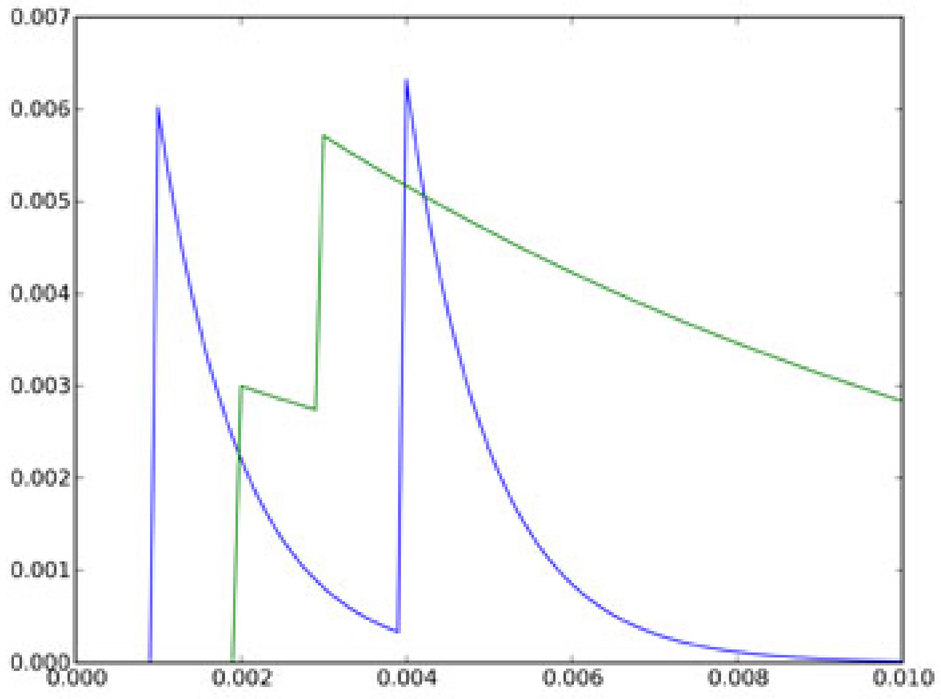
So far, this only declares our intention to connect neurons in group G1 to neurons in group G2, because the connection matrix is initially all zeros. Now, with connection C1 we connect neuron 0 in group G1 to neuron 0 in group G2, with weight 3 mV. This means that when neuron 0 in group G1 fires, the state variable Va of the neuron in group G2 will be increased by 6 mV. Then we use connection C2 to connection neuron 1 in group G1 to neuron 0 in group G2, this time with weight 3 mV.

```
C1[0,0] = 6*mV
C2[1,0] = 3*mV
```

The net effect of this is that when neuron 0 of G1 fires, Va for the neuron in G2 will increase 6 mV, and when neuron 1 of G1 fires, Vb for the neuron in G2 will increase 3 mV.

Now we set up monitors to record the activity of the network, run it and plot it.

```
Ma = StateMonitor(G2,'Va',record=True)
Mb = StateMonitor(G2,'Vb',record=True)

run(10*ms)

plot(Ma.times,Ma[0])
plot(Mb.times,Mb[0])
show()
```



The two plots show the state variables `Va` and `Vb` for the single neuron in group `G2`. `Va` is shown in blue, and `Vb` in green. According to the differential equations, `Va` decays much faster than `Vb` (time constant 1 ms rather than 10 ms), but we have set it up (through the connection strengths) that an incoming spike from neuron 0 of `G1` causes a large increase of 6 mV to `Va`, whereas a spike from neuron 1 of `G1` causes a smaller increase of 3 mV to Vb. The value for `Va` then jumps at times 1 ms and 4 ms, when we defined neuron 0 of `G1` to fire, and decays almost back to rest in between. The value for `Vb` jumps at times 2 ms and 3 ms, and because the times are closer together and the time constant is longer, they add together.

In the next part of this tutorial, we'll see how to use this system to do something useful.

Exercises

1. Try playing with the parameters `tau_a`, `tau_b` and the connection strengths, `C1[0,0]` and `C2[0,1]`. Try changing the list of spike times.
2. In this part of the tutorial, the states `Va` and `Vb` are independent of one another. Try rewriting the differential equations so that they're not independent and play around with that.
3. Write a network with inhibitory and excitatory neurons. Hint: you only need one connection.
4. Write a network with inhibitory and excitatory neurons whose actions have different time constants (for example, excitatory neurons have a slower effect than inhibitory ones).

Solutions

1. Simple write `C[i,j]=-3*mV` to make the connection from neuron i to neuron j inhibitory.
2. See the next part of this tutorial.

Tutorial 2b: Excitatory and inhibitory currents

In this tutorial, we use multiple connections to solve a real problem, how to implement two types of synapses with excitatory and inhibitory currents with different time constants.

The scheme

The scheme we implement is the following diffential equations:

> taum dV/dt = -V + ge - gi
> taue dge/dt = -ge
> taui dgi/dt = -gi

An excitatory neuron connects to state ge, and an inhibitory neuron connects to state gi. When an excitatory spike arrives, ge instantaneously increases, then decays exponentially. Consequently, V will initially but continuously rise and then fall. Solving these equations, if V(0)=0, ge(0)=g0 corresponding to an excitatory spike arriving at time 0, and gi(0)=0 then:

> gi = 0
> ge = g0 exp(-t/taue)
> V = (exp(-t/taum) - exp(-t/taue)) taue g0 / (taum-taue)

We use a very short time constant for the excitatory currents, a longer one for the inhibitory currents, and an even longer one for the membrane potential.

```
from brian import *

taum = 20*ms
taue =  1*ms
taui = 10*ms
Vt   = 10*mV
Vr   =  0*mV

model = Model(equations = '''
        dV/dt  = (-V+ge-gi)/taum : volt
        dge/dt = -ge/taue        : volt
        dgi/dt = -gi/taui        : volt
        ''', threshold=Vt, reset=Vr)
```

Connections

As before, we'll have a group of two neurons under direct control, the first of which will be excitatory this time, and the second will be inhibitory. To demonstrate the effect, we'll have two excitatory spikes reasonably close together, followed by an inhibitory spike later on, and then shortly after that two excitatory spikes close together.

```
spiketimes = [(0,1*ms),(0,10*ms),
              (1,40*ms),
              (0,50*ms),(0,55*ms)]

G1 = SpikeGeneratorGroup(2,spiketimes)
G2 = NeuronGroup(N=1,model=model)
```

```
C1 = Connection(G1,G2,'ge')
C2 = Connection(G1,G2,'gi')
```

The weights are the same - when we increase `ge` the effect on `V` is excitatory and when we increase `gi` the effect on `V` is inhibitory.

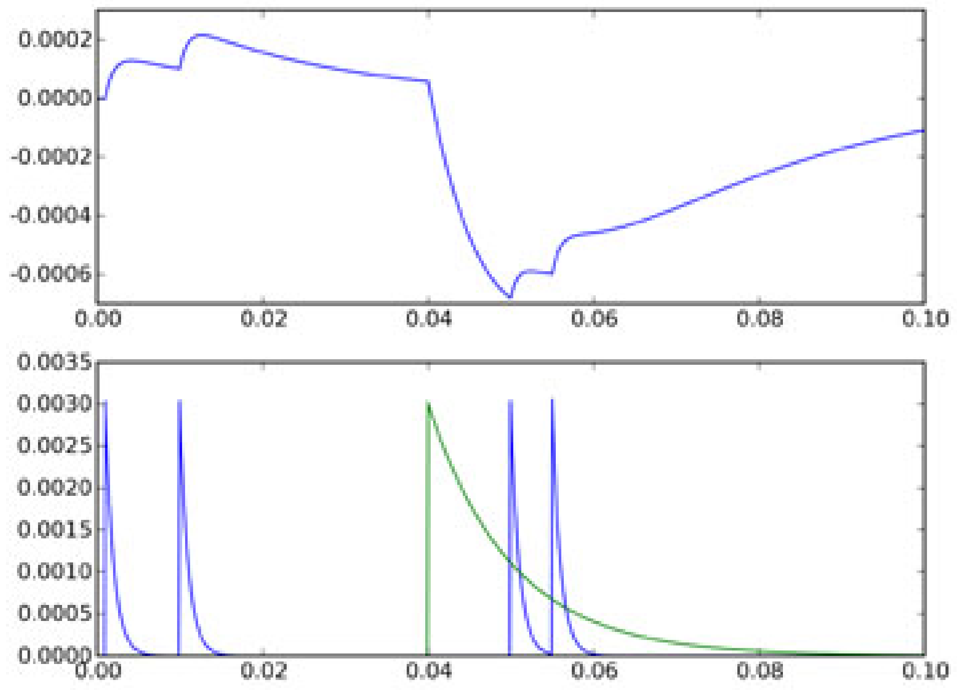
```
C1[0,0] = 3*mV
C2[1,0] = 3*mV
```

We set up monitors and run as normal.

```
Mv  = StateMonitor(G2,'V',record=True)
Mge = StateMonitor(G2,'ge',record=True)
Mgi = StateMonitor(G2,'gi',record=True)

run(100*ms)
```

This time we do something a little bit different when plotting it. We want a plot with two subplots, the top one will show `V`, and the bottom one will show both `ge` and `gi`. We use the `subplot` command from pylab which mimics the same command from Matlab.

```
figure()
subplot(211)
plot(Mv.times,Mv[0])
subplot(212)
plot(Mge.times,Mge[0])
plot(Mgi.times,Mgi[0])
show()
```



The top figure shows the voltage trace, and the bottom figure shows `ge` in blue and `gi` in green. You can see that although the inhibitory and excitatory weights are the same, the inhibitory current is much more powerful. This is because the effect of `ge` or `gi` on `V` is related to the integral of the differential equation for those variables, and `gi` decays much more slowly than `ge`. Thus the size of the negative deflection at 40 ms is much bigger than the excitatory ones, and even the double excitatory spike after the inhibitory one can't cancel it out.

In the next part of this tutorial, we set up our first serious network, with 4000 neurons, excitatory and inhibitory.

Exercises

1. Try changing the parameters and spike times to get a feel for how it works.
2. Try an equivalent implementation with the equation taum dV/dt = -V+ge+gi
3. Verify that the differential equation has been solved correctly.

Solutions

Solution for 2:

Simply use the line `C2[1,0] = -3*mV` to get the same effect.

Solution for 3:

First, set up the situation we described at the top for which we already know the solution of the differential equations, by changing the spike times as follows:

```
spiketimes = [(0,0*ms)]
```

Now we compute what the values ought to be as follows:

```
t = Mv.times
Vpredicted = (exp(-t/taum) - exp(-t/taue))*taue*(3*mV) / (taum-taue)
```

Now we can compute the difference between the predicted and actual values:

```
Vdiff = abs(Vpredicted - Mv[0])
```

This should be zero:

```
print max(Vdiff)
```

Sure enough, it's as close as you can expect on a computer. When I run this it gives me the value 1.3 aV, which is 1.3 * 10^-18 volts, i.e. effectively zero given the finite precision of the calculations involved.

Tutorial 2c: The CUBA network

In this part of the tutorial, we set up our first serious network that actually does something. It implements the CUBA network, Benchmark 2 from:

> Simulation of networks of spiking neurons: A review of tools and strategies (2006). Brette, Rudolph, Carnevale, Hines, Beeman, Bower, Diesmann, Goodman, Harris, Zirpe, Natschlager, Pecevski, Ermentrout, Djurfeldt, Lansner, Rochel, Vibert, Alvarez, Muller, Davison, El Boustani and Destexhe. Journal of Computational Neuroscience

This is a network of 4000 neurons, of which 3200 excitatory, and 800 inhibitory, with exponential synaptic currents. The neurons are randomly connected with probability 0.02.

```
from brian import *

taum =  20*ms           # membrane time constant
taue =   5*ms           # excitatory synaptic time constant
taui =  10*ms           # inhibitory synaptic time constant
Vt   = -50*mV           # spike threshold
Vr   = -60*mV           # reset value
El   = -49*mV           # resting potential
we   = (60*0.27/10)*mV # excitatory synaptic weight
wi   =  (20*4.5/10)*mV # inhibitory synaptic weight

model = Model(equations = '''
        dV/dt  = (ge-gi-(V-El))/taum : volt
        dge/dt = -ge/taue            : volt
        dgi/dt = -gi/taui            : volt
        ''', threshold=Vt, reset=Vr)
```

So far, this has been pretty similar to the previous part, the only difference is we have a couple more parameters, and we've added a resting potential `El` into the equation for `V`.

Now we make lots of neurons:

```
G = NeuronGroup(4000, model=model)
```

Next, we divide them into subgroups. The `subgroup()` method of a `NeuronGroup` returns a new `NeuronGroup` that can be used in exactly the same way as its parent group. At the moment, the subgrouping mechanism can only be used to create contiguous groups of neurons (so you can't have a subgroup consisting of neurons 0-100 and also 200-300 say). We designate the first 3200 neurons as `Ge` and the second 800 as `Gi`, these will be the excitatory and inhibitory neurons.

```
Ge = G.subgroup(3200) # Excitatory neurons
Gi = G.subgroup(800)  # Inhibitory neurons
```

Now we define the connections. As in the previous part of the tutorial, `ge` is the excitatory current and `gi` is the inhibitory one. `Ce` says that an excitatory neuron can synapse onto any neuron in `G`, be it excitatory or inhibitory. Similarly for inhibitory neurons.

```
Ce=Connection(Ge, G, 'ge')
Ci=Connection(Gi, G, 'gi')
```

We randomly connect `Ge` and `Gi` to the whole of `G` with probability 0.02 and the weights given in the list of parameters at the top.

```
Ce.connect_random(Ge, G, 0.02, weight=we)
Ci.connect_random(Gi, G, 0.02, weight=wi)
```

Set up some monitors as usual. The line `record=0` in the `StateMonitor` declarations indicates that we only want to record the activity of neuron 0. This saves time and memory.

```
M   = SpikeMonitor(G)
MV  = StateMonitor(G, 'V', record=0)
Mge = StateMonitor(G, 'ge', record=0)
Mgi = StateMonitor(G, 'gi', record=0)
```

And in order to start the network off in a somewhat more realistic state, we initialise the membrane potentials uniformly randomly between the reset and the threshold.

```
G.V = Vr + (Vt-Vr) * rand(len(G))
```

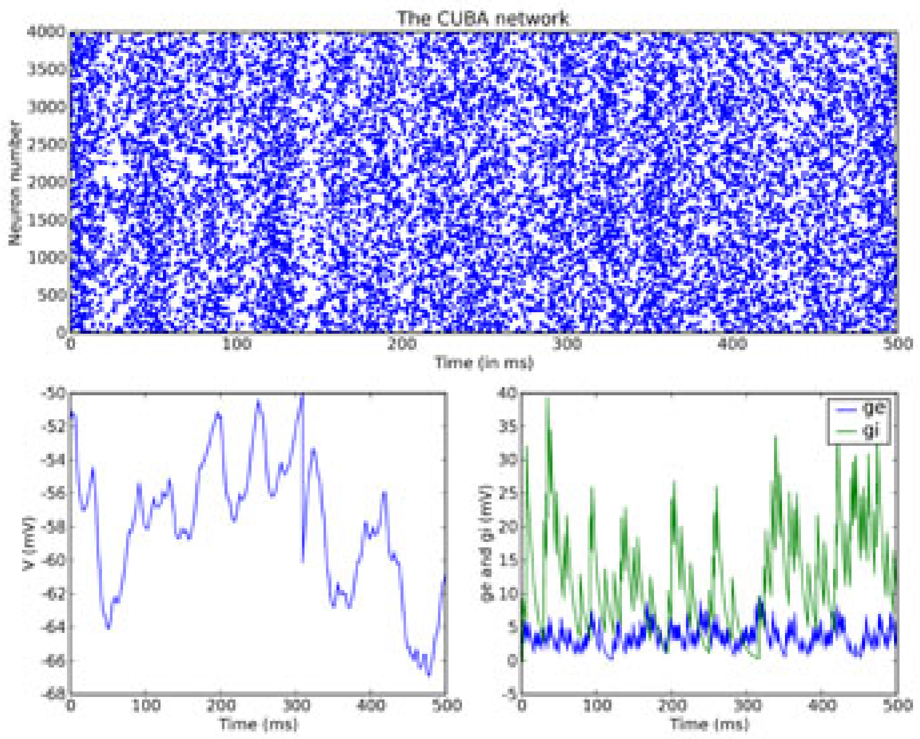
Now we run.

```
run(500*ms)
```

And finally we plot the results. Just for fun, we do a rather more complicated plot than we've been doing so far, with three subplots. The upper one is the raster plot of the whole network, and the lower two are the values of `V` (on the left) and `ge` and `gi` (on the right) for the neuron we recorded from. See the PyLab documentation for an explanation of the plotting functions, but note that the `raster_plot()` keyword `newfigure=False` instructs the (Brian) function `raster_plot()` not to create a new figure (so that it can be placed as a subplot of a larger figure).

```
subplot(211)
raster_plot(M, title='The CUBA network', newfigure=False)
subplot(223)
```

```
    plot(MV.times/ms, MV[0]/mV)
    xlabel('Time (ms)')
    ylabel('V (mV)')
    subplot(224)
    plot(Mge.times/ms, Mge[0]/mV)
    plot(Mgi.times/ms, Mgi[0]/mV)
    xlabel('Time (ms)')
    ylabel('ge and gi (mV)')
    legend(('ge','gi'), 'upper right')
    show()
```



3.2 Examples

These examples cover some basic topics in writing Brian scripts in Python. The complete source code for the examples is available in the examples folder in the extras package.

3.2.1 Example: adaptive

An adaptive neuron model

```
from brian import *

PG = PoissonGroup(1,500*Hz)
eqs='''
dv/dt = (-w-v)/(10*ms) : volt # the membrane equation
```

```
dw/dt = -w/(30*ms) : volt # the adaptation current
'''
def myreset(P,spikes):
    P.v[spikes]=0*mV # Faster: P.v_[spikes]=0*mV
    P.w[spikes]+=3*mV # the adaptation variable increases with each spike
IF = NeuronGroup(1,model=eqs,reset=myreset,threshold=20*mV)

C = Connection(PG,IF,'v')
C.connect_full(PG,IF,3*mV)

MS = SpikeMonitor(PG,True)
Mv = StateMonitor(IF,'v',record=True)
Mw = StateMonitor(IF,'w',record=True)

run(100*ms)

plot(Mv.times/ms,Mv[0]/mV)
plot(Mw.times/ms,Mw[0]/mV)

show()
```

3.2.2 Example: adaptive_threshold

A model with adaptive threshold (increases with each spike)

```
from brian import *

eqs='''
dv/dt = -v/(10*ms) : volt
dvt/dt = (10*mV-vt)/(15*ms) : volt
'''

def myreset(P, spikes):
    P.v[spikes]=0*mV
    P.vt[spikes]+=3*mV

IF = NeuronGroup(1, model=eqs,
        reset=myreset,
        threshold=lambda v,vt:v>=vt)
IF.rest()
PG = PoissonGroup(1, 500*Hz)

C = Connection(PG, IF, 'v')
C.connect_full(PG, IF, 3*mV)

Mv = StateMonitor(IF, 'v', record=True)
Mvt = StateMonitor(IF, 'vt', record=True)

run(100*ms)

plot(Mv.times/ms, Mv[0]/mV)
plot(Mvt.times/ms, Mvt[0]/mV)

show()
```

3.2.3 Example: cable

Dendrite with 100 compartments

```
from brian import *
from brian.compartments import *
from brian.library.ionic_currents import *

length=1*mm
nseg=100
dx=length/nseg
Cm=1*uF/cm**2
gl=0.02*msiemens/cm**2
diam=1*um
area=pi*diam*dx
El=0*mV
Ri=100*ohm*cm
ra=Ri*4/(pi*diam**2)

print "Time constant =",Cm/gl
print "Space constant =",.5*(diam/(gl*Ri))**.5

segments={}
for i in range(nseg):
    segments[i]=MembraneEquation(Cm*area)+leak_current(gl*area,El)

segments[0]+=Current('I:nA')

cable=Compartments(segments)
for i in range(nseg-1):
    cable.connect(i,i+1,ra*dx)

neuron=NeuronGroup(1,model=cable)
#neuron.vm_0=10*mV
neuron.I_0=.05*nA

trace=[]
for i in range(10):
    trace.append(StateMonitor(neuron,'vm_'+str(10*i),record=True))

run(200*ms)

for i in range(10):
    plot(trace[i].times/ms,trace[i][0]/mV)
show()
```

3.2.4 Example: COBA

This is a Brian script implementing a benchmark described in the following review paper:

Simulation of networks of spiking neurons: A review of tools and strategies (2007). Brette, Rudolph, Carnevale, Hines, Beeman, Bower, Diesmann, Goodman, Harris, Zirpe, Natschlager, Pecevski, Ermentrout, Djurfeldt, Lansner, Rochel, Vibert, Alvarez, Muller, Davison, El Boustani and Destexhe. Journal of Computational Neuroscience 23(3):349-98

Benchmark 1: random network of integrate-and-fire neurons with exponential synaptic conductances

Clock-driven implementation with Euler integration (no spike time interpolation)

R. Brette - Dec 2007

Brian is a simulator for spiking neural networks written in Python, developed by R. Brette and D. Goodman. http://brian.di.ens.fr

```
from brian import *
import time

# Time constants
taum=20*msecond
taue=5*msecond
taui=10*msecond
# Reversal potentials
Ee=(0.+60.)*mvolt
Ei=(-80.+60.)*mvolt

start_time=time.time()
eqs=Equations('''
dv/dt  =  (-v+ge*(Ee-v)+gi*(Ei-v))*(1./taum) : volt
dge/dt = -ge*(1./taue) : 1
dgi/dt = -gi*(1./taui) : 1
''')
# NB 1: conductances are in units of the leak conductance
# NB 2: multiplication is faster than division

P=NeuronGroup(4000,model=eqs,threshold=10*mvolt,\
              reset=0*mvolt,refractory=5*msecond,
              order=1,compile=True)
Pe=P.subgroup(3200)
Pi=P.subgroup(800)
Ce=Connection(Pe,P,'ge')
Ci=Connection(Pi,P,'gi')
we=6./10. # excitatory synaptic weight (voltage)
wi=67./10. # inhibitory synaptic weight
Ce.connect_random(Pe, P, 0.02,weight=we)
Ci.connect_random(Pi, P, 0.02,weight=wi)
# Initialization
P.v=(randn(len(P))*5-5)*mvolt
P.ge=randn(len(P))*1.5+4
P.gi=randn(len(P))*12+20

# Record the number of spikes
Me=PopulationSpikeCounter(Pe)
Mi=PopulationSpikeCounter(Pi)

print "Network construction time:",time.time()-start_time,"seconds"
print "Simulation running..."
start_time=time.time()

run(1*second)
duration=time.time()-start_time
print "Simulation time:",duration,"seconds"
print Me.nspikes,"excitatory spikes"
print Mi.nspikes,"inhibitory spikes"
```

3.2.5 Example: COBAHH

This is a Brian script implementing a benchmark described in the following review paper:

Simulation of networks of spiking neurons: A review of tools and strategies (2007). Brette, Rudolph, Carnevale, Hines, Beeman, Bower, Diesmann, Goodman, Harris, Zirpe, Natschlager, Pecevski, Ermentrout, Djurfeldt, Lansner, Rochel, Vibert, Alvarez, Muller, Davison, El Boustani and Destexhe. Journal of Computational Neuroscience 23(3):349-98

Benchmark 3: random network of HH neurons with exponential synaptic conductances

Clock-driven implementation with exponential Euler integration (no spike time interpolation)

R. Brette - Dec 2007

Brian is a simulator for spiking neural networks written in Python, developed by R. Brette and D. Goodman. http://brian.di.ens.fr

```
from brian import *
import time

# Parameters
area=20000*umetre**2
Cm=(1*ufarad*cm**-2)*area
gl=(5e-5*siemens*cm**-2)*area
El=-60*mV
EK=-90*mV
ENa=50*mV
g_na=(100*msiemens*cm**-2)*area
g_kd=(30*msiemens*cm**-2)*area
VT=-63*mV
# Time constants
taue=5*ms
taui=10*ms
# Reversal potentials
Ee=0*mV
Ei=-80*mV
we=6*nS # excitatory synaptic weight (voltage)
wi=67*nS # inhibitory synaptic weight

start_time=time.time()
# The model
eqs=Equations('''
dv/dt = (gl*(El-v)+ge*(Ee-v)+gi*(Ei-v)-g_na*(m*m*m)*h*(v-ENa)-g_kd*(n*n*n*n)*(v-EK))/Cm : volt
dm/dt = alpham*(1-m)-betam*m : 1
dn/dt = alphan*(1-n)-betan*n : 1
dh/dt = alphah*(1-h)-betah*h : 1
dge/dt = -ge*(1./taue) : siemens
dgi/dt = -gi*(1./taui) : siemens
alpham = 0.32*(mV**-1)*(13*mV-v+VT)/(exp((13*mV-v+VT)/(4*mV))-1.)/ms : Hz
betam = 0.28*(mV**-1)*(v-VT-40*mV)/(exp((v-VT-40*mV)/(5*mV))-1)/ms : Hz
alphah = 0.128*exp((17*mV-v+VT)/(18*mV))/ms : Hz
betah = 4./(1+exp((40*mV-v+VT)/(5*mV)))/ms : Hz
alphan = 0.032*(mV**-1)*(15*mV-v+VT)/(exp((15*mV-v+VT)/(5*mV))-1.)/ms : Hz
betan = .5*exp((10*mV-v+VT)/(40*mV))/ms : Hz
''')

P=NeuronGroup(4000,model=eqs,\
              threshold=EmpiricalThreshold(threshold=-20*mV,refractory=3*ms),\
              implicit=True,freeze=True,compile=False)
Pe=P.subgroup(3200)
Pi=P.subgroup(800)
Ce=Connection(Pe,P,'ge')
Ci=Connection(Pi,P,'gi')
Ce.connect_random(Pe, P, 0.02,weight=we)
Ci.connect_random(Pi, P, 0.02,weight=wi)
# Initialization
P.v=El+(randn(len(P))*5-5)*mV
P.ge=(randn(len(P))*1.5+4)*10.*nS
P.gi=(randn(len(P))*12+20)*10.*nS

# Record the number of spikes and a few traces
Me=PopulationSpikeCounter(Pe)
Mi=PopulationSpikeCounter(Pi)
trace=StateMonitor(P,'v',record=[1,10,100])

print "Network construction time:",time.time()-start_time,"seconds"
print "Simulation running..."
run(1*msecond)
start_time=time.time()

run(1000*msecond)
duration=time.time()-start_time
print "Simulation time:",duration,"seconds"
print Me.nspikes,"excitatory spikes"
print Mi.nspikes,"inhibitory spikes"

plot(trace.times/ms,trace[1]/mV)
plot(trace.times/ms,trace[10]/mV)
plot(trace.times/ms,trace[100]/mV)
show()
```

3.2.6 Example: cobahh_simplified

This is an implementation of a benchmark described in the following review paper:

Simulation of networks of spiking neurons: A review of tools and strategies (2006). Brette, Rudolph, Carnevale, Hines, Beeman, Bower, Diesmann, Goodman, Harris, Zirpe, NatschlAger, Pecevski, Ermentrout, Djurfeldt, Lansner, Rochel, Vibert, Alvarez, Muller, Davison, El Boustani and Destexhe. Journal of Computational Neuroscience

Benchmark 3: random network of HH neurons with exponential synaptic conductances

Clock-driven implementation (no spike time interpolation)

R. Brette - Dec 2007

70s for dt=0.1 ms with exponential Euler

```
from brian import *

# Parameters
area=20000*umetre**2
Cm=(1*ufarad*cm**-2)*area
gl=(5e-5*siemens*cm**-2)*area
El=-60*mV
EK=-90*mV
ENa=50*mV
```

```
g_na=(100*msiemens*cm**-2)*area
g_kd=(30*msiemens*cm**-2)*area
VT=-63*mV
# Time constants
taue=5*ms
taui=10*ms
# Reversal potentials
Ee=0*mV
Ei=-80*mV
we=6*nS # excitatory synaptic weight (voltage)
wi=67*nS # inhibitory synaptic weight

# The model
eqs=Equations('''
dv/dt = (gl*(El-v)+ge*(Ee-v)+gi*(Ei-v)-\
    g_na*(m*m*m)*h*(v-ENa)-\
    g_kd*(n*n*n*n)*(v-EK))/Cm : volt
dm/dt = alpham*(1-m)-betam*m : 1
dn/dt = alphan*(1-n)-betan*n : 1
dh/dt = alphah*(1-h)-betah*h : 1
dge/dt = -ge*(1./taue) : siemens
dgi/dt = -gi*(1./taui) : siemens
alpham = 0.32*(mV**-1)*(13*mV-v+VT)/ \
    (exp((13*mV-v+VT)/(4*mV))-1.)/ms : Hz
betam = 0.28*(mV**-1)*(v-VT-40*mV)/ \
    (exp((v-VT-40*mV)/(5*mV))-1)/ms : Hz
alphah = 0.128*exp((17*mV-v+VT)/(18*mV))/ms : Hz
betah = 4./(1+exp((40*mV-v+VT)/(5*mV)))/ms : Hz
alphan = 0.032*(mV**-1)*(15*mV-v+VT)/ \
    (exp((15*mV-v+VT)/(5*mV))-1.)/ms : Hz
betan = .5*exp((10*mV-v+VT)/(40*mV))/ms : Hz
''')

P=NeuronGroup(4000,model=eqs,
    threshold=EmpiricalThreshold(threshold=-20*mV,
                                 refractory=3*ms),
    implicit=True,freeze=True)
Pe=P.subgroup(3200)
Pi=P.subgroup(800)
Ce=Connection(Pe,P,'ge')
Ci=Connection(Pi,P,'gi')
Ce.connect_random(Pe, P, 0.02,weight=we)
Ci.connect_random(Pi, P, 0.02,weight=wi)
# Initialization
P.v=El+(randn(len(P))*5-5)*mV
P.ge=(randn(len(P))*1.5+4)*10.*nS
P.gi=(randn(len(P))*12+20)*10.*nS

# Record the number of spikes and a few traces
trace=StateMonitor(P,'v',record=[1,10,100])

run(1*second)

plot(trace[1])
plot(trace[10])
plot(trace[100])
show()
```

3.2.7 Example: correlated_inputs

An example with correlated spike trains From: Brette, R. (2007). Generation of correlated spike trains.

```
from brian import *
from brian.correlatedspikes import *

input=HomogeneousCorrelatedSpikeTrains(1000,r=30*Hz,c=0.05,tauc=10*ms)

S=SpikeMonitor(input)
S2=PopulationRateMonitor(input)
M=StateMonitor(input,'rate',record=True)
run(1000*ms)
subplot(211)
raster_plot(S)
subplot(212)
plot(S2.times/ms,S2.smooth_rate(5*ms))
plot(M.times/ms,M[0]/Hz)
show()
```

3.2.8 Example: CUBA

This is a Brian script implementing a benchmark described in the following review paper:

Simulation of networks of spiking neurons: A review of tools and strategies (2007). Brette, Rudolph, Carnevale, Hines, Beeman, Bower, Diesmann, Goodman, Harris, Zirpe, Natschlager, Pecevski, Ermentrout, Djurfeldt, Lansner, Rochel, Vibert, Alvarez, Muller, Davison, El Boustani and Destexhe. Journal of Computational Neuroscience 23(3):349-98

Benchmark 2: random network of integrate-and-fire neurons with exponential synaptic currents

Clock-driven implementation with exact subthreshold integration (but spike times are aligned to the grid)

R. Brette - Oct 2007

Brian is a simulator for spiking neural networks written in Python, developed by R. Brette and D. Goodman. http://brian.di.ens.fr

```
from brian import *
import time

start_time=time.time()
taum=20*ms
taue=5*ms
taui=10*ms
Vt=-50*mV
Vr=-60*mV
El=-49*mV

eqs= Equations('''
dv/dt  = (ge+gi-(v-El))/taum : volt
dge/dt = -ge/taue : volt
dgi/dt = -gi/taui : volt
''')

P=NeuronGroup(4000,model=eqs,threshold=Vt,reset=Vr,refractory=5*ms)
P.v=Vr
```

```
P.ge=0*mV
P.gi=0*mV

Pe=P.subgroup(3200)
Pi=P.subgroup(800)
Ce=Connection(Pe,P,'ge')
Ci=Connection(Pi,P,'gi')
we=(60*0.27/10)*mV # excitatory synaptic weight (voltage)
wi=(-20*4.5/10)*mV # inhibitory synaptic weight
Ce.connect_random(Pe, P, 0.02,weight=we)
Ci.connect_random(Pi, P, 0.02,weight=wi)
P.v=Vr+rand(len(P))*(Vt-Vr)

# Record the number of spikes
Me=PopulationSpikeCounter(Pe)
Mi=PopulationSpikeCounter(Pi)
# A population rate monitor
M = PopulationRateMonitor(P)

print "Network construction time:",time.time()-start_time,"seconds"
print len(P),"neurons in the network"
print "Simulation running..."
run(1*msecond)
start_time=time.time()

run(1*second)

duration=time.time()-start_time
print "Simulation time:",duration,"seconds"
print Me.nspikes,"excitatory spikes"
print Mi.nspikes,"inhibitory spikes"
plot(M.times/ms,M.smooth_rate(2*ms,'gaussian'))
show()
```

3.2.9 Example: current_clamp

An example of single-electrode current clamp recording with bridge compensation (using the electrophysiology library).

```
from brian import *
from brian.library.electrophysiology import *

taum=20*ms         # membrane time constant
gl=1./(50*Mohm)    # leak conductance
Cm=taum*gl         # membrane capacitance
Re=50*Mohm         # electrode resistance
Ce=0.5*ms/Re       # electrode capacitance

eqs=Equations('''
dvm/dt=(-gl*vm+i_inj)/Cm : volt
Rbridge:ohm # bridge resistance
I:amp # command current
''')
eqs+=current_clamp(i_cmd='I',Re=Re,Ce=Ce,bridge='Rbridge')
setup=NeuronGroup(1,model=eqs)
soma=StateMonitor(setup,'vm',record=True)
```

```
recording=StateMonitor(setup,'v_rec',record=True)

# No compensation
run(50*ms)
setup.I=.5*nA
run(100*ms)
setup.I=0*nA
run(50*ms)

# Full compensation
setup.Rbridge=Re
run(50*ms)
setup.I=.5*nA
run(100*ms)
setup.I=0*nA
run(50*ms)

plot(recording.times/ms,recording[0]/mV,'b')
plot(soma.times/ms,soma[0]/mV,'r')
show()
```

3.2.10 Example: delays

Random network with external noise and transmission delays

```
from brian import *
tau=10*ms
sigma=5*mV
eqs='dv/dt = -v/tau+sigma*xi/tau**.5 : volt'
P=NeuronGroup(4000,model=eqs,threshold=10*mV,reset=0*mV,\
              refractory=5*ms)
P.v=-60*mV
Pe=P.subgroup(3200)
Pi=P.subgroup(800)
C=Connection(P,P,'v',delay=2*ms)
C.connect_random(Pe, P, 0.05,weight=.7*mV)
C.connect_random(Pi, P, 0.05,weight=-2.8*mV)
M=SpikeMonitor(P,True)
run(1*second)
print 'Mean rate =',M.nspikes/4000./second
raster_plot(M)
show()
```

3.2.11 Example: expIF_network

A network of exponential IF models with synaptic conductances

```
from brian import *
from brian.library.IF import *
from brian.library.synapses import *
import time

C=200*pF
taum=10*msecond
```

```
gL=C/taum
EL=-70*mV
VT=-55*mV
DeltaT=3*mV

# Synapse parameters
Ee=0*mvolt
Ei=-80*mvolt
taue=5*msecond
taui=10*msecond

eqs=exp_IF(C,gL,EL,VT,DeltaT)
# Two different ways of adding synaptic currents:
eqs+=Current('''
Ie=ge*(Ee-vm) : amp
dge/dt=-ge/taue : siemens
''')
eqs+=exp_conductance('gi',Ei,taui) # from library.synapses

P=NeuronGroup(4000,model=eqs,threshold=-20*mvolt,reset=EL,refractory=2*ms)
Pe=P.subgroup(3200)
Pi=P.subgroup(800)
Ce=Connection(Pe,P,'ge')
Ci=Connection(Pi,P,'gi')
we=1.5*nS # excitatory synaptic weight
wi=2.5*we # inhibitory synaptic weight
Ce.connect_random(Pe, P, 0.05,weight=we)
Ci.connect_random(Pi, P, 0.05,weight=wi)
# Initialization
P.vm=randn(len(P))*10*mV-70*mV
P.ge=(randn(len(P))*2+5)*we
P.gi=(randn(len(P))*2+5)*wi

# Excitatory input to a subset of excitatory and inhibitory neurons
# Excitatory neurons are excited for the first 200 ms
# Inhibitory neurons are excited for the first 100 ms
input_layer1=Pe.subgroup(200)
input_layer2=Pi.subgroup(200)
input1=PoissonGroup(200,rates=lambda t: (t<200*ms and 2000*Hz) or 0*Hz)
input2=PoissonGroup(200,rates=lambda t: (t<100*ms and 2000*Hz) or 0*Hz)
input_co1=IdentityConnection(input1,input_layer1,'ge',weight=we)
input_co2=IdentityConnection(input2,input_layer2,'ge',weight=we)

# Record the number of spikes
M=SpikeMonitor(P)

print "Simulation running..."
start_time=time.time()
run(500*ms)
duration=time.time()-start_time
print "Simulation time:",duration,"seconds"
print M.nspikes/4000.,"spikes per neuron"
raster_plot(M)
show()
```

3.2.12 Example: gap_junctions

Network of noisy IF neurons with gap junctions

```
from brian import *

N=300
v0=5*mV
tau=20*ms
sigma=5*mV
vt=10*mV
vr=0*mV
g_gap=1./N
beta=60*mV*2*ms
delta=vt-vr

eqs='''
dv/dt=(v0-v)/tau+g_gap*(u-N*v)/tau : volt
du/dt=(N*v0-u)/tau : volt # input from other neurons
'''

def myreset(P,spikes):
    P.v_[spikes]=vr # reset
    P.v_+=g_gap*beta*len(spikes) # spike effect
    P.u_-=delta*len(spikes)

group=NeuronGroup(N,model=eqs,threshold=vt,reset=myreset)

@network_operation
def noise(cl):
    x=randn(N)*sigma*(cl.dt/tau)**.5
    group.v_+=x
    group.u_+=sum(x)

trace=StateMonitor(group,'v',record=[0,1])
spikes=SpikeMonitor(group)
rate=PopulationRateMonitor(group)

run(1*second)
subplot(311)
raster_plot(spikes)
subplot(312)
plot(trace.times/ms,trace[0]/mV)
plot(trace.times/ms,trace[1]/mV)
subplot(313)
plot(rate.times/ms,rate.smooth_rate(5*ms)/Hz)
show()
```

3.2.13 Example: HodgkinHuxley

Hodgkin-Huxley model Assuming area 1*cm**2

```
#import brian_no_units
from brian import *
from brian.library.ionic_currents import *
```

```
#c=Clock(dt=.01*ms) # more precise
El=10.6*mV
EK=-12*mV
ENa=120*mV
eqs=MembraneEquation(1*uF)+leak_current(.3*msiemens,El)
eqs+=K_current_HH(36*msiemens,EK)+Na_current_HH(120*msiemens,ENa)
eqs+=Current('I:amp')

neuron=NeuronGroup(1,eqs,implicit=True,freeze=True)

trace=StateMonitor(neuron,'vm',record=True)

run(100*ms)
neuron.I=10*uA
run(100*ms)
plot(trace.times/ms,trace[0]/mV)
show()
```

3.2.14 Example: I-F_curve

Input-Frequency curve of a neuron (cortical RS type) Network: 1000 unconnected integrate-and-fire neurons (Brette-Gerstner) with an input parameter I. The input is set differently for each neuron. Spikes are sent to a 'neuron' group with the same size and variable n, which has the role of a spike counter.

```
from brian import *
from brian.library.IF import *

N=1000
eqs=Brette_Gerstner()+Current('I:amp')
group=NeuronGroup(N,model=eqs,threshold=-20*mV,reset=AdaptiveReset())
group.vm=-70*mV
group.I=linspace(0*nA,1*nA,N)

counter=NeuronGroup(N,model='n:1')
C=IdentityConnection(group,counter,'n')

i=N*8/10
trace=StateMonitor(group,'vm',record=i)

duration=5*second
run(duration)
subplot(211)
plot(group.I/nA,counter.n/duration)
xlabel('I (nA)')
ylabel('Firing rate (Hz)')
subplot(212)
plot(trace.times/ms,trace[i]/mV)
xlabel('Time (ms)')
ylabel('Vm (mV)')
show()
```

3.2.15 Example: I-F_curve2

Input-Frequency curve of a IF model Network: 1000 unconnected integrate-and-fire neurons (Brette-Gerstner) with an input parameter I. The input is set differently for each neuron. Spikes are sent to a 'neuron' group with the same size and variable n, which has the role of a spike counter.

```
from brian import *

N=1000
tau=10*ms
eqs='''
dv/dt=(v0-v)/tau : volt
v0 : volt
'''
group=NeuronGroup(N,model=eqs,threshold=10*mV,reset=0*mV,refractory=5*ms)
group.v=0*mV
group.v0=linspace(0*mV,20*mV,N)

counter=SpikeCounter(group)

duration=5*second
run(duration)
plot(group.v0/mV,counter.count/duration)
show()
```

3.2.16 Example: if

A very simple example Brian script to show how to implement an integrate and fire model. In this example, we also drive the single integrate and fire neuron with regularly spaced spikes from the `SpikeGeneratorGroup`.

```
from brian import *

tau = 10*ms
Vr = -70*mV
Vt = -55*mV

model = Model(equations='''
    V : volt
    ''', threshold=Vt, reset=Vr)
G = NeuronGroup(1,model)

input = SpikeGeneratorGroup(1,[(0,t*ms) for t in linspace(10,100,25)])

C = Connection(input, G)
C[0,0] = 2*mV

M = StateMonitor(G, 'V', record=True)

G.V = Vr
run(100*ms)
plot(M.times/ms,M[0]/mV)
show()
```

3.2.17 Example: leaky_if

A very simple example Brian script to show how to implement a leaky integrate and fire model. In this example, we also drive the single leaky integrate and fire neuron with regularly spaced spikes from the `SpikeGeneratorGroup`.

```
from brian import *

tau = 10*ms
Vr = -70*mV
Vt = -55*mV

model = Model(equations='''
    dV/dt = -(V-Vr)/tau : volt
    ''', threshold=Vt, reset=Vr)
G = NeuronGroup(1,model)

spikes = linspace(10*ms,100*ms,25)
input = MultipleSpikeGeneratorGroup([spikes])

C = Connection(input, G)
C[0,0] = 5*mV

M = StateMonitor(G, 'V', record=True)

G.V = Vr
run(100*ms)
plot(M.times/ms,M[0]/mV)
show()
```

3.2.18 Example: minimalexample

Very short example program.

```
from brian import *

eqs='''
dv/dt = (ge+gi-(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)
P.v=-60*mV+10*mV*rand(len(P))
Pe=P.subgroup(3200)
Pi=P.subgroup(800)

Ce=Connection(Pe,P,'ge')
Ci=Connection(Pi,P,'gi')
Ce.connect_random(Pe, P, 0.02,weight=1.62*mV)
Ci.connect_random(Pi, P, 0.02,weight=-9*mV)

M=SpikeMonitor(P)

run(1*second)
```

```
raster_plot(M)
show()
```

3.2.19 Example: mirollo_strogatz

Mirollo-Strogatz network

```
from brian import *

tau=10*ms
v0=11*mV
N=20
w=.1*mV

group=NeuronGroup(N,model='dv/dt=(v0-v)/tau : volt',threshold=10*mV,reset=0*mV)

W=Connection(group,group,'v')
W.connect_full(group,group,weight=w)

group.v=rand(N)*10*mV

S=SpikeMonitor(group)

run(300*ms)

raster_plot(S)
show()
```

3.2.20 Example: multipleclocks

This example demonstrates using different clocks for different objects in the network. The clock `simclock` is the clock used for the underlying simulation. The clock `monclock` is the clock used for monitoring the membrane potential. This monitoring takes place less frequently than the simulation update step to save time and memory. Finally, the clock `inputclock` controls when the external 'current' `Iext` should be updated. In this case, we update it infrequently so we can see the effect on the network.

This example also demonstrates the @network_operation decorator. A function with this decorator will be run as part of the network update step, in sync with the clock provided (or the default one if none is provided).

```
from brian import *
# define the three clocks
simclock   = Clock(dt=0.1*ms)
monclock   = Clock(dt=0.3*ms)
inputclock = Clock(dt=100*ms)
# simple leaky I&F model with external 'current' Iext as a parameter
tau = 10*ms
eqs='''
dV/dt = (-V+Iext)/tau : volt
Iext: volt
'''
# A single leaky I&F neuron with simclock as its clock
model = Model(equation=eqs, reset=0*mV, threshold=10*mV, clock=simclock)
G = NeuronGroup(1, model=model)
G.V=5*mV
```

```
# This function will be run in sync with inputclock i.e. every 100 ms
@network_operation(clock=inputclock)
def update_Iext():
    G.Iext = rand(len(G)) * 20 * mV
# V is monitored in sync with monclock
MV = StateMonitor(G, 'V', record=0, clock=monclock)
# run and plot
run(1000*ms)
plot(MV.times/ms, MV[0]/mV)
show()
# You should see 10 different regions, sometimes Iext will be above threshold
# in which case you will see regular spiking at different rates, and sometimes
# it will be below threshold in which case you'll see exponential decay to that
# value
```

3.2.21 Example: named_threshold

Example with named threshold and reset variables

```
from brian import *
eqs='''
dge/dt = -ge/(5*ms) : volt
dgi/dt = -gi/(10*ms) : volt
dx/dt = (ge+gi-(x+49*mV))/(20*ms) : volt
'''
P=NeuronGroup(4000,model=eqs,threshold=Threshold(-50*mV,state='x'),\
              reset=Refractoriness(-60*mV,5*ms,state='x'))
#P=NeuronGroup(4000,model=eqs,threshold=Threshold(-50*mV,state='x'),\
#              reset=Reset(-60*mV,state='x')) # without refractoriness
P.x=-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, 0.02,weight=1.62*mV)
Ci.connect_random(Pi, P, 0.02,weight=-9*mV)
M=SpikeMonitor(P)
run(1*second)
raster_plot(M)
show()
```

3.2.22 Example: noisy_ring

Integrate-and-fire neurons with noise

```
from brian import *

tau=10*ms
sigma=.5
N=100
J=-1
mu=2

eqs="""
```

```
dv/dt=mu/tau+sigma/tau**.5*xi : 1
"""

group=NeuronGroup(N,model=eqs,threshold=1,reset=0)

C=Connection(group,group,'v')
for i in range(N):
    C[i,(i+1) % N]=J

#C.connect_full(group,group,weight=J)
#for i in range(N):
#    C[i,i]=0

S=SpikeMonitor(group)
trace=StateMonitor(group,'v',record=True)

run(500*ms)
i,t=S.spikes[-1]

subplot(211)
raster_plot(S)
subplot(212)
plot(trace.times/ms,trace[0])
show()
```

3.2.23 Example: parallelpython

Example of using Parallel Python 'pp' module for running multiple jobs

See (limited) documentation for PP at their website:

> http://www.parallelpython.com/

Each job server must have an up to date copy of Brian installed on it, and must run the pp jobserver script as follows:

> ppserver.py -a -s "He's not the Messiah, he's a very naughty boy"

This ppserver.py script is installed in the Scripts/ folder of your Python installation when you install pp. The -a option sets it to auto-discovery mode, so that nodes on your cluster running the ppserver can be automatically found by a process submitting jobs to it. The -s option is a shared secret, basically a password to prevent external access.

```
from brian import *
import pp

# We create a pp job server in one of the following ways (see pp documentation for more info):

#js = pp.Server(ppservers=('computer1.complete.domain.name','computer2.complete.domain.name')) # For
#js = pp.Server(ppservers=('computer1','computer2')) # For running over the local network
#js = pp.Server(ppservers=('*',)) # For running with autodiscovery mode over the local network
js = pp.Server(ppservers=()) # For running only on your own computer (but using multiple CPU cores)

# Now we write a function which defines the job to be executed. Note that
# there are some annoying features of pp: functions cannot use any global
# variables, so we have to import all the Brian functions etc. inside the
# function. However, we have a function decorator @ppfunction which does
# the work for you. Unfortunately, it needs to create an external file
# which will be named modulename_functionname_parallelpythonised.py, so
# in this example it will be called:
#   parallelpython_howmanyspikes_parallelpythonised.py
# This file contains the transformed code to make it work smoothly with
# parallelpython.

@ppfunction
def howmanyspikes(excitatory_weight):
    eqs='''
    dv/dt = (ge+gi-(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)
    P.v=-60*mV+10*mV*rand(len(P))
    Pe=P.subgroup(3200)
    Pi=P.subgroup(800)
    Ce=Connection(Pe,P,'ge')
    Ci=Connection(Pi,P,'gi')
    Ce.connect_random(Pe, P, 0.02,weight=excitatory_weight)
    Ci.connect_random(Pi, P, 0.02,weight=-9*mV)
    M=SpikeMonitor(P)
    run(100*ms)
    return M.nspikes

# Now we submit jobs. See the pp documentation details of what is going on here.
# In short write j = js.submit(func, args, depfuncs, modules) to submit function
# func with arguments args (which should be a tuple of values), depending on
# functions depfuncs (a tuple of functions), relying on modules (another tuple
# of strings). The job is submitted. To get the result of a job, you write
# val = j(), but executing this line will wait until the job is complete.

# Single job

#f = js.submit(howmanyspikes, (1.62*mV,), (), ('brian','numpy'))
#print f()

# Multiple jobs, and results plotted

excitatory_weight_range = linspace(0,4,20)
jobs = [ js.submit(howmanyspikes, (ew*mV,), (), ('brian','numpy')) for ew in excitatory_weight_range
numspikes = [ j() for j in jobs ]

js.print_stats()

plot(excitatory_weight_range, numspikes)
show()
```

3.2.24 Example: phase_locking

Phase locking of IF neurons to a periodic input

```
from brian import *

tau=20*ms
```

```
N=100
b=1.2 # constant current mean, the modulation varies
f=10*Hz

eqs='''
dv/dt=(-v+a*sin(2*pi*f*t)+b)/tau : 1
a : 1
'''

neurons=NeuronGroup(N,model=eqs,threshold=1,reset=0)
neurons.v=rand(N)
neurons.a=linspace(.05,0.75,N)
S=SpikeMonitor(neurons)
trace=StateMonitor(neurons,'v',record=50)

run(1000*ms)
subplot(211)
raster_plot(S)
subplot(212)
plot(trace.times/ms,trace[50])
show()
```

3.2.25 Example: pickle_loadnet

Pickling example, see also pickle_savenet.py

```
from brian import *
import pickle

inputfile = open('data.pkl','rb')
obj = pickle.load(inputfile)
inputfile.close()

clk, eqs, P, Pe, Pi, Ce, Ci, M, net = obj

net.run(100*ms)
raster_plot(M)
show()
```

3.2.26 Example: pickle_savenet

Pickling example, see also pickle_loadnet.py

```
from brian import *
import pickle

clk = Clock()
eqs='''
dv/dt = (ge+gi-(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)
P.v=-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, 0.02,weight=1.62*mV)
Ci.connect_random(Pi, P, 0.02,weight=-9*mV)
M=SpikeMonitor(P)
net = Network(P, Ce, Ci, M)
net.run(100*ms)

obj = (clk, eqs, P, Pe, Pi, Ce, Ci, M, net)

output = open('data.pkl', 'wb')
pickle.dump(obj,output,-1)
output.close()

# show what we've computed so far...
raster_plot(M)
show()
```

3.2.27 Example: poisson

This example demonstrates the PoissonGroup object. Here we have used a custom function to generate different rates at different times.

This example also demonstrates a custom SpikeMonitor.

```
#import brian_no_units # uncomment to run faster
from brian import *

# Rates

r1 = arange(101, 201)*0.1*Hz
r2 = arange(1, 101)*0.1*Hz

def myrates(t):
    if t<10*second:
        return r1
    else:
        return r2
# More compact: myrates=lambda t: (t<10*second and r1) or r2

# Neuron group
P=PoissonGroup(100,myrates)

# Calculation of rates

ns=zeros(len(P))

def ratemonitor(spikes):
    ns[spikes]+=1

Mf = SpikeMonitor(P,function=ratemonitor)
M  = SpikeMonitor(P)

# Simulation and plotting
```

```
run(10*second)
print "Rates after 10s:"
print ns/(10*second)

ns[:] = 0
run(10*second)
print "Rates after 20s:"
print ns/(10*second)

raster_plot()
show()
```

3.2.28 Example: poissongroup

Poisson input to an IF model

```
from brian import *

PG = PoissonGroup(1,lambda t:200*Hz*(1+cos(2*pi*t*50*Hz)))
IF = NeuronGroup(1,model='dv/dt=-v/(10*ms) : volt',reset=0*volt,threshold=10*mV)

C = Connection(PG,IF,'v')
C.connect_full(PG,IF,3*mV)

MS = SpikeMonitor(PG,True)
Mv = StateMonitor(IF,'v',record=True)
rates = StateMonitor(PG,'rate',record=True)

run(100*ms)

subplot(211)
plot(rates.times/ms,rates[0]/Hz)
subplot(212)
plot(Mv.times/ms,Mv[0]/mV)

show()
```

3.2.29 Example: pulsepacket

This example basically replicates what the Brian PulsePacket object does, and then compares to that object.

```
from brian import *
from random import gauss, shuffle

# Generator for pulse packet
def pulse_packet(t, n, sigma):
    # generate a list of n times with Gaussian distribution, sort them in time, and
    # then randomly assign the neuron numbers to them
    times = [gauss(t, sigma) for i in range(n)]
    times.sort()
    neuron = range(n)
    shuffle(neuron)
    return zip(neuron, times) # returns a list of pairs (i,t)
```

```
G1 = SpikeGeneratorGroup(1000, pulse_packet(50*ms, 1000, 5*ms))
M1 = SpikeMonitor(G1)
PRM1 = PopulationRateMonitor(G1,bin=1*ms)

G2 = PulsePacket(50*ms, 1000, 5*ms)
M2 = SpikeMonitor(G2)
PRM2 = PopulationRateMonitor(G2,bin=1*ms)

run(100*ms)

subplot(221)
raster_plot(M1)
subplot(223)
plot(PRM1.rate)
subplot(222)
raster_plot(M2)
subplot(224)
plot(PRM2.rate)
show()
```

3.2.30 Example: rate_model

A rate model

```
from brian import *

N=50000
tau=20*ms
I=10*Hz
eqs='''
dv/dt=(I-v)/tau : Hz # note the unit here: this is the output rate
'''
group=NeuronGroup(N,eqs,threshold=PoissonThreshold())
S=PopulationRateMonitor(group,bin=1*ms)

run(100*ms)

plot(S.rate)
show()
```

3.2.31 Example: ring

A ring of integrate-and-fire neurons.

```
from brian import *

tau=10*ms
v0=11*mV
N=20
w=1*mV

ring=NeuronGroup(N,model='dv/dt=(v0-v)/tau : volt',threshold=10*mV,reset=0*mV)
```

```
W=Connection(ring,ring,'v')
for i in range(N):
    W[i,(i+1) % N]=w

ring.v=rand(N)*10*mV

S=SpikeMonitor(ring)

run(300*ms)

raster_plot(S)
show()
```

3.2.32 Example: sfc

Implementation of synfire chain from Diesmann et al. 1999

Dan Goodman - Dec. 2007

```
#import brian_no_units
from brian import *
import time

from brian.library.IF import *
from brian.library.synapses import *

def minimal_example():
    # Neuron model parameters
    Vr = -70*mV
    Vt = -55*mV
    taum = 10*ms
    taupsp = 0.325*ms
    weight = 4.86 * mV
    # Neuron model
    equations = Equations('''
        dV/dt = (-(V-Vr)+x)*(1./taum)                             : volt
        dx/dt = (-x+y)*(1./taupsp)                                : volt
        dy/dt = -y*(1./taupsp)+25.27*mV/ms+(39.24*mV/ms**0.5)*xi : volt
        ''')

    # Neuron groups
    P = NeuronGroup(N=1000, model=equations,
                  threshold=Vt,reset=Vr,refractory=1*ms)
#    P = NeuronGroup(N=1000, model=(dV,dx,dy),init=(0*volt,0*volt,0*volt),
#                  threshold=Vt,reset=Vr,refractory=1*ms)

    Pinput = PulsePacket(t=50*ms,n=85,sigma=1*ms)
    # The network structure
    Pgp = [ P.subgroup(100) for i in range(10)]
    C = Connection(P,P,'y')
    for i in range(9):
        C.connect_full(Pgp[i],Pgp[i+1],weight)
    Cinput = Connection(Pinput,P,'y')
    Cinput.connect_full(Pinput,Pgp[0],weight)
    # Record the spikes
    Mgp = [SpikeMonitor(p,record=True) for p in Pgp]
    Minput = SpikeMonitor(Pinput,record=True)
    monitors = [Minput]+Mgp
    # Setup the network, and run it
    P.V = Vr + rand(len(P)) * (Vt-Vr)
    run(100*ms)
    # Plot result
    raster_plot(showgrouplines=True,*monitors)
    show()


# DEFAULT PARAMATERS FOR SYNFIRE CHAIN
# Approximates those in Diesman et al. 1999
model_params = Parameters(
    # Simulation parameters
    dt = 0.1*ms,
    duration = 100 * ms,
    # Neuron model parameters
    taum = 10*ms,
    taupsp = 0.325*ms,
    Vt = -55*mV,
    Vr = -70*mV,
    abs_refrac = 1*ms,
    we = 34.7143,
    wi = -34.7143,
    psp_peak = 0.14 * mV,
    # Noise parameters
    noise_neurons = 20000,
    noise_exc = 0.88,
    noise_inh = 0.12,
    noise_exc_rate = 2 * Hz,
    noise_inh_rate = 12.5 * Hz,
    computed_model_parameters = """
    noise_mu = noise_neurons * (noise_exc * noise_exc_rate - noise_inh * noise_inh_rate ) * psp_peak
    noise_sigma = (noise_neurons * (noise_exc * noise_exc_rate + noise_inh * noise_inh_rate ))**.5 *
    """
    )

# MODEL FOR SYNFIRE CHAIN
# Excitatory PSPs only
def Model(p):
    equations = Equations('''
        dV/dt = (-(V-Vr)+x)*(1./taum)                            : volt
        dx/dt = (-x+y)*(1./taupsp)                               : volt
        dy/dt = -y*(1./taupsp)+25.27*mV/ms+(39.24*mV/ms**0.5)*xi : volt
        ''')
    return Model(equations=equations,threshold=p.Vt,reset=p.Vr,refractory=p.abs_refrac,\
                  init=(0*volt,0*volt,0*volt))

default_params = Parameters(
    # Network parameters
    num_layers = 10,
    neurons_per_layer = 100,
    neurons_in_input_layer = 100,
    # Initiating burst parameters
    initial_burst_t = 50 * ms,
    initial_burst_a = 85,
    initial_burst_sigma = 1 * ms,
    # these values are recomputed whenever another value changes
    computed_network_parameters = """
    total_neurons = neurons_per_layer * num_layers
    """,
    # plus we also use the default model parameters
    **model_params
    )

# DEFAULT NETWORK STRUCTURE
# Single input layer, multiple chained layers
class DefaultNetwork(Network):
    def __init__(self,p):
        # define groups
        chaingroup = NeuronGroup(N=p.total_neurons, model=Model(p))
        inputgroup = PulsePacket(p.initial_burst_t,p.neurons_in_input_layer,p.initial_burst_sigma)
        layer = [ chaingroup.subgroup(p.neurons_per_layer) for i in range(p.num_layers) ]
        # connections
        chainconnect = Connection(chaingroup,chaingroup,2)
        for i in range(p.num_layers-1):
            chainconnect.connect_full(layer[i],layer[i+1],p.psp_peak*p.we)
        inputconnect = Connection(inputgroup,chaingroup,2)
        inputconnect.connect_full(inputgroup,layer[0],p.psp_peak*p.we)
        # monitors
        chainmon = [SpikeMonitor(g,True) for g in layer]
        inputmon = SpikeMonitor(inputgroup,True)
        mon = [inputmon]+chainmon
        # network
        Network.__init__(self,chaingroup,inputgroup,chainconnect,inputconnect,mon)
        # add additional attributes to self
        self.mon = mon
        self.inputgroup = inputgroup
        self.chaingroup = chaingroup
        self.layer = layer
        self.params = p
    def prepare(self):
        Network.prepare(self)
        self.reinit()
    def reinit(self,p=None):
        Network.reinit(self)
        q = self.params
        if p is None: p = q
        self.inputgroup.generate(p.initial_burst_t,p.initial_burst_a,p.initial_burst_sigma)
        self.chaingroup.V=q.Vr+rand(len(self.chaingroup))*(q.Vt-q.Vr)
    def run(self):
        Network.run(self,self.params.duration)
    def plot(self):
        raster_plot(ylabel="Layer",title="Synfire chain raster plot",
                    color=(1,0,0),markersize=3,
                    showgrouplines=True,spacebetweengroups=0.2,grouplinecol=(0.5,0.5,0.5),
                    *self.mon)

def estimate_params(mon,time_est):
    # Quick and dirty algorithm for the moment, for a more decent algorithm
    # use leastsq algorithm from scipy.optimize.minpack to fit const+Gaussian
    # http://www.scipy.org/doc/api_docs/SciPy.optimize.minpack.html#leastsq
    i, times = zip(*mon.spikes)
    times = qarray(times)
    times = times[abs(times-time_est)<15*ms]
    if len(times)==0:
        return (0,0*ms)
    better_time_est = times.mean()
    times = times[abs(times-time_est)<5*ms]
    if len(times)==0:
        return (0,0*ms)
    return (len(times),times.std())

def single_sfc():
    net = DefaultNetwork(default_params)
    net.run()
    net.plot()

def state_space(grid, neuron_multiply, verbose=True):
    amin = 0
    amax = 100
    sigmamin = 0.*ms
    sigmamax = 3.*ms

    params = default_params()
    params.num_layers = 1
    params.neurons_per_layer = params.neurons_per_layer * neuron_multiply

    net = DefaultNetwork(params)

    i=0
    # uncomment these 2 lines for TeX labels
    #import pylab
    #pylab.rc_params.update({'text.usetex': True})
    if verbose:
        print "Completed:"
    start_time = time.time()
    figure()
    for ai in range(grid+1):
        for sigmai in range(grid+1):
            a = int(amin + (ai * (amax-amin)) / grid)
            if a>amax: a=amax
            sigma = sigmamin + sigmai * (sigmamax-sigmamin) / grid
            params.initial_burst_a, params.initial_burst_sigma = a, sigma
            net.reinit(params)
            net.run()
            (newa,newsigma) = estimate_params(net.mon[-1],params.initial_burst_t)
            newa = float(newa)/float(neuron_multiply)
            col = (float(ai)/float(grid),float(sigmai)/float(grid),0.5)
            plot([sigma/ms,newsigma/ms],[a,newa],color=col)
            plot([sigma/ms],[a],marker='.',color=col,markersize=15)
            i+=1
            if verbose:
                print str(int(100.*float(i)/float((grid+1)**2)))+"%",
        if verbose:
            print
    if verbose:
        print "Evaluation time:", time.time()-start_time,"seconds"
    xlabel(r'$\sigma$ (ms)')
    ylabel('a')
    title('Synfire chain state space')
    axis([sigmamin/ms,sigmamax/ms,amin,amax])
```

```
minimal_example()
#print 'Computing SFC with multiple layers'
#single_sfc()
#print 'Plotting SFC state space'
#state_space(3,1)
#state_space(8,10)
#state_space(10,50)
#state_space(10,150)
#show())
```

3.2.33 Example: short_term_plasticity

Example with Tsodyks STP model Neurons with regular inputs and depressing synapses

```
from brian import *

U_SE=.67
tau_e=3*ms
taum=50*ms
tau_rec=800*ms
A_SE=250*pA
Rm=100*Mohm
N=10

eqs='''
dx/dt=rate : 1
dR/dt=(1-R)/tau_rec : 1
rate : Hz
'''

def reset_STP(P,spikes):
    P.R_[spikes]-=U_SE*P.R_[spikes]
    P.x[spikes]=0

input=NeuronGroup(N,model=eqs,threshold=1.,reset=reset_STP)
MR=StateMonitor(input,'R',record=[0,N-1])
input.R=1
input.rate=linspace(5*Hz,30*Hz,N)

eqs_neuron='''
dv/dt=(Rm*i-v)/taum:volt
di/dt=-i/tau_e:amp
'''
neuron=NeuronGroup(N,model=eqs_neuron)

C=Connection(input,neuron,'i',modulation='R')
C.connect_one_to_one(input,neuron,A_SE*U_SE)
trace=StateMonitor(neuron,'v',record=[0,N-1])

run(1000*ms)
subplot(221)
plot(MR.times/ms,MR[0])
title('R')
subplot(223)
plot(trace.times/ms,trace[0]/mV)
title('Vm')
```

```
subplot(222)
plot(MR.times/ms,MR[N-1])
title('R')
subplot(224)
plot(trace.times/ms,trace[N-1]/mV)
title('Vm')
show()
```

3.2.34 Example: short_term_plasticity2

Network (CUBA) with depressing synapses Excitatory synapses are depressing, inhibitory ones are not

```
from brian import *

U_SE=.2
tau_rec=500*ms

eqs='''
dv/dt = (ge+gi-(v+49*mV))/(20*ms) : volt
dge/dt = -ge/(5*ms) : volt
dgi/dt = -gi/(10*ms) : volt
dR/dt=(1-R)/tau_rec : 1 # synaptic resource (in [0,1])
'''

def reset_STP(P,spikes):
    P.R_[spikes]-=U_SE*P.R_[spikes]
    P.v_[spikes]=-60*mV

P=NeuronGroup(4000,model=eqs,threshold=-50*mV,reset=reset_STP)
P.v=-60*mV+rand(4000)*10*mV
P.R=1
Pe=P.subgroup(3200)
Pi=P.subgroup(800)
Ce=Connection(Pe,P,'ge',modulation='R')
Ci=Connection(Pi,P,'gi')
Ce.connect_random(Pe, P, 0.02,weight=1.62*mV)
Ci.connect_random(Pi, P, 0.02,weight=-9*mV)
M=SpikeMonitor(P)
trace=StateMonitor(P,'R',record=0)
rate=PopulationRateMonitor(P)
run(1*second)
print M.nspikes,"spikes"
subplot(311)
raster_plot(M)
subplot(312)
plot(trace.times/ms,trace[0])
subplot(313)
plot(rate.times/ms,rate.smooth_rate(5*ms))
show()
```

3.2.35 Example: STDP1

Spike-timing dependent plasticity Adapted from Song, Miller and Abbott (2000) Takes a long time!

```
from brian import *
from time import time
#set_global_preferences(useweave=True)
taum=20*ms
tau_post=20*ms
tau_pre=20*ms
Ee=0*mV
vt=-54*mV
vr=-60*mV
El=-70*mV
taue=5*ms
gmax=0.015
dA_pre=gmax*.005
dA_post=-dA_pre*1.05

eqs_poisson='''
rate : Hz
dA_pre/dt=-A_pre/tau_pre : 1
'''

eqs_neurons='''
dv/dt=(ge*(Ee-v)+El-v)/taum : volt
dge/dt=-ge/taue : 1
dA_post/dt=-A_post/tau_post : 1
'''

def poisson_reset(P,spikes):
    for i in spikes:
        synapses[i,:]=clip(synapses[i,:]+neurons.A_post_,0,gmax)
    P.A_pre_[spikes]+=dA_pre

def neurons_reset(P,spikes):
    P.v_[spikes]=vr
    for i in spikes:
        synapses[:,i]=clip(synapses[:,i]+input.A_pre_,0,gmax)
    P.A_post_[spikes]+=dA_post

input=NeuronGroup(1000,model=eqs_poisson,threshold=PoissonThreshold(),reset=poisson_reset)
neurons=NeuronGroup(1,model=eqs_neurons,threshold=vt,reset=neurons_reset)
synapses=Connection(input,neurons,'ge',structure='dense')
synapses.connect(input,neurons,rand(len(input),len(neurons))*gmax)
neurons.v=vr
input.rate=10*Hz

rate=PopulationRateMonitor(neurons)

start_time=time()
run(100*second)
#run(2*second)
print "Simulation time:",time()-start_time

subplot(211)
plot(rate.times/ms,rate.smooth_rate(500*ms))
subplot(212)
plot(synapses.W.squeeze(),'.')
show()
```

3.2.36 Example: stim2d

Example of a 2D stimulus, see the complete description at the Brian Cookbook.

```python
from brian import *
import scipy.ndimage as im

__all__ = ['bar','StimulusArrayGroup']

def bar(width, height, thickness, angle):
    '''
    An array of given dimensions with a bar of given thickness and angle
    '''
    stimulus = zeros((width, height))
    stimulus[:,int(height/2.-thickness/2.):int(height/2.+thickness/2.)] = 1.
    stimulus = im.rotate(stimulus, angle, reshape=False)
    return stimulus

class StimulusArrayGroup(PoissonGroup):
    '''
    A group of neurons which fire with a given stimulus at a given rate

    The argument ``stimulus`` should be a 2D array with values between 0 and 1.
    The point in the stimulus array at position (y,x) will correspond to the
    neuron with index i=y*width+x. This neuron will fire Poisson spikes at
    ``rate*stimulus[y,x]`` Hz. The stimulus will start at time ``onset``
    for ``duration``.
    '''
    def __init__(self, stimulus, rate, onset, duration):
        height, width = stimulus.shape
        stim = stimulus.ravel()*rate
        self.stimulus = stim
        def stimfunc(t):
            if onset<t<(onset+duration):
                return stim
            else:
                return 0.*Hz
        PoissonGroup.__init__(self, width*height, stimfunc)

if __name__=='__main__':
    import pylab
    subplot(121)
    stim = bar(100,100,10,90)*0.9+0.1
    pylab.imshow(stim, origin='lower')
    pylab.gray()
    G = StimulusArrayGroup(stim, 50*Hz, 100*ms, 100*ms)
    M = SpikeMonitor(G)
    run(300*ms)
    subplot(122)
    raster_plot(M)
    axis(xmin=0,xmax=300)
    show()
```

3.2.37 Example: stopping

Network to demonstrate stopping a simulation during a run

Have a fully connected network of integrate and fire neurons with input fed by a group of Poisson neurons with a steadily increasing rate, want to determine the point in time at which the network of integrate and fire neurons switches from no firing to all neurons firing, so we have a network_operation called stop_condition that calls the stop() function if the monitored network firing rate is above a minimum threshold.

```
from brian import *

clk = Clock()

Vr = 0*mV
El = 0*mV
Vt = 10*mV
tau = 10*ms
weight = 0.2*mV
duration = 100*msecond
max_input_rate = 10000*Hz
num_input_neurons = 1000
input_connection_p = 0.1
rate_per_neuron = max_input_rate/(num_input_neurons*input_connection_p)

model = Model(equations='''
    dV/dt=-(V-El)/tau : volt
    ''',
    threshold=Vt,
    reset=Vr)

P = PoissonGroup(num_input_neurons, lambda t: rate_per_neuron*(t/duration))

G = NeuronGroup(1000, model=model)
G.V = Vr+(Vt-Vr)*rand(len(G))

CPG = Connection(P, G)
CPG.connect_random(P, G, p=input_connection_p, weight=weight)

CGG = Connection(G, G)
CGG.connect_full(G, G, weight=weight)

MP = PopulationRateMonitor(G, bin=1*ms)

@network_operation
def stop_condition():
    if MP.rate[-1]*Hz>10*Hz:
        stop()

run(duration)

print "Reached population rate>10 Hz by time", clk.t, "+/- 1 ms."
```

3.2.38 Example: synfire_chains

Synfire chains (from Diesmann et al, 1999)

```
from brian import *
# Neuron model parameters
Vr = -70*mV
Vt = -55*mV
```

```
taum = 10*ms
taupsp = 0.325*ms
weight = 4.86 * mV
# Neuron model
eqs=Equations('''
dV/dt=(-(V-Vr)+x)*(1./taum) : volt
dx/dt=(-x+y)*(1./taupsp) : volt
dy/dt=-y*(1./taupsp)+25.27*mV/ms+\
    (39.24*mV/ms**0.5)*xi : volt
''')
# Neuron groups
P = NeuronGroup(N=1000, model=eqs,
    threshold=Vt,reset=Vr,refractory=1*ms)
Pinput = PulsePacket(t=50*ms,n=85,sigma=1*ms)
# The network structure
Pgp = [ P.subgroup(100) for i in range(10)]
C = Connection(P,P,'y')
for i in range(9):
    C.connect_full(Pgp[i],Pgp[i+1],weight)
Cinput = Connection(Pinput,P,'y')
Cinput.connect_full(Pinput,Pgp[0],weight)
# Record the spikes
Mgp = [SpikeMonitor(p,record=True) for p in Pgp]
Minput = SpikeMonitor(Pinput,record=True)
monitors = [Minput]+Mgp
# Setup the network, and run it
P.V = Vr + rand(len(P)) * (Vt-Vr)
run(100*ms)
# Plot result
raster_plot(showgrouplines=True,*monitors)
show()
```

3.2.39 Example: topographic_map

Topographic map - an example of complicated connections. Two layers of neurons. The first layer is connected randomly to the second one in a topographical way. The second layer has random lateral connections.

```
from brian import *

N=100
tau=10*ms
tau_e=2*ms # AMPA synapse
eqs='''
dv/dt=(I-v)/tau : volt
dI/dt=-I/tau_e : volt
'''

rates=zeros(N)*Hz
rates[N/2-10:N/2+10]=ones(20)*30*Hz
layer1=PoissonGroup(N,rates=rates)
layer2=NeuronGroup(N,model=eqs,threshold=10*mV,reset=0*mV)

topomap=lambda i,j:exp(-abs(i-j)*.1)*3*mV
feedforward=Connection(layer1,layer2)
feedforward.connect_random(layer1,layer2,.5,weight=topomap)
#feedforward[2,3]=1*mV
```

```
lateralmap=lambda i,j:exp(-abs(i-j)*.05)*0.5*mV
recurrent=Connection(layer2,layer2)
recurrent.connect_random(layer2,layer2,.5,weight=lateralmap)

spikes=SpikeMonitor(layer2)

run(1*second)
subplot(211)
raster_plot(spikes)
subplot(223)
imshow(array(feedforward.W.todense()), interpolation='nearest', origin='lower')
title('Feedforward connection strengths')
subplot(224)
imshow(array(recurrent.W.todense()), interpolation='nearest', origin='lower')
title('Recurrent connection strengths')
show()
```

3.2.40 Example: topographic_map2

Topographic map - an example of complicated connections. Two layers of neurons. The first layer is connected randomly to the second one in a topographical way. The second layer has random lateral connections. Each neuron has a position x[i].

```
from brian import *

N=100
tau=10*ms
tau_e=2*ms # AMPA synapse
eqs='''
dv/dt=(I-v)/tau : volt
dI/dt=-I/tau_e : volt
'''

rates=zeros(N)*Hz
rates[N/2-10:N/2+10]=ones(20)*30*Hz
layer1=PoissonGroup(N,rates=rates)
layer1.x=linspace(0.,1.,len(layer1)) # abstract position between 0 and 1
layer2=NeuronGroup(N,model=eqs,threshold=10*mV,reset=0*mV)
layer2.x=linspace(0.,1.,len(layer2))

# Generic connectivity function
topomap=lambda i,j,x,y,sigma: exp(-abs(x[i]-y[j])/sigma)

feedforward=Connection(layer1,layer2)
feedforward.connect_random(layer1,layer2,.5,
                           weight=lambda i,j:topomap(i,j,layer1.x,layer2.x,.3)*3*mV)

recurrent=Connection(layer2,layer2)
recurrent.connect_random(layer2,layer2,.5,
                         weight=lambda i,j:topomap(i,j,layer1.x,layer2.x,.2)*.5*mV)

spikes=SpikeMonitor(layer2)

run(1*second)
subplot(211)
```

```
raster_plot(spikes)
subplot(223)
imshow(feedforward.W.todense(), interpolation='nearest', origin='lower')
title('Feedforward connection strengths')
subplot(224)
imshow(recurrent.W.todense(), interpolation='nearest', origin='lower')
title('Recurrent connection strengths')
show()
```

3.2.41 Example: transient_sync

Transient synchronisation in a population of noisy IF neurons with distance-dependent synaptic weights (organised as a ring)

```
from brian import *

tau=10*ms
N=100
v0=5*mV
sigma=4*mV
group=NeuronGroup(N,model='dv/dt=(v0-v)/tau + sigma*xi/tau**.5 : volt',\
                  threshold=10*mV,reset=0*mV)
C=Connection(group,group,'v',structure='dense') # use a dense matrix
#f=lambda i,j:.5*mV*exp(-abs(i-j)*.1)
#C.connect_full(group,group,weight=lambda i,j:f(i,j)+f(i+N,j)+f(i,j+N))
C.connect_full(group,group,weight=lambda i,j:.4*mV*cos(2.*pi*(i-j)*1./N))
S=SpikeMonitor(group)
R=PopulationRateMonitor(group)
group.v=rand(N)*10*mV

run(5000*ms)
subplot(211)
raster_plot(S)
subplot(223)
imshow(C.W, interpolation='nearest')
title('Synaptic connections')
subplot(224)
plot(R.times/ms,R.smooth_rate(2*ms,filter='flat'))
title('Firing rate')
show()
```

3.2.42 Example: two_neurons

Two connected neurons with delays

```
from brian import *
tau=10*ms
w=-1*mV
v0=11*mV
neurons=NeuronGroup(2,model='dv/dt=(v0-v)/tau : volt',threshold=10*mV,reset=0*mV,\
                    max_delay=5*ms)
neurons.v=rand(2)*10*mV
W=Connection(neurons,neurons,'v',delay=2*ms)
W[0,1]=w
```

```
W[1,0]=w
S=StateMonitor(neurons,'v',record=True)
#mymonitor=SpikeMonitor(neurons[0])
mymonitor=PopulationSpikeCounter(neurons)

run(500*ms)
plot(S.times/ms,S[0]/mV)
plot(S.times/ms,S[1]/mV)
save('trace.txt',(S.times/ms,S[0]/mV))
print mymonitor.nspikes
show()
```

CHAPTER

FOUR

User manual

The SciPy, NumPy and PyLab packages are documented on the following web sites:

- http://www.scipy.org/Getting_Started
- http://www.scipy.org/Documentation
- http://matplotlib.sourceforge.net/matplotlib.pylab.html

Brian itself is documented in the following sections:

4.1 Units

4.1.1 Basics

Brian has a system for physical quantities with units built in, and most of the library functions require that variables have the right units. This restriction is useful in catching hard to find errors based on using incorrect units, and ensures that simulated models are physically meaningful. For example, running the following code causes an error:

```
>>> from brian import *
>>> c = Clock(t=0)

Traceback (most recent call last):
  File "<pyshell#1>", line 1, in <module>
    c = Clock(t=0)
  File "C:\Documents and Settings\goodman\Mes documents\Programming\Python simulator\Brian\units.py",
    raise DimensionMismatchError("Function " + f.__name__ + " variable " + k + " should have dimensio
DimensionMismatchError: Function __init__ variable t should have dimensions of s, dimensions were (1)
```

You can see that Brian raises a `DimensionMismatchError` exception, because the `Clock` object expects `t` to have units of time. The correct thing to write is:

```
>>> from brian import *
>>> c = Clock(t=0*second)
```

Similarly, attempting to do numerical operations with inconsistent units will raise an error:

```
>>> from brian import *
>>> 3*second+2*metre

Traceback (most recent call last):
  File "<pyshell#38>", line 1, in <module>
    3*second+2*metre
  File "C:\Documents and Settings\goodman\Mes documents\Programming\Python simulator\Brian\units.py",
    if dim==self.dim:
DimensionMismatchError: Addition, dimensions were (s) (m)
```

4.1.2 Units defined in Brian

The following fundamental SI unit names are defined:

> `metre`, `meter` (US spelling), `kilogram`, `second`, `amp`, `kelvin`, `mole`, `candle`

These derived SI unit names are also defined:

> `radian`, `steradian`, `hertz`, `newton`, `pascal`, `joule`, `watt`, `coulomb`, `volt`, `farad`, `ohm`, `siemens`, `weber`, `tesla`, `henry`, `celsius`, `lumen`, `lux`, `becquerel`, `gray`, `sievert`, `katal`

In addition, you can form scaled versions of these units with any of the standard SI prefixes:

Factor	Name	Symbol	Factor	Name	Symbol
10^24	yotta	Y	10^-24	yocto	y
10^21	zetta	Z	10^-21	zepto	z
10^18	exa	E	10^-21	zepto	z
10^15	peta	P	10^-15	femto	f
10^12	tera	T	10^-12	pico	p
10^9	giga	G	10^-9	nano	n
10^6	mega	M	10^-6	micro	u (mu in SI)
10^3	kilo	k	10^-3	milli	m
10^2	hecto	h	10^-2	centi	c
10^1	deka	da	10^-1	deci	d

So for example, you could write `fnewton` for femto-newtons, `Mwatt` for megawatt, etc.

There are also units for 2nd and 3rd powers of each of the above units, for example `metre3 = metre**3`, `watt2 = watt*watt`, etc.

You can optionally use short names for some units derived from volts, amps, farads, siemens, seconds, hertz and metres: `mV, mA, uA, nA, pA, mF, uF, nF, mS, uS, ms, Hz, kHz, MHz, cm, cm2, cm3, mm, mm2, mm3, um, um2, um3`. Since these names are so short, there is a danger that they might clash with your own variables names, so watch out for that.

4.1.3 Arrays and units

Versions of Brian before 1.0 had a system for allowing arrays to have units, this has been removed for the 1.0 release because of stability problems - as new releases of NumPy, SciPy and PyLab came out it required changes to the units code. Now all arrays used by Brian are standard NumPy arrays and have no units.

4.1.4 Checking units

Units are automatically checked when arithmetic operations are performed, and when a neuron group is initialised (the consistency of the differential equations is checked). They can also be checked explictly when a user-defined function is called by using the decorator `@check_units`, which can be used as follows:

```
@check_units(I=amp,R=ohm,wibble=metre,result=volt)
def getvoltage(I,R,**k):
    return I*R
```

Remarks:

- not all arguments need to be checked
- keyword arguments may be checked
- the result can optionnally be checked
- no error is raised if the values are strings.

4.1.5 Disabling units

Unit checking can slow down the simulations. The units system can be disabled by inserting `import brian_no_units` as the *first line* of the script, e.g.:

```
import brian_no_units
from brian import *
# etc
```

Internally, physical quantities are floats with an additional units information. The float value is the value in the SI system. For example, `float(mV)` returns `0.001`. After importing `brian_no_units`, all units are converted to their float values. For example, `mV` is simply the number `0.001`. This may also be a solution when using external libraries which are not compatible with units (but see next section).

A good practice is to develop the script with units on, then switch them off once the script runs correctly.

4.1.6 Converting quantities

In many situations, physical quantities need to be expressed with given units. For example, one might want to plot a graph of the membrane potential in mV as a function of time in ms. The following code:

```
plot(t,V)
```

displays the trace with time in seconds and potential in volts. The simplest solution to have time in ms and potential in mV is to use units operations:

```
plot(t/ms,V/mV)
```

Here, t/ms is a unitless array containing the values of t in ms. The same trick may be applied to use external functions which do not work with units (convert the arguments to unitless quantities as above).

4.2 Models and neuron groups

4.2.1 `Equations`

`Equations` objects are initialised with a string as follows:

```
eqs=Equations('''
dx/dt=(y-x)/tau + a : volt   # differential equation
y=2*x : volt                 # equation
z=x                          # alias
a : volt/second              # parameter
''')
```

It is possible to pass a string instead of an `Equations` object when initialising a neuron group. In that case, the string is implicitly converted to an `Equations` object. There are 4 different types of equations:

- Differential equations: a differential equation, also defining the variable as a state variable in neuron groups.
- Equations: a non-differential equation, which is useful for defining complicated models. The variables are also accessible for reading in neuron groups, which is useful for monitoring. The graph of dependencies of all equations must have no cycle.
- Aliases: the two variables are equivalent. This is implemented as an equation, with write access in neuron groups.
- Parameters: these are constant variables, but their values can differ from one neuron to the next. They are implemented internally as differential equations with zero derivative.

Right hand sides must be valid Python expressions, possibly including comments and multiline characters (`\`).

The units of all variables except aliases must be specified. Note that in first line, the units *volt* are meant for x, not dx/dt. The consistency of all units is checked with the method `check_units()`, which is automatically called when initialising a neuron group (through the method `prepare()`).

When an `Equations` object is finalised (through the method `prepare()`, automatically called the `NeuronGroup` initialiser), the names of variables defined by non-differential equations are replaced by their (string) values, so that differential equations are self-consistent. In the process, names of external variables are also modified to avoid conflicts (by adding a prefix).

4.2.2 Neuron groups

The key idea for efficient simulations is to update synchronously the state variables of all identical neuron models. A neuron group is defined by the model equations, and optionnally a threshold condition and a reset. For example for 100 neurons:

```
eqs=Equations('dv/dt=-v/tau : volt')
group=NeuronGroup(100,model=eqs,reset=0*mV,threshold=10*mV)
```

The `model` keyword also accepts strings (in that case it is converted to an `Equations` object), e.g.:

```
group=NeuronGroup(100,model='dv/dt=-v/tau : volt',reset=0*mV,threshold=10*mV)
```

The units of both the reset and threshold are checked for consistency with the equations. The code above defines a group of 100 integrate-and-fire neurons with threshold 10 mV and reset 0 mV. The second line defines an object named `group` which contains all the state variables, which can be accessed with the dot notation, i.e. `group.v` is a vector with the values of variable `v` for all of the 100 neurons. It is an array with units as defined in the equations (here, volt). By default, all state variables are initialised at value 0. It can be initialised by the user as in the following example:

```
group.v=linspace(0*mV,10*mV,100)
```

Here the values of `v` for all the neurons are evenly spaced between 0 mV and 10 mV (`linspace` is a NumPy function). The method `group.rest()` may also be used to set the resting point of the equations, but convergence is not always guaranteed.

Important options

- `refractory`: a refractory period (default 0 ms), to be used in combination with the `reset` value.
- `implicit` (default `False`): if True, then an implicit method is used. This is useful for Hodgkin-Huxley equations, which are stiff.

Subgroups

Subgroups can be created with the slice operator:

```
subgroup1=group[0:50]
subgroup2=group[50:100]
```

Then `subgroup2.v[i]` equals `group.v[50+i]`. An alternative equivalent method is the following:

```
subgroup1=group.subgroup(50)
subgroup2=group.subgroup(50)
```

The parent group keeps track of the allocated subgroups. But note that the two methods are mutually exclusive, e.g. in the following example:

```
subgroup1=group[0:50]
subgroup2=group.subgroup(50)
```

both subgroups are actually identical.

Subgroups are useful when creating connections or monitoring the state variables or spikes. The best practice is to define groups as large as possible, then divide them in subgroups if necessary. Indeed, the larger the groups are, the faster the simulation runs. For example, for a network with a feedforward architecture, one should first define one group holding all the neurons in the network, then define the layers as subgroups of this big group.

4.2.3 Reset

More complex resets can be defined. The value of the `reset` keyword can be:

- a quantity (`0*mV`)
- a function
- a `Reset` object, which can be used for resetting a specific state variable or for resetting a state variable to the value of another variable.

Functional reset

To define a specific reset, the generic method is define a function as follows:

```
def myreset(P,spikes):
  P.v[spikes]=rand(len(spikes))*5*mV
group=NeuronGroup(100,model=eqs,reset=myreset,threshold=10*mV)
```

or faster:

```
def myreset(P,spikes):
  P.v_[spikes]=rand(len(spikes))*5*mV
```

Every time step, the user-defined function is called with arguments `P`, the neuron group, and `spikes`, the list of indexes of the neurons that just spiked. The function above resets the neurons that just spiked to a random value.

Resetting another variable

It is possible to specify the reset variable explicitly:

```
group=NeuronGroup(100,model=eqs,reset=Reset(0*mV,state='w'),threshold=10*mV)
```

Here the variable `w` is reset.

Resetting to the value of another variable

The value of the reset can be given by another state variable:

```
group=NeuronGroup(100,model=eqs,reset=VariableReset(0*mV,state='v',resetvaluestate='w'),threshold=10
```

Here the value of the variable `w` is used to reset the variable `v`.

4.2.4 Threshold

As for the reset, the threshold can be customised.

Functional threshold

The generic method to define a custom threshold condition is to pass a function of the state variables which returns a boolean (true if the threshold condition is met), for example:

```
eqs='''
dv/dt=-v/tau : volt
dw/dt=(v-w)/tau : volt
'''
group=NeuronGroup(100,model=eqs,reset=0*mV,threshold=lambda v,w:v>=w)
```

Here we used an anonymous function (`lambda` keyword) but of course a named function can also be used. In this example, spikes are generated when v is greater than w. Note that the arguments of the function must be the state variables with the same order as in the `Equations` string.

Thresholding another variable

It is possible to specify the threshold variable explicitly:

```
group=NeuronGroup(100,model=eqs,reset=0*mV,threshold=Threshold(0*mV,state='w'))
```

Here the variable `w` is checked.

Using another variable as the threshold value

The same model as in the functional threshold example can be defined as follows:

```
group=NeuronGroup(100,model=eqs,reset=0*mV,threshold=\
      VariableThreshold(state='v',threshold_state='w'))
```

Empirical threshold

For Hodgkin-Huxley models, one needs to determine the threshold empirically. Here the *threshold* should really be understood rather as the onset of the spikes (used to propagate the spikes to the other neurons), since there is no explicit reset. There is a `Threshold` subclass for this purpose:

```
group=NeuronGroup(100,model=eqs,threshold=EmpiricalThreshold(threshold=-20*mV,refractory=3*ms))
```

Spikes are triggered when the membrane potential reaches the value -20 mV, but only if it has not spiked in the last 3 ms (otherwise there would be spikes every time step during the action potential). The `state` keyword may be used to specify the state variable which should be checked for the threshold condition.

Poisson threshold

It is possible to generate spikes with a given probability rather than when a threshold condition is met, by using the class `PoissonThreshold`, as in the following example:

```
group=NeuronGroup(100,model='x : Hz',threshold=PoissonThreshold(state='x'))
x=linspace(0*Hz,10*Hz,100)
```

Here spikes are generated as Poisson processes with rates given by the variable x (the `state` keyword is optional: default = first variable defined). Note that x can change over time (inhomogeneous Poisson processes). The units of variable x must be Hertz.

4.3 Connections

4.3.1 Building connections

First, one must define which neuron groups are connected and which state variable receives the spikes. The following instruction:

```
myconnection=Connection(group1,group2,'ge')
```

defines a connection from group `group1` to `group2`, acting on variable `ge`. When neurons from group `group1` spike, the variable `ge` of the target neurons in group `group2` are incremented. When the connection object is initialised, the list of connections is empty. It can be created in several ways. First, explicitly:

```
myconnection[2,5]=3*nS
```

This instruction connects neuron 2 from `group1` to neuron 5 from `group2` with synaptic weight 3 nS. Units should match the units of the variable defined at initialisation time (`ge`).

The matrix of synaptic weights can be defined directly with the method `Connection.connect()`:

```
W=rand(len(group1),len(group2))*nS
myconnection.connect(group1,group2,W)
```

Here a matrix with random elements is used to define the synaptic weights from `group1` to `group2`. It is possible to build the matrix by block by using subgroups, e.g.:

```
W=rand(20,30)*nS
myconnection.connect(group1[0:20],group2[10:40],W)
```

There are several handy functions available to set the synaptic weights: `connect_full()`, `connect_random()` and `connect_one_to_one()`. The first one is used to set uniform weights for all pairs of neurons in the (sub)groups:

```
myconnection.connect_full(group1[0:20],group2[10:40],weight=5*nS)
```

The second one is used to set uniform weights for random pairs of neurons in the (sub)groups:

```
myconnection.connect_random(group1[0:20],group2[10:40],0.02,weight=5*nS)
```

Here the third argument (0.02) is the probability that a synaptic connection exists between two neurons. The number of presynaptic neurons can be made constant by setting the keyword `fixed=True` (probability * number of neurons in `group1`). Finally, the method `connect_one_to_one()` connects neuron i from the first group to neuron i from the second group:

```
myconnection.connect_one_to_one(group1,group2,weight=3*nS)
```

Both groups must have the same number of neurons.

Building connections with connectivity functions

There is a simple and efficient way to build heterogeneous connections, by passing functions instead of constants to the methods `connect_full()` and `connect_random()`. The function must return the synaptic weight for a given pair of neuron (i,j). For example:

```
myconnection.connect_full(group1,group2,weight=lambda i,j:(1+cos(i-j))*2*nS)
```

where i (j) indexes neurons in `group1` (`group2`). This is the same as doing by hand:

```
for i in range(len(group1)):
  for j in range(len(group2)):
    myconnection[i,j]=(1+cos(i-j))*2*nS
```

but it is much faster because the construction is vectorised, i.e., the function is called for every i with j being the entire row of target indexes. Thus, the implementation is closer to:

```
for i in range(len(group1)):
    myconnection[i,j]=(1+cos(i-arange(len(group2)))*2*nS
```

The method `connect_random()` also accepts functional arguments for the weights (not the connection probability yet). For that method, it is possible to pass a function with no argument, as in the following example:

```
myconnection.connect_random(group1,group2,0.1,weight=lambda:rand()*nS)
```

Here each synaptic weight is random (between 0 and 1 nS).

4.3.2 Delays

Transmission delays can be introduced with the keyword `delay`, passed at initialisation time:

```
myconnection=Connection(group1,group2,'ge',delay=3*ms)
```

Note that all synaptic connections have the same delay. To define connections with different delays, several Connection objects must be introduced, e.g.:

```
myconnection_fast=Connection(group1,group2,'ge',delay=1*ms)
myconnection_slow=Connection(group1,group2,'ge',delay=5*ms)
```

4.3.3 Connection structure

The underlying data structure used to store the synaptic connections is by default a sparse matrix. If the connections are dense, it is more efficient to use a dense matrix, which can be set at initialisation time:

```
myconnection=Connection(group1,group2,'ge',structure='dense')
```

Currently, long-term plasticity (STDP) can only be implemented with dense matrices. The `structure` keyword can take the following values: sparse (default), dense and computed. The last one correspond to synaptic connections which are calculated on the fly, but this feature is not implemented yet.

4.3.4 Modulation

The synaptic weights can be modulated by a state variable of the presynaptic neurons with the keyword `modulation`:

```
myconnection=Connection(group1,group2,'ge',modulation='u')
```

When a spike is produced by a presynaptic neuron (`group1`), the variable ge of each postsynaptic neuron (`group2`) is incremented by the synaptic weight multiplied by the value of the variable u of the presynaptic neuron. This is useful to implement short-term plasticity.

4.3.5 Direct connection

In some cases, it is useful to connect a group directly to another one, in a one-to-one fashion. The most efficient way to implement it is with the class `IdentityConnection`:

```
myconnection=IdentityConnection(group1,group2,'ge',weight=1*nS)
```

With this structure, the synaptic weights are homogeneous (it is not possible to define them independently). When neuron i from `group1` spikes, the variable ge of neuron i from `group2` is increased by 1 nS. A typical application is when defining inputs to a network.

4.4 Recording

The activity of the network can be recorded by defining *monitors*.

4.4.1 Recording spikes

To record the spikes from a given group, define a `SpikeMonitor` object:

```
M=SpikeMonitor(group)
```

At the end of the simulation, the spike times are stored in the variable `spikes` as a list of pairs (i,t) where neuron i fired at time t. For example, the following code extracts the list of spike times for neuron 3:

```
spikes3=[t for i,t in M.spikes if i==3]
```

but this operation can be done directly as follows:

```
spikes3=M[3]
```

The total number of spikes is `M.nspikes`.

Custom monitoring

To process the spikes in a specific way, one can pass a function at initialisation of the `SpikeMonitor` object:

```
def f(spikes):
  print spikes

M=SpikeMonitor(group,function=f)
```

The function `f` is called every time step with the argument `spikes` being the list of indexes of neurons that just spiked.

4.4.2 Recording state variables

State variables can be recorded continuously by defining a `StateMonitor` object, as follows:

```
M=StateMonitor(group,'v')
```

Here the state variables v of the defined group are monitored. By default, only the statistics are recorded. The list of time averages for all neurons is M.mean; the standard deviations are stored in M.std and the variances in M.var. Note that these are averages over time, not over the neurons.

To record the values of the state variables over the whole simulation, use the keyword record:

```
M1=StateMonitor(group,'v',record=True)
M2=StateMonitor(group,'v',record=[3,5,9])
```

The first monitor records the value of v for all neurons while the second one records v for neurons 3, 5 and 9 only. The list of times is stored in M1.times and the lists of values are stored in M1[i], where i the index of the neuron. By default, the values of the state variables are recorded every timestep, but one may record every n timesteps by setting the keyword timestep:

```
M=StateMonitor(group,'v',record=True,timestep=n)
```

4.4.3 Counting spikes

To count the total number of spikes produced by a group, use a PopulationSpikeCounter object:

```
M=PopulationSpikeCounter(group)
```

Then the number of spikes after the simulation is M.nspikes. If you need to count the spikes separately for each neuron, use a SpikeCounter object:

```
M=SpikeCounter(group)
```

Then M[i] is the number of spikes produced by neuron i.

4.4.4 Recording population rates

The population rate can be monitored with a PopulationRateMonitor object:

```
M=PopulationRateMonitor(group)
```

After the simulation, M.times contains the list of recording times and M.rate is the list of rate values (where the rate is meant in the spatial sense: average rate over the whole group at some given time). The bin size is set with the bin keyword (in seconds):

```
M=PopulationRateMonitor(group,bin=1*ms)
```

Here the averages are calculated over 1 ms time windows. Alternatively, one can use the smooth_rate() method to smooth the rates:

```
rates=M.smooth_rate(width=1*ms,filter='gaussian')
```

The rates are convolved with a linear filter, which is either a Gaussian function (gaussian, default) or a box function ('flat').

4.5 Inputs

Some specific types of neuron groups are available to provide inputs to a network.

4.5.1 Poisson inputs

Poisson spike trains can be generated as follows:

```
group=PoissonGroup(100,rates=10*Hz)
```

Here 100 neurons are defined, which emit spikes independently according to Poisson processes with rates 10 Hz. To have different rates across the group, initialise with an array of rates:

group=PoissonGroup(100,rates=linspace(0*Hz,10*Hz,100))

Inhomogeneous Poisson processes can be defined by passing a function of time that returns the rates:

```
group=PoissonGroup(100,rates=lambda t:(1+cos(t))*10*Hz)
```

or:

```
r0=linspace(0*Hz,10*Hz,100)
group=PoissonGroup(100,rates=lambda t:(1+cos(t))*r0)
```

4.5.2 Correlated inputs

Generation of correlated spike trains is partially implemented, using algorithms from the the following paper: Brette, R. (2008) Generation of correlated spike trains, Neural Computation.

To generate correlated spike trains with identical rates and homogeneous exponential correlations, use the class `HomogeneousCorrelatedSpikeTrains`:

```
group=HomogeneousCorrelatedSpikeTrains(100,r=10*Hz,c=0.1,tauc=10*ms)
```

where `r` is the rate, `c` is the total correlation strength and `tauc` is the correlation time constant. The implementation uses Cox processes (or doubly stochastic processes) to generate the spike trains.

Heterogeneous spike trains have not been implemented yet (but will be).

4.5.3 Input spike trains

A set of spike trains can be explicitly defined as list of pairs (i,t) (meaning neuron i fires at time t), which used to initialise a `SpikeGeneratorGroup`:

```
spiketimes=[(0,1*ms), (1,2*ms)]
input=SpikeGeneratorGroup(5,spiketimes)
```

The neuron 0 fires at time 1 ms and neuron 1 fires at time 2 ms (there are 5 neurons, but 3 of them never spike). One may also pass a generator instead of a list (in that case the pairs should be ordered in time).

Spike times may also be provided separately for each neuron, using the `MultipleSpikeGeneratorGroup` class:

```
S0=[1*ms, 2*ms]
S1=[3*ms]
S2=[1*ms, 3*ms, 5*ms]
input=MultipleSpikeGeneratorGroup([S0,S1,S2])
```

The object is initialised with a list of spike containers, one for each neuron. Each container can be a sorted list of spike times or any iterable object returning the spike times (ordered in time).

Gaussian spike packets

There is a subclass of `SpikeGeneratorGroup` for generating spikes with a Gaussian distribution:

```
input=PulsePacket(t=10*ms,n=10,sigma=3*ms)
```

Here 10 spikes are produced, with spike times distributed according a Gaussian distribution with mean 10 ms and standard deviation 3 ms.

4.5.4 Direct input

Inputs may also be defined by accessing directly the state variables of a neuron group. The standard way to do this is to insert parameters in the equations:

```
eqs='''
dv/dt=(I-x)/tau : volt
I : volt
'''
group=NeuronGroup(100,model=eqs,reset=0*mV,threshold=15*mV)
group.I=linspace(0*mV,20*mV,100)
```

Here the value of the parameter I for each neuron is provided at initialisation time (evenly distributed between 0 mV and 20 mV). It is possible to change the value of I every timestep by using a user-defined operation (see next section).

4.6 User-defined operations

In addition to neuron models, the user can provide functions that are to be called every timestep during the simulation, using the decorator `network_operation()`:

```
@network_operation
def myoperation():
    do_something_every_timestep()
```

The operation may be called at regular intervals by defining a clock:

```
myclock=Clock(dt=1*ms)

@network_operation(myclock)
def myoperation():
    do_something_every_ms()
```

4.7 Analysis and plotting

Most plotting should be done with the PyLab commands, all of which are loaded when you import Brian. See:

> http://matplotlib.sourceforge.net/matplotlib.pylab.html

for help on PyLab. The scientific library Scipy is also automatically imported by the instruction `from brian import *`.

The most useful plotting instruction is the Pylab function `plot`. A typical use with Brian is:

```
plot(t/ms,vm/mV)
```

where t is a vector of times with units ms and vm is a vector of voltage values with units mV. To display the figures on the screen, the function `show()` must be called once (this should be the last line of your script), except when using IPython with the Pylab mode (`ipython -pylab`).

Brian currently defines just two plotting functions of its own, `raster_plot()` and `hist_plot()`.

4.7.1 Raster plots

Spike trains recorded by a `SpikeMonitor` can be displayed as raster plots:

```
S=SpikeMonitor(group)
...
raster_plot(S)
```

Usual options of the `plot` command can also be passed to `raster_plot()`. One may also pass several spike monitors as arguments.

4.8 Clocks

Brian is a clock-based simulator: operations are done synchronously at each tick of a clock.

Many Brian objects store a clock object, passed in the initialiser with the optional keyword `clock`. For example, to simulate a neuron group with time step dt=1 ms:

```
myclock=Clock(dt=1*ms)
group=NeuronGroup(100,model='dx/dt=1*mV/ms : volt',clock=myclock)
```

If no clock is specified, the program uses the global default clock. When Brian is initially imported, this is the object `defaultclock`, and it has a default time step of 0.1 ms. In a simple script, you can override this by writing (for example):

```
defaultclock.dt = 1*ms
```

You may wish to use multiple clocks in your program. In this case, for each object which requires one, you have to pass a copy of its `Clock` object. The network run function automatically handles objects with different clocks, updating them all at the appropriate time according to their time steps (value of `dt`).

Multiple clocks can be useful, for example, for defining a simulation that runs with a very small `dt`, but with some computationally expensive operation running at a lower frequency. In the following example, the model is simulated with dt=0.01 ms and the variable x is recorded every ms:

```
simulation_clock=Clock(dt=0.01*ms)
record_clock=Clock(dt=1*ms)
group=NeuronGroup(100,model='dx/dt=-x/tau : volt',clock=simulation_clock)
M=StateMonitor(group,'x',record='True',clock=record_clock)
```

The current time of a clock is stored in the attribute `t` (`simulation_clock.t`) and the timestep is stored in the attribute `dt`.

4.9 Simulation control

4.9.1 The update schedule

When a simulation is run, the operations are done in the following order by default:

1. Update every `NeuronGroup`, this typically performs an integration time step for the differential equations defining the neuron model.
2. Check the threshold condition and propagate the spikes to the target neurons.
3. Reset all neurons that spiked.
4. Call all user-defined operations and state monitors.

The user-defined operations and state monitors can be placed at other places in this schedule, by using the keyword `when`. The values can be `start`, `before_groups`, `after_groups`, `middle`, `before_connections`, `after_connections`, `before_resets`, `after_resets` or `end` (default: end). For example, to call a function `f` at the beginning of every timestep:

```
@network_operation(when='start')
def f():
  do_something()
```

or to record the value of a state variable just before the resets:

```
M=StateMonitor(group,'x',record=True,when='before_resets')
```

4.9.2 Basic simulation control

The simulation is run simply as follows:

```
run(1000*ms)
```

where 1000 ms is the duration of the run. It can be stopped during the simulation with the instruction `stop()`, and the network can be reinitialised with the instruction `reinit()`.

When the `run()` function is called, Brian looks for all relevant objects in the namespace (groups, connections, monitors, user operations), and runs them. In complex scripts, the user might want to run only selected objects. In that case, a `Network` object needs to be created.

4.9.3 The Network class

A `Network` object holds a collection of objets that can be run, i.e., objects with class `NeuronGroup`, `Connection`, `SpikeMonitor`, `StateMonitor` (or subclasses) or any user-defined operation with the decorator `network_operation()`. Thoses objects can then be simulated. Example:

```
G = NeuronGroup(...)
C = Connection(...)
net = Network(G,C)
net.run(1*second)
```

You can also pass lists of objects. The simulation can be controlled with the methods `stop` and `reinit`.

4.10 More on equations

The `Equations` class is a central part of Brian, since models are generally specified with an `Equations` object. Here we explain advanced aspects of this class.

4.10.1 External variables

Equations may contain external variables. When an `Equations` object is initialised, a dictionary is built with the values of all external variables. These values are taken from the namespace where the `Equations` object was defined. It is possible to go one or several levels up in the namespaces by specifying the keyword `level` (default=0). The value of these parameters can in general be changed during the simulation and the modifications are taken into account, except in two situations: when the equations are frozen (see below) or when the integration is exact (linear equations). In those cases, the values of the parameters are the ones at initialisation time.

Alternatively, the string defining the equations can be evaluated within a given namespace by providing keywords at initialisation time, e.g.:

```
eqs=Equations('dx/dt=-x/tau : volt',tau=10*ms)
```

In that case, the values of all external variables are taken from the specified dictionary (given by the keyword arguments), even if variables with the same name exist in the namespace where the string was defined. The two methods for passing the values of external variables are mutually exclusive, that is, either all external variables are explicitly specified with keywords (if not, they are left unspecified even if there are variables with the same names in the namespace where the string was defined), or all values are taken from the calling namespace.

More can be done with keyword arguments. If the value is a string, then the name of the variable is replaced, e.g.:

```
eqs=Equations('dx/dt=-x/tau : volt',tau=10*ms,x='Vm')
```

changes the variable name x to Vm. This is useful for writing functions which return equations where the variable name is provided by the user.

Finally, if the value is `None` then the name of the variable is replaced by a unique name, e.g.:

```
eqs=Equations('dx/dt=-x/tau : volt',tau=10*ms,x=None)
```

This is useful to avoid conflicts in the names of hidden variables.

Issues

- There can be problems if a variable with the same name as the variable of a differential equation exists in the namespace where the `Equations` object was defined.

4.10.2 Combining equations

`Equations` can be combined using the sum operator. For example:

```
eqs=Equations('dx/dt=(y-x)/tau : volt')
eqs+=Equations('dy/dt=-y/tau: volt')
```

Note that some variables may be undefined when defining the first equation. No error is raised when variables are undefined and absent from the calling namespace. When two `Equations` objects are added, the consistency is checked. For example it is not possible to add two `Equations` objects which define the same variable.

4.10.3 Which variable is the membrane potential?

Several objects, such as `Threshold` or `Reset` objects can be initialised without specifying which variable is the membrane potential, in which case it is assumed that it is the first variable. Internally, the variables of an `Equations` object are reorderered so that the first one is most likely to be the membrane potential (using `Equations.get_Vm()`). The first variable is, with decreasing priority :

- v
- V
- vm
- Vm
- the first defined variable.

4.10.4 Numerical integration

The currently available integration methods are:

- Exact integration when the equations are linear.
- Euler integration (explicit, first order).
- Runge-Kutta integration (explicit, second order).
- Exponential Euler integration (implicit, first order).

The method is selected when a `NeuronGroup` is initialized. If the equations are linear, exact integration is automatically selected. Otherwise, Euler integration is selected by default, unless the keyword `implicit=True` is passed, which selects the exponential Euler method. A second-order method can be selected using the keyword `order=2` (explicit Runge-Kutta method, midpoint estimation). It is possible to override this behaviour with the `method` keyword when initialising a `NeuronGroup`. Possible values are `linear`, `nonlinear`, `Euler`, `RK`, `exponential_Euler`.

Exact integration

If the differential equations are linear, then the update phase X(t)->X(t+dt) can be calculated exactly with a matrix product. First, the equations are examined to determine whether they are linear with the method `islinear()` and the function `is_affine()` (this is currently done using dynamic typing). Second, the matrix M and the vector B such that dX/dt=M(X-B) are calculated with the function `get_linear_equations()` [1]. Third, the matrix A such that X(t+dt)=A*(X(t)-B)+B is calculated at initialisation of a specific state updater object, `LinearStateUpdater`, as A=expm(M*dt), where expm is the matrix exponential.

Important remark: since the update matrix and vector are precalculated, the values of all external variables in the equations are frozen at initialisation. If external variables are modified after initialisation, those modifications are *not* taken into account during the simulation.

Inexact exact integration: If the equation cannot be put into the form dX/dt=M(X-B), for example if the equation is dX/dt=MX+A where M is not invertible, then the equations are not integrated exactly, but using a system equivalent to Euler integration but with dt 100 times smaller than specified. Updates are of the form X(t+dt)=A*X(t)+C where the matrix A and vector C are computed by applying Euler integration 100 times to the differential equations.

Euler integration

The Euler is a first order explicit integration method. It is the default one for nonlinear equations. It is simply implemented as X(t+dt)=X(t)+f(X)*dt.

Exponential Euler integration

The exponential Euler method is used for Hodgkin-Huxley type equations, are which stiff. Equations of that type are conditionally linear, that is, the differential equation for each variable is linear in that variable (i.e., linear if all other variables are considered constant). The idea is thus to solve the differential equation for each variable over one time step, assuming that all other variables are constant over that time step. The numerical scheme is still first order, but it is more stable than the forward Euler method. Each equation can be written as dx/dt=a*x+b, where a and b depend on the other variables and thus change after each time step. The values of a and b are obtained during the update phase by calculating a*x+b for x=0 and x=1 (note that these values are different for every neuron, thus we calculate vectors A and B). Then x(t+dt) is calculated in the same way as for the exact integration method above.

4.10.5 Stochastic differential equations

Noise is introduced in differential equations with the keyword `xi`, which means normalised gaussian noise (the derivative of the Brownian term). Currently, this is implemented simply by adding a normal random number to the variable at the end of the integration step (independently for each neuron). The unit of white noise is non-trivial, it is `second**(-.5)`. Thus, a typical stochastic equation reads:

```
dx/dt=-x/tau+sigma*xi/tau**.5
```

where `sigma` is in the same units as `x`. We note the following two facts:

- The noise term is independent between neurons. Thus, one cannot use this method to analyse the response to frozen noise (where all neurons receive the same input noise). One would need to use an external variable representing the input, updated by a user-defined operation.
- The noise term is independent between equations. This can however be solved by the following trick:

```
dx/dt=-x/tau+sigmax*u/tau**.5 : volt
dy/dt=-y/tau+sigmay*u/tau**.5 : volt
u=xi : second**(-.5)
```

4.10.6 Non-autonomous equations

The time variable `t` can be directly inserted into an equation string. It is replaced at run time by the current value of the time variable for the relevant neuron group, and also appears as a state variable of the neuron group.

4.10.7 Freezing

External variables can be frozen by passing the keyword `freeze=True` (default = `False`) at initialization of a `NeuronGroup` object. Then when the string defining the equations are compiled into Python functions (method `compile_functions()`), the external variables are replaced by their float values (units are discarded). This can result in a significant speed-up.

TODO: more on the implementation.

4.10.8 Compilation

State updates can be compiled into Python code objects by passing the keyword `compile=True` at initialization of a a `NeuronGroup`. Note that this is different from the method `compile_functions()`, which compiles the equation for every variable into a Python function (not the whole state update process).

When the `compile` keyword is set, the method `forward_euler_code()` or `exponential_euler_code()` is called. It generates a string containing the Python code for the update of all state variables (one time step), then compiles it into Python code object. That compiled object is then called at every time step. All external variables are frozen in the process (regardless of the value of the `freeze` keyword). This results in a significant speed-up (although the exponential Euler code is not quite optimised yet). Note that only Python code is generated, thus a C compiler is not required.

4.10.9 Working with equations

`Equations` object can also be used outside simulations. In the following, we suppose that an `Equations` object is defined as follows:

```
eqs=Equations('''
dx/dt=(y-x)/(10*ms) : volt
dy/dt=-z/(5*ms) : volt
z=2*(x+y) : volt
''')
```

Applying an equation

The value of z can be calculated using the `apply()` method:

```
z=eqs.apply('z',dict(x=3*mV,y=5*mV))
```

The second argument is a dictionary containing the values of all dependent variables (here the result is `8*mV`). The right-hand side of differential equations can also be calculated in the same way:

```
x=eqs.apply('x',dict(x=2*mV,y=3*mV))
y=eqs.apply('y',dict(x=2*mV,y=3*mV))
```

Note in the second case that only the values of the dynamic variables should be passed.

Calculating a fixed point

A fixed point of the equations can be calculated as follows:

```
fp=eqs.fixedpoint(x=2*mV,y=3*mV)
```

where the optional keywords give the initial point (zero if not provided). Internally, the function `optimize.fsolve` from the Scipy package is used to find a zero of the set of differential equations (thus, convergence is not guaranteed; in that case, the initial values are returned). A dictionary with the values of the dynamic variables at the fixed point is returned.

Issues

- If the equations were previously frozen, then the units disappear from the equations and unit consistency problems may arise.
- `Equations` objects need to be "prepared" before use, as follows:

  ```
  eqs.prepare()
  ```

  This is automatically called by the NeuronGroup initialiser.

For more detailed information, see the reference chapter.

[1] Note that this approach raises an issue when dX/dt=B. We currently (temporarily) solve this problem by adding a small diagonal matrix to M to make it invertible.

CHAPTER

FIVE

The library

A number of standard models is defined in the library folder. To use library elements, use the following syntax:

```
from brian.library.module_name import *
```

For example, to import electrophysiology models:

```
from brian.library.electrophysiology import *
```

5.1 Library models

5.1.1 Membrane equations

Library models are defined using the `MembraneEquation` class. This is a subclass of `Equations` which is defined by a capacitance C and a sum of currents. The following instruction:

```
eqs=MembraneEquation(200*pF)
```

defines the equation C*dvm/dt=0*amp, with the membrane capacitance C=200 pF. The name of the membrane potential variable can be changed as follows:

```
eqs=MembraneEquation(200*pF,vm='V')
```

The main interest of this class is that one can use it to build models by adding currents to a membrane equation. The `Current` class is a subclass of `Equations` which defines a current to be added to a membrane equation. For example:

```
eqs=MembraneEquation(200*pF)+Current(I='(V0-vm)/R : amp',current_name='I')
```

defines the same equation as:

```
eqs=Equations('''
dvm/dt=I/(200*pF) : volt
I=(V0-vm)/R : amp
''')
```

The keyword `current_name` is optional if there is no ambiguity, i.e., if there is only one variable or only one variable with amp units. As for standard equations, `Current` objects can be initialised with a multiline string (several equations). By default, the convention for the current direction is the one for injected current. For the ionic current convention, use the `IonicCurrent` class:

```
eqs=MembraneEquation(200*pF)+IonicCurrent(I='(vm-V0)/R : amp')
```

5.1.2 Integrate-and-Fire models

A few standard Integrate-and-Fire models are implemented in the `IF` library module:

```
from brian.library.IF import *
```

All these functions return `Equations` objects (more precisely, `MembraneEquation` objects).

- Leaky integrate-and-fire model (`dvm/dt=(El-vm)/tau : volt`):

  ```
  eqs=leaky_IF(tau=10*ms,El=-70*mV)
  ```

- Perfect integrator (`dvm/dt=Im/tau : volt`):

  ```
  eqs=perfect_IF(tau=10*ms)
  ```

- Quadratic integrate-and-fire model (`C*dvm/dt=a*(vm-El)*(vm-VT) : volt`):

  ```
  eqs=quadratic_IF(C=200*pF,a=10*nS/mV,EL=-70*mV,VT=-50*mV)
  ```

- Exponential integrate-and-fire model (`C*dvm/dt=gL*(EL-vm)+gL*DeltaT*exp((vm-VT)/DeltaT) :volt`):

  ```
  eqs=exp_IF(C=200*pF,gL=10*nS,EL=-70*mV,VT=-55*mV,DeltaT=3*mV)
  ```

In general, it is possible to define a neuron group with different parameter values for each neuron, by passing strings at initialisation. For example, the following code defines leaky integrate-and-fire models with heterogeneous resting potential values:

```
eqs=leaky_IF(tau=10*ms,El='V0')+Equations('V0:volt')
group=NeuronGroup(100,model=eqs,reset=0*mV,threshold=15*mV)
```

5.1.3 Two-dimensional IF models

Integrate-and-fire models with two variables can display a very rich set of electrophysiological behaviours. In Brian, two such models have been implemented: Izhikevich model and Brette-Gerstner adaptive exponential integrate-and-fire model (also included in the `IF` module). The equations are obtained in the same way as for one-dimensional models:

```
eqs=Izhikevich(a=0.02/ms,b=0.2/ms)
eqs=Brette_Gerstner(C=281*pF,gL=30*nS,EL=-70.6*mV,VT=-50.4*mV,DeltaT=2*mV,tauw=144*ms,a=4*nS)
eqs=aEIF(C=281*pF,gL=30*nS,EL=-70.6*mV,VT=-50.4*mV,DeltaT=2*mV,tauw=144*ms,a=4*nS) # equivalent
```

and two state variables are defined: `vm` (membrane potential) and `w` (adaptation variable). The equivalent equations for Izhikevich model are:

```
dvm/dt=(0.04/ms/mV)*vm**2+(5/ms)*vm+140*mV/ms-w : volt/second
dw/dt=a*(b*vm-w)                               : volt/second
```

and for Brette-Gerstner model:

```
C*dvm/dt=gL*(EL-vm)+gL*DeltaT*exp((vm-VT)/DeltaT)-w :volt
dw/dt=(a*(vm-EL)-w)/tauw : amp
```

To simulate these models, one needs to specify a threshold value, and a good choice is `VT+4*DeltaT`. The reset is particular in these models since it is bidimensional: vm->Vr and w->w+b. A specific reset class has been implemented for this purpose: `AdaptiveReset`, initialised with Vr and b. Thus, a typical construction of a group of such models is:

```
eqs=Brette_Gerstner(C=281*pF,gL=30*nS,EL=-70.6*mV,VT=-50.4*mV,DeltaT=2*mV,tauw=144*ms,a=4*nS)
group=NeuronGroup(100,model=eqs,threshold=-43*mV,reset=AdaptiveReset(Vr=-70.6*mvolt,b=0.0805*nA))
```

5.1.4 Synapses

A few simple synaptic models are implemented in the module `synapses`:

```
from brian.library.synapses import *
```

All the following functions need to be passed the name of the variable upon which the received spikes will act, and the name of the variable representing the current or conductance. The simplest one is the exponential synapse:

```
eqs=exp_synapse(input='x',tau=10*ms,unit=amp,output='x_current')
```

It is equivalent to:

```
eqs=Equations('''
dx/dt=-x/tau : amp
x_out=x
''')
```

Here, `x` is the variable which receives the spikes and `x_current` is the variable to be inserted in the membrane equation (since it is a one-dimensional synaptic model, the variables are the same). If the output variable name is not defined, then it will be automatically generated by adding the suffix `_out` to the input name.

Two other types of synapses are implemented. The alpha synapse (`x(t)=alpha*(t/tau)*exp(1-t/tau)`, where `alpha` is a normalising factor) is defined with the same syntax by:

```
eqs=alpha_synapse(input='x',tau=10*ms,unit=amp)
```

and the bi-exponential synapse is defined by (`x(t)=(tau2/(tau2-tau1))*(exp(-t/tau1)-exp(-t/tau2))`, up to a normalising factor):

```
eqs=biexp_synapse(input='x',tau1=10*ms,tau2=5*ms,unit=amp)
```

For all types of synapses, the normalising factor is such that the maximum of x(t) is 1. These functions can be used as in the following example:

```
eqs=MembraneEquation(C=200*pF)+Current('I=gl*(El-vm)+ge*(Ee-vm):amp')
eqs+=alpha_synapse(input='ge_in',tau=10*ms,unit=siemens,output='ge')
```

where alpha conductances have been inserted in the membrane equation.

One can directly insert synaptic currents with the functions `exp_current`, `alpha_current` and `biexp_current`:

```
eqs=MembraneEquation(C=200*pF)+Current('I=gl*(El-vm):amp')+\
    alpha_current(input='ge',tau=10*ms)
```

(the units is amp by default), or synaptic conductances with the functions `exp_conductance`, `alpha_conductance` and `biexp_conductance`:

```
eqs=MembraneEquation(C=200*pF)+Current('I=gl*(El-vm):amp')+\
    alpha_conductance(input='ge',E=0*mV,tau=10*ms)
```

where `E` is the reversal potential.

5.1.5 Ionic currents

A few standard ionic currents have implemented in the module `ionic_currents`:

```
from brian.library.ionic_currents import *
```

When the current name is not specified, a unique name is generated automatically. Models can be constructed by adding currents to a `MembraneEquation`.

- Leak current (`gl*(El-vm)`):

  ```
  current=leak_current(gl=10*nS,El=-70*mV,current_name='I')
  ```

- Hodgkin-Huxley K+ current:

  ```
  current=K_current_HH(gmax,EK,current_name='IK'):
  ```

- Hodgkin-Huxley Na+ current:

  ```
  current=Na_current_HH(gmax,ENa,current_name='INa'):
  ```

5.2 Random processes

To import the random processes library:

```
from brian.library.random_processes import *
```

For the moment, only the Ornstein-Uhlenbeck process has been included. The function `OrnsteinUhlenbeck()` returns an `Equations` object. The following example defines a membrane equation with an Ornstein-Uhlenbeck current `I` (= coloured noise):

```
eqs=Equations('dv/dt=-v/tau+I/C : volt')
eqs+=OrnsteinUhlenbeck('I',mu=1*nA,sigma=2*nA,tau=10*ms)
```

where `mu` is the mean of the current, `sigma` is the standard deviation and `tau` is autocorrelation time constant.

5.3 Electrophysiology

5.4 Extending the library

For names, we try to follow the standard Python convention, that is, `function_and_variable_names` and `ClassNames`.

CHAPTER

SIX

Advanced concepts

6.1 Parallel computing

ppfunction(*f*)

Convenience wrapper for writing functions to use with parallelpython

The parallel python module `pp` allows you to write code that runs simultaneously on multiple cores on a single machine, or multiple machines on a cluster. You can download the module at http://www.parallelpython.com/

One annoying feature of `pp` is that you cannot use data values that are in the global namespace as part of your code, only modules and functions. This means that you could not execute a function with the code `3*mV` for example, because `mV` is a data value in the `brian` namespace. Instead you would have to import the `brian` module and write `3*brian.mV` which is annoying in long chunks of code. This decorator simply generates a new version of your code with every name `x` from the `brian` namespace replaced by `brian.x`. As part of this process, the rewritten code has to be saved to a file (because of how `pp` works) and this file is named according to the scheme `basename_funcname_parallelpythonised.py`, where `basename` is the current module name and `funcname` is the name of the function being rewritten.

Example

```
@ppfunction
def testf():
    return 3*mV
```

6.2 How to write efficient Brian code

There are a few keys to writing fast and efficient Brian code. The first is to use Brian itself efficiently. The second is to write good vectorised code, which is using Python and NumPy efficiently.

6.2.1 Brian specifics

You can switch off Brian's entire unit checking module by including the line:

```
import brian_no_units
```

before importing Brian itself. Good practice is to leave unit checking on most of the time when developing and debugging a model, but switching it off for long runs once the basic model is stable.

Another way to speed up code is to store references to arrays rather than extracting them from Brian objects each time you need them. For example, if you know the custom reset object in the code above is only ever applied to a group `custom_group` say, then you could do something like this:

```
def myreset(P, spikes):
        custom_group_V_[spikes] = 0*mV
        custom_group_Vt_[spikes] = 2*mV

custom_group = ...
custom_group_V_ = custom_group.V_
custom_group_Vt_ = custom_group.Vt_
```

In this case, the speed increase will be quite small, and probably not worth doing because it makes it less readable, but in more complicated examples where you repeatedly refer to `custom_group.V_` it could add up.

6.2.2 Vectorisation

Python is a fast language, but each line of Python code has an associated overhead attached to it. Sometimes you can get considerable increases in speed by writing a vectorised version of it. A good guide to this in general is the Performance Python page. Here we will do a single worked example in Brian.

Suppose you wanted to multiplicatively depress the connection strengths every time step by some amount, you might do something like this:

```
C = Connection(G1, G2, 'V', structure='dense')
...
@network_operation(when='end')
def depress_C():
        for i in range(len(G1)):
                for j in range(len(G2)):
                        C[i,j] = C[i,j]*depression_factor
```

This will work, but it will be very, very slow.

The first thing to note is that the Python expression `range(N)` actually constructs a list `[0,1,2,...,N-1]` each time it is called, which is not really necessary if you are only iterating over the list. Instead, use the `xrange` iterator which doesn't construct the list explicitly:

```
for i in xrange(len(G1)):
        for j in xrange(len(G2)):
                C[i,j] = C[i,j]*depression_factor
```

The next thing to note is that when you call C[i,j] you are doing an operation on the `Connection` object, not directly on the underlying matrix. Instead, do something like this:

```
C = Connection(G1, G2, 'V', structure='dense')
C_matrix = asarray(C.W)
...
@network_operation(when='end')
def depress_C():
        for i in xrange(len(G1)):
                for j in xrange(len(G2)):
                        C_matrix[i,j] *= depression_factor
```

What's going on here? First of all, `C.W` refers to the `ConnectionMatrix` object, which is a 2D NumPy array with some extra stuff - we don't need the extra stuff so we convert it to a straight NumPy array `asarray(C.W)`. We also store a copy of this as the variable `C_matrix` so we don't need to do this every time step. The other thing we do is to use the `*=` operator instead of the `*` operator.

The most important step of all though is to vectorise the entire operation. You don't need to loop over i and j at all, you can manipulate the array object with a single NumPy expression:

```
C = Connection(G1, G2, 'V', structure='dense')
C_matrix = asarray(C.W)
...
@network_operation(when='end')
def depress_C():
        C_matrix *= depression_factor
```

This final version will probably be hundreds if not thousands of times faster than the original. It's usually possible to work out a way using NumPy expressions only to do whatever you want in a vectorised way, but in some very rare instances it might be necessary to have a loop. In this case, if this loop is slowing your code down, you might want to try writing that loop in inline C++ using the SciPy Weave package. See the documentation at that link for more details, but as an example we could rewrite the code above using inline C++ as follows:

```
from scipy import weave
...
C = Connection(G1, G2, 'V', structure='dense')
C_matrix = asarray(C.W)
...
@network_operation(when='end')
def depress_C():
        n = len(G1)
        m = len(G2)
        code = '''
                for(int i=0;i<n;i++)
                        for(int j=0;j<m;j++)
                                C_matrix(i,j) *= depression_factor
                '''
        weave.inline(code,
                ['C_matrix', 'n', 'm', 'depression_factor'],
                type_converters=weave.converters.blitz,
                compiler='gcc',
                extra_compile_args=['-O3'])
```

The first time you run this it will be slower because it compiles the C++ code and stores a copy, but the second time will be much faster as it just loads the saved copy. The way it works is that Weave converts the listed Python and NumPy variables (C_matrix, n, m and depression_factor) into C++ compatible data types. n and m are turned into int‘‘s, ‘‘depression_factor is turned into a double, and C_matrix is turned into a Weave Array class. The only thing you need to know about this is that elements of a Weave array are referenced with parentheses rather than brackets, i.e. C_matrix(i,j) rather than C_matrix[i,j]. In this example, I have used the gcc compiler and added the optimisation flag -O3 for maximum optimisations. Again, in this case it's much simpler to just use the C_matrix *= depression_factor NumPy expression, but in some cases using inline C++ might be necessary, and as you can see above, it's very easy to do this with Weave, and the C++ code for a snippet like this is often almost as simple as the Python code would be.

6.3 Projects with multiple files or functions

Brian works with the minimal hassle if the whole of your code is in a single Python module (.py file). This is fine when learning Brian or for quick projects, but for larger, more realistic projects with the source code separated into multiple files, there are some small issues you need to be aware of. These issues essentially revolve around the use of the ‘’magic” functions run(), etc. The way these functions work is to look for objects of the required type that have been instantiated (created) in the same ‘’execution frame” as the run() function. In a small script, that is normally just any objects that have been defined in that script. However, if you define objects in a different module, or in a function, then the magic functions won't be able to find them.

There are three main approaches then to splitting code over multiple files (or functions).

6.3.1 Use the `Network` object explicitly

The magic `run()` function works by creating a `Network` object automatically, and then running that network. Instead of doing this automatically, you can create your own `Network` object. Rather than writing something like:

```
group1 = ...
group2 = ...
C = Connection(group1,group2)
...
run(1*second)
```

You do this:

```
group1 = ...
group2 = ...
C = Connection(group1, group2)
...
net = Network(group1, group2, C)
net.run(1*second)
```

In other words, you explicitly say which objects are in your network. Note that any `NeuronGroup`, `Connection`, `Monitor` or function decorated with `network_operation()` should be included in the `Network`. See the documentation for `Network` for more details.

This is the preferred solution for almost all cases. You may want to use either of the following two solutions if you think your code may be used by someone else, or if you want to make it into an extension to Brian.

6.3.2 Use the `magic_return()` decorator or `magic_register()` function

The `magic_return()` decorator is used as follows:

```
@magic_return
def f():
        ...
        return obj
```

Any object returned by a function decorated by `magic_return()` will be considered to have been instantiated in the execution frame that called the function. In other words, the magic functions will find that object even though it was really instantiated in a different execution frame.

In more complicated scenarios, you may want to use the `magic_register()` function. For example:

```
def f():
        ...
        magic_register(obj1, obj2)
        return (obj1, obj2)
```

This does the same thing as `magic_return()` but can be used with multiple objects. Also, you can specify a `level` (see documentation on `magic_register()` for more details).

6.3.3 Use derived classes

Rather than writing a function which returns an object, you could instead write a derived class of the object type. So, suppose you wanted to have an object that emitted N equally spaced spikes, with an interval dt between them, you could use the `SpikeGeneratorGroup` class as follows:

```
@magic_return
def equally_spaced_spike_group(N, dt):
        spikes = [(0,i*dt) for i in range(N)]
        return SpikeGeneratorGroup(spikes)
```

Or alternatively, you could derive a class from `SpikeGeneratorGroup` as follows:

```
class EquallySpacedSpikeGroup(SpikeGeneratorGroup):
        def __init__(self, N, t):
                spikes = [(0,i*dt) for i in range(N)]
                SpikeGeneratorGroup.__init__(self, spikes)
```

You would use these objects in the following ways:

```
obj1 = equally_spaced_spike_group(100, 10*ms)
obj2 = EquallySpacedSpikeGroup(100, 10*ms)
```

For simple examples like the one above, there's no particular benefit to using derived classes, but using derived classes allows you to add methods to your derived class for example, which might be useful. For more experienced Python programmers, or those who are thinking about making their code into an extension for Brian, this is probably the preferred approach. Finally, it may be useful to note that there is a protocol for one object to 'contain' other objects. That is, suppose you want to have an object that can be treated as a simple `NeuronGroup` by the person using it, but actually instantiates several objects (perhaps internal `Connection` objects). These objects need to be added to the `Network` object in order for them to be run with the simulation, but the user shouldn't need to have to know about them. To this end, for any object added to a `Network`, if it has an attribute `contained_objects`, then any objects in that container will also be added to the network.

6.4 Parameters

Brian includes a simple tool for keeping track of parameters. If you only need something simple, then a dict or an empty class could be used. The point of the parameters class is that allows you to define a cascade of computed parameters that depend on the values of other parameters, so that changing one will automatically update the others. See the synfire chain example `examples/sfc.py` for a demonstration of how it can be used.

class Parameters(***kwds*)

A storage class for keeping track of parameters

Example usage:

```
p = Parameters(
    a = 5,
    b = 6,
    computed_parameters = '''
    c = a + b
    ''')
print p.c
p.a = 1
print p.c
```

The first `print` statement will give 11, the second gives 7.

Details:

Call as:

```
p = Parameters(...)
```

Where the `...` consists of a list of keyword / value pairs (like a `dict`). Keywords must not start with the underscore _ character. Any keyword that starts with `computed_` should be a string of valid Python statements that compute new values based on the given ones. Whenever a non-computed value is changed, the computed parameters are recomputed, in alphabetical order of their keyword names (so `computed_a` is computed before `computed_b` for example). Non-computed values can be accessed and set via `p.x`, `p.x=1` for example, whereas computed values can only be accessed and not set. New parameters can be added after the `Parameters` object is created, including new `computed_*` parameters. You can 'derive' a new parameters object from a given one as follows:

```
p1 = Parameters(x=1)
p2 = Parameters(y=2,**p1)
print p2.x
```

Note that changing the value of `x` in `p2` will not change the value of `x` in `p1` (this is a copy operation).

6.5 Preferences

6.5.1 Functions

Setting and getting global preferences is done with the following functions:

`set_global_preferences`(***kwds*)
Set global preferences for Brian

Usage:

```
``set_global_preferences(...)``
```

where ... is a list of keyword assignments.

`get_global_preference`(*k*)
Get the value of the named global preference

The currently known global preferences are:

6.5.2 Global preferences for Brian

The following global preferences have been defined:

`defaultclock = Clock(dt=0.1*msecond)` The default clock to use if none is provided or defined in any enclosing scope.

`useweave_linear_diffeq = False` Whether to use weave C++ acceleration for the solution of linear differential equations. Note that on some platforms, typically older ones, this is faster and on some platforms, typically new ones, this is actually slower.

`useweave = False` Defines whether or not functions should use inlined compiled C code where defined. Requires a compatible C++ compiler. The `gcc` and `g++` compilers are probably the easiest option (use Cygwin on Windows machines). See also the `weavecompiler` global preference.

weavecompiler = gcc Defines the compiler to use for weave compilation. On Windows machines, installing Cygwin is the easiest way to get access to the gcc compiler.

magic_useframes = True Defines whether or not the magic functions should search for objects defined only in the calling frame or if they should find all objects defined in any frame. This should be set to `False` if you are using Brian from an interactive shell like IDLE or IPython where each command has its own frame, otherwise set it to `True`.

6.6 Logging

Brian uses the standard Python `logging` package to generate information and warnings. All messages are sent to the logger named `brian` or loggers derived from this one, and you can use the standard logging functions to set options, write the logs to files, etc. Alternatively, Brian has four simple functions to set the level of the displayed log (see below). There are four different levels for log messages, in decreasing order of severity they are ERROR, WARN, INFO and DEBUG. By default, Brian displays only the WARN and ERROR level messages. Some useful information is at the INFO level, so if you are having problems with your program, setting the level to INFO may help.

log_level_error()
Shows log messages only of level ERROR or higher.

log_level_warn()
Shows log messages only of level WARNING or higher (including ERROR level).

log_level_info()
Shows log messages only of level INFO or higher (including WARNING and ERROR levels).

log_level_debug()
Shows log messages only of level DEBUG or higher (including INFO, WARNING and ERROR levels).

CHAPTER

SEVEN

Extending Brian

TODO: Description of how to extend Brian, add new model types, and maybe at some point how to upload them to a database, share with others, etc.

For the moment, see the documentation on *Projects with multiple files or functions*.

CHAPTER

EIGHT

Reference

For an overview of Brian, see the *User manual* section.

8.1 Units system

have_same_dimensions(*obj1, obj2*)

Tests if two scalar values have the same dimensions, returns a `bool`.

Note that the syntax may change in later releases of Brian, with tighter integration of scalar and array valued quantities.

is_dimensionless(*obj*)

Tests if a scalar value is dimensionless or not, returns a `bool`.

Note that the syntax may change in later releases of Brian, with tighter integration of scalar and array valued quantities.

exception DimensionMismatchError

Exception class for attempted operations with inconsistent dimensions

For example, `3*mvolt + 2*amp` raises this exception. The purpose of this class is to help catch errors based on incorrect units. The exception will print a representation of the dimensions of the two inconsistent objects that were operated on. If you want to check for inconsistent units in your code, do something like:

```
try:
    ...
    your code here
    ...
except DimensionMismatchError, inst:
    ...
    cleanup code here, e.g.
    print "Found dimension mismatch, details:", inst
    ...
```

check_units(***au*)

Decorator to check units of arguments passed to a function

Sample usage:

```
@check_units(I=amp,R=ohm,wibble=metre,result=volt)
def getvoltage(I,R,**k):
    return I*R
```

You don't have to check the units of every variable in the function, and you can define what the units should be for variables that aren't explicitly named in the definition of the function. For example, the code above checks that the variable wibble should be a length, so writing:

```
getvoltage(1*amp,1*ohm,wibble=1)
```

would fail, but:

```
getvoltage(1*amp,1*ohm,wibble=1*metre)
```

would pass. String arguments are not checked (e.g. `getvoltage(wibble='hello')` would pass).

The special name `result` is for the return value of the function.

An error in the input value raises a `DimensionMismatchError`, and an error in the return value raises an `AssertionError` (because it is a code problem rather than a value problem).

Notes

This decorator will destroy the signature of the original function, and replace it with the signature `(*args, **kwds)`. Other decorators will do the same thing, and this decorator critically needs to know the signature of the function it is acting on, so it is important that it is the first decorator to act on a function. It cannot be used in combination with another decorator that also needs to know the signature of the function.

Typically, you shouldn't need to use any details about the following two classes, and their implementations are subject to change in future releases of Brian.

class `Quantity`(*value*)

A number with an associated physical dimension.

In most cases, it is not necessary to create a `Quantity` object by hand, instead use the constant unit names `second`, `kilogram`, etc. The details of how `Quantity` objects work is subject to change in future releases of Brian, as we plan to reimplement it in a more efficient manner, more tightly integrated with numpy. The following can be safely used:

- `Quantity`, this name will not change, and the usage `isinstance(x,Quantity)` should be safe.
- The standard unit objects, `second`, `kilogram`, etc. documented in the main documentation will not be subject to change (as they are based on SI standardisation).
- Scalar arithmetic will work with future implementations.

class `Unit`(*value*)

A physical unit

Normally, you do not need to worry about the implementation of units. They are derived from the `Quantity` object with some additional information (name and string representation). You can define new units which will be used when generating string representations of quantities simply by doing an arithmetical operation with only units, for example:

```
Nm = newton * metre
```

Note that operations with units are slower than operations with `Quantity` objects, so for efficiency if you do not need the extra information that a `Unit` object carries around, write `1*second` in preference to `second`.

8.2 Clocks

Many Brian objects store a clock object (always passed in the initialiser with the keyword `clock=...`). If no clock is specified, the program uses the global default clock. When Brian is initially imported, this is the object `defaultclock`, and it has a default time step of 0.1ms. In a simple script, you can override this by writing (for example):

```
defaultclock.dt = 1*ms
```

However, there are other ways to access or redefine the default clock (see functions below). You may wish to use multiple clocks in your program. In this case, for each object which requires one, you have to pass a copy of its `Clock` object. The network run function automatically handles objects with different clocks, updating them all at the appropriate time according to their time steps (value of `dt`).

Multiple clocks can be useful, for example, for defining a simulation that runs with a very small `dt`, but with some computationally expensive operation running at a lower frequency.

8.2.1 The `Clock` class

class `Clock` (*dt=0.1 ms, t=0.0 s, makedefaultclock=False*)

An object that holds the simulation time and the time step.

Initialisation arguments:

`dt` The time step of the simulation.

`t` The current time of the clock.

`makedefaultclock` Set to `True` to make this clock the default clock.

Methods

`reinit` (*[t=0*second]*)

Reinitialises the clock time to zero (or to your specified time).

Attributes

`t`
`dt`

Current time and time step with units.

Advanced

Attributes

`end`

The time at which the current simulation will end, set by the `Network.run()` method.

Methods

`tick` ()

Advances the clock by one time step.

`set_t` (*t*)
`set_dt` (*dt*)
`set_end` (*end*)

Set the various parameters.

`get_duration` ()

The time until the current simulation ends.

`set_duration` (*duration*)

Set the time until the current simulation ends.

`still_running` ()

Returns a `bool` to indicate whether the current simulation is still running.

For reasons of efficiency, we recommend using the methods `tick()`, `set_duration()` and `still_running()` (which bypass unit checking internally).

8.2.2 The default clock

defaultclock

The default clock object

Note that this is only the default clock object if you haven't redefined it with the `define_default_clock()` function or the `makedefaultclock=True` option of a `Clock` object. A safe way to get hold of the default clock is to use the functions:

- `get_default_clock()`
- `reinit_default_clock()`

However, it is suitable for short scripts, e.g.:

```
defaultclock.dt = 1*ms
...
```

define_default_clock(***kwds*)

Create a new default clock

Uses the keywords of the `Clock` initialiser.

Sample usage:

```
define_default_clock(dt=1*ms)
```

reinit_default_clock(*t=0.0 s*)

Reinitialise the default clock (to zero or a specified time)

get_default_clock()

Returns the default clock object.

8.3 Neuron models and groups

8.3.1 The `Equations` object

class **Equations**(*expr=", level=0, **kwds*)

Container that stores equations from which models can be created

Initialised as:

```
Equations(expr[,level=0[,keywords...]])
```

with arguments:

expr An expression, which can each be a string representing equations, an `Equations` objects, or a list of strings and `Equations` objects. See below for details of the string format.

level Indicates how many levels back in the stack the namespace for string equations is found, so that e.g. `level=0` looks in the namespace of the function where the `Equations` object was created, `level=1` would look in the namespace of the function that called the function where the `Equations` object was created, etc. Normally you can just leave this out.

keywords Any sequence of keyword pairs `key=value` where the string `key` in the string equations will be replaced with `value` which can be either a string, value or `None`, in the latter case a unique name will be generated automatically (but it won't be pretty).

Systems of equations can be defined by passing lists of `Equations` to a new `Equations` object, or by adding `Equations` objects together (the usage is similar to that of a Python `list`).

String equations

String equations can be of any of the following forms:

1. `dx/dt = f : unit` (differential equation)
2. `x = f : unit` (equation)
3. `x = y` (alias)
4. `x : unit` (parameter)

Here each of `x` and `y` can be any valid Python variable name, `f` can be any valid Python expression, and `unit` should be the unit of the corresponding `x`. You can also include multi-line expressions by appending a `\` character at the end of each line which is continued on the next line (following the Python standard), or comments by including a `#` symbol.

These forms mean:

Differential equation A differential equation with variable `x` which has physical units `unit`. The variable `x` will become one of the state variables of the model.

Equation An equation defining the meaning of `x` can be used for building systems of complicated differential equations.

Alias The variable `x` becomes equivalent to the variable `y`, useful for connecting two separate systems of equations together.

Parameter The variable `x` will have physical units `unit` and will be one of the state variables of the model (but will not evolve dynamically, instead it should be set by the user).

Noise

String equations can also use the reserved term `xi` for a Gaussian white noise with mean 0 and variance 1.

Example usage

```
eqs=Equations('''
dv/dt=(u-v)/tau : volt
u=3*v : volt
w=v
''')
```

For information on integration methods, and the `StateUpdater` class, see *Integration*.

8.3.2 The `Model` object

class **`Model`**(***kwds*)

Stores properties that define a model neuron

The purpose of this class is to store the parameters that define a model neuron, but not actually create any neurons themselves. That is done by the `NeuronGroup` object. The parameters for initialising this object are the same as for `NeuronGroup` less `N` and with the addition of `equation` and `equations` as alternative keywords for `model` (for readability of code).

At the moment, this object simply stores a copy of these keyword assignments and passes them on to a `NeuronGroup` when you instantiate it with this model, so the definitive reference point is the `NeuronGroup`. For convenience, we include a copy of these arguments to initiate a `Model` here:

`model`, `equation` or `equations` An object defining the neuron model. It can be an `Equations` object, a string defining an `Equations` object, a `StateUpdater` object, or a list or tuple of `Equations` and strings.

threshold=None A Threshold object, a function or a scalar quantity. If threshold is a function with one argument, it will be converted to a SimpleFunThreshold, otherwise it will be a FunThreshold. If threshold is a scalar, then a constant single valued threshold with that value will be used. In this case, the variable to apply the threshold to will be guessed. If there is only one variable, or if you have a variable named one of V, Vm, v or vm it will be used.

reset=None A Reset object, a function or a scalar quantity. If it's a function, it will be converted to a FunReset object. If it's a scalar, then a constant single valued reset with that value will be used. In this case, the variable to apply the reset to will be guessed. If there is only one variable, or if you have a variable named one of V, Vm, v or vm it will be used.

refractory=0*ms A refractory period, used in combination with the reset value if it is a scalar.

order=1 The order to use for nonlinear differential equation solvers. TODO: more details.

implicit=False Whether to use an implicit method for solving the differential equations. TODO: more details.

max_delay=0*ms The maximum allowable delay (larger values use more memory). TODO: more details.

compile=False Whether or not to attempt to compile the differential equation solvers into C++ code.

freeze=False If True, parameters are replaced by their values at the time of initialization.

Usage

You can either pass a Model as an argument to initialise a NeuronGroup or initialise a NeuronGroup by writing:

```
group = model * N
```

to create a NeuronGroup of N neurons based on that model.

Example

Starting with a model defined like this:

```
model = Model(equations='''
dv/dt = (ge+gi-(v+49*mV))/(20*ms) : volt
dge/dt = -ge/(5*ms) : volt
dgi/dt = -gi/(10*ms) : volt
''', threshold=-50*mV, reset=-60*mV)
```

The following two lines are equivalent:

```
P = NeuronGroup(4000, model=model)
P = 4000*model
```

8.3.3 The NeuronGroup object

class NeuronGroup(*N, model=None, threshold=None, reset=No reset, init=None, refractory=0.0 s, clock=None, order=1, implicit=False, max_delay=0.0 s, compile=False, freeze=False, method=None, **args*)

Group of neurons

Initialised as:

```
NeuronGroup(N,model[,threshold[,reset[,refractory[,clock[,
        order[,implicit[,max_delay[,compile[,freeze[,method]]]]]]]]]])
```

with arguments:

N The number of neurons in the group.

model An object defining the neuron model. It can be a `Model` object, an `Equations` object, a string defining an `Equations` object, a `StateUpdater` object, or a list or tuple of `Equations` and strings.

threshold=None A `Threshold` object, a function or a scalar quantity. If `threshold` is a function with one argument, it will be converted to a `SimpleFunThreshold`, otherwise it will be a `FunThreshold`. If `threshold` is a scalar, then a constant single valued threshold with that value will be used. In this case, the variable to apply the threshold to will be guessed. If there is only one variable, or if you have a variable named one of `V`, `Vm`, `v` or `vm` it will be used.

reset=None A `Reset` object, a function or a scalar quantity. If it's a function, it will be converted to a `FunReset` object. If it's a scalar, then a constant single valued reset with that value will be used. In this case, the variable to apply the reset to will be guessed. If there is only one variable, or if you have a variable named one of `V`, `Vm`, `v` or `vm` it will be used.

refractory=0*ms A refractory period, used in combination with the `reset` value if it is a scalar.

clock A clock to use for scheduling this `NeuronGroup`, if omitted the default clock will be used.

order=1 The order to use for nonlinear differential equation solvers. TODO: more details.

implicit=False Whether to use an implicit method for solving the differential equations. TODO: more details.

max_delay=0*ms The maximum allowable delay (larger values use more memory). TODO: more details.

compile=False Whether or not to attempt to compile the differential equation solvers into `C++` code.

freeze=False If True, parameters are replaced by their values at the time of initialization.

`method=None If not None, the integration method is forced. Possible values are linear, nonlinear, Euler, exponential_Euler (overrides implicit and order keywords).

Methods

subgroup(*N*)
Returns the next sequential subgroup of `N` neurons. See the section on subgroups below.

state(*var*)
state_(*var*)
Returns the `qarray` or `array` respectively for state variable `var`. This is the array of values for that state variable, with length the number of neurons in the group. The `qarray` form has units and checks for unit consistency, the `array` form doesn't. Normally, you should use the unit checking form, but it is slower so if speed is a serious problem, you can use the other form.

The following usages are also possible for a group `G`:

G[i:j] Returns the subgroup of neurons from `i` to `j`.

len(G) Returns the number of neurons in `G`.

G.x, G.x_ For any valid Python variable name `x` corresponding to a state variable of the the `NeuronGroup`, this returns the `qarray` or `array` of values for the state variable `x`, as for the `state()` and `state_()` methods above.

Subgroups

A subgroup is a view on a group. It isn't a new group, it's just a convenient way of referring to a subset of the neurons in an already defined group. The subset has to be a continguous set of neurons. They can be overlapping if defined with the slice notation, or consecutive if defined with the `subgroup()` method. Subgroups can themselves be subgrouped. Subgroups can be used in almost all situations exactly as if they were groups, except that they cannot be passed to the `Network` object.

Details

TODO: details of other methods and properties for people wanting to write extensions?

8.3.4 Resets

Reset objects are called each network update step to reset specified state variables of neurons that have fired.

class `Reset` (*resetvalue=0.0 V, state=0*)

Resets specified state variable to a fixed value

Initialise as:

```
R = Reset([resetvalue=0*mvolt[, state=0]])
```

with arguments:

`resetvalue` The value to reset to.

`state` The name or number of the state variable to reset.

This will reset all of the neurons that have just spiked. The given state variable of the neuron group will be set to value `resetvalue`.

class `VariableReset` (*resetvaluestate=1, state=0*)

Resets specified state variable to the value of another state variable

Initialised with arguments:

`resetvaluestate` The state variable which contains the value to reset to.

`state` The name or number of the state variable to reset.

This will reset all of the neurons that have just spiked. The given state variable of the neuron group will be set to the value of the state variable `resetvaluestate`.

class `Refractoriness` (*resetvalue=0.0 V, period=5.0 ms, state=0*)

Holds the state variable at the reset value for a fixed time after a spike.

Initialised as:

```
Refractoriness([resetvalue=0*mV[,period=5*ms[,state=0]]])
```

with arguments:

`resetvalue` The value to reset and hold to.

`period` The length of time to hold at the reset value.

`state` The name or number of the state variable to reset and hold.

class `SimpleCustomRefractoriness` (*resetfun, period=5.0 ms, state=0*)

Holds the state variable at the custom reset value for a fixed time after a spike.

Initialised as:

```
SimpleCustomRefractoriness(resetfunc[,period=5*ms[,state=0]])
```

with arguments:

`resetfun` The custom reset function `resetfun(P, spikes)` for `P` a `NeuronGroup` and `spikes` a list of neurons that fired spikes.

`period` The length of time to hold at the reset value.

`state` The name or number of the state variable to reset and hold, it is your responsibility to check that this corresponds to the custom reset function.

The assumption is that `resetfun(P, spikes)` will reset the state variable `state` on the group `P` for the spikes with indices `spikes`. The values assigned by the custom reset function are stored by this object, and they are clamped at these values for `period`. This object does not introduce refractoriness for more than the one specified variable `state` or for spike indices other than those in the variable `spikes` passed to the custom reset function.

class **`CustomRefractoriness`**(*resetfun, period=5.0 ms, refracfunc=None*)

Holds the state variable at the custom reset value for a fixed time after a spike.

Initialised as:

```
CustomRefractoriness(resetfunc[,period=5*ms[,refracfunc=resetfunc]])
```

with arguments:

`resetfunc` The custom reset function `resetfunc(P, spikes)` for `P` a `NeuronGroup` and `spikes` a list of neurons that fired spikes.

`refracfunc` The custom refractoriness function `refracfunc(P, indices)` for `P` a `NeuronGroup` and `indices` a list of neurons that are in their refractory periods. In some cases, you can choose not to specify this, and it will use the reset function.

`period` The length of time to hold at the reset value.

class **`FunReset`**(*resetfun*)

A reset with a user-defined function.

Initialised as:

```
FunReset(resetfun)
```

with argument:

`resetfun` A function `f(G,spikes)` where `G` is the `NeuronGroup` and `spikes` is an array of the indexes of the neurons to be reset.

class **`NoReset`**()

Absence of reset mechanism.

Initialised as:

```
NoReset()
```

8.3.5 Thresholds

A threshold mechanism checks which neurons have fired a spike.

class **`Threshold`**(*threshold=1.0 mV, state=0*)

All neurons with a specified state variable above a fixed value fire a spike.

Initialised as:

```
Threshold([threshold=1*mV[,state=0])
```

with arguments:

`threshold` The value above which a neuron will fire.

`state` The state variable which is checked.

Compilation

Note that if the global variable `useweave` is set to `True` then this function will use a `C++` accelerated version which runs approximately 3x faster.

class `VariableThreshold`(*threshold_state=1, state=0*)

Threshold mechanism where one state variable is compared to another.

Initialised as:

```
VariableThreshold([threshold_state=1[,state=0]])
```

with arguments:

`threshold_state` The state holding the lower bound for spiking.

`state` The state that is checked.

If `x` is the value of state variable `threshold_state` on neuron `i` and `y` is the value of state variable `state` on neuron `i` then neuron `i` will fire if `y>x`.

Typically, using this class is more time efficient than writing a custom thresholding operation.

Compilation

Note that if the global variable `useweave` is set to `True` then this function will use a `C++` accelerated version.

class `EmpiricalThreshold`(*threshold=1.0 mV, refractory=1.0 ms, state=0, clock=None*)

Empirical threshold, e.g. for Hodgkin-Huxley models.

In empirical models such as the Hodgkin-Huxley method, after a spike neurons are not instantaneously reset, but reset themselves as part of the dynamical equations defining their behaviour. This class can be used to model that. It is a simple threshold mechanism that checks e.g. `V>=Vt` but it only does so for neurons that haven't recently fired (giving the dynamical equations time to reset the values naturally). It should be used in conjunction with the `NoReset` object.

Initialised as:

```
EmpiricalThreshold([threshold=1*mV[,refractory=1*ms[,state=0[,clock]]]])
```

with arguments:

`threshold` The lower bound for the state variable to induce a spike.

`refractory` The time to wait after a spike before checking for spikes again.

`state` The name or number of the state variable to check.

`clock` If this object is being used for a `NeuronGroup` which doesn't use the default clock, you need to specify its clock here.

class `SimpleFunThreshold`(*thresholdfun, state=0*)

Threshold mechanism with a user-specified function.

Initialised as:

```
FunThreshold(thresholdfun[,state=0])
```

with arguments:

`thresholdfun` A function with one argument, the array of values for the specified state variable. For efficiency, this is a numpy array, and there is no unit checking.

`state` The name or number of the state variable to pass to the threshold function.

Sample usage:

```
FunThreshold(lambda V:V>=Vt,state='V')
```

class **`FunThreshold`**(*thresholdfun*)

Threshold mechanism with a user-specified function.

Initialised as:

```
FunThreshold(thresholdfun)
```

where `thresholdfun` is a function with one argument, the 2d state value array, where each row is an array of values for one state, of length N for N the number of neurons in the group. For efficiency, data are numpy arrays and there is no unit checking.

Note: if you only need to consider one state variable, use the `SimpleFunThreshold` object instead.

class **`NoThreshold`**()

No thresholding mechanism.

Initialised as:

```
NoThreshold()
```

8.4 Integration

See *Numerical integration* for an overview.

8.4.1 StateUpdaters

Typically you don't need to worry about `StateUpdater` objects because they are automatically created from the differential equations defining your model. TODO: more details about this.

class **`LinearStateUpdater`**(*M, B=None, clock=None*)

A linear model with dynamics dX/dt = M(X-B) or dX/dt = MX.

Initialised as:

```
LinearStateUpdater(M[,B[,clock]])
```

with arguments:

`M` Matrix defining the differential equation.

`B` Optional linear term in the differential equation.

`clock` Optional clock.

Computes an update matrix A=exp(M dt) for the linear system, and performs the update step.

TODO: more mathematical details?

class **`LazyStateUpdater`**(*numstatevariables=1, clock=None*)

A StateUpdater that does nothing.

Initialised as:

```
LazyStateUpdater([numstatevariables=1[,clock]])
```

with arguments:

`numstatevariables` The number of state variables to create.

`clock` An optional clock to determine when it updates, although the update function does nothing so...

TODO: write docs for these StateUpdaters:

- StateUpdater, LinearStateUpdater more details, NonlinearStateUpdater, NonlinearStateUpdater2, ExponentialEulerStateUpdater, NonlinearStateUpdaterRK2, NonlinearStateUpdaterBE, SynapticNoise

8.5 Standard Groups

Some standard types of `NeuronGroup` have already been defined. `PoissonGroup` to generate spikes with Poisson statistics, `PulsePacket` to generate pulse packets with specified parameters, `SpikeGeneratorGroup` and `MultipleSpikeGeneratorGroup` to generate spikes which fire at prespecified times.

class `PoissonGroup`(*N, rates=0.0 Hz, clock=None*)

A group that generates independent Poisson spike trains.

Initialised as:

```
PoissonGroup(N,rates[,clock])
```

with arguments:

`N` The number of neurons in the group

`rates` A scalar, array or function returning a scalar or array. The array should have the same length as the number of neurons in the group. The function should take one argument `t` the current simulation time.

`clock` The clock which the group will update with, do not specify to use the default clock.

class `PulsePacket`(*t, n, sigma, clock=None*)

Fires a Gaussian distributed packet of n spikes with given spread

Initialised as:

```
PulsePacket(t,n,sigma[,clock])
```

with arguments:

`t` The mean firing time

`n` The number of spikes in the packet

`sigma` The standard deviation of the firing times.

`clock` The clock to use (omit to use default or local clock)

Methods

This class is derived from `SpikeGeneratorGroup` and has all its methods as well as one additional method:

`generate`(*t, n, sigma*)

Change the parameters and/or generate a new pulse packet.

class `SpikeGeneratorGroup`(*N, spiketimes, clock=None, period=None*)

Emits spikes at given times

Initialised as:

```
SpikeGeneratorGroup(N,spiketimes[,clock[,period]])
```

with arguments:

`N` The number of neurons in the group.

spiketimes An object specifying which neurons should fire and when. It can be a container such as a `list`, containing tuples `(i,t)` meaning neuron `i` fires at time `t`, or a callable object which returns such a container (which allows you to use generator objects, see below). If `spiketimes` is not a list or tuple, the pairs `(i,t)` need to be sorted in time. You can also pass a numpy array `spiketimes` where the first column of the array is the neuron indices, and the second column is the times in seconds. WARNING: units are not checked in this case, and you need to ensure that the spikes are sorted.

clock An optional clock to update with (omit to use the default clock).

period Optionally makes the spikes recur periodically with the given period. Note that iterator objects cannot be used as the `spikelist` with a period as they cannot be reinitialised.

Sample usages

The simplest usage would be a list of pairs `(i,t)`:

```
spiketimes = [(0,1*ms), (1,2*ms)]
SpikeGeneratorGroup(N,spiketimes)
```

A more complicated example would be to pass a generator:

```
import random
def nextspike():
    nexttime = random.uniform(0*ms,10*ms)
    while True:
        yield (random.randint(0,9),nexttime)
        nexttime = nexttime + random.uniform(0*ms,10*ms)
P = SpikeGeneratorGroup(10,nextspike())
```

This would give a neuron group `P` with 10 neurons, where a random one of the neurons fires at an average rate of one every 5ms.

Notes

Note that if a neuron fires more than one spike in a given interval `dt`, additional spikes will be discarded. If you want them to stack, consider using the less efficient `MultipleSpikeGeneratorGroup` object instead. A warning will be issued if this is detected.

Also note that if you pass a generator, then reinitialising the group will not have the expected effect because a generator object cannot be reinitialised. Instead, you should pass a callable object which returns a generator. In the example above, that would be done by calling:

```
P = SpikeGeneratorGroup(10,nextspike)
```

Whenever P is reinitialised, it will call `nextspike()` to create the required spike container.

class MultipleSpikeGeneratorGroup(*spiketimes, clock=None, period=None*)

Emits spikes at given times

Initialised as:

```
MultipleSpikeGeneratorGroup(spiketimes[,clock[,period]])
```

with arguments:

spiketimes a list of spike time containers, one for each neuron in the group, although note that elements of `spiketimes` can also be callable objects which return spike time containers if you want to be able to reinitialise (see below). At it's simplest, `spiketimes` could be a list of lists, where `spiketimes[0]` contains the firing times for neuron 0, `spiketimes[1]` for neuron 1, etc. But, any iterable object can be passed, so `spiketimes[0]` could be a generator for example. Each spike time container should be sorted in time. If the containers are numpy arrays units will not be checked (times should be in seconds).

clock A clock, if omitted the default clock will be used.

period Optionally makes the spikes recur periodically with the given period. Note that iterator objects cannot be used as the `spikelist` with a period as they cannot be reinitialised.

Note that if two or more spike times fall within the same `dt`, spikes will stack up and come out one per dt until the stack is exhausted. A warning will be generated if this happens.

Also note that if you pass a generator, then reinitialising the group will not have the expected effect because a generator object cannot be reinitialised. Instead, you should pass a callable object which returns a generator, this will be called each time the object is reinitialised by calling the `reinit()` method.

Sample usage:

```
spiketimes = [[1*msecond, 2*msecond]]
P = MultipleSpikeGeneratorGroup(spiketimes)
```

8.6 Connections

The best way to understand the concept of a `Connection` in Brian is to work through Tutorial 2: Connections.

class Connection(*source, target, state=0, delay=0.0 s, modulation=None, structure='sparse', **kwds*)

Mechanism for propagating spikes from one group to another

A Connection object declares that when spikes in a source group are generated, certain neurons in the target group should have a value added to specific states. See Tutorial 2: Connections to understand this better.

Initialised as:

```
Connection(source, target[, state=0[, delay=0*ms[, modulation=None]]])
```

With arguments:

source The group from which spikes will be propagated.

target The group to which spikes will be propagated.

state The state variable name or number that spikes will be propagated to in the target group.

delay The delay between a spike being generated at the source and received at the target. At the moment, the mechanism for delays only works for relatively short delays (an error will be generated for delays that are too long).

modulation The state variable name from the source group that scales the synaptic weights (for short-term synaptic plasticity).

structure Data structure: sparse (default), dense or computed (no storing).

Methods

connect_random(P,Q,p[,weight=1[,fixed=False[,seed=None]]]) Connects each neuron in `P` to each neuron in `Q` with independent probability `p` and weight `weight` (this is the amount that gets added to the target state variable). If `fixed` is True, then the number of presynaptic neurons per neuron is constant. If `seed` is given, it is used as the seed to the random number generators, for exactly repeatable results.

connect_full(P,Q[,weight=1]) Connect every neuron in `P` to every neuron in `Q` with the given weight.

connect_one_to_one(P,Q) If `P` and `Q` have the same number of neurons then neuron `i` in `P` will be connected to neuron `i` in `Q` with weight 1.

connect(P,Q,W) You can specify a matrix of weights directly (can be in any format recognised by NumPy). Note that due to internal implementation details, passing a full matrix rather than a sparse one may slow down your code (because zeros will be propagated as well as nonzero values). **WARNING:** No unit checking is done at the moment.

Additionally, you can directly access the matrix of weights by writing:

```
C = Connection(P,Q)
print C[i,j]
C[i,j] = ...
```

Where here `i` is the source neuron and `j` is the target neuron. Note: if `C[i,j]` should be zero, it is more efficient not to write `C[i,j]=0`, if you write this then when neuron `i` fires all the targets will have the value 0 added to them rather than just the nonzero ones. **WARNING:** No unit checking is currently done if you use this method. Take care to set the right units.

Advanced information

The following methods are also defined and used internally, if you are writing your own derived connection class you need to understand what these do.

`propagate(spikes)` Action to take when source neurons with indices in `spikes` fired.

`do_propagate()` The method called by the `Network` `update()` step, typically just propagates the spikes obtained by calling the `get_spikes` method of the `source` `NeuronGroup`.

8.6.1 Connection matrix types

Computed connections

The following two connection matrix types can be given for a `Connection` object.

class **`UserComputedConnectionMatrix`**(*dims, row_func*)

A computed connection matrix defined by a user-specified function

Normally this matrix will be initialised by passing the class object to the `Connection` object. In the initialisation of the `Connection` specify `structure=UserComputedConnectionMatrix` and add the keyword `row_func=...`, e.g.:

```
def f(i):
    return max_weight*ones(N)/(1+(arange(N)-i)**2)
C = Connection(G1, G2, structure=UserComputedConnectionMatrix, row_func=f)
```

Initialisation arguments:

`dims` The pair `(N,M)` specifying the dimensions of the matrix.

`row_func` The function `f(i)` which returns an array of length `M`, the weight matrix for row `i`. Note that you are responsible for making sure the function returns consistent results (so random functions should be initialised with a seed based on the row `i`).

Limitations

This type of connection matrix cannot be changed during a run, and cannot be used with methods like `Connection.connect_random`.

Efficiency considerations

This connection matrix is for dense connectivity, if the connectivity is sparse you might get better performance with `UserComputedSparseConnectionMatrix`.

class **`UserComputedSparseConnectionMatrix`**(*dims, row_func*)

A computed sparse connection matrix defined by a user-specified function

Normally this matrix will be initialised by passing the class object to the `Connection` object. In the initialisation of the `Connection` specify `structure=UserComputedSparseConnectionMatrix` and add the keyword `row_func=...`, e.g.:

```
def f(i):
    if 0<i<N-1:
        return ([i-1,i+1], weight*ones(2))
    elif i>0:
        return ([i-1], weight*ones(1))
    else:
        return ([i+1], weight*ones(1))
C = Connection(G1, G2, structure=UserComputedSparseConnectionMatrix, row_func=f)
```

Initialisation arguments:

dims The pair (N,M) specifying the dimensions of the matrix.

row_func The function f(i) which for a row i returns a pair (indices, values)) consisting of a list or array indices with the indices of the nonzero elements of the row, and an array of the same length values giving the weight matrix for those indices. Note that you are responsible for making sure the function returns consistent results (so random functions should be initialised with a seed based on the row i).

Limitations

This type of connection matrix cannot be changed during a run, and cannot be used with methods like Connection.connect_random.

Efficiency considerations

This connection matrix is for sparse connectivity, if the connectivity is dense you might get better performance with UserComputedConnectionMatrix.

These standard functions can be used to define their behaviour as an alternative to specifying your own.

random_row_func(*N, p, weight=1.0, initseed=None*)

Returns a random connectivity row_func for use with UserComputedConnectionMatrix

Gives equivalent output to the Connection.connect_random() method.

Arguments:

N The number of target neurons.

p The probability of a synapse.

weight The connection weight (must be a single value).

initseed The initial seed value (for reproducible results).

random_sparse_row_func(*N, p, weight=1.0, initseed=None*)

Returns a random connectivity row_func for use with UserComputedSparseConnectionMatrix

Gives equivalent output to the Connection.connect_random() method.

Arguments:

N The number of target neurons.

p The probability of a synapse.

weight The connection weight (must be a single value).

initseed The initial seed value (for reproducible results).

8.7 Network

The Network object stores simulation objects and runs simulations. Usage is described in detail below. For simple scripts, you don't even need to use the Network object itself, just directly use the ''magic'' functions run() and reinit() described below.

class **Network** (**args, **kwds*)

Contains simulation objects and runs simulations

Initialised as:

```
Network(...)
```

with `...` any collection of objects that should be added to the `Network`. You can also pass lists of objects, lists of lists of objects, etc. Objects that need to passed to the `Network` object are:

- `NeuronGroup` and anything derived from it such as `PoissonGroup`.
- `Connection` and anything derived from it.
- Any monitor such as `SpikeMonitor` or `StateMonitor`.
- Any network operation defined with the `network_operation()` decorator.

Models, equations, etc. do not need to be passed to the `Network` object.

The most important method is the `run(duration)` method which runs the simulation for the given length of time (see below for details about what happens when you do this).

Example usage:

```
G = NeuronGroup(...)
C = Connection(...)
net = Network(G,C)
net.run(1*second)
```

Methods

`add(...)` Add additional objects after initialisation, works the same way as initialisation.

`run(duration)` Runs the network for the given duration. See below for details about what happens when you do this.

`reinit()` Reinitialises the network, runs each object's `reinit()` and each clock's `reinit()` method (resetting them to 0).

`stop()` Can be called from a `network_operation()` for example to stop the network from running.

`__len__()` Returns the number of neurons in the network.

`__call__(obj)` Similar to `add`, but you can only pass one object and that object is returned. You would only need this in obscure circumstances where objects needed to be added to the network but were either not stored elsewhere or were stored in a way that made them difficult to extract, for example below the NeuronGroup object is only added to the network if certain conditions hold:

```
net = Network(...)
if some_condition:
    x = net(NeuronGroup(...))
```

What happens when you run

For an overview, see the Concepts chapter of the main documentation.

When you run the network, the first thing that happens is that it checks if it has been prepared and calls the `prepare()` method if not. This just does various housekeeping tasks and optimisations to make the simulation run faster. Also, an update schedule is built at this point (see below).

Now the `update()` method is repeatedly called until every clock has run for the given length of time. After each call of the `update()` method, the clock is advanced by one tick, and if multiple clocks are being used, the next clock is determined (this is the clock whose value of `t` is minimal amongst all the clocks). For example, if you had two clocks in operation, say `clock1` with `dt=3*ms` and `clock2` with `dt=5*ms` then this will happen:

1. `update()` for `clock1`, tick `clock1` to `t=3*ms`, next clock is `clock2` with `t=0*ms`.
2. `update()` for `clock2`, tick `clock2` to `t=5*ms`, next clock is `clock1` with `t=3*ms`.
3. `update()` for `clock1`, tick `clock1` to `t=6*ms`, next clock is `clock2` with `t=5*ms`.
4. `update()` for `clock2`, tick `clock2` to `t=10*ms`, next clock is `clock1` with `t=6*ms`.
5. `update()` for `clock1`, tick `clock1` to `t=9*ms`, next clock is `clock1` with `t=9*ms`.
6. `update()` for `clock1`, tick `clock1` to `t=12*ms`, next clock is `clock2` with `t=10*ms`. etc.

The `update()` method simply runs each operation in the current clock's update schedule. See below for details on the update schedule.

Update schedules

An update schedule is the sequence of operations that are called for each `update()` step. The standard update schedule is:

- Network operations with `when = 'start'`
- Network operations with `when = 'before_groups'`
- Call `update()` method for each `NeuronGroup`, this typically performs an integration time step for the differential equations defining the neuron model.
- Network operations with `when = 'after_groups'`
- Network operations with `when = 'middle'`
- Network operations with `when = 'before_connections'`
- Call `do_propagate()` method for each `Connection`, this typically adds a value to the target state variable of each neuron that a neuron that has fired is connected to. See Tutorial 2: Connections for a more detailed explanation of this.
- Network operations with `when = 'after_connections'`
- Network operations with `when = 'before_resets'`
- Call `reset()` method for each `NeuronGroup`, typically resets a given state variable to a given reset value for each neuron that fired in this update step.
- Network operations with `when = 'after_resets'`
- Network operations with `when = 'end'`

There is one predefined alternative schedule, which you can choose by calling the `update_schedule_groups_resets_connections()` method before running the network for the first time. As the name suggests, the reset operations are done before connections (and the appropriately named network operations are called relative to this rearrangement). You can also define your own update schedule with the `set_update_schedule` method (see that method's API documentation for details). This might be useful for example if you have a sequence of network operations which need to be run in a given order.

`network_operation`(**args, **kwds*)

Decorator to make a function into a `NetworkOperation`

A `NetworkOperation` is a callable class which is called every time step by the `Network` `run` method. Sometimes it is useful to just define a function which is to be run every update step. This decorator can be used to turn a function into a `NetworkOperation` to be added to a `Network` object.

Example usages

Operation doesn't need a clock:

```
@network_operation
def f():
    ...
```

Automagically detect clock:

```
@network_operation
def f(clock):
    ...
```

Specify a clock:

```
@network_operation(specifiedclock)
def f(clock):
    ...
```

Specify when the network operation is run (default is `'end'`):

```
@network_operation(when='start')
def f():
    ...
```

Then add to a network as follows:

```
net = Network(f,...)
```

class `NetworkOperation`(*function, clock=None, when='end'*)

Callable class for operations that should be called every update step

Typically, you should just use the `network_operation()` decorator, but if you can't for whatever reason, use this. Note: current implementation only works for functions, not any callable object.

Initialisation:

```
NetworkOperation(function[,clock])
```

If your function takes an argument, the clock will be passed as that argument.

The ''magic'' functions `run()` and `reinit()` work by searching for objects which could be added to a network, constructing a network with all these objects, and working with that. They are suitable for simple scripts only. If you have problems where objects are unexpectedly not being added to the network, the best thing to do would probably be to just use an explicit `Network` object as above rather than trying to tweak your program to make the magic functions work. However, details are available in the `brian/magic.py` source code.

`run`(*duration, threads=1*)

Run a network created from any suitable objects that can be found

Usage:

```
run(duration)
```

where `duration` is the length of time to run the network for.

Works by constructing a `MagicNetwork` object from all the suitable objects that could be found (`NeuronGroup`, `Connection`, etc.) and then running that network. Not suitable for repeated runs or situations in which you need precise control.

`reinit`()

Reinitialises any suitable objects that can be found

Usage:

```
reinit()
```

Works by constructing a `MagicNetwork` object from all the suitable objects that could be found (`NeuronGroup`, `Connection`, etc.) and then calling `reinit()` for each of them. Not suitable for repeated runs or situations in which you need precise control.

stop()

Globally stops any running network, this is reset the next time a network is run

class **MagicNetwork**(*verbose=False, level=1*)

Creates a `Network` object from any suitable objects

Initialised as:

```
MagicNetwork()
```

The object returned can then be used just as a regular `Network` object. It works by finding any object in the ''execution frame" (i.e. in the same function, script or section of module code where the `MagicNetwork` was created) derived from `NeuronGroup`, `Connection` or `NetworkOperation`.

Sample usage:

```
G = NeuronGroup(...)
C = Connection(...)
@network_operation
def f():
    ...
net = MagicNetwork()
```

Each of the objects `G`, `C` and `f` are added to `net`.

Advanced usage:

```
MagicNetwork([verbose=False[,level=1]])
```

with arguments:

verbose Set to `True` to print out a list of objects that were added to the network, for debugging purposes.

level Where to find objects. `level=1` means look for objects where the `MagicNetwork` object was created. The `level` argument says how many steps back in the stack to look.

8.8 Monitors

Monitors are used to record properties of your network. The two most important are `SpikeMonitor` which records spikes, and `StateMonitor` which records values of state variables. These objects are just added to the network like a `NeuronGroup` or `Connection`.

Implementation note: monitors that record spikes are classes derived from `Connection`, and overwrite the `propagate` method to store spikes. If you want to write your own custom spike monitors, you can do the same (or just use `SpikeMonitor` with a custom function). Monitors that record values are classes derived from `NetworkOperation` and implement the `__call__` method to store values each time the network updates. Custom state monitors are most easily written by just writing your own network operation using the `network_operation` decorator.

class **SpikeMonitor**(*source, record=True, delay=0, function=None*)

Counts or records spikes from a `NeuronGroup`

Initialised as one of:

```
SpikeMonitor(source(,record=True))
SpikeMonitor(source,function=function)
```

Where:

source A `NeuronGroup` to record from

record `True` or `False` to record all the spikes or just summary statistics.

function A function `f(spikes)` which is passed the array of neuron numbers that have fired called each step, to define custom spike monitoring.

Has two attributes:

nspikes The number of recorded spikes

spikes A time ordered list of pairs `(i,t)` where neuron `i` fired at time `t`.

For `M` a `SpikeMonitor`, you can also write:

M[i] A qarray of the spike times of neuron `i`.

Notes:

`SpikeMonitor` is subclassed from `Connection`. To define a custom monitor, either define a subclass and rewrite the `propagate` method, or pass the monitoring function as an argument (`function=myfunction`, with `def myfunction(spikes):...`)

class SpikeCounter(*source*)

Counts spikes from a `NeuronGroup`

Initialised as:

```
SpikeCounter(source)
```

With argument:

source A `NeuronGroup` to record from

Has two attributes:

nspikes The number of recorded spikes

count An array of spike counts for each neuron

For a `SpikeCounter` `M` you can also write `M[i]` for the number of spikes counted for neuron `i`.

class PopulationSpikeCounter(*source, delay=0*)

Counts spikes from a `NeuronGroup`

Initialised as:

```
PopulationSpikeCounter(source)
```

With argument:

source A `NeuronGroup` to record from

Has one attribute:

nspikes The number of recorded spikes

class StateSpikeMonitor(*source, var*)

Counts or records spikes and state variables at spike times from a `NeuronGroup`

Initialised as:

```
StateSpikeMonitor(source, var)
```

Where:

source A `NeuronGroup` to record from

var The variable name or number to record from, or a tuple of variable names or numbers if you want to record multiple variables for each spike.

Has two attributes:

nspikes
The number of recorded spikes

spikes
A time ordered list of tuples `(i,t,v)` where neuron `i` fired at time `t` and the specified variable had value `v`. If you specify multiple variables, each tuple will be of the form `(i,t,v0,v1,v2,...)` where the `vi` are the values corresponding in order to the variables you specified in the `var` keyword.

And two methods:

times(*i=None*)
Returns a `qarray` of the spike times for the whole monitored group, or just for neuron `i` if specified.

values(*var, i=None*)
Returns a `qarray` of the values of variable `var` for the whole monitored group, or just for neuron `i` if specified.

class **StateMonitor**(*P, varname, clock=None, record=False, timestep=1, when='end'*)
Records the values of a state variable from a `NeuronGroup`.

Initialise as:

```
StateMonitor(P,varname(,record=False)
    (,when='end)(,timestep=1)(,clock=clock))
```

Where:

P The group to be recorded from

varname The state variable name or number to be recorded

record What to record. The default value is `False` and the monitor will only record summary statistics for the variable. You can choose `record=integer` to record every value of the neuron with that number, `record="list of integers to record every value of each of those neurons, or "record=True` to record every value of every neuron (although beware that this may use a lot of memory).

when When the recording should be made in the network update, possible values are any of the strings: `'start'`, `'before_groups'`, `'after_groups'`, `'before_connections'`, `'after_connections'`, `'before_resets'`, `'after_resets'`, `'end'` (in order of when they are run).

timestep A recording will be made each timestep clock updates (so `timestep` should be an integer).

clock A clock for the update schedule, use this if you have specified a clock other than the default one in your network, or to update at a lower frequency than the update cycle. Note though that if the clock here is different from the main clock, the when parameter will not be taken into account, as network updates are done clock by clock. Use the `timestep` parameter if you need recordings to be made at a precise point in the network update step.

The `StateMonitor` object has the following properties (where names without an underscore return `QuantityArray` objects with appropriate units and names with an underscore return `array` objects without units):

times, times_ The times at which recordings were made

mean, mean_ The mean value of the state variable for every neuron in the group (not just the ones specified in the `record` keyword)

var, var_ The unbiased estimate of the variances, as in `mean`

std, std_ The square root of `var`, as in `mean`

values, values_ A 2D array of the values of all the recorded neurons, each row is a single neuron's values.

In addition, if `M`` is a `StateMonitor` object, you write:

```
M[i]
```

for the recorded values of neuron `i` (if it was specified with the `record` keyword). It returns a `QuantityArray` object with units. Downcast to an array without units by writing `asarray(M[i])`.

class **FileSpikeMonitor**(*source, filename, record=False, delay=0*)

Records spikes to a file

Initialised as:

```
FileSpikeMonitor(source, filename[, record=False])
```

Does everything that a `SpikeMonitor` does except also records the spikes to the named file. note that spikes are recorded as an ASCII file of lines each of the form:

```
    i, t
```

Where `i` is the neuron that fired, and `t` is the time in seconds.

Has one additional method:

close_file() Closes the file manually (will happen automatically when the program ends).

class **ISIHistogramMonitor**(*source, bins, delay=0*)

Records the interspike interval histograms of a group.

Initialised as:

```
ISIHistogramMonitor(source, bins)
```

source The source group to record from.

bins The lower bounds for each bin, so that e.g. `bins = [0*ms, 10*ms, 20*ms]` would correspond to bins with intervals 0-10ms, 10-20ms and 20+ms.

Has properties:

bins The `bins` array passed at initialisation.

count An array of length `len(bins)` counting how many ISIs were in each bin.

This object can be passed directly to the plotting function `hist_plot()`.

class **PopulationRateMonitor**(*source, bin=None*)

Monitors and stores the (time-varying) population rate

Initialised as:

```
PopulationRateMonitor(source,bin)
```

Records the average activity of the group for every bin.

Properties:

rate, rate_ A `qarray` of the rates in Hz.

times, times_ The times of the bins.

bin The duration of a bin (in second).

8.9 Plotting

Most plotting should be done with the PyLab commands, all of which are loaded when you import Brian. See:

> http://matplotlib.sourceforge.net/matplotlib.pylab.html

for help on PyLab.

Brian currently defines just two plotting functions of its own, `raster_plot()` and `hist_plot()`.

`raster_plot`(**monitors, **plotoptions*)

Raster plot of a `SpikeMonitor`

Usage

`raster_plot(monitor,options...)` Plots the spike times of the monitor on the x-axis, and the neuron number on the y-axis

`raster_plot(monitor0,monitor1,...,options...)` Plots the spike times for all the monitors given, with y-axis defined by placing a spike from neuron n of m in monitor i at position i+n/m

`raster_plot(options...)` Guesses the monitors to plot automagically

Options

Any of PyLab options for the `plot` command can be given, as well as:

`showplot=False` set to `True` to run pylab's `show()` function

`newfigure=True` set to `False` not to create a new figure with pylab's `figure()` function

`xlabel` label for the x-axis

`ylabel` label for the y-axis

`title` title for the plot

`showgrouplines=False` set to `True` to show a line between each monitor

`grouplinecol` colour for group lines

`spacebetweengroups` value between 0 and 1 to insert a space between each group on the y-axis

`hist_plot`(*histmon=None, **plotoptions*)

Plot a histogram

Usage

`hist_plot(histmon,options...)` Plot the given histogram monitor

`hist_plot(options...)` Guesses which histogram monitor to use

with argument:

`histmon` is a monitor of histogram type

Notes

Plots only the first n-1 of n bars in the histogram, because the nth bar is for the interval (-,infinity).

Options

Any of PyLab options for bar can be given, as well as:

`showplot=False` set to `True` to run pylab's `show()` function

`newfigure=True` set to `False` not to create a new figure with pylab's `figure()` function

`xlabel` label for the x-axis

`ylabel` label for the y-axis

`title` title for the plot

8.10 Magic in Brian

magic_return (*f*)

Decorator to ensure that the returned object from a function is recognised by magic functions

Usage example:

```
@magic_return
def f():
    return PulsePacket(50*ms, 100, 10*ms)
```

Explanation

Normally, code like the following wouldn't work:

```
def f():
    return PulsePacket(50*ms, 100, 10*ms)
pp = f()
M = SpikeMonitor(pp)
run(100*ms)
raster_plot()
show()
```

The reason is that the magic function `run()` only recognises objects created in the same execution frame that it is run from. The `magic_return()` decorator corrects this, it registers the return value of a function with the magic module. The following code will work as expected:

```
@magic_return
def f():
    return PulsePacket(50*ms, 100, 10*ms)
pp = f()
M = SpikeMonitor(pp)
run(100*ms)
raster_plot()
show()
```

Technical details

The `magic_return()` function uses `magic_register()` with the default `level=1` on just the object returned by a function. See details for `magic_register()`.

magic_register (**args, **kwds*)

Declare that a magically tracked object should be put in a particular frame

Standard usage

If `A` is a tracked class (derived from `InstanceTracker`), then the following wouldn't work:

```
def f():
    x = A('x')
    return x
objs = f()
print get_instances(A,0)[0]
```

Instead you write:

```
def f():
    x = A('x')
    magic_register(x)
    return x
```

```
objs = f()
print get_instances(A,0)[0]
```

Definition

Call as:

```
magic_register(...[,level=1])
```

The `...` can be any sequence of tracked objects or containers of tracked objects, and each tracked object will have its instance id (the execution frame in which it was created) set to that of its parent (or to its parent at the given level). This is equivalent to calling:

```
x.set_instance_id(level=level)
```

For each object `x` passed to `magic_register()`.

See Also:

Projects with multiple files or functions Describes difficulties and solutions for using magic functions on projects with multiple files or functions.

8.11 Tests

`run_all_tests``()`
Run all of Brian's test functions

TODO: Reference documentation that still needs written:

- Connection matrix types (dense, sparse, etc.)
- STDP
- STP
- numpywrappers (and generally, the units stuff is incomplete)

CHAPTER

NINE

Typical Tasks

TODO: typical things you want to achieve in running your simulation, and how to go about doing them.

9.1 Projects with multiple files or functions

Brian works with the minimal hassle if the whole of your code is in a single Python module (`.py` file). This is fine when learning Brian or for quick projects, but for larger, more realistic projects with the source code separated into multiple files, there are some small issues you need to be aware of. These issues essentially revolve around the use of the ''magic" functions `run()`, etc. The way these functions work is to look for objects of the required type that have been instantiated (created) in the same ''execution frame" as the `run()` function. In a small script, that is normally just any objects that have been defined in that script. However, if you define objects in a different module, or in a function, then the magic functions won't be able to find them.

There are three main approaches then to splitting code over multiple files (or functions).

9.1.1 Use the `Network` object explicitly

The magic `run()` function works by creating a `Network` object automatically, and then running that network. Instead of doing this automatically, you can create your own `Network` object. Rather than writing something like:

```
group1 = ...
group2 = ...
C = Connection(group1,group2)
...
run(1*second)
```

You do this:

```
group1 = ...
group2 = ...
C = Connection(group1, group2)
...
net = Network(group1, group2, C)
net.run(1*second)
```

In other words, you explicitly say which objects are in your network. Note that any `NeuronGroup`, `Connection`, `Monitor` or function decorated with `network_operation()` should be included in the `Network`. See the documentation for `Network` for more details.

This is the preferred solution for almost all cases. You may want to use either of the following two solutions if you think your code may be used by someone else, or if you want to make it into an extension to Brian.

9.1.2 Use the `magic_return()` decorator or `magic_register()` function

The `magic_return()` decorator is used as follows:

```
@magic_return
def f():
        ...
        return obj
```

Any object returned by a function decorated by `magic_return()` will be considered to have been instantiated in the execution frame that called the function. In other words, the magic functions will find that object even though it was really instantiated in a different execution frame.

In more complicated scenarios, you may want to use the `magic_register()` function. For example:

```
def f():
        ...
        magic_register(obj1, obj2)
        return (obj1, obj2)
```

This does the same thing as `magic_return()` but can be used with multiple objects. Also, you can specify a `level` (see documentation on `magic_register()` for more details).

9.1.3 Use derived classes

Rather than writing a function which returns an object, you could instead write a derived class of the object type. So, suppose you wanted to have an object that emitted N equally spaced spikes, with an interval dt between them, you could use the `SpikeGeneratorGroup` class as follows:

```
@magic_return
def equally_spaced_spike_group(N, dt):
        spikes = [(0,i*dt) for i in range(N)]
        return SpikeGeneratorGroup(spikes)
```

Or alternatively, you could derive a class from `SpikeGeneratorGroup` as follows:

```
class EquallySpacedSpikeGroup(SpikeGeneratorGroup):
        def __init__(self, N, t):
                spikes = [(0,i*dt) for i in range(N)]
                SpikeGeneratorGroup.__init__(self, spikes)
```

You would use these objects in the following ways:

```
obj1 = equally_spaced_spike_group(100, 10*ms)
obj2 = EquallySpacedSpikeGroup(100, 10*ms)
```

For simple examples like the one above, there's no particular benefit to using derived classes, but using derived classes allows you to add methods to your derived class for example, which might be useful. For more experienced Python programmers, or those who are thinking about making their code into an extension for Brian, this is probably the preferred approach. Finally, it may be useful to note that there is a protocol for one object to 'contain' other objects. That is, suppose you want to have an object that can be treated as a simple `NeuronGroup` by the person using it, but actually instantiates several objects (perhaps internal `Connection` objects). These objects need to be added to the `Network` object in order for them to be run with the simulation, but the user shouldn't need to have to know about them. To this end, for any object added to a `Network`, if it has an attribute `contained_objects`, then any objects in that container will also be added to the network.

MODULE INDEX

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