Brian Documentation

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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.

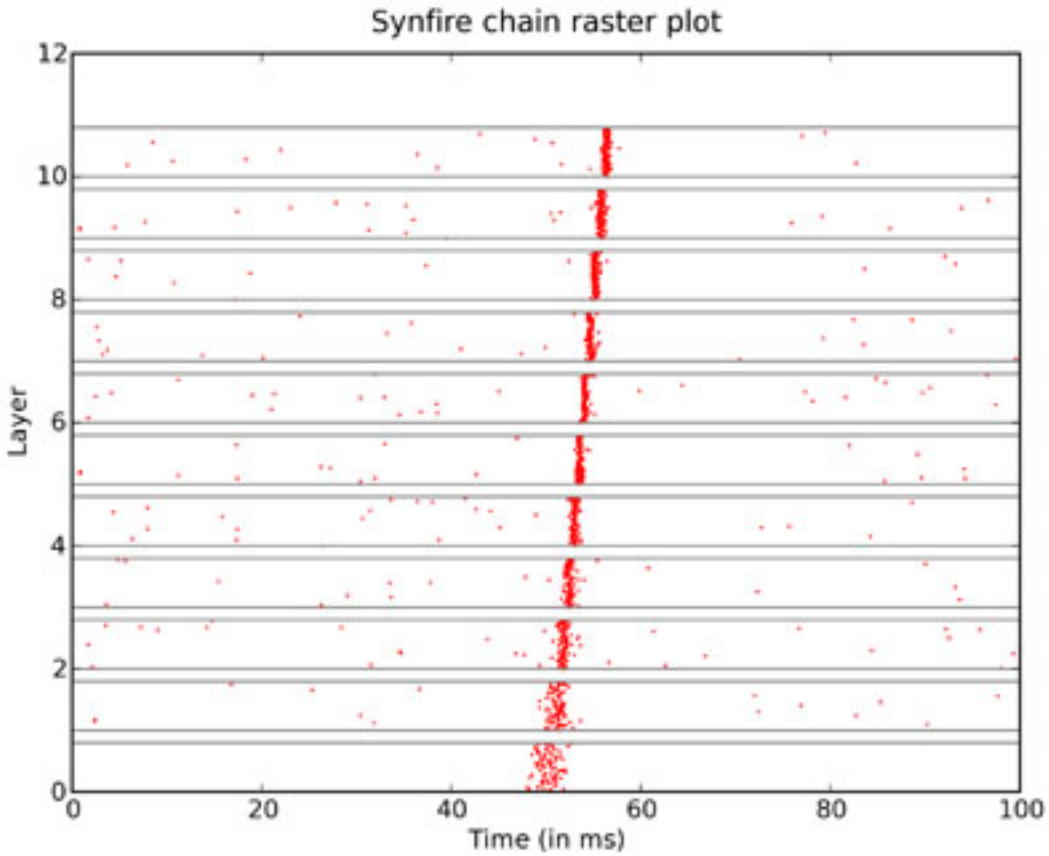
Here's what the Python web site has to say about themselves:

> 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.

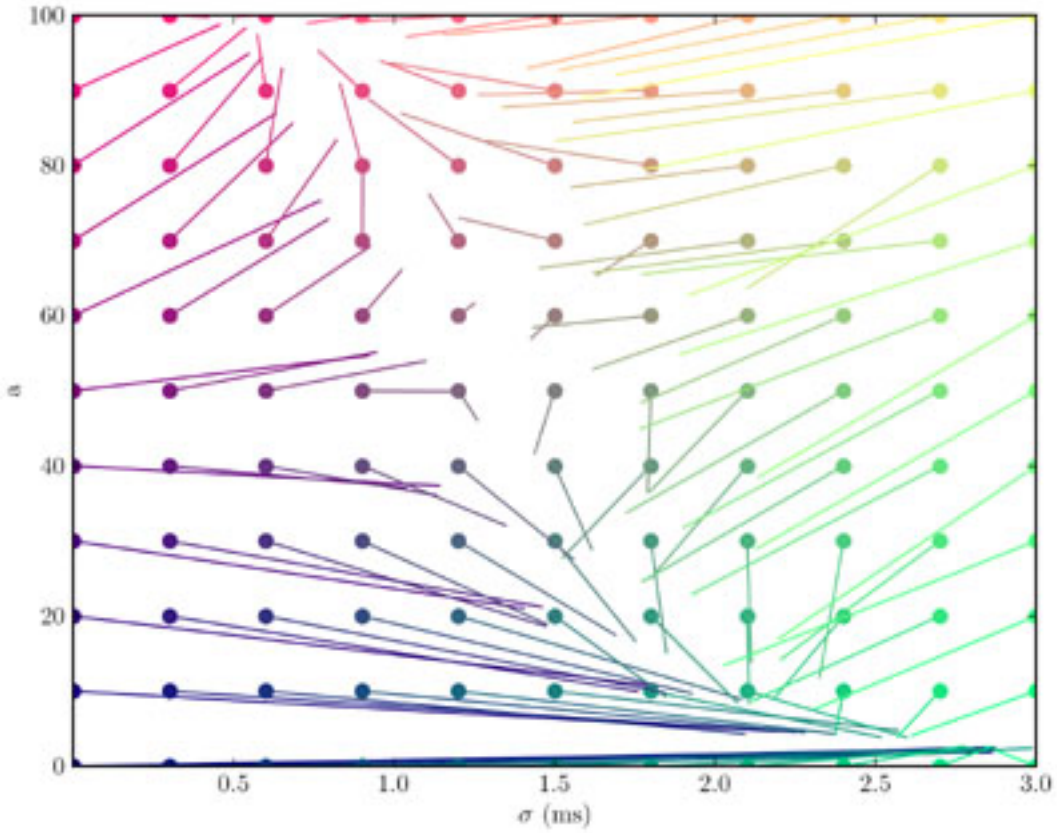
As an example of the ease of use and clarity of programs written in Brian, the following script defines and runs a randomly connected network of 4000 integrate and fire neurons with exponential currents:

```
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',weight=1.62*mV,sparseness=0.02)
Ci=Connection(Pi,P,'gi',weight=-9*mV,sparseness=0.02)
M=SpikeMonitor(P)
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 2.5-2.7, 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 2.5-2.7 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.).

Note that there are some optimisations you can make after installation, see the section below on Optimisations.

2.2 Manual installation

Installing Brian requires the following components:

1. Python version 2.5-2.7.
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). 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.

Windows users: the Python(x,y) distribution includes all the packages (including Eclipse and IPython) above except Brian (which is available as an optional plugin).

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. See also the section on *Compiled code*.

2.3 Testing

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

```
from brian import *
brian_sample_run()
```

A sample network should run and produce a raster plot.

2.4 Optimisations

After a successful installation, there are some optimisations you can make to your Brian installation to get it running faster using compiled C code. We do not include these as standard because they do not work on all computers, and we want Brian to install without problems on all computers. Note that including all the optimisations can result in significant speed increases (around 30%).

These optimisations are described in detail in the section on *Compiled code*.

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

The first place to look is the SciPy documentation website. 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:

- `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 and create a group of 40 neurons with this model.

```
G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)
```

The statement creates a new object 'G' which is an instance of the Brian class `NeuronGroup`, initialised with the values in the line above and 40 neurons. 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.

For the moment, we leave the neurons 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)

G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)
```

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:

```
G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)

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)

G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)

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:

```
G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)
```

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(sparseness=0.1, weight=psp)
```

These two previous lines could be done in one line:

```
C = Connection(G,G,sparseness=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.

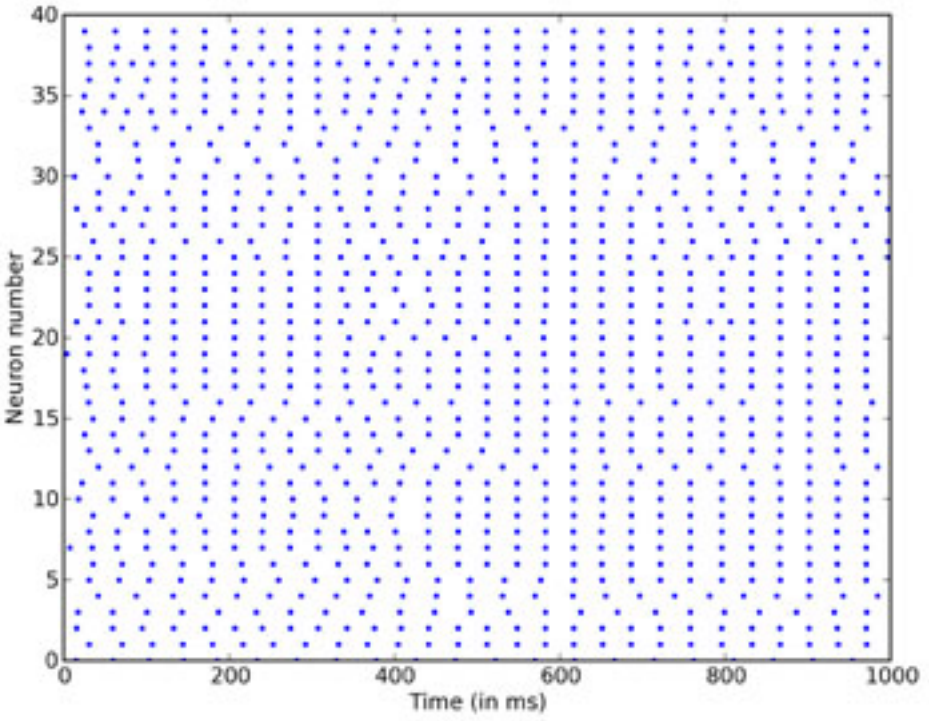
Tutorial 1f: Recording spikes

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

G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)

C = Connection(G, G)
C.connect_random(sparseness=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

G = NeuronGroup(N=40, model='dV/dt = -(V-El)/tau : volt',
                threshold=Vt, reset=Vr)

C = Connection(G, G)
C.connect_random(sparseness=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)
```

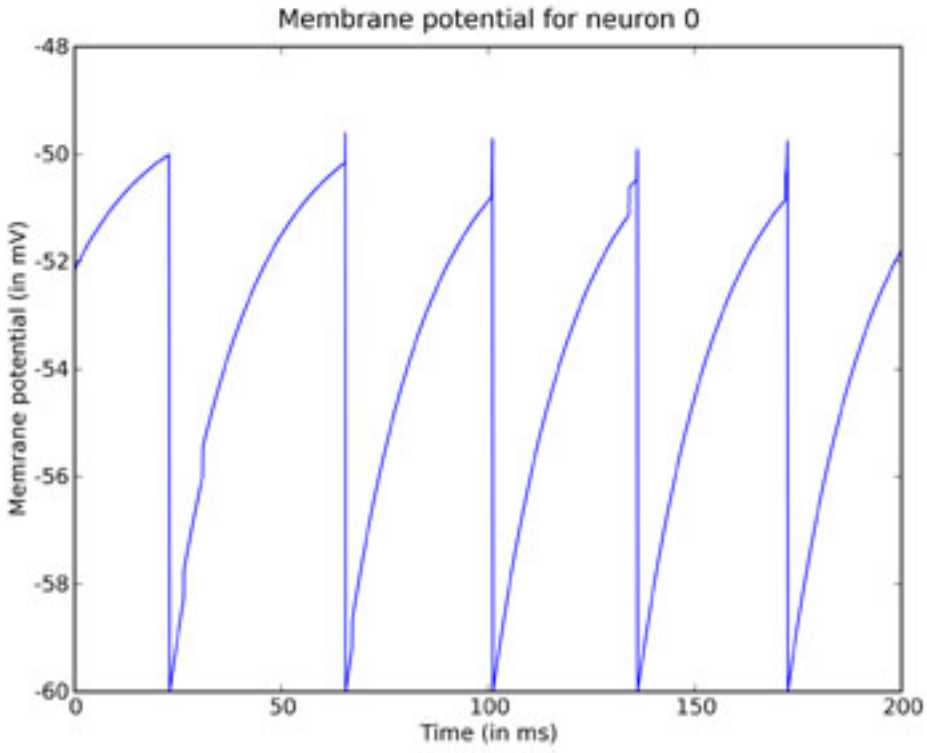
But this time we run it for a shorter time so we can look at the output in more detail:

```
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 / ms, M[0] / mV)
xlabel('Time (in ms)')
ylabel('Membrane 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 a `Connection` in Brian.

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 `NeuronGroup` 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
      ''')
```

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=eqs, threshold=Vt, reset=Vr)
```

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')
```

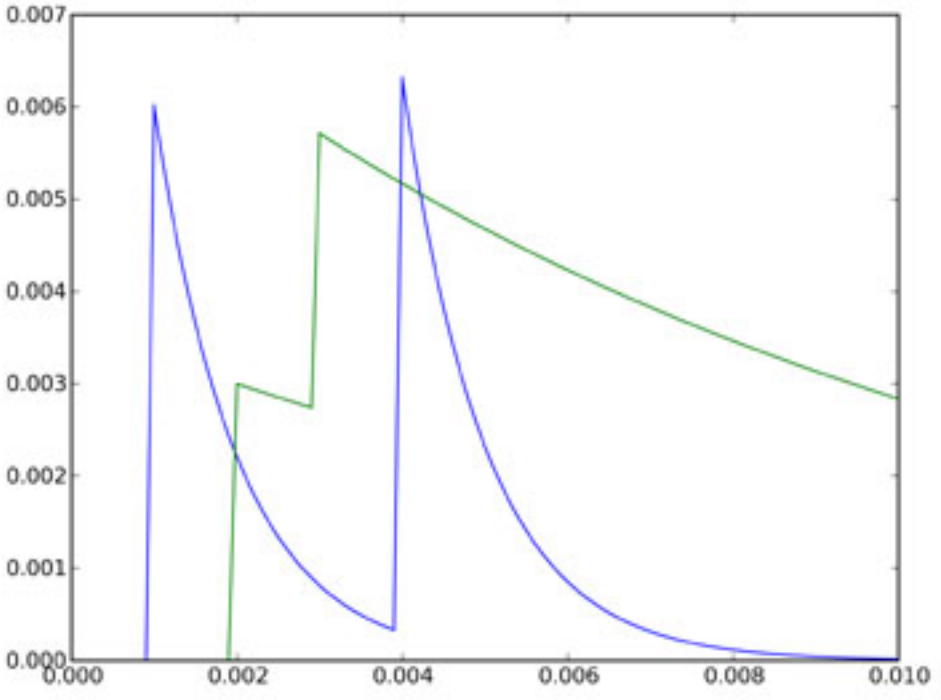
So far, this only declares our intention to connect neurons in group G1 to neurons in group G2, because the connection matrix is initially all zeros. Now, with connection C1 we connect neuron 0 in group G1 to neuron 0 in group G2, with weight 3 mV. This means that when neuron 0 in group G1 fires, the 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

3. Simple write `C[i,j]=-3*mV` to make the connection from neuron i to neuron j inhibitory.
4. 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

eqs = Equations('''
      dV/dt  = (-V+ge-gi)/taum : volt
      dge/dt = -ge/taue        : volt
      dgi/dt = -gi/taui        : volt
      ''')
```

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=eqs, threshold=Vt, reset=Vr)

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.

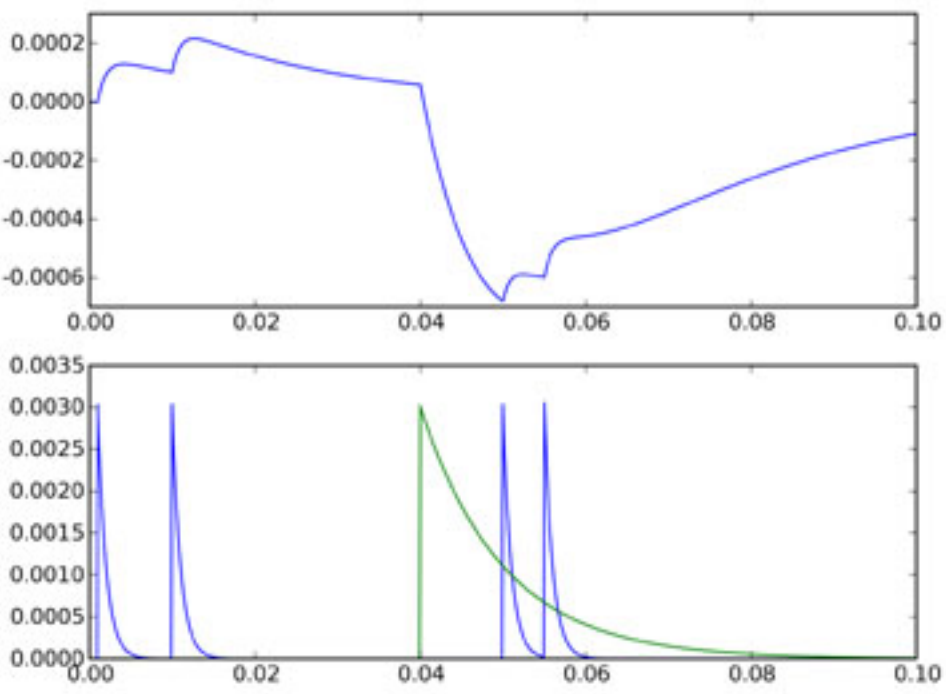
```
C1[0, 0] = 3 * mV
C2[1, 0] = 3 * mV
```

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

eqs = Equations('''
        dV/dt  = (ge-gi-(V-El))/taum : volt
        dge/dt = -ge/taue            : volt
        dgi/dt = -gi/taui            : volt
        ''')
```

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=eqs, threshold=Vt, reset=Vr)
```

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. We also 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 = Connection(Ge, G, 'ge', sparseness=0.02, weight=we)
Ci = Connection(Gi, G, 'gi', sparseness=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.

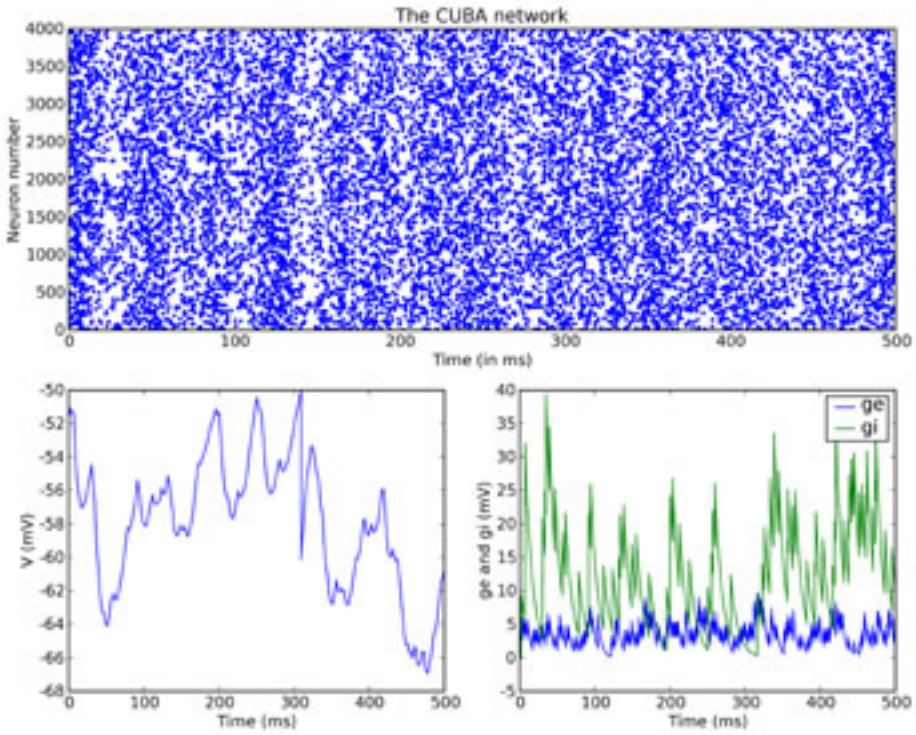
```
G.V = Vr + (Vt - Vr) * rand(len(G))
```

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 plasticity

Example: short_term_plasticity (plasticity)

Example with short term plasticity model Neurons with regular inputs and depressing synapses

```
from brian import *

tau_e = 3 * ms
taum = 10 * ms
A_SE = 250 * pA
Rm = 100 * Mohm
N = 10

eqs = '''
dx/dt=rate : 1
rate : Hz
'''

input = NeuronGroup(N, model=eqs, threshold=1., reset=0)
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')
C.connect_one_to_one(weight=A_SE)
stp = STP(C, taud=1 * ms, tauf=100 * ms, U=.1) # facilitation
#stp=STP(C,taud=100*ms,tauf=10*ms,U=.6) # depression
trace = StateMonitor(neuron, 'v', record=[0, N - 1])

run(1000 * ms)
subplot(211)
plot(trace.times / ms, trace[0] / mV)
title('Vm')
subplot(212)
plot(trace.times / ms, trace[N - 1] / mV)
title('Vm')
show()
```

Example: short_term_plasticity2 (plasticity)

Network (CUBA) with short-term synaptic plasticity for excitatory synapses (Depressing at long timescales, facilitating at short timescales)

```
from brian import *
from time import time

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 + rand(4000) * 10 * mV
Pe = P.subgroup(3200)
Pi = P.subgroup(800)
Ce = Connection(Pe, P, 'ge', weight=1.62 * mV, sparseness=.02)
Ci = Connection(Pi, P, 'gi', weight= -9 * mV, sparseness=.02)
```

```
stp = STP(Ce, taud=200 * ms, tauf=20 * ms, U=.2)
M = SpikeMonitor(P)
rate = PopulationRateMonitor(P)
t1 = time()
run(1 * second)
t2 = time()
print "Simulation time:", t2 - t1, "s"
print M.nspikes, "spikes"
subplot(211)
raster_plot(M)
subplot(212)
plot(rate.times / ms, rate.smooth_rate(5 * ms))
show()
```

Example: STDP1 (plasticity)

Spike-timing dependent plasticity Adapted from Song, Miller and Abbott (2000) and Song and Abbott (2001)

This simulation takes a long time!

```
from brian import *
from time import time

N = 1000
taum = 10 * ms
tau_pre = 20 * ms
tau_post = tau_pre
Ee = 0 * mV
vt = -54 * mV
vr = -60 * mV
El = -74 * mV
taue = 5 * ms
F = 15 * Hz
gmax = .01
dA_pre = .01
dA_post = -dA_pre * tau_pre / tau_post * 1.05

eqs_neurons = '''
dv/dt=(ge*(Ee-vr)+El-v)/taum : volt   # the synaptic current is linearized
dge/dt=-ge/taue : 1
'''

input = PoissonGroup(N, rates=F)
neurons = NeuronGroup(1, model=eqs_neurons, threshold=vt, reset=vr)
synapses = Connection(input, neurons, 'ge', weight=rand(len(input), len(neurons)) * gmax)
neurons.v = vr

#stdp=ExponentialSTDP(synapses,tau_pre,tau_post,dA_pre,dA_post,wmax=gmax)
## Explicit STDP rule
eqs_stdp = '''
dA_pre/dt=-A_pre/tau_pre : 1
dA_post/dt=-A_post/tau_post : 1
'''
dA_post *= gmax
dA_pre *= gmax
stdp = STDP(synapses, eqs=eqs_stdp, pre='A_pre+=dA_pre;w+=A_post',
            post='A_post+=dA_post;w+=A_pre', wmax=gmax)
```

```
rate = PopulationRateMonitor(neurons)

start_time = time()
run(100 * second, report='text')
print "Simulation time:", time() - start_time

subplot(311)
plot(rate.times / second, rate.smooth_rate(100 * ms))
subplot(312)
plot(synapses.W.todense() / gmax, '.')
subplot(313)
hist(synapses.W.todense() / gmax, 20)
show()
```

Example: STDP2 (plasticity)

Spike-timing dependent plasticity Adapted from Song, Miller and Abbott (2000), Song and Abbott (2001) and van Rossum et al (2000).

This simulation takes a long time!

```
from brian import *
from time import time

N = 1000
taum = 10 * ms
tau_pre = 20 * ms
tau_post = tau_pre
Ee = 0 * mV
vt = -54 * mV
vr = -60 * mV
El = -74 * mV
taue = 5 * ms
gmax = 0.01
F = 15 * Hz
dA_pre = .01
dA_post = -dA_pre * tau_pre / tau_post * 2.5

eqs_neurons = '''
dv/dt=(ge*(Ee-vr)+El-v)/taum : volt   # the synaptic current is linearized
dge/dt=-ge/taue : 1
'''

input = PoissonGroup(N, rates=F)
neurons = NeuronGroup(1, model=eqs_neurons, threshold=vt, reset=vr)
synapses = Connection(input, neurons, 'ge', weight=rand(len(input), len(neurons)) * gmax,
                      structure='dense')
neurons.v = vr

stdp = ExponentialSTDP(synapses, tau_pre, tau_post, dA_pre, dA_post, wmax=gmax, update='mixed')

rate = PopulationRateMonitor(neurons)

start_time = time()
run(100 * second, report='text')
print "Simulation time:", time() - start_time
```

```
subplot(311)
plot(rate.times / second, rate.smooth_rate(100 * ms))
subplot(312)
plot(synapses.W.todense() / gmax, '.')
subplot(313)
hist(synapses.W.todense() / gmax, 20)
show()
```

3.2.2 multiprocessing

Example: multiple_runs_simple (multiprocessing)

Example of using Python multiprocessing module to distribute simulations over multiple processors.

The general procedure for using multiprocessing is to define and run a network inside a function, and then use multiprocessing.Pool.map to call the function with multiple parameter values. Note that on Windows, any code that should only run once should be placed inside an if __name__=='__main__' block.

```
from brian import *
import multiprocessing

# This is the function that we want to compute for various different parameters
def how_many_spikes(excitatory_weight):
    # These two lines reset the clock to 0 and clear any remaining data so that
    # memory use doesn't build up over multiple runs.
    reinit_default_clock()
    clear(True)
    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, 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

if __name__ == '__main__':
    # Note that on Windows platforms, all code that is executed rather than
    # just defining functions and classes has to be in the if __name__=='__main__'
    # block, otherwise it will be executed by each process that starts. This
    # isn't a problem on Linux.
    pool = multiprocessing.Pool() # uses num_cpu processes by default
    weights = linspace(0, 3.5, 100) * mV
    args = [w * volt for w in weights]
    results = pool.map(how_many_spikes, args) # launches multiple processes
    plot(weights, results, '.')
    show()
```

Example: multiple_runs_with_gui (multiprocessing)

A complicated example of using multiprocessing for multiple runs of a simulation with different parameters, using a GUI to monitor and control the runs.

This example features:

- An indefinite number of runs, with a set of parameters for each run generated at random for each run.
- A plot of the output of all the runs updated as soon as each run is completed.
- A GUI showing how long each process has been running for and how long until it completes, and with a button allowing you to terminate the runs.

A simpler example is in `examples/multiprocessing/multiple_runs_simple.py`.

```
# We use Tk as the backend for the GUI and matplotlib so as to avoid any
# threading conflicts
import matplotlib
matplotlib.use('TkAgg')

from brian import *
import Tkinter, time, multiprocessing, os
from brian.utils.progressreporting import make_text_report
from Queue import Empty as QueueEmpty


class SimulationController(Tkinter.Tk):
    '''
    GUI, uses Tkinter and features a progress bar for each process, and a callback
    function for when the terminate button is clicked.
    '''
    def __init__(self, processes, terminator, width=600):
        Tkinter.Tk.__init__(self, None)
        self.parent = None
        self.grid()
        button = Tkinter.Button(self, text='Terminate simulation',
                                command=terminator)
        button.grid(column=0, row=0)
        self.pb_width = width
        self.progressbars = []
        for i in xrange(processes):
            can = Tkinter.Canvas(self, width=width, height=30)
            can.grid(column=0, row=1 + i)
            can.create_rectangle(0, 0, width, 30, fill='#aaaaaa')
            r = can.create_rectangle(0, 0, 0, 30, fill='#ffaaaa', width=0)
            t = can.create_text(width / 2, 15, text='')
            self.progressbars.append((can, r, t))
        self.results_text = Tkinter.Label(self, text='Computed 0 results, time taken: 0s')
        self.results_text.grid(column=0, row=processes + 1)
        self.title('Simulation control')

    def update_results(self, elapsed, complete):
        '''
        Method to update the total number of results computed and the amount of time taken.
        '''
        self.results_text.config(text='Computed ' + str(complete) + ', time taken: ' + str(int(elapse
        self.update()

    def update_process(self, i, elapsed, complete, msg):
```

```
        '''
        Method to update the status of a given process.
        '''
        can, r, t = self.progressbars[i]
        can.itemconfigure(t, text='Process ' + str(i) + ': ' + make_text_report(elapsed, complete) +
        can.coords(r, 0, 0, int(self.pb_width * complete), 30)
        self.update()

def sim_mainloop(pool, results, message_queue):
    '''
    Monitors results of a simulation as they arrive

    pool is the multiprocessing.Pool that the processes are running in,
    results is the AsyncResult object returned by Pool.imap_unordered which
    returns simulation results asynchronously as and when they are ready,
    and message_queue is a multiprocessing.Queue used to communicate between
    child processes and the server process. In this case, we use this Queue to
    send messages about the percent complete and time elapsed for each run.
    '''
    # We use this to enumerate the processes, mapping their process IDs to an int
    # in the range 0:num_processes.
    pid_to_id = dict((pid, i) for i, pid in enumerate([p.pid for p in pool._pool]))
    num_processes = len(pid_to_id)
    start = time.time()
    stoprunningsim = [False]
    # This function terminates all the pool's child processes, it is used as
    # the callback function called when the terminate button on the GUI is clicked.
    def terminate_sim():
        pool.terminate()
        stoprunningsim[0] = True
    controller = SimulationController(num_processes, terminate_sim)
    for i in range(num_processes):
        controller.update_process(i, 0, 0, 'no info yet')
    i = 0
    while True:
        try:
            # If there is a new result (the 0.1 means wait 0.1 seconds for a
            # result before giving up) then this try clause will execute, otherwise
            # a TimeoutError will occur and the except clause afterwards will
            # execute.
            weight, numspikes = results.next(0.1)
            # if we reach here, we have a result to plot, so we plot it and
            # update the GUI
            plot_result(weight, numspikes)
            i = i + 1
            controller.update_results(time.time() - start, i)
        except multiprocessing.TimeoutError:
            # if we're still waiting for a new result, we can process events in
            # the message_queue and update the GUI if there are any.
            while not message_queue.empty():
                try:
                    # messages here are of the form: (pid, elapsed, complete)
                    # where pid is the process ID of the child process, elapsed
                    # is the amount of time elapsed, and complete is the
                    # fraction of the run completed. See function how_many_spikes
                    # to see where these messages come from.
                    pid, elapsed, complete = message_queue.get_nowait()
                    controller.update_process(pid_to_id[pid], elapsed, complete, '')
```

```
                except QueueEmpty:
                    break
            controller.update()
            if stoprunningsim[0]:
                print 'Terminated simulation processes'
                break
    controller.destroy()

def plot_result(weight, numspikes):
    plot([weight], [numspikes], '.', color=(0, 0, 0.5))
    axis('tight')
    draw() # this forces matplotlib to redraw

# Note that how_many_spikes only takes one argument, which is a tuple of
# its actual arguments. The reason for this is that Pool.imap_unordered can only
# pass a single argument to the function its applied to, but that argument can
# be a tuple...
def how_many_spikes((excitatory_weight, message_queue)):
    reinit_default_clock()
    clear(True)

    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, 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)

    # This reporter function is called every second, and it sends a message to
    # the server process updating the status of the current run.
    def reporter(elapsed, complete):
        message_queue.put((os.getpid(), elapsed, complete))

    run(4000 * ms, report=reporter, report_period=1 * second)

    return (excitatory_weight, M.nspikes)


if __name__ == '__main__':
    numprocesses = None # number of processes to use, set to None to have one per CPU
    # We have to use a Queue from the Manager to send messages from client
    # processes to the server process
    manager = multiprocessing.Manager()
    message_queue = manager.Queue()
    pool = multiprocessing.Pool(processes=numprocesses)
    # This generator function repeatedly generates random sets of parameters
    # to pass to the how_many_spikes function
    def args():
        while True:
            weight = rand()*3.5 * mV
```

```
            yield (weight, message_queue)
    # imap_unordered returns an AsyncResult object which returns results as
    # and when they are ready, we pass this results object which is returned
    # immediately to the sim_mainloop function which monitors this, updates the
    # GUI and plots the results as they come in.
    results = pool.imap_unordered(how_many_spikes, args())
    ion() # this puts matplotlib into interactive mode to plot as we go
    sim_mainloop(pool, results, message_queue)
```

3.2.3 modelfitting

Example: modelfitting (modelfitting)

Model fitting example. Fit an integrate-and-fire model to an in-vitro electrophysiological recording during one second.

```
from brian import loadtxt, ms, Equations
from brian.library.modelfitting import *

if __name__ == '__main__':
    equations = Equations('''
        dV/dt=(R*I-V)/tau : 1
        I : 1
        R : 1
        tau : second
    ''')
    input = loadtxt('current.txt')
    spikes = loadtxt('spikes.txt')
    results = modelfitting( model = equations,
                            reset = 0,
                            threshold = 1,
                            data = spikes,
                            input = input,
                            dt = .1*ms,
                            popsize = 1000,
                            maxiter = 3,
                            delta = 4*ms,
                            R = [1.0e9, 9.0e9],
                            tau = [10*ms, 40*ms],
                            refractory = [0*ms, 10*ms])
    print_table(results)
```

Example: modelfitting_groups (modelfitting)

Example showing how to fit a single model with different target spike trains (several groups).

```
from brian import loadtxt, ms, Equations, second
from brian.library.modelfitting import *

if __name__ == '__main__':

    model = Equations('''
        dV/dt=(R*I-V)/tau : 1
        I : 1
        R : 1
        tau : second
```

```
    ''')

    input = loadtxt('current.txt')
    spikes0 = loadtxt('spikes.txt')
    spikes = []
    for i in xrange(2):
        spikes.extend([(i, spike*second + 5*i*ms) for spike in spikes0])

    results = modelfitting( model = model,
                            reset = 0,
                            threshold = 1,
                            data = spikes,
                            input = input,
                            dt = .1*ms,
                            popsize = 1000,
                            maxiter = 3,
                            cpu = 1,
                            delta = 4*ms,
                            R = [1.0e9, 9.0e9],
                            tau = [10*ms, 40*ms],
                            delays = [-10*ms, 10*ms])
    print_table(results)
```

Example: modelfitting_machines (modelfitting)

Model fitting example using several machines. Before running this example, you must start the Playdoh server on the remote machines.

```
from brian import loadtxt, ms, Equations
from brian.library.modelfitting import *

if __name__ == '__main__':
    # List of machines IP addresses
    machines = ['bobs-machine.university.com',
                'jims-machine.university.com']

    equations = Equations('''
        dV/dt=(R*I-V)/tau : 1
        I : 1
        R : 1
        tau : second
    ''')
    input = loadtxt('current.txt')
    spikes = loadtxt('spikes.txt')
    results = modelfitting( model = equations,
                            reset = 0,
                            threshold = 1,
                            data = spikes,
                            input = input,
                            dt = .1*ms,
                            popsize = 1000,
                            maxiter = 3,
                            delta = 4*ms,
                            unit_type = 'CPU',
                            machines = machines,
                            R = [1.0e9, 9.0e9],
                            tau = [10*ms, 40*ms],
```

```
                            refractory = [0*ms, 10*ms])
    print_table(results)
```

3.2.4 misc

Example: adaptive (misc)

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
'''
# The adaptation variable increases with each spike
IF = NeuronGroup(1, model=eqs, threshold=20 * mV,
                 reset='''v  = 0*mV
                          w += 3*mV ''')

C = Connection(PG, IF, 'v', weight=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()
```

Example: adaptive_threshold (misc)

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
'''

reset = '''
v=0*mV
vt+=3*mV
'''

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

C = Connection(PG, IF, 'v', weight=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()
```

Example: after_potential (misc)

A model with depolarizing after-potential.

```
from brian import *

v0=20.5*mV
eqs = '''
dv/dt = (v0-v)/(30*ms) : volt # the membrane equation
dAP/dt = -AP/(3*ms) : volt # the after-potential
vm = v+AP : volt # total membrane potential
'''
IF = NeuronGroup(1, model=eqs, threshold='vm>20*mV',
                 reset='v=0*mV; AP=10*mV')
Mv = StateMonitor(IF, 'vm', record=True)

run(500 * ms)
plot(Mv.times / ms, Mv[0] / mV)
show()
```

Example: cable (misc)

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()
```

Example: COBA (misc)

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)
we = 6. / 10. # excitatory synaptic weight (voltage)
wi = 67. / 10. # inhibitory synaptic weight
Ce = Connection(Pe, P, 'ge', weight=we, sparseness=0.02)
Ci = Connection(Pi, P, 'gi', weight=wi, sparseness=0.02)
# 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"
```

Example: COBAHH (misc)

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)

18. 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', weight=we, sparseness=0.02)
Ci = Connection(Pi, P, 'gi', weight=wi, sparseness=0.02)
# 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()
```

Example: correlated_inputs (misc)

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

```
from brian import *
```

```
N = 100
#input = HomogeneousCorrelatedSpikeTrains(N, r=10 * Hz, c=0.1, tauc=10 * ms)

c = .2
nu = linspace(1*Hz, 10*Hz, N)
P = c*dot(nu.reshape((N,1)), nu.reshape((1,N)))/mean(nu**2)
tauc = 5*ms

spikes = mixture_process(nu, P, tauc, 1*second)
#spikes = [(i,t*second) for i,t in spikes]
input = SpikeGeneratorGroup(N, spikes)

S = SpikeMonitor(input)
#S2 = PopulationRateMonitor(input)
#M = StateMonitor(input, 'rate', record=0)
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()
```

Example: correlated_inputs2 (misc)

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

```
from brian import *

N = 100
c = .2
nu = linspace(1*Hz, 10*Hz, N)
P = c*dot(nu.reshape((N,1)), nu.reshape((1,N)))/mean(nu**2)
tauc = 5*ms

spikes = mixture_process(nu, P, tauc, 1*second)
input = SpikeGeneratorGroup(N, spikes)

S = SpikeMonitor(input)
run(1000 * ms)

raster_plot(S)
show()
```

Example: CUBA (misc)

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)
we = (60 * 0.27 / 10) * mV # excitatory synaptic weight (voltage)
wi = (-20 * 4.5 / 10) * mV # inhibitory synaptic weight
Ce = Connection(Pe, P, 'ge', weight=we, sparseness=0.02)
Ci = Connection(Pi, P, 'gi', weight=wi, sparseness=0.02)
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()
```

Example: current_clamp (misc)

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()
```

Example: delays (misc)

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()
```

Example: expIF_network (misc)

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)
we = 1.5 * nS # excitatory synaptic weight
wi = 2.5 * we # inhibitory synaptic weight
Ce = Connection(Pe, P, 'ge', weight=we, sparseness=0.05)
Ci = Connection(Pi, P, 'gi', weight=wi, sparseness=0.05)
# 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()
```

Example: gap_junctions (misc)

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()
```

Example: heterogeneous_delays (misc)

Script demonstrating use of a `Connection` with homogenenous delays

The network consists of a 'starter' neuron which fires a single spike at time t=0, connected to 100 leaky integrate and fire neurons with different delays for each target neuron, with the delays forming a quadratic curve centred at neuron 50. The longest delay is 10ms, and the network is run for 40ms. At the end, the delays are plotted above a colour plot of the membrane potential of each of the target neurons as a function of time (demonstrating the delays).

```
from brian import *
# Starter neuron, threshold is below 0 so it fires immediately, reset is below
# threshold so it fires only once.
G = NeuronGroup(1, model='V:1', threshold= -1.0, reset= -2.0)
# 100 LIF neurons, no reset or threshold so they will not spike
H = NeuronGroup(100, model='dV/dt=-V/(10*ms):volt')
# Connection with delays, here the delays are specified as a function of (i,j)
# giving the delay from neuron i to neuron j. In this case there is only one
# presynaptic neuron so i will be 0.
C = Connection(G, H, weight=5 * mV, max_delay=10 * ms,
               delay=lambda i, j:10 * ms * (j / 50. - 1) ** 2)
M = StateMonitor(H, 'V', record=True)
run(40 * ms)
subplot(211)
# These are the delays from neuron 0 to neuron i in ms
plot([C.delay[0, i] / ms for i in range(100)])
ylabel('Delay (ms)')
title('Delays')
subplot(212)
# M.values is an array of all the recorded values, here transposed to make
# it fit with the plot above.
imshow(M.values.T, aspect='auto', extent=(0, 100, 40, 0))
xlabel('Neuron number')
ylabel('Time (ms)')
title('Potential')
show()
```

Example: HodgkinHuxley (misc)

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

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

#defaultclock.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()
```

Example: I-F_curve (misc)

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')
print eqs
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()
```

Example: I-F_curve2 (misc)

Input-Frequency curve of a IF model Network: 1000 unconnected integrate-and-fire neurons (leaky IF) with an input parameter v0. The input is set differently for each neuron. Spikes are sent to a spike counter (counts the spikes emitted by each neuron).

```
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()
```

Example: if (misc)

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

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

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()
```

Example: leaky_if (misc)

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

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

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()
```

Example: linked_var (misc)

Example showing `linked_var()`, connecting two different `NeuronGroup` variables. Here we show something like a simplified haircell and auditory nerve fibre model where the hair cells and ANFs are implemented as two separate `NeuronGroup` objects. The hair cells filter their inputs via a differential equation, and then emit graded amounts of neurotransmitter (variable 'y') to the auditory nerve fibres input current (variable 'I').

```
from brian import *

N = 5
f = 50 * Hz
a_min = 1.0
a_max = 100.0
tau_haircell = 50 * ms
tau = 10 * ms
duration = 100 * ms

eqs_haircells = '''
input = a*sin(2*pi*f*t) : 1
x = clip(input, 0, Inf)**(1.0/3.0) : 1
a : 1
dy/dt = (x-y)/tau_haircell : 1
'''

haircells = NeuronGroup(N, eqs_haircells)
haircells.a = linspace(a_min, a_max, N)
M_haircells = MultiStateMonitor(haircells, vars=('input', 'y'), record=True)

eqs_nervefibres = '''
dV/dt = (I-V)/tau : 1
I : 1
'''
nervefibres = NeuronGroup(N, eqs_nervefibres, reset=0, threshold=1)
nervefibres.I = linked_var(haircells, 'y')
M_nervefibres = MultiStateMonitor(nervefibres, record=True)

run(duration)

subplot(221)
M_haircells['input'].plot()
ylabel('haircell.input')
subplot(222)
M_haircells['y'].plot()
ylabel('haircell.y')
subplot(223)
M_nervefibres['I'].plot()
ylabel('nervefibres.I')
subplot(224)
```

```
M_nervefibres['V'].plot()
ylabel('nervefibres.V')
show()
```

Example: minimalexample (misc)

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', weight=1.62 * mV, sparseness=0.02)
Ci = Connection(Pi, P, 'gi', weight= -9 * mV, sparseness=0.02)

M = SpikeMonitor(P)

run(1 * second)
i = 0
while len(M[i]) <= 1:
    i += 1
print "The firing rate of neuron", i, "is", firing_rate(M[i]) * Hz
print "The coefficient of variation neuron", i, "is", CV(M[i])
raster_plot(M)
show()
```

Example: mirollo_strogatz (misc)

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', weight=w)

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

S = SpikeMonitor(group)

run(300 * ms)
```

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

Example: multipleclocks (misc)

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
G = NeuronGroup(1, model=eqs, reset=0 * mV, threshold=10 * mV, clock=simclock)
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
```

Example: named_threshold (misc)

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='x>-50*mV', \
              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', weight=1.62 * mV, sparseness=0.02)
Ci = Connection(Pi, P, 'gi', weight= -9 * mV, sparseness=0.02)
M = SpikeMonitor(P)
run(1 * second)
raster_plot(M)
show()
```

Example: noisy_ring (misc)

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()
```

Example: non_reliability (misc)

Reliability of spike timing. See e.g. Mainen & Sejnowski (1995) for experimental results in vitro.

Here: a constant current is injected in all trials.

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```
from brian import *

N = 25
tau = 20 * ms
sigma = .015
eqs_neurons = '''
dx/dt=(1.1-x)/tau+sigma*(2./tau)**.5*xi:1
'''
neurons = NeuronGroup(N, model=eqs_neurons, threshold=1, reset=0, refractory=5 * ms)
spikes = SpikeMonitor(neurons)

run(500 * ms)
raster_plot(spikes)
show()
```

Example: phase_locking (misc)

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()
```

Example: poisson (misc)

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()
```

Example: poissongroup (misc)

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', weight=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()
```

Example: pulsepacket (misc)

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()
```

Example: rate_model (misc)

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()
```

Example: realtime_plotting (misc)

Realtime plotting example

```
# These lines are necessary for interactive plotting when launching from the
# Eclipse IDE, they may not be necessary in every environment.
import matplotlib
matplotlib.use('WXAgg') # You may need to experiment, try WXAgg, GTKAgg, QTAgg, TkAgg

from brian import *
###### Set up the standard CUBA example ######
N = 4000
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(N, 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', weight=1.62 * mV, sparseness=0.02)
Ci = Connection(Pi, P, 'gi', weight= -9 * mV, sparseness=0.02)

M = SpikeMonitor(P)
trace = RecentStateMonitor(P, 'v', record=range(5), duration=200 * ms)

ion()
subplot(211)
raster_plot(M, refresh=10 * ms, showlast=200 * ms, redraw=False)
subplot(212)
trace.plot(refresh=10 * ms, showlast=200 * ms)

run(1 * second)

ioff() # switch interactive mode off
show() # and wait for user to close the window before shutting down
```

Example: reliability (misc)

Reliability of spike timing. See e.g. Mainen & Sejnowski (1995) for experimental results in vitro.

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```
from brian import *

# The common noisy input
N = 25
tau_input = 5 * ms
input = NeuronGroup(1, model='dx/dt=-x/tau_input+(2./tau_input)**.5*xi:1')
```

```
# The noisy neurons receiving the same input
tau = 10 * ms
sigma = .015
eqs_neurons = '''
dx/dt=(0.9+.5*I-x)/tau+sigma*(2./tau)**.5*xi:1
I : 1
'''
neurons = NeuronGroup(N, model=eqs_neurons, threshold=1, reset=0, refractory=5 * ms)
neurons.x = rand(N)
neurons.I = linked_var(input,'x') # input.x is continuously fed into neurons.I
spikes = SpikeMonitor(neurons)

run(500 * ms)
raster_plot(spikes)
show()
```

Example: remotecontrolclient (misc)

Example of using `RemoteControlServer` and `RemoteControlClient` to control a simulation as it runs in Brian.

Run the script remotecontrolserver.py before running this.

```
from brian import *
import time

client = RemoteControlClient()

time.sleep(1)

subplot(121)
plot(*client.evaluate('(M.times, M.values)'))

client.execute('G.I = 1.1')

time.sleep(1)

subplot(122)
plot(*client.evaluate('(M.times, M.values)'))

client.stop()

show()
```

Example: remotecontrolserver (misc)

Example of using `RemoteControlServer` and `RemoteControlClient` to control a simulation as it runs in Brian.

After running this script, run remotecontrolclient.py or paste the code from that script into an IPython shell for interactive control.

```
from brian import *

eqs = '''
dV/dt = (I-V)/(10*ms)+0.1*xi*(2/(10*ms))**.5 : 1
```

```
I : 1
'''

G = NeuronGroup(3, eqs, reset=0, threshold=1)
M = RecentStateMonitor(G, 'V', duration=50*ms)

server = RemoteControlServer()

run(1e10*second)
```

Example: ring (misc)

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()
```

Example: stim2d (misc)

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

```
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()
```

Example: stopping (misc)

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)
```

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

G = NeuronGroup(1000, model='dV/dt=-(V-El)/tau : volt', threshold=Vt, reset=Vr)
G.V = Vr + (Vt - Vr) * rand(len(G))

CPG = Connection(P, G, weight=weight, sparseness=input_connection_p)

CGG = Connection(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."
```

Example: timed_array (misc)

An example of the `TimedArray` class used for applying input currents to neurons.

```
from brian import *

N = 5
duration = 100 * ms
Vr = -60 * mV
Vt = -50 * mV
tau = 10 * ms
Rmin = 1 * Mohm
Rmax = 10 * Mohm
freq = 50 * Hz
k = 10 * nA

eqs = '''
dV/dt = (-(V-Vr)+R*I)/tau : volt
R : ohm
I : amp
'''

G = NeuronGroup(N, eqs, reset='V=Vr', threshold='V>Vt')
G.R = linspace(Rmin, Rmax, N)

t = linspace(0 * second, duration, int(duration / defaultclock.dt))
I = clip(k * sin(2 * pi * freq * t), 0, Inf)
G.I = TimedArray(I)

M = MultiStateMonitor(G, record=True)

run(duration)

subplot(211)
M['I'].plot()
ylabel('I (amp)')
subplot(212)
```

```
M['V'].plot()
ylabel('V (volt)')
show()
```

Example: topographic_map (misc)

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, sparseness=.5, weight=topomap)
#feedforward[2,3]=1*mV

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

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()
```

Example: topographic_map2 (misc)

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

recurrent = Connection(layer2, layer2, sparseness=.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()
```

Example: transient_sync (misc)

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', 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.todense(), interpolation='nearest')
title('Synaptic connections')
```

```
subplot(224)
plot(R.times / ms, R.smooth_rate(2 * ms, filter='flat'))
title('Firing rate')
show()
```

Example: two_neurons (misc)

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)
show()
```

Example: using_classes (misc)

Example of using derived classes in Brian

Using a class derived from one of Brian's classes can be a useful way of organising code in complicated simulations. A class such as a `NeuronGroup` can itself create further `NeuronGroup`, `Connection` and `NetworkOperation` objects. In order to have these objects included in the simulation, the derived class has to include them in its `contained_objects` list (this tells Brian to add these to the `Network` when the derived class object is added to the network).

```
from brian import *


class PoissonDrivenGroup(NeuronGroup):
    '''
    This class is a group of leaky integrate-and-fire neurons driven by
    external Poisson inputs. The class creates the Poisson inputs and
    connects them to itself.
    '''
    def __init__(self, N, rate, weight):
        tau = 10 * ms
        eqs = '''
        dV/dt = -V/tau : 1
        '''
        # It's essential to call the initialiser of the base class
        super(PoissonDrivenGroup, self).__init__(N, eqs, reset=0, threshold=1)
        self.poisson_group = PoissonGroup(N, rate)
        self.conn = Connection(self.poisson_group, self, 'V')
```

```
        self.conn.connect_one_to_one(weight=weight)
        self.contained_objects += [self.poisson_group,
                                   self.conn]

G = PoissonDrivenGroup(100, 100 * Hz, .3)

M = SpikeMonitor(G)
M_pg = SpikeMonitor(G.poisson_group)
trace = StateMonitor(G, 'V', record=0)

run(1 * second)

subplot(311)
raster_plot(M_pg)
title('Input spikes')
subplot(312)
raster_plot(M)
title('Output spikes')
subplot(313)
plot(trace.times, trace[0])
title('Sample trace')
show()
```

Example: van_rossum_metric (misc)

Example of how to use the van Rossum metric.

The VanRossumMetric function, which is defined as a monitor and therefore works online, computes the metric between every neuron in a given population. The present example show the concept of phase locking: N neurons are driven by sinusoidal inputs with different amplitude.

> Use: output=VanRossumMetric(source, tau=4 * ms)
>
> source is a NeuronGroup of N neurons tau is the time constant of the kernel used in the metric
>
> output is a monitor with attribute distance which is the distance matrix between the neurons in source

```
from brian import *
from time import time

tau=20*ms
N=100
b=1.2 # constant current mean, the modulation varies
f=10*Hz
delta =2*ms

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)

van_rossum_metric=VanRossumMetric(neurons, tau=4 * ms)
```

```
run(1000*ms)

raster_plot(S)
title('Raster plot')

figure()
title('Distance matrix between spike trains')
imshow(van_rossum_metric.distance)
colorbar()
show()
```

3.2.5 interface

Example: interface (interface)

Interface example Install cherrypy for this example Then run the script and go to http://localhost:8080 on your web browser You can use cherrypy to write html interfaces to your code.

```
from brian import *
import cherrypy
import os.path

# The server is defined here
class MyInterface(object):
    @cherrypy.expose
    def index(self): # redirect to the html page we wrote
        return '<meta HTTP-EQUIV="Refresh" content="0;URL=index.html">'

    @cherrypy.expose
    def runscript(self, we="1.62", wi="-9", **kwd): # 'runscript' is the script name
        # we and wi are the names of form fields
        we = float(we)
        wi = float(wi)
        # From minimalexample
        reinit_default_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 + 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=we * mV)
        Ci.connect_random(Pi, P, 0.02, weight=wi * mV)
        M = SpikeMonitor(P)
        run(.5 * second)
        clf()
        raster_plot(M)
        savefig('image.png')
        # Redirect to the html page we wrote
        return '<meta HTTP-EQUIV="Refresh" content="0;URL=results.html">'
```

```
# Set the directory for static files
current_dir = os.path.dirname(os.path.abspath(__file__))
conf = {'/': {'tools.staticdir.on':True,
              'tools.staticdir.dir':current_dir}}

# Start the server
cherrypy.quickstart(MyInterface(), config=conf)
```

3.2.6 hears

Example: approximate_gammatone (hears)

Example of the use of the class `ApproximateGammatone` available in the library. It implements a filterbank of approximate gammatone filters as described in Hohmann, V., 2002, "Frequency analysis and synthesis using a Gammatone filterbank", Acta Acustica United with Acustica. In this example, a white noise is filtered by a gammatone filterbank and the resulting cochleogram is plotted.

```
from brian import *
from brian.hears import *

level=50*dB # level of the input sound in rms dB SPL
sound = whitenoise(100*ms).ramp() # generation of a white noise
sound = sound.atlevel(level) # set the sound to a certain dB level

nbr_center_frequencies = 50  # number of frequency channels in the filterbank
# center frequencies with a spacing following an ERB scale
center_frequencies = erbspace(100*Hz, 1000*Hz, nbr_center_frequencies)
# bandwidth of the filters (different in each channel)
bw = 10**(0.037+0.785*log10(center_frequencies))

gammatone = ApproximateGammatone(sound, center_frequencies, bw, order=3)

gt_mon = gammatone.process()

figure()
imshow(flipud(gt_mon.T), aspect='auto')
show()
```

Example: artificial_vowels (hears)

This example implements the artificial vowels from Culling, J. F. and Summerfield, Q. (1995a). "Perceptual segregation of concurrent speech sounds: absence of across-frequency grouping by common interaural delay" J. Acoust. Soc. Am. 98, 785-797.

```
from brian import *
from brian.hears import *

duration = 409.6*ms
width = 150*Hz/2
samplerate = 10*kHz

set_default_samplerate(samplerate)

centres = [225*Hz, 625*Hz, 975*Hz, 1925*Hz]
vowels = {
```

```
    'ee':[centres[0], centres[3]],
    'ar':[centres[1], centres[2]],
    'oo':[centres[0], centres[2]],
    'er':[centres[1], centres[3]]
    }

def generate_vowel(vowel):
    vowel = vowels[vowel]
    x = whitenoise(duration)
    y = fft(asarray(x).flatten())
    f = fftfreq(len(x), 1/samplerate)
    I = zeros(len(f), dtype=bool)
    for cf in vowel:
        I = I|((abs(f)<cf+width)&(abs(f)>cf-width))
    I = -I
    y[I] = 0
    x = ifft(y)
    return Sound(x.real)

v1 = generate_vowel('ee').ramp()
v2 = generate_vowel('ar').ramp()
v3 = generate_vowel('oo').ramp()
v4 = generate_vowel('er').ramp()

for s in [v1, v2, v3, v4]:
    s.play(normalise=True, sleep=True)

s1 = Sound((v1, v2))
#s1.play(normalise=True, sleep=True)

s2 = Sound((v3, v4))
#s2.play(normalise=True, sleep=True)

v1.save('mono_sound.wav')
s1.save('stereo_sound.wav')

subplot(211)
plot(v1.times, v1)
subplot(212)
v1.spectrogram()
show()
```

Example: butterworth (hears)

Example of the use of the class `Butterworth` available in the library. In this example, a white noise is filtered by a bank of butterworth bandpass filters and lowpass filters which are different for every channels. The centre or cutoff frequency of the filters are linearly taken between 100kHz and 1000kHz and its bandwidth frequency increases linearly with frequency.

```
from brian import *
from brian.hears import *

level = 50*dB  # level of the input sound in rms dB SPL
sound = whitenoise(100*ms).ramp()
sound = sound.atlevel(level)
order = 2 #order of the filters
```

```
#### example of a bank of bandpass filter ################
nchannels = 50
center_frequencies = linspace(100*Hz, 1000*Hz, nchannels)
bw = linspace(50*Hz, 300*Hz, nchannels) # bandwidth of the filters
#arrays of shape (2 x nchannels) defining the passband frequencies (Hz)
fc = vstack((center_frequencies-bw/2, center_frequencies+bw/2))

filterbank = Butterworth(sound, nchannels, order, fc, 'bandpass')

filterbank_mon = filterbank.process()

figure()
subplot(211)
imshow(flipud(filterbank_mon.T), aspect='auto')

### example of a bank of lowpass filter ################
nchannels = 50
cutoff_frequencies = linspace(200*Hz, 1000*Hz, nchannels)

filterbank = Butterworth(sound, nchannels, order, cutoff_frequencies, 'low')

filterbank_mon = filterbank.process()

subplot(212)
imshow(flipud(filterbank_mon.T), aspect='auto')
show()
```

Example: cochleagram (hears)

Example of basic filtering of a sound with Brian hears. This example implements a cochleagram based on a gammatone filterbank followed by halfwave rectification, cube root compression and 10 Hz low pass filtering.

```
from brian import *
from brian.hears import *

sound1 = tone(1*kHz, .1*second)
sound2 = whitenoise(.1*second)

sound = sound1+sound2
sound = sound.ramp()

cf = erbspace(20*Hz, 20*kHz, 3000)
gammatone = Gammatone(sound, cf)
cochlea = FunctionFilterbank(gammatone, lambda x: clip(x, 0, Inf)**(1.0/3.0))
lowpass = LowPass(cochlea, 10*Hz)
output = lowpass.process()

imshow(output.T, origin='lower left', aspect='auto', vmin=0)
show()
```

Example: cochlear_models (hears)

Example of the use of the cochlear models (DRNL and DCGC) available in the library.

```
from brian import *
from brian.hears import *
```

```
simulation_duration = 50*ms
set_default_samplerate(50*kHz)
sound = whitenoise(simulation_duration)
sound = sound.atlevel(50*dB) # level in rms dB SPL
cf = erbspace(100*Hz, 1000*Hz, 50) # centre frequencies

## DNRL
param_drnl = {}
param_drnl['lp_nl_cutoff_m'] = 1.1
drnl_filter=DRNL(sound, cf, type='human', param=param_drnl)
drnl = drnl_filter.process()

## DCGC
param_dcgc = {}
param_dcgc['c1'] = -2.96
interval = 1
dcgc_filter = DCGC(sound, cf, interval, param=param_dcgc)
dcgc = dcgc_filter.process()

figure()
subplot(211)
imshow(flipud(drnl.T), aspect='auto')
subplot(212)
imshow(flipud(dcgc.T), aspect='auto')
show()
```

Example: dcgc (hears)

Implementation example of the compressive gammachirp auditory filter as described in Irino, T. and Patterson R., "A compressive gammachirp auditory filter for both physiological and psychophysical data", JASA 2001.

A class called DCGC implementing this model is available in the library.

Technical implementation details and notation can be found in Irino, T. and Patterson R., "A Dynamic Compressive Gammachirp Auditory Filterbank", IEEE Trans Audio Speech Lang Processing.

```
from brian import *
from brian.hears import *

simulation_duration = 50*ms
samplerate = 50*kHz
level = 50*dB # level of the input sound in rms dB SPL
sound = whitenoise(simulation_duration, samplerate).ramp()
sound = sound.atlevel(level)

nbr_cf = 50 # number of centre frequencies
# center frequencies with a spacing following an ERB scale
cf = erbspace(100*Hz, 1000*Hz, nbr_cf)

c1 = -2.96 #glide slope of the first filterbank
b1 = 1.81  #factor determining the time constant of the first filterbank
c2 = 2.2   #glide slope of the second filterbank
b2 = 2.17  #factor determining the time constant of the second filterbank

order_ERB = 4
ERBrate = 21.4*log10(4.37*cf/1000+1)
ERBwidth = 24.7*(4.37*cf/1000 + 1)
```

```
ERBspace = mean(diff(ERBrate))

# the filter coefficients are updated every update_interval (here in samples)
update_interval = 1



#bank of passive gammachirp filters. As the control path uses the same passive
#filterbank than the signal path (but shifted in frequency)
#this filterbank is used by both pathway.
pGc = LogGammachirp(sound, cf, b=b1, c=c1)

fp1 = cf + c1*ERBwidth*b1/order_ERB #centre frequency of the signal path

#### Control Path ####

#the first filterbank in the control path consists of gammachirp filters
#value of the shift in ERB frequencies of the control path with respect to the signal path
lct_ERB = 1.5
n_ch_shift = round(lct_ERB/ERBspace) #value of the shift in channels
#index of the channel of the control path taken from pGc
indch1_control = minimum(maximum(1, arange(1, nbr_cf+1)+n_ch_shift), nbr_cf).astype(int)-1
fp1_control = fp1[indch1_control]
#the control path bank pass filter uses the channels of pGc indexed by indch1_control
pGc_control = RestructureFilterbank(pGc, indexmapping=indch1_control)

#the second filterbank in the control path consists of fixed asymmetric compensation filters
frat_control = 1.08
fr2_control = frat_control*fp1_control
asym_comp_control = AsymmetricCompensation(pGc_control, fr2_control, b=b2, c=c2)

#definition of the pole of the asymmetric comensation filters
p0 = 2
p1 = 1.7818*(1-0.0791*b2)*(1-0.1655*abs(c2))
p2 = 0.5689*(1-0.1620*b2)*(1-0.0857*abs(c2))
p3 = 0.2523*(1-0.0244*b2)*(1+0.0574*abs(c2))
p4 = 1.0724

#definition of the parameters used in the control path output levels computation
#(see IEEE paper for details)
decay_tcst = .5*ms
order = 1.
lev_weight = .5
level_ref = 50.
level_pwr1 = 1.5
level_pwr2 = .5
RMStoSPL = 30.
frat0 = .2330
frat1 = .005
exp_deca_val = exp(-1/(decay_tcst*samplerate)*log(2))
level_min = 10**(-RMStoSPL/20)

#definition of the controller class. What is does it take the outputs of the
#first and second fitlerbanks of the control filter as input, compute an overall
#intensity level for each frequency channel. It then uses those level to update
#the filter coefficient of its target, the asymmetric compensation filterbank of
#the signal path.
class CompensensationFilterUpdater(object):
```

```
    def __init__(self, target):
        self.target = target
        self.level1_prev = -100
        self.level2_prev = -100

    def __call__(self, *input):
         value1 = input[0][-1,:]
         value2 = input[1][-1,:]
         #the current level value is chosen as the max between the current
         #output and the previous one decreased by a decay
         level1 = maximum(maximum(value1, 0), self.level1_prev*exp_deca_val)
         level2 = maximum(maximum(value2, 0), self.level2_prev*exp_deca_val)

         self.level1_prev = level1 #the value is stored for the next iteration
         self.level2_prev = level2
         #the overall intensity is computed between the two filterbank outputs
         level_total = lev_weight*level_ref*(level1/level_ref)**level_pwr1+\
                   (1-lev_weight)*level_ref*(level2/level_ref)**level_pwr2
         #then it is converted in dB
         level_dB = 20*log10(maximum(level_total, level_min))+RMStoSPL
         #the frequency factor is calculated
         frat = frat0 + frat1*level_dB
         #the centre frequency of the asymmetric compensation filters are updated
         fr2 = fp1*frat
         coeffs = asymmetric_compensation_coeffs(samplerate, fr2,
                        self.target.filt_b, self.target.filt_a, b2, c2,
                        p0, p1, p2, p3, p4)
         self.target.filt_b, self.target.filt_a = coeffs

#### Signal Path ####
#the signal path consists of the passive gammachirp filterbank pGc previously
#defined followed by a asymmetric compensation filterbank
fr1 = fp1*frat0
varyingfilter_signal_path = AsymmetricCompensation(pGc, fr1, b=b2, c=c2)
updater = CompensensationFilterUpdater(varyingfilter_signal_path)
 #the controler which takes the two filterbanks of the control path as inputs
 #and the varying filter of the signal path as target is instantiated
control = ControlFilterbank(varyingfilter_signal_path,
                            [pGc_control, asym_comp_control],
                            varyingfilter_signal_path, updater, update_interval)

#run the simulation
#Remember that the controler are at the end of the chain and the output of the
#whole path comes from them
signal = control.process()

figure()
imshow(flipud(signal.T), aspect='auto')
show()
```

Example: drnl (hears)

Implementation example of the dual resonance nonlinear (DRNL) filter with parameters fitted for human as described in Lopez-Paveda, E. and Meddis, R., A human nonlinear cochlear filterbank, JASA 2001.

A class called `DRNL` implementing this model is available in the library.

The entire pathway consists of the sum of a linear and a nonlinear pathway.

The linear path consists of a bank of bandpass filters (second order gammatone), a low pass function, and a gain/attenuation factor, g, in a cascade.

The nonlinear path is a cascade consisting of a bank of gammatone filters, a compression function, a second bank of gammatone filters, and a low pass function, in that order.

The parameters are given in the form `10**(p0+mlog10(cf))`.

```
from brian import *
from brian.hears import *

simulation_duration = 50*ms
samplerate = 50*kHz
level = 50*dB  # level of the input sound in rms dB SPL
sound = whitenoise(simulation_duration, samplerate).ramp()
sound.level = level

nbr_cf = 50  #number of centre frequencies
#center frequencies with a spacing following an ERB scale
center_frequencies = erbspace(100*Hz,1000*Hz, nbr_cf)

#conversion to stape velocity (which are the units needed by the following centres)
sound = sound*0.00014

#### Linear Pathway ####

#bandpass filter (second order gammatone filter)
center_frequencies_linear = 10**(-0.067+1.016*log10(center_frequencies))
bandwidth_linear = 10**(0.037+0.785*log10(center_frequencies))
order_linear = 3
gammatone = ApproximateGammatone(sound, center_frequencies_linear,
                                 bandwidth_linear, order=order_linear)

#linear gain
g = 10**(4.2-0.48*log10(center_frequencies))
func_gain = lambda x:g*x
gain = FunctionFilterbank(gammatone, func_gain)

#low pass filter(cascade of 4 second order lowpass butterworth filters)
cutoff_frequencies_linear = center_frequencies_linear
order_lowpass_linear = 2
lp_l = LowPass(gain, cutoff_frequencies_linear)
lowpass_linear = Cascade(gain, lp_l, 4)

#### Nonlinear Pathway ####

#bandpass filter (third order gammatone filters)
center_frequencies_nonlinear = center_frequencies
bandwidth_nonlinear = 10**(-0.031+0.774*log10(center_frequencies))
order_nonlinear = 3
bandpass_nonlinear1 = ApproximateGammatone(sound, center_frequencies_nonlinear,
                                           bandwidth_nonlinear,
                                           order=order_nonlinear)

#compression (linear at low level, compress at high level)
a = 10**(1.402+0.819*log10(center_frequencies))  #linear gain
b = 10**(1.619-0.818*log10(center_frequencies))
v = .2 #compression exponent
func_compression = lambda x: sign(x)*minimum(a*abs(x), b*abs(x)**v)
```

```
compression = FunctionFilterbank(bandpass_nonlinear1, func_compression)

#bandpass filter (third order gammatone filters)
bandpass_nonlinear2 = ApproximateGammatone(compression,
                                           center_frequencies_nonlinear,
                                           bandwidth_nonlinear,
                                           order=order_nonlinear)

#low pass filter
cutoff_frequencies_nonlinear = center_frequencies_nonlinear
order_lowpass_nonlinear = 2
lp_nl = LowPass(bandpass_nonlinear2, cutoff_frequencies_nonlinear)
lowpass_nonlinear = Cascade(bandpass_nonlinear2, lp_nl, 3)

#adding the two pathways
dnrl_filter = lowpass_linear+lowpass_nonlinear

dnrl = dnrl_filter.process()

figure()
imshow(flipud(dnrl.T), aspect='auto')
show()
```

Example: gammatone (hears)

Example of the use of the class `Gammatone` available in the library. It implements a fitlerbank of IIR gammatone filters as described in Slaney, M., 1993, "An Efficient Implementation of the Patterson-Holdsworth Auditory Filter Bank". Apple Computer Technical Report #35. In this example, a white noise is filtered by a gammatone filterbank and the resulting cochleogram is plotted.

```
from brian import *
from brian.hears import *
from matplotlib import pyplot

sound = whitenoise(100*ms).ramp()
sound.level = 50*dB

nbr_center_frequencies = 50
b1 = 1.019  #factor determining the time constant of the filters
#center frequencies with a spacing following an ERB scale
center_frequencies = erbspace(100*Hz, 1000*Hz, nbr_center_frequencies)
gammatone = Gammatone(sound, center_frequencies, b=b1)

gt_mon = gammatone.process()

figure()
imshow(gt_mon.T, aspect='auto', origin='lower left',
       extent=(0, sound.duration/ms,
               center_frequencies[0], center_frequencies[-1]))
pyplot.yscale('log')
title('Cochleogram')
ylabel('Frequency (Hz)')
xlabel('Time (ms)')

show()
```

Example: IIRfilterbank (hears)

Example of the use of the class `IIRFilterbank` available in the library. In this example, a white noise is filtered by a bank of chebyshev bandpass filters and lowpass filters which are different for every channels. The centre frequencies of the filters are linearly taken between 100kHz and 1000kHz and its bandwidth or cutoff frequency increases linearly with frequency.

```
from brian import *
from brian.hears import *

sound = whitenoise(100*ms).ramp()
sound.level = 50*dB

### example of a bank of bandpass filter ################
nchannels = 50
center_frequencies = linspace(200*Hz, 1000*Hz, nchannels)  #center frequencies
bw = linspace(50*Hz, 300*Hz, nchannels)  #bandwidth of the filters
# The maximum loss in the passband in dB. Can be a scalar or an array of length
# nchannels
gpass = 1.*dB
# The minimum attenuation in the stopband in dB. Can be a scalar or an array
# of length nchannels
gstop = 10.*dB
#arrays of shape (2 x nchannels) defining the passband frequencies (Hz)
passband = vstack((center_frequencies-bw/2, center_frequencies+bw/2))
#arrays of shape (2 x nchannels) defining the stopband frequencies (Hz)
stopband = vstack((center_frequencies-1.1*bw, center_frequencies+1.1*bw))

filterbank = IIRFilterbank(sound, nchannels, passband, stopband, gpass, gstop,
                           'bandstop', 'cheby1')
filterbank_mon = filterbank.process()

figure()
subplot(211)
imshow(flipud(filterbank_mon.T), aspect='auto')

#### example of a bank of lowpass filter ################
nchannels = 50
cutoff_frequencies = linspace(100*Hz, 1000*Hz, nchannels)
#bandwidth of the transition region between the en of the pass band and the
#begin of the stop band
width_transition = linspace(50*Hz, 300*Hz, nchannels)
# The maximum loss in the passband in dB. Can be a scalar or an array of length
# nchannels
gpass = 1*dB
# The minimum attenuation in the stopband in dB. Can be a scalar or an array of
# length nchannels
gstop = 10*dB
passband = cutoff_frequencies-width_transition/2
stopband = cutoff_frequencies+width_transition/2

filterbank = IIRFilterbank(sound, nchannels, passband, stopband, gpass, gstop,
                           'low','cheby1')
filterbank_mon=filterbank.process()

subplot(212)
imshow(flipud(filterbank_mon.T), aspect='auto')
show()
```

Example: ircam_hrtf (hears)

Example showing the use of HRTFs in Brian hears. Note that you will need to download the `IRCAM_LISTEN` database.

```
from brian import *
from brian.hears import *
# Load database
hrtfdb = IRCAM_LISTEN(r'F:\HRTF\IRCAM')
hrtfset = hrtfdb.load_subject(1002)
# Select only the horizontal plane
hrtfset = hrtfset.subset(lambda elev: elev==0)
# Set up a filterbank
sound = whitenoise(10*ms)
fb = hrtfset.filterbank(sound)
# Extract the filtered response and plot
img = fb.process().T
img_left = img[:img.shape[0]/2, :]
img_right = img[img.shape[0]/2:, :]
subplot(121)
imshow(img_left, origin='lower left', aspect='auto',
       extent=(0, sound.duration/ms, 0, 360))
xlabel('Time (ms)')
ylabel('Azimuth')
title('Left ear')
subplot(122)
imshow(img_right, origin='lower left', aspect='auto',
       extent=(0, sound.duration/ms, 0, 360))
xlabel('Time (ms)')
ylabel('Azimuth')
title('Right ear')
show()
```

Example: linear_gammachirp (hears)

Example of the use of the class `LinearGammachirp` available in the library. It implements a filterbank of FIR gammatone filters with linear frequency sweeps as described in Wagner et al. 2009, "Auditory responses in the barn owl's nucleus laminaris to clicks: impulse response and signal analysis of neurophonic potential", J. Neurophysiol. In this example, a white noise is filtered by a gammachirp filterbank and the resulting cochleogram is plotted. The different impulse responses are also plotted.

```
from brian import *
from brian.hears import *

sound = whitenoise(100*ms).ramp()
sound.level = 50*dB

nbr_center_frequencies = 10  #number of frequency channels in the filterbank
#center frequencies with a spacing following an ERB scale
center_frequencies = erbspace(100*Hz, 1000*Hz, nbr_center_frequencies)

c = 0.0 #glide slope
time_constant = linspace(3, 0.3, nbr_center_frequencies)*ms

gamma_chirp = LinearGammachirp(sound, center_frequencies, time_constant, c)

gamma_chirp_mon = gamma_chirp.process()
```

```
figure()

imshow(gamma_chirp_mon.T, aspect='auto')
figure()
plot(gamma_chirp.impulse_response.T)
show()
```

Example: log_gammachirp (hears)

Example of the use of the class `LogGammachirp` available in the library. It implements a filterbank of IIR gammachirp filters as Unoki et al. 2001, "Improvement of an IIR asymmetric compensation gammachirp filter". In this example, a white noise is filtered by a linear gammachirp filterbank and the resulting cochleogram is plotted. The different impulse responses are also plotted.

```
from brian import *
from brian.hears import *

sound = whitenoise(100*ms).ramp()
sound.level = 50*dB

nbr_center_frequencies = 50  #number of frequency channels in the filterbank

c1 = -2.96 #glide slope
b1 = 1.81  #factor determining the time constant of the filters

#center frequencies with a spacing following an ERB scale
cf = erbspace(100*Hz, 1000*Hz, nbr_center_frequencies)

gamma_chirp = LogGammachirp(sound, cf, c=c1, b=b1)

gamma_chirp_mon = gamma_chirp.process()

figure()
imshow(flipud(gamma_chirp_mon.T), aspect='auto')
show()
```

Example: online_computation (hears)

Example of online computation using `process()`. Plots the RMS value of each channel output by a gammatone filterbank.

```
from brian import *
from brian.hears import *

sound1 = tone(1*kHz, .1*second)
sound2 = whitenoise(.1*second)

sound = sound1+sound2
sound = sound.ramp()

sound.level = 60*dB

cf = erbspace(20*Hz, 20*kHz, 3000)
fb = Gammatone(sound, cf)
```

```
def sum_of_squares(input, running):
    return running+sum(input**2, axis=0)

rms = sqrt(fb.process(sum_of_squares)/sound.nsamples)

sound_rms = sqrt(mean(sound**2))

axhline(sound_rms, ls='--')
plot(cf, rms)
xlabel('Frequency (Hz)')
ylabel('RMS')
show()
```

Example: simple_anf (hears)

Example of a simple auditory nerve fibre model with Brian hears.

```
from brian import *
from brian.hears import *

sound1 = tone(1*kHz, .1*second)
sound2 = whitenoise(.1*second)

sound = sound1+sound2
sound = sound.ramp()

cf = erbspace(20*Hz, 20*kHz, 3000)
cochlea = Gammatone(sound, cf)

# Half-wave rectification and compression [x]^(1/3)
ihc = FunctionFilterbank(cochlea, lambda x: 3*clip(x, 0, Inf)**(1.0/3.0))

# Leaky integrate-and-fire model with noise and refractoriness
eqs = '''
dv/dt = (I-v)/(1*ms)+0.2*xi*(2/(1*ms))**.5 : 1
I : 1
'''
anf = FilterbankGroup(ihc, 'I', eqs, reset=0, threshold=1, refractory=5*ms)

M = SpikeMonitor(anf)
run(sound.duration)
raster_plot(M)
show()
```

Example: sounds (hears)

Example of basic use and manipulation of sounds with Brian hears.

```
from brian import *
from brian.hears import *

sound1 = tone(1*kHz, 1*second)
sound2 = whitenoise(1*second)

sound = sound1+sound2
sound = sound.ramp()
```

```
# Comment this line out if you don't have pygame installed
sound.play()

# The first 20ms of the sound
startsound = sound[:20*ms]

subplot(121)
plot(startsound.times, startsound)
subplot(122)
sound.spectrogram()
show()
```

Example: sound_localisation_model (hears)

Example demonstrating the use of many features of Brian hears, including HRTFs, restructuring filters and integration with Brian. Implements a simplified version of the "ideal" sound localisation model from Goodman and Brette (2010).

The sound is played at a particular spatial location (indicated on the final plot by a red +). Each location has a corresponding assembly of neurons, whose summed firing rates give the sizes of the blue circles in the plot. The most strongly responding assembly is indicated by the green x, which is the estimate of the location by the model.

Reference:

Goodman DFM, Brette R (2010). Spike-timing-based computation in sound localization. PLoS Comput. Biol. 6(11).

```
from brian import *
from brian.hears import *

# Download the IRCAM database, and replace this filename with the location
# you downloaded it to
hrtfdb = IRCAM_LISTEN(r'F:\HRTF\IRCAM')
subject = 1002
hrtfset = hrtfdb.load_subject(subject)
# This gives the number of spatial locations in the set of HRTFs
num_indices = hrtfset.num_indices
# Choose a random location for the sound to come from
index = randint(hrtfset.num_indices)
# A sound to test the model with
sound = Sound.whitenoise(500*ms)
# This is the specific HRTF for the chosen location
hrtf = hrtfset.hrtf[index]
# We apply the chosen HRTF to the sound, the output has 2 channels
hrtf_fb = hrtf.filterbank(sound)
# We swap these channels (equivalent to swapping the channels in the
# subsequent filters, but simpler to do it with the inputs)
swapped_channels = RestructureFilterbank(hrtf_fb, indexmapping=[1, 0])
# Now we apply all of the possible pairs of HRTFs in the set to these
# swapped channels, which means repeating them num_indices times first
hrtfset_fb = hrtfset.filterbank(Repeat(swapped_channels, num_indices))
# Now we apply cochlear filtering (logically, this comes before the HRTF
# filtering, but since convolution is commutative it is more efficient to
# do the cochlear filtering afterwards
cfmin, cfmax, cfN = 150*Hz, 5*kHz, 40
cf = erbspace(cfmin, cfmax, cfN)
# We repeat each of the HRTFSet filterbank channels cfN times, so that
# for each location we will apply each possible cochlear frequency
gfb = Gammatone(Repeat(hrtfset_fb, cfN),
```

```
                tile(cf, hrtfset_fb.nchannels))
# Half wave rectification and compression
cochlea = FunctionFilterbank(gfb, lambda x:15*clip(x, 0, Inf)**(1.0/3.0))
# Leaky integrate and fire neuron model
eqs = '''
dV/dt = (I-V)/(1*ms)+0.1*xi/(0.5*ms)**.5 : 1
I : 1
'''
G = FilterbankGroup(cochlea, 'I', eqs, reset=0, threshold=1, refractory=5*ms)
# The coincidence detector (cd) neurons
cd = NeuronGroup(num_indices*cfN, eqs, reset=0, threshold=1, clock=G.clock)
# Each CD neuron receives precisely two inputs, one from the left ear and
# one from the right, for each location and each cochlear frequency
C = Connection(G, cd, 'V')
for i in xrange(num_indices*cfN):
    C[i, i] = 0.5                 # from right ear
    C[i+num_indices*cfN, i] = 0.5 # from left ear
# We want to just count the number of CD spikes
counter = SpikeCounter(cd)
# Run the simulation, giving a report on how long it will take as we run
run(sound.duration, report='stderr')
# We take the array of counts, and reshape them into a 2D array which we sum
# across frequencies to get the spike count of each location-specific assembly
count = counter.count
count.shape = (num_indices, cfN)
count = sum(count, axis=1)
count = array(count, dtype=float)/amax(count)
# Our guess of the location is the index of the strongest firing assembly
index_guess = argmax(count)
# Now we plot the output, using the coordinates of the HRTFSet
coords = hrtfset.coordinates
azim, elev = coords['azim'], coords['elev']
scatter(azim, elev, 100*count)
plot([azim[index]], [elev[index]], '+r', ms=15, mew=2)
plot([azim[index_guess]], [elev[index_guess]], 'xg', ms=15, mew=2)
xlabel('Azimuth (deg)')
ylabel('Elevation (deg)')
xlim(-5, 350)
ylim(-50, 95)
show()
```

Example: time_varying_filter1 (hears)

This example implements a band pass filter whose center frequency is modulated by an Ornstein-Uhlenbeck. The white noise term used for this process is output by a FunctionFilterbank. The bandpass filter coefficients update is an example of how to use a `ControlFilterbank`. The bandpass filter is a basic biquadratic filter for which the Q factor and the center frequency must be given. The input is a white noise.

```
from brian import *
from brian.hears import *

samplerate = 20*kHz
SoundDuration = 300*ms
sound = whitenoise(SoundDuration, samplerate).ramp()

#number of frequency channel (here it must be one as a spectrogram of the
#output is plotted)
```

```
nchannels = 1

fc_init = 5000*Hz   #initial center frequency of the band pass filter
Q = 5               #quality factor of the band pass filter
update_interval = 4 # the filter coefficients are updated every 4 samples

#parameters of the Ornstein-Uhlenbeck process
s_i = 1200*Hz
tau_i = 100*ms
mu_i = fc_init/tau_i
sigma_i = sqrt(2)*s_i/sqrt(tau_i)
deltaT = defaultclock.dt

#this function  is used in a FunctionFilterbank. It outputs a noise term that
#will be later used by the controler to update the center frequency
noise = lambda x: mu_i*deltaT+sigma_i*randn(1)*sqrt(deltaT)
noise_generator = FunctionFilterbank(sound, noise)

#this class will take as input the output of the noise generator and as target
#the bandpass filter center frequency
class CoeffController(object):
    def __init__(self, target):
        self.target = target
        self.deltaT = 1./samplerate
        self.BW = 2*arcsinh(1./2/Q)*1.44269
        self.fc = fc_init

    def __call__(self, input):
        #the control variables are taken as the last of the buffer
        noise_term = input[-1,:]
        #update the center frequency by updateing the OU process
        self.fc = self.fc-self.fc/tau_i*self.deltaT+noise_term

        w0 = 2*pi*self.fc/samplerate
        #update the coefficient of the biquadratic filterbank
        alpha = sin(w0)*sinh(log(2)/2*self.BW*w0/sin(w0))
        self.target.filt_b[:, 0, 0] = sin(w0)/2
        self.target.filt_b[:, 1, 0] = 0
        self.target.filt_b[:, 2, 0] = -sin(w0)/2

        self.target.filt_a[:, 0, 0] = 1+alpha
        self.target.filt_a[:, 1, 0] = -2*cos(w0)
        self.target.filt_a[:, 2, 0] = 1-alpha

# In the present example the time varying filter is a LinearFilterbank therefore
#we must initialise the filter coefficients; the one used for the first buffer computation
w0 = 2*pi*fc_init/samplerate
BW = 2*arcsinh(1./2/Q)*1.44269
alpha = sin(w0)*sinh(log(2)/2*BW*w0/sin(w0))

filt_b = zeros((nchannels, 3, 1))
filt_a = zeros((nchannels, 3, 1))
filt_b[:, 0, 0] = sin(w0)/2
filt_b[:, 1, 0] = 0
filt_b[:, 2, 0] = -sin(w0)/2
filt_a[:, 0, 0] = 1+alpha
filt_a[:, 1, 0] = -2*cos(w0)
filt_a[:, 2, 0] = 1-alpha
```

```
#the filter which will have time varying coefficients
bandpass_filter = LinearFilterbank(sound, filt_b, filt_a)
#the updater
updater = CoeffController(bandpass_filter)

#the controller. Remember it must be the last of the chain
control = ControlFilterbank(bandpass_filter, noise_generator, bandpass_filter,
                            updater, update_interval)

time_varying_filter_mon = control.process()

figure(1)
pxx, freqs, bins, im = specgram(squeeze(time_varying_filter_mon),
                                NFFT=256, Fs=samplerate, noverlap=240)
imshow(flipud(pxx), aspect='auto')

show()
```

Example: time_varying_filter2 (hears)

This example implements a band pass filter whose center frequency is modulated by a sinusoid function. This modulator is implemented as a `FunctionFilterbank`. One state variable (here time) must be kept; it is therefore implemented with a class. The bandpass filter coefficients update is an example of how to use a `ControlFilterbank`. The bandpass filter is a basic biquadratic filter for which the Q factor and the center frequency must be given. The input is a white noise.

```
from brian import *
from brian.hears import *


samplerate = 20*kHz
SoundDuration = 300*ms
sound = whitenoise(SoundDuration, samplerate).ramp()

#number of frequency channel (here it must be one as a spectrogram of the
#output is plotted)
nchannels = 1

fc_init = 5000*Hz   #initial center frequency of the band pass filter
Q = 5               #quality factor of the band pass filter
update_interval = 1 # the filter coefficients are updated every sample

mean_center_freq = 4*kHz #mean frequency around which the CF will oscillate
amplitude = 1500*Hz      #amplitude of the oscillation
frequency = 10*Hz        #frequency of the oscillation

#this class is used in a FunctionFilterbank (via its __call__). It outputs the
#center frequency of the band pass filter. Its output is thus later passed as
#input to the controler.
class CenterFrequencyGenerator(object):
    def __init__(self):
        self.t=0*second

    def __call__(self, input):
        #update of the center frequency
        fc = mean_center_freq+amplitude*sin(2*pi*frequency*self.t)
```

```
        #update of the state variable
        self.t = self.t+1./samplerate
        return fc

center_frequency = CenterFrequencyGenerator()

fc_generator = FunctionFilterbank(sound, center_frequency)

#the updater of the controller generates new filter coefficient of the band pass
#filter based on the center frequency it receives from the fc_generator
#(its input)
class CoeffController(object):
    def __init__(self, target):
        self.BW = 2*arcsinh(1./2/Q)*1.44269
        self.target=target

    def __call__(self, input):
        fc = input[-1,:] #the control variables are taken as the last of the buffer
        w0 = 2*pi*fc/array(samplerate)
        alpha = sin(w0)*sinh(log(2)/2*self.BW*w0/sin(w0))

        self.target.filt_b[:, 0, 0] = sin(w0)/2
        self.target.filt_b[:, 1, 0] = 0
        self.target.filt_b[:, 2, 0] = -sin(w0)/2

        self.target.filt_a[:, 0, 0] = 1+alpha
        self.target.filt_a[:, 1, 0] = -2*cos(w0)
        self.target.filt_a[:, 2, 0] = 1-alpha

# In the present example the time varying filter is a LinearFilterbank therefore
#we must initialise the filter coefficients; the one used for the first buffer computation
w0 = 2*pi*fc_init/samplerate
BW = 2*arcsinh(1./2/Q)*1.44269
alpha = sin(w0)*sinh(log(2)/2*BW*w0/sin(w0))

filt_b = zeros((nchannels, 3, 1))
filt_a = zeros((nchannels, 3, 1))

filt_b[:, 0, 0] = sin(w0)/2
filt_b[:, 1, 0] = 0
filt_b[:, 2, 0] = -sin(w0)/2

filt_a[:, 0, 0] = 1+alpha
filt_a[:, 1, 0] = -2*cos(w0)
filt_a[:, 2, 0] = 1-alpha

#the filter which will have time varying coefficients
bandpass_filter = LinearFilterbank(sound, filt_b, filt_a)
#the updater
updater = CoeffController(bandpass_filter)

#the controller. Remember it must be the last of the chain
control = ControlFilterbank(bandpass_filter, fc_generator, bandpass_filter,
                            updater, update_interval)

time_varying_filter_mon = control.process()

figure(1)
```

```
pxx, freqs, bins, im = specgram(squeeze(time_varying_filter_mon),
                                NFFT=256, Fs=samplerate, noverlap=240)
imshow(flipud(pxx), aspect='auto')

show()
```

3.2.7 frompapers

Example: Brette_Gerstner_2005 (frompapers)

Adaptive exponential integrate-and-fire model. http://www.scholarpedia.org/article/Adaptive_exponential_integrate-and-fire_model

Introduced in Brette R. and Gerstner W. (2005), Adaptive Exponential Integrate-and-Fire Model as an Effective Description of Neuronal Activity, J. Neurophysiol. 94: 3637 - 3642.

```
from brian import *

# Parameters
C = 281 * pF
gL = 30 * nS
taum = C / gL
EL = -70.6 * mV
VT = -50.4 * mV
DeltaT = 2 * mV
Vcut = VT + 5 * DeltaT

# Pick an electrophysiological behaviour
tauw, a, b, Vr = 144 * ms, 4 * nS, 0.0805 * nA, -70.6 * mV # Regular spiking (as in the paper)
#tauw,a,b,Vr=20*ms,4*nS,0.5*nA,VT+5*mV # Bursting
#tauw,a,b,Vr=144*ms,2*C/(144*ms),0*nA,-70.6*mV # Fast spiking

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

neuron = NeuronGroup(1, model=eqs, threshold=Vcut, reset="vm=Vr;w+=b", freeze=True)
neuron.vm = EL
trace = StateMonitor(neuron, 'vm', record=0)
spikes = SpikeMonitor(neuron)

run(20 * ms)
neuron.I = 1 * nA
run(100 * ms)
neuron.I = 0 * nA
run(20 * ms)

# We draw nicer spikes
vm = trace[0]
for _, t in spikes.spikes:
    i = int(t / defaultclock.dt)
    vm[i] = 20 * mV

plot(trace.times / ms, vm / mV)
show()
```

Example: Diesmann_et_al_1999 (frompapers)

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, Pgp[0], 'y')
Cinput.connect_full(weight=weight)
# Record the spikes
Mgp = [SpikeMonitor(p) for p in Pgp]
Minput = SpikeMonitor(Pinput)
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()
```

Example: Diesmann_et_al_1999_longer (frompapers)

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-p.Vr)+x)*(1./p.taum)                          : volt
        dx/dt = (-x+y)*(1./p.taupsp)                               : volt
        dy/dt = -y*(1./p.taupsp)+25.27*mV/ms+(39.24*mV/ms**0.5)*xi : volt
        ''')
    return Parameters(model=equations, threshold=p.Vt, reset=p.Vr, refractory=p.abs_refrac)

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(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 = array(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()
```

Example: Rothman_Manis_2003 (frompapers)

Cochlear neuron model of Rothman & Manis

Rothman JS, Manis PB (2003) The roles potassium currents play in regulating the electrical activity of ventral cochlear nucleus neurons. J Neurophysiol 89:3097-113.

All model types differ only by the maximal conductances.

Adapted from their Neuron implementation by Romain Brette

```
from brian import *

#defaultclock.dt=0.025*ms # for better precision

'''
Simulation parameters: choose current amplitude and neuron type
(from type1c, type1t, type12, type 21, type2, type2o)
'''
```

```
neuron_type = 'type1c'
Ipulse = 250 * pA

C = 12 * pF
Eh = -43 * mV
EK = -70 * mV # -77*mV in mod file
El = -65 * mV
ENa = 50 * mV
nf = 0.85 # proportion of n vs p kinetics
zss = 0.5 # steady state inactivation of glt
celsius = 22. # temperature
q10 = 3. ** ((celsius - 22) / 10.)
# hcno current (octopus cell)
frac = 0.0
qt = 4.5 ** ((celsius - 33.) / 10.)

# Maximal conductances of different cell types in nS
maximal_conductances = dict(
type1c=(1000, 150, 0, 0, 0.5, 0, 2),
type1t=(1000, 80, 0, 65, 0.5, 0, 2),
type12=(1000, 150, 20, 0, 2, 0, 2),
type21=(1000, 150, 35, 0, 3.5, 0, 2),
type2=(1000, 150, 200, 0, 20, 0, 2),
type2o=(1000, 150, 600, 0, 0, 40, 2) # octopus cell
)
gnabar, gkhtbar, gkltbar, gkabar, ghbar, gbarno, gl = [x * nS for x in maximal_conductances[neuron_ty

# Classical Na channel
eqs_na = """
ina = gnabar*m**3*h*(ENa-v) : amp
dm/dt=q10*(minf-m)/mtau : 1
dh/dt=q10*(hinf-h)/htau : 1
minf = 1./(1+exp(-(vu + 38.) / 7.)) : 1
hinf = 1./(1+exp((vu + 65.) / 6.)) : 1
mtau =  ((10. / (5*exp((vu+60.) / 18.) + 36.*exp(-(vu+60.) / 25.))) + 0.04)*ms : ms
htau =  ((100. / (7*exp((vu+60.) / 11.) + 10.*exp(-(vu+60.) / 25.))) + 0.6)*ms : ms
"""

# KHT channel (delayed-rectifier K+)
eqs_kht = """
ikht = gkhtbar*(nf*n**2 + (1-nf)*p)*(EK-v) : amp
dn/dt=q10*(ninf-n)/ntau : 1
dp/dt=q10*(pinf-p)/ptau : 1
ninf =   (1 + exp(-(vu + 15) / 5.))**-0.5 : 1
pinf =  1. / (1 + exp(-(vu + 23) / 6.)) : 1
ntau =  ((100. / (11*exp((vu+60) / 24.) + 21*exp(-(vu+60) / 23.))) + 0.7)*ms : ms
ptau = ((100. / (4*exp((vu+60) / 32.) + 5*exp(-(vu+60) / 22.))) + 5)*ms : ms
"""

# Ih channel (subthreshold adaptive, non-inactivating)
eqs_ih = """
ih = ghbar*r*(Eh-v) : amp
dr/dt=q10*(rinf-r)/rtau : 1
rinf = 1. / (1+exp((vu + 76.) / 7.)) : 1
rtau = ((100000. / (237.*exp((vu+60.) / 12.) + 17.*exp(-(vu+60.) / 14.))) + 25.)*ms : ms
"""

# KLT channel (low threshold K+)
```

```
eqs_klt = """
iklt = gkltbar*w**4*z*(EK-v) : amp
dw/dt=q10*(winf-w)/wtau : 1
dz/dt=q10*(zinf-z)/wtau : 1
winf = (1. / (1 + exp(-(vu + 48.) / 6.)))**0.25 : 1
zinf = zss + ((1.-zss) / (1 + exp((vu + 71.) / 10.))) : 1
wtau = ((100. / (6.*exp((vu+60.) / 6.) + 16.*exp(-(vu+60.) / 45.))) + 1.5)*ms : ms
ztau = ((1000. / (exp((vu+60.) / 20.) + exp(-(vu+60.) / 8.))) + 50)*ms : ms
"""

# Ka channel (transient K+)
eqs_ka = """
ika = gkabar*a**4*b*c*(EK-v): amp
da/dt=q10*(ainf-a)/atau : 1
db/dt=q10*(binf-b)/btau : 1
dc/dt=q10*(cinf-c)/ctau : 1
ainf = (1. / (1 + exp(-(vu + 31) / 6.)))**0.25 : 1
binf = 1. / (1 + exp((vu + 66) / 7.))**0.5 : 1
cinf = 1. / (1 + exp((vu + 66) / 7.))**0.5 : 1
atau =  ((100. / (7*exp((vu+60) / 14.) + 29*exp(-(vu+60) / 24.))) + 0.1)*ms : ms
btau =  ((1000. / (14*exp((vu+60) / 27.) + 29*exp(-(vu+60) / 24.))) + 1)*ms : ms
ctau = ((90. / (1 + exp((-66-vu) / 17.))) + 10)*ms : ms
"""

# Leak
eqs_leak = """
ileak = gl*(El-v) : amp
"""

# h current for octopus cells
eqs_hcno = """
ihcno = gbarno*(h1*frac + h2*(1-frac))*(Eh-v) : amp
dh1/dt=(hinfno-h1)/tau1 : 1
dh2/dt=(hinfno-h2)/tau2 : 1
hinfno = 1./(1+exp((vu+66.)/7.)) : 1
tau1 = bet1/(qt*0.008*(1+alp1))*ms : ms
tau2 = bet2/(qt*0.0029*(1+alp2))*ms : ms
alp1 = exp(1e-3*3*(vu+50)*9.648e4/(8.315*(273.16+celsius))) : 1
bet1 = exp(1e-3*3*0.3*(vu+50)*9.648e4/(8.315*(273.16+celsius))) : 1
alp2 = exp(1e-3*3*(vu+84)*9.648e4/(8.315*(273.16+celsius))) : 1
bet2 = exp(1e-3*3*0.6*(vu+84)*9.648e4/(8.315*(273.16+celsius))) : 1
"""

eqs = """
dv/dt=(ileak+ina+ikht+iklt+ika+ih+ihcno+I)/C : volt
vu = v/mV : 1 # unitless v
I : amp
"""
eqs += eqs_leak + eqs_ka + eqs_na + eqs_ih + eqs_klt + eqs_kht + eqs_hcno

neuron = NeuronGroup(1, eqs, implicit=True)
neuron.v = El

run(50 * ms) # Go to rest

M = StateMonitor(neuron, 'v', record=0)
neuron.I = Ipulse
```

```
run(100 * ms, report='text')

plot(M.times / ms, M[0] / mV)
show()
```

Example: Sturzl_et_al_2000 (frompapers)

Adapted from Theory of Arachnid Prey Localization W. Sturzl, R. Kempter, and J. L. van Hemmen PRL 2000

Poisson inputs are replaced by integrate-and-fire neurons

Romain Brette

```
from brian import *

# Parameters
degree = 2 * pi / 360.
duration = 500 * ms
R = 2.5 * cm # radius of scorpion
vr = 50 * meter / second # Rayleigh wave speed
phi = 144 * degree # angle of prey
A = 250 * Hz
deltaI = .7 * ms # inhibitory delay
gamma = (22.5 + 45 * arange(8)) * degree # leg angle
delay = R / vr * (1 - cos(phi - gamma))  # wave delay

# Wave (vector w)
t = arange(int(duration / defaultclock.dt) + 1) * defaultclock.dt
Dtot = 0.
w = 0.
for f in range(150, 451):
    D = exp(-(f - 300) ** 2 / (2 * (50 ** 2)))
    xi = 2 * pi * rand()
    w += 100 * D * cos(2 * pi * f * t + xi)
    Dtot += D
w = .01 * w / Dtot

# Rates from the wave
def rates(t):
    return w[array(t / defaultclock.dt, dtype=int)]

# Leg mechanical receptors
tau_legs = 1 * ms
sigma = .01
eqs_legs = """
dv/dt=(1+rates(t-d)-v)/tau_legs+sigma*(2./tau_legs)**.5*xi:1
d : second
"""
legs = NeuronGroup(8, model=eqs_legs, threshold=1, reset=0, refractory=1 * ms)
legs.d = delay
spikes_legs = SpikeCounter(legs)

# Command neurons
tau = 1 * ms
taus = 1 * ms
wex = 7
winh = -2
eqs_neuron = '''
```

```
dv/dt=(x-v)/tau : 1
dx/dt=(y-x)/taus : 1 # alpha currents
dy/dt=-y/taus : 1
'''
neurons = NeuronGroup(8, model=eqs_neuron, threshold=1, reset=0)
synapses_ex = IdentityConnection(legs, neurons, 'y', weight=wex)
synapses_inh = Connection(legs, neurons, 'y', delay=deltaI)
for i in range(8):
    synapses_inh[i, (4 + i - 1) % 8] = winh
    synapses_inh[i, (4 + i) % 8] = winh
    synapses_inh[i, (4 + i + 1) % 8] = winh
spikes = SpikeCounter(neurons)

run(duration)
nspikes = spikes.count
x = sum(nspikes * exp(gamma * 1j))
print "Angle (deg):", arctan(imag(x) / real(x)) / degree
polar(concatenate((gamma, [gamma[0] + 2 * pi])), concatenate((nspikes, [nspikes[0]])) / duration)
show()
```

3.2.8 electrophysiology

Example: AEC (electrophysiology)

AEC experiment (current-clamp)

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

myclock = Clock(dt=.1 * ms)
clock_rec = Clock(dt=.1 * ms)

#log_level_debug()

taum = 20 * ms
gl = 20 * nS
Cm = taum * gl
Re = 50 * Mohm
Ce = 0.1 * ms / Re

eqs = Equations('''
dvm/dt=(-gl*vm+i_inj)/Cm : volt
I:amp
''')
eqs += electrode(.6 * Re, Ce)
eqs += current_clamp(vm='v_el', i_inj='i_cmd', i_cmd='I', Re=.4 * Re, Ce=Ce)
setup = NeuronGroup(1, model=eqs, clock=myclock)
board = AEC(setup, 'v_rec', 'I', clock_rec)
recording = StateMonitor(board, 'record', record=True, clock=myclock)
soma = StateMonitor(setup, 'vm', record=True, clock=myclock)

run(50 * ms)
board.command = .5 * nA
run(200 * ms)
board.command = 0 * nA
```

```
run(150 * ms)
board.start_injection()
t1 = time()
run(1 * second)
t2 = time()
print 'Duration:', t2 - t1, 's'
board.stop_injection()
run(100 * ms)
board.estimate()
print 'Re=', sum(board.Ke) * ohm
board.switch_on()
run(50 * ms)
board.command = .5 * nA
run(200 * ms)
board.command = 0 * nA
run(150 * ms)
board.switch_off()
figure()
plot(recording.times / ms, recording[0] / mV, 'b')
plot(soma.times / ms, soma[0] / mV, 'r')
figure()
plot(board.Ke)
show()
```

Example: bridge (electrophysiology)

Bridge experiment (current-clamp)

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

defaultclock.dt = .01 * ms

#log_level_debug()

taum = 20 * ms
gl = 20 * nS
Cm = taum * gl
Re = 50 * Mohm
Ce = 0.5 * ms / Re
N = 10

eqs = Equations('''
dvm/dt=(-gl*vm+i_inj)/Cm : volt
#Rbridge:ohm
CC:farad
I:amp
''')
eqs += electrode(.6 * Re, Ce)
#eqs+=current_clamp(vm='v_el',i_inj='i_cmd',i_cmd='I',Re=.4*Re,Ce=Ce,
#                   bridge='Rbridge')
eqs += current_clamp(vm='v_el', i_inj='i_cmd', i_cmd='I', Re=.4 * Re, Ce=Ce,
                     bridge=Re, capa_comp='CC')
setup = NeuronGroup(N, model=eqs)
setup.I = 0 * nA
setup.v = 0 * mV
#setup.Rbridge=linspace(0*Mohm,60*Mohm,N)
```

```
setup.CC = linspace(0 * Ce, Ce, N)
recording = StateMonitor(setup, 'v_rec', record=True)

run(50 * ms)
setup.I = .5 * nA
run(200 * ms)
setup.I = 0 * nA
run(150 * ms)
for i in range(N):
    plot(recording.times / ms + i * 400, recording[i] / mV, 'k')
show()
```

Example: DCC (electrophysiology)

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

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

defaultclock.dt = 0.01 * ms

taum = 20 * ms          # membrane time constant
gl = 1. / (50 * Mohm)   # leak conductance
Cm = taum * gl          # membrane capacitance
Re = 50 * Mohm          # electrode resistance
Ce = 0.1 * 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)
setup = NeuronGroup(1, model=eqs)
ampli = DCC(setup, 'v_rec', 'I', 1 * kHz)
soma = StateMonitor(setup, 'vm', record=True)
recording = StateMonitor(setup, 'v_rec', record=True)
DCCrecording = StateMonitor(ampli, 'record', record=True)

# No compensation
run(50 * ms)
ampli.command = .5 * nA
run(100 * ms)
ampli.command = 0 * nA
run(50 * ms)

ampli.set_frequency(2 * kHz)
ampli.command = .5 * nA
run(100 * ms)
ampli.command = 0 * nA
run(50 * ms)

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

Example: SEVC (electrophysiology)

Voltage-clamp experiment (SEVC)

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

defaultclock.dt = .01 * ms

taum = 20 * ms          # membrane time constant
gl = 1. / (50 * Mohm)   # leak conductance
Cm = taum * gl          # membrane capacitance
Re = 50 * Mohm          # electrode resistance
Ce = 0.1 * ms / Re      # electrode capacitance

eqs = Equations('''
dvm/dt=(-gl*vm+i_inj)/Cm : volt
I:amp
''')
eqs += current_clamp(i_cmd='I', Re=Re, Ce=Ce)
setup = NeuronGroup(1, model=eqs)
ampli = SEVC(setup, 'v_rec', 'I', 1 * kHz, gain=250 * nS, gain2=50 * nS / ms)
recording = StateMonitor(ampli, 'record', record=True)
soma = StateMonitor(setup, 'vm', record=True)

ampli.command = 20 * mV
run(200 * ms)
figure()
plot(recording.times / ms, recording[0] / nA, 'k')
figure()
plot(soma.times / ms, soma[0] / mV, 'b')
show()
```

Example: voltageclamp (electrophysiology)

Voltage-clamp experiment

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

defaultclock.dt = .01 * ms

taum = 20 * ms
gl = 20 * nS
Cm = taum * gl
Re = 50 * Mohm
Ce = 0.2 * ms / Re
N = 1
Rs = .9 * Re
tauc = Rs * Ce # critical tau_u

eqs = Equations('''
dvm/dt=(-gl*vm+i_inj)/Cm : volt
''')
eqs += electrode(.2 * Re, Ce)
eqs += voltage_clamp(vm='v_el', v_cmd=20 * mV, i_inj='i_cmd', i_rec='ic',
                     Re=.8 * Re, Rs=.9 * Re, tau_u=.2 * ms)
```

```
setup = NeuronGroup(N, model=eqs)
setup.v = 0 * mV
recording = StateMonitor(setup, 'ic', record=True)
soma = StateMonitor(setup, 'vm', record=True)

run(200 * ms)
figure()
plot(recording.times / ms, recording[0] / nA, 'k')
figure()
plot(soma.times / ms, soma[0] / mV, 'b')
show()
```

3.2.9 audition

Example: filterbank (audition)

An auditory filterbank implemented with Poisson neurons

The input sound has a missing fundamental (only harmonics 2 and 3)

```
from brian import *

defaultclock.dt = .01 * ms

N = 1500
tau = 1 * ms # Decay time constant of filters = 2*tau
freq = linspace(100 * Hz, 2000 * Hz, N) # characteristic frequencies
f_stimulus = 500 * Hz # stimulus frequency
gain = 500 * Hz

eqs = '''
dv/dt=(-a*w-v+I)/tau : Hz
dw/dt=(v-w)/tau : Hz # e.g. linearized potassium channel with conductance a
a : 1
I = gain*(sin(4*pi*f_stimulus*t)+sin(6*pi*f_stimulus*t)) : Hz
'''

neurones = NeuronGroup(N, model=eqs, threshold=PoissonThreshold())
neurones.a = (2 * pi * freq * tau) ** 2

spikes = SpikeMonitor(neurones)
counter = SpikeCounter(neurones)
run(100 * ms)

subplot(121)
CF = array([freq[i] for i, _ in spikes.spikes])
timings = array([t for _, t in spikes.spikes])
plot(timings / ms, CF, '.')
xlabel('Time (ms)')
ylabel('Characteristic frequency (Hz)')
subplot(122)
plot(counter.count / (300 * ms), freq)
xlabel('Firing rate (Hz)')
show()
```

Example: jeffress (audition)

Jeffress model, adapted with spiking neuron models. A sound source (white noise) is moving around the head. Delay differences between the two ears are used to determine the azimuth of the source. Delays are mapped to a neural place code using delay lines (each neuron receives input from both ears, with different delays).

Romain Brette

```
from brian import *

defaultclock.dt = .02 * ms
dt = defaultclock.dt

# Sound
sound = TimedArray(10 * randn(50000)) # white noise

# Ears and sound motion around the head (constant angular speed)
sound_speed = 300 * metre / second
interaural_distance = 20 * cm # big head!
max_delay = interaural_distance / sound_speed
print "Maximum interaural delay:", max_delay
angular_speed = 2 * pi * radian / second # 1 turn/second
tau_ear = 1 * ms
sigma_ear = .1
eqs_ears = '''
dx/dt=(sound(t-delay)-x)/tau_ear+sigma_ear*(2./tau_ear)**.5*xi : 1
delay=distance*sin(theta) : second
distance : second # distance to the centre of the head in time units
dtheta/dt=angular_speed : radian
'''
ears = NeuronGroup(2, model=eqs_ears, threshold=1, reset=0, refractory=2.5 * ms)
ears.distance = [-.5 * max_delay, .5 * max_delay]
traces = StateMonitor(ears, 'x', record=True)

# Coincidence detectors
N = 300
tau = 1 * ms
sigma = .1
eqs_neurons = '''
dv/dt=-v/tau+sigma*(2./tau)**.5*xi : 1
'''
neurons = NeuronGroup(N, model=eqs_neurons, threshold=1, reset=0)
synapses = Connection(ears, neurons, 'v', structure='dense', delay=True, max_delay=1.1 * max_delay)
synapses.connect_full(ears, neurons, weight=.5)
synapses.delay[0, :] = linspace(0 * ms, 1.1 * max_delay, N)
synapses.delay[1, :] = linspace(0 * ms, 1.1 * max_delay, N)[::-1]
spikes = SpikeMonitor(neurons)

run(1000 * ms)
raster_plot(spikes)
show()
```

Example: licklider (audition)

Spike-based adaptation of Licklider's model of pitch processing (autocorrelation with delay lines) with phase locking.

Romain Brette

```
from brian import *

defaultclock.dt = .02 * ms

# Ear and sound
max_delay = 20 * ms # 50 Hz
tau_ear = 1 * ms
sigma_ear = .1
eqs_ear = '''
dx/dt=(sound-x)/tau_ear+sigma_ear*(2./tau_ear)**.5*xi : 1
sound=5*sin(2*pi*frequency*t)**3 : 1 # nonlinear distorsion
#sound=5*(sin(4*pi*frequency*t)+.5*sin(6*pi*frequency*t)) : 1 # missing fundamental
frequency=(200+200*t*Hz)*Hz : Hz # increasing pitch
'''
receptors = NeuronGroup(2, model=eqs_ear, threshold=1, reset=0, refractory=2 * ms)
traces = StateMonitor(receptors, 'x', record=True)
sound = StateMonitor(receptors, 'sound', record=0)

# Coincidence detectors
min_freq = 50 * Hz
max_freq = 1000 * Hz
N = 300
tau = 1 * ms
sigma = .1
eqs_neurons = '''
dv/dt=-v/tau+sigma*(2./tau)**.5*xi : 1
'''
neurons = NeuronGroup(N, model=eqs_neurons, threshold=1, reset=0)
synapses = Connection(receptors, neurons, 'v', structure='dense', max_delay=1.1 * max_delay, delay=T
synapses.connect_full(receptors, neurons, weight=.5)
synapses.delay[1, :] = 1. / exp(linspace(log(min_freq / Hz), log(max_freq / Hz), N))
spikes = SpikeMonitor(neurons)

run(500 * ms)
raster_plot(spikes)
ylabel('Frequency')
yticks([0, 99, 199, 299], array(1. / synapses.delay.todense()[1, [0, 99, 199, 299]], dtype=int))
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://docs.scipy.org/
- http://matplotlib.sourceforge.net/

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).

Unit checking can also be turned down locally when initializing a neuron group by passing the argument `check_units=False`. In that case, no error is raised if the differential equations are not homogeneous.

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 optionally 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.

Details

For details, see the reference documentation for `NeuronGroup`.

4.2.3 Reset

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

- a quantity (`0*mV`)
- a string
- 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.

Reset as Python code

The simplest way to customise the reset is to define it as a Python statement, e.g.:

```
eqs='''
dv/dt=-v/tau : volt
dw/dt=-w/tau : volt
'''
group=NeuronGroup(100,model=eqs,reset="v=0*mV;w+=3*mV",threshold=10*mV)
```

The string must be a valid Python statement (possibly a multiline string). It can contain variables from the neuron group, units and any variable defined in the namespace (e.g. tau), as for equations. Be aware that if a variable in the namespace has the same name as a neuron group variable, then it masks the neuron variable. The way it works is that the code is evaluated with each neuron variable `v` replaced by `v[spikes]`, where `spikes` is the array of indexes of the neurons that just spiked.

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.

Threshold as Python expression

The simplest way to customise the threshold is to define it as a Python expression, e.g.:

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

The string must be an expression which evaluates to a boolean. It can contain variables from the neuron group, units and any variable defined in the namespace (e.g. tau), as for equations. Be aware that if a variable in the namespace has the same name as a neuron group variable, then it masks the neuron variable. The way it works is that the expression is evaluated with the neuron variables replaced by their vector values (values for all neurons), so that the expression returns a boolean vector.

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=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],sparseness=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.

If you are connecting the whole groups, you can omit the first two arguments, e.g.:

```
myconnection.connect_full(weight=5*nS)
```

connects `group1` to `group2` with weights 5 nS.

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 and connection probability. 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). Alternatively, the connection probability can also be a function, e.g.:

```
myconnection.connect_random(group1,group2,0.1,weight=1*nS,sparseness=lambda i,j:exp(-abs(i-j)*.1))
```

The weight or the connection probability may both be functions (with 0 or 2 arguments).

4.3.2 Delays

Transmission delays can be introduced with the keyword `delay`, passed at initialisation time. There are two types of delays, homogeneous (all synapses have the same delay) and heterogeneous (all synapses can have different delays). The former is more computationally efficient than the latter. An example of homogeneous delays:

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

If you have limited heterogeneity, you can use several Connection objects, e.g.:

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

For a highly heterogeneous set of delays, initialise the connection with `delay=True`, set a maximum delay with for example `max_delay=5*ms` and then use the `delay` keyword in the `connect_random()` and `connect_full()` methods:

```
myconnection=Connection(group1,group2,'ge',delay=True,max_delay=5*ms)
myconnection.connect_full(group1,group2,weight=3*nS,delay=(0*ms,5*ms))
```

The code above initialises the delays uniformly randomly between 0ms and 5ms. You can also set `delay` to be a function of no variables, where it will be called once for each synapse, or of two variables `i, j` where it will be called once for each row, as in the case of the weights in the section above.

Alternatively, you can set the delays as follows:

```
myconnection.delay[i,j] = 3*ms
```

See the reference documentation for `Connection` and `DelayConnection` for more details.

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')
```

The sparse matrix structure is fixed during a run, new synapses cannot be added or deleted, but there is a dynamic sparse matrix structure. It is less computationally efficient, but allows runtime adding and deleting of synaptic connections. Use the `structure='dynamic'` keyword. For more details see the reference documentation for `Connection`.

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.

4.3.6 Simple connections

If your connection just connects one group to another in a simple way, you can initialise the weights and delays at the time you initialise the `Connection` object by using the `weight`, `sparseness` and `delay` keywords. For example:

```
myconnection = Connection(group1, group2, 'ge', weight=1*nS, sparseness=0.1,
                          delay=(0*ms, 5*ms), max_delay=5*ms)
```

This would be equivalent to:

```
myconnection = Connection(group1, group2, 'ge', delay=True, max_delay=5*ms)
myconnection.connect_random(group1, group2, weight=1*nS, delay=(0*ms, 5*ms))
```

If the `sparseness` value is omitted or set to value 1, full connectivity is assumed, otherwise random connectivity.

NOTE: in this case the `delay` keyword used without the `weight` keyword has no effect.

4.4 Spike-timing-dependent plasticity

Synaptic weights can be modified by spiking activity. Weight modifications at a given synapse depend on the relative timing between presynaptic and postsynaptic spikes. Down to the biophysical level, there is a number of synaptic

variables which are continuously evolving according to some differential equations, and those variables can be modified by presynaptic and postsynaptic spikes. In spike-timing-dependent plasticity (STDP) rules, the synaptic weight changes at the times of presynaptic and postsynaptic spikes only, as a function of the other synaptic variables. In Brian, an STDP rule can be specified by defining an `STDP` object, as in the following example:

```
eqs_stdp='''
dA_pre/dt=-A_pre/tau_pre : 1
dA_post/dt=-A_post/tau_post : 1
'''
stdp=STDP(myconnection,eqs=eqs_stdp,pre='A_pre+=dA_pre;w+=A_post',
          post='A_post+=dA_post;w+=A_pre',wmax=gmax)
```

The `STDP` object acts on the `Connection` object `myconnection`. Equations of the synaptic variables are given in a string (argument `eqs`) as for defining neuron models. When a presynaptic (postsynaptic) spike is received, the code `pre` (`post`) is executed, where the special identifier `w` stands for the synaptic weight (from the specified connection matrix). Optionally, an upper limit can be specified for the synaptic weights (`wmax`).

The example above defines an exponential STDP rule with hard bounds and all-to-all pair interactions.

4.4.1 Current limitations

- The differential equations must be linear.
- Presynaptic and postsynaptic variables must not interact, that is, a variable cannot be modified by both presynaptic and postsynaptic spikes. However, synaptic weight modifications can depend on all variables.
- STDP currently works only with homogeneous delays, not heterogeneous ones.

Exponential STDP

In many applications, the STDP function is piecewise exponential. In that case, one can use the `ExponentialSTDP` class:

```
stdp=ExponentialSTDP(synapses,taup,taum,Ap,Am,wmax=gmax,interactions='all',update='additive')
```

Here the synaptic weight modification function is:

```
f(s) = Ap*exp(-s/taup) if s >0
       Am*exp(s/taum) if s <0
```

where s is the time of the postsynaptic spike minus the time of the presynaptic spike. The modification is generally relative to the maximum weight `wmax` (see below). The `interactions` keyword determines how pairs of pre/post synaptic spikes interact: `all` if contributions from all pairs are added, `nearest` for only nearest neighbour interactions, `nearest_pre` if only the nearest presynaptic spike and all postsynaptic spikes are taken into account and `nearest_post` for the symmetrical situation. The weight update can be `additive`, i.e., w=w+wmax*f(s), or `multiplicative`: w=w+w*f(s) for depression (usually s<0) and w=w+(wmax-w)*f(s) for potentiation (usually s>0). It can also be `mixed`: multiplicative for depression, additive for potentiation.

Delays

By default, transmission delays are assumed to be axonal, i.e., synapses are located on the soma: if the delay of the connection C is d, then presynaptic spikes act after a delay d while postsynaptic spikes act immediately. This behaviour can be overriden with the keywords `delay_pre` and `delay_post`, in both classes `STDP` and `Exponential STDP`.

4.5 Short-term plasticity

Brian implements the short-term plasticity model described in: Markram et al (1998). Differential signaling via the same axon of neocortical pyramidal neurons, PNAS 95(9):5323-8. Synaptic dynamics is described by two variables x and u, which follows the following differential equations:

```
dx/dt=(1-x)/taud   (depression)
du/dt=(U-u)/tauf   (facilitation)
```

where taud, tauf are time constants and U is a parameter in 0..1. Each a presynaptic spike triggers modifications of the variables:

```
x->x*(1-u)
u->u+U*(1-u)
```

Note that the update order is important. Synaptic weights are modulated by the product u*x (in 0..1), which is taken before updating the variables. This model describes both depression and facilitation.

To introduce short-term plasticity into an existing connection C, use the class `STP`:

```
mystp=STP(C,taud=100*ms,tauf=5*ms,U=.6)
```

4.6 Recording

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

4.6.1 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.

4.6.2 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. Means and variances are no longer recorded if you record traces.

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)
```

Recording spike triggered state values

You can record the value of a state variable at each spike using `StateSpikeMonitor`:

```
M = StateSpikeMonitor(group, 'V')
```

The `spikes` attribute of `M` consists of a series of tuples `(i,t,V)` where `V` is the value at the time of the spike.

Recording multiple state variables

You can either use multiple `StateMonitor` objects or use the `MultiStateMonitor` object:

```
M = MultiStateMonitor(group, record=True)
...
run(...)
...
plot(M['V'].times, M['V'][0])
figure()
for name, m in M.iteritems():
    plot(m.times, m[0], label=name)
legend()
show()
```

Recording only recent values

You can use the `RecentStateMonitor` object, e.g.:

```
G = NeuronGroup(1, 'dV/dt = xi/(10*ms)**0.5 : 1')
MR = RecentStateMonitor(G, 'V', duration=5*ms)
run(7*ms)
MR.plot()
show()
```

4.6.3 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.

4.6.4 Counting coincidences

To count the number of coincident spikes between the neurons of a group and given target spike trains, use a `CoincidenceCounter` object:

```
C=CoincidenceCounter(source=group, data=data, delta=delta)
```

`data` is a list of pairs (neuron_index, spike time), and delta is the time window in second. To get the number of coincidences for each neuron of the group, use

```
coincidences = C.coincidences
```

The gamma precision factor can be obtained with

```
gamma = C.gamma
```

4.6.5 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').

4.6.6 Van Rossum Metric

The Van Rossum metric can be computed by monitoring a group with a `VanRossumMetric` object:

```
M = VanRossumMetric(G, tau=4*ms)
...
imshow(M.distance)
```

4.7 Inputs

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

4.7.1 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)
```

4.7.2 Correlated inputs

Generation of correlated spike trains is partially implemented, using algorithms from the the following paper: Brette, R. (2009) Generation of correlated spike trains, Neural Computation 21(1): 188-215. Currently, only the method with Cox processes (or doubly stochastic processes, first method in the paper) is fully implemented.

Doubly stochastic processes

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 cross-covariance functions are *(c*r/tauc)*exp(-|s|/tauc)*. To generate correlated spike trains with arbitrary rates r(i) and cross-covariance functions *c(i,j)*exp(-|s|/tauc)*, use the class `CorrelatedSpikeTrains`:

```
group=CorrelatedSpikeTrains(rates,C,tauc)
```

where `rates` is the vector of rates r(i), `C` is the correlation matrix (which must be symmetrical) and `tauc` is the correlation time constant. Note that distortions are introduced with strong correlations and short correlation time constants. For short time constants, the mixture method is more appropriate (see the paper above). The two classes `HomogeneousCorrelatedSpikeTrains` and `CorrelatedSpikeTrains` define neuron groups, which can be directly used with `Connection` objects.

Mixture method

The mixture method to generate correlated spike trains is only partially implemented and the interface may change in future releases. Currently, one can use the function `mixture_process()` to generate spike trains:

```
spiketrains=mixture_process(nu,P,tauc,t)
```

where `nu` is the vector of rates of the source spike trains, `P` is the mixture matrix (entries between 0 and 1), `tauc` is the correlation time constant, `t` is the duration. It returns a list of (neuron_number,spike_time), which can be passed to `SpikeGeneratorGroup`. This method is appropriate for short time constants and is explained in the paper mentioned above.

4.7.3 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.

4.7.4 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-v)/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).

Time varying inputs

It is possible to change the value of I every timestep by using a user-defined operation (see next section). Alternatively, you can use a `TimedArray` to specify the values the variable will have at each time interval, for example:

```
eqs = '''
dv/dt = (I-v)/tau : volt
I : volt
'''
group = NeuronGroup(1, model=eqs, reset=0*mV, threshold=15*mV)
group.I = TimedArray(linspace(0*mV, 20*mV, 100), dt=10*ms)
```

Here `I` will have value `0*mV` for t between 0 and `10*ms`‘, ‘`0.2*mV` between `10*ms` and `20*ms`, and so on. A more intuitive syntax is:

```
I = TimedArray(linspace(0*mV, 20*mV, 100), dt=10*ms)
eqs = '''
dv/dt = (I(t)-v)/tau : volt
'''
group = NeuronGroup(1, model=eqs, reset=0*mV, threshold=15*mV)
```

Note however that the more efficient exact linear differential equations solver won’t be used in this case because `I(t)` could be any function, so the previous mechanism is often preferable.

Linked variables

Another option is to link the variable of one group to the variables of another group using `linked_var()`, for example:

```
G = NeuronGroup(...)
H = NeuronGroup(...)
G.V = linked_var(H, 'W')
```

In this scenario, the variable V in group G will always be updated with the values from variable W in group H. The groups G and H must be the same size (although subgroups can be used if they are not the same size).

4.8 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()
```

4.9 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()`. In addition, the `StateMonitor` object has a `plot()` method.

4.9.1 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.

4.9.2 State variable plots

State values recorded by a `StateMonitor` can also be plotted as follows:

```
M = StateMonitor(group, 'V', record=[0,1,2])
...
M.plot()
```

4.9.3 Realtime plotting

Both `raster_plot()` and `StateMonitor.plot()` have real-time versions which update as the simulation runs, for example:

```
G = NeuronGroup(...)
spikemon = SpikeMonitor(G)
statemon = StateMonitor(G, 'V', record=range(5))
ion()
subplot(211)
raster_plot(spikemon, refresh=10*ms, showlast=200*ms)
subplot(212)
statemon.plot(refresh=10*ms, showlast=200*ms)
run(1*second)
ioff()
show()
```

The `ion()` and `ioff()` command activate and deactivate Pylab's interactive plotting mode. The `refresh` parameter specifies how often (in simulation time) to refresh the plot - smaller values will slow down the simulation. The `showlast` option only plots the most recent values.

With some IDEs, you may need to do something like the following at the beginning of your script to make interactive mode work:

```
import matplotlib
matplotlib.use('WXAgg')
```

This is because the default graphical backend can sometimes interact badly with the IDE. Other options to try are `GTKAgg`, `QTAgg`, `TkAgg`.

4.9.4 Statistics

Here are a few functions to analyse first and second order statistical properties of spike trains, defined as ordered lists of spike times:

- Firing rate: `firing_rate(spikes)` where `spikes` is a spike train (list of spike times).
- Coefficient of variation: `CV(spikes)`.
- Cross-correlogram: `correlogram(T1,T2,width=20*ms,bin=1*ms,T=None)` returns the cross-correlogram of spike trains T1 and T2 with lag in [-width,width] and given bin size. T is the total duration (optional) and should be greater than the duration of T1 and T2. The result the rate of coincidences in each bin, returned as an array.
- Autocorrelogram: `autocorrelogram(T0,width=20*ms,bin=1*ms,T=None)` is the same as `correlogram(T0,T0,width=20*ms,bin=1*ms,T=None)`.
- Cross-correlation function: `CCF(T1,T2,width=20*ms,bin=1*ms,T=None)` returns the cross-correlation function of T1 and T2, which is the same as the cross-correlogram divided by the bin size (which makes the result independent of the bin size).
- Autocorrelation function: `ACF(T0,width=20*ms,bin=1*ms,T=None)`, same as `CCF(T0,T0,width=20*ms,bin=1*ms,T=None)`.
- Cross-covariance function: `CCVF(T1,T2,width=20*ms,bin=1*ms,T=None)` is the cross-correlation function of T1 and T2 minus for the cross-correlation of independent spike trains with the same rates (product of rates).
- Auto-covariance function: `ACVF(T0,width=20*ms,bin=1*ms,T=None)` is the same as `CCVF(T0,T0,width=20*ms,bin=1*ms,T=None)`.
- Total correlation coefficient: `total_correlation(T1,T2,width=20*ms,T=None)` is the integral of the cross-covariance function divided by the rate of T1, typically (but not always) between 0 and 1.
- Vector strength: `vector_strength(spikes,period)` returns the vector strength of the given spike train with respect to the period. If each spike time with phase phi is represented by a vector with angle phi, then the vector strength is the length of the average vector. It equals 1 for spikes with constant phase and 0 for homogeneous phase distributions.
- Gamma precision factor: `gamma_factor(source, target, delta)` returns the gamma precision factor between source and target trains, with precision delta.

These functions return NaN (not a number) when a spike train is empty.

4.10 Realtime control

A running Brian simulation can be controlled, for example using an IPython shell. This can work either on a single computer, or over IP from another computer. The process running the simulation calls something like:

```
server = RemoteControlServer()
```

and the IPython shell calls:

```
client = RemoteControlClient()
```

The shell can now execute and evaluate in the server process via:

```
spikes = client.evaluate('M.spikes')
i, t = zip(*spikes)
plot(t, i, '.')
client.stop()
```

Parameters can be changed as the simulation runs. For more details, see the reference documentation for `RemoteControlServer` and `RemoteControlClient`.

4.11 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`.

When using multiple clocks, it can be important to specify the order in which they evaluated, which you can using the `order` keyword of the `Clock` object, e.g.:

```
clock_first = Clock(dt=1*ms, order=0)
clock_second = Clock(dt=5*ms, order=1)
```

Every 5ms, these two clocks will coincide, and the order attribute means that `clock_first` will always be evaluated before `clock_second`.

4.11.1 Other clocks

The default clock uses an underlying integer representation. This behaviour was changed in Brian 1.3 from earlier versions which used a float representation. To recover the earlier behaviour if it is important, you can use `FloatClock` or `NaiveClock`.

You may want to have events that happen at regular times, but still want to use the default clock for all other objects, in which case you can use the `EventClock` for a `network_operation()` and it will not create any clock ambiguities, e.g.:

```
from brian import *

...

G = NeuronGroup(N, eqs, ...)

...

@network_operation(clock=EventClock(dt=1*second))
def do_something():
    ...
```

4.12 Simulation control

4.12.1 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')
```

4.12.2 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()`. The `run()` function also has some options for reporting the progress of the simulation as it runs, for example this will print out the elapsed time, percentage of the simulation this is complete, and an estimate of the remaining time every 10s:

```
run(100*second, report='text')
```

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, there are two options. The first is to create a `Network` object (see next section). The second is to use the `forget()` function on objects you want to exclude from being used. These can then be later added back using the `recall()` function.

Users of `ipython` may also want to make use of the `clear()` function which removes all Brian objects and deletes their data. This is useful because `ipython` keeps persistent references to these objects which stops memory from being freed.

4.12.3 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`.

4.12.4 The `MagicNetwork` object

When `run()`, `reinit()` and `stop()` are called, they act on the "magic network" (the network consisting of all relevant objects such as groups, connections, monitors and user operations). This "magic network" can be explicitly constructed using the `MagicNetwork` object:

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

4.13 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.

4.13.1 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.

4.13.2 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.

4.13.3 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.

4.13.4 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.

[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.

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.

4.13.5 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)
```

Important notice

It is not possible to modulate the noise term with a variable (e.g. `v*xi/tau**.5`). One reason is that, with multiplicative noise, there is an ambiguity between the Ito and the Stratonovich interpretation. Unfortunately, this limitation also applies to parameters, i.e., `sigma*xi/tau**.5` is not possible if sigma is a parameter, as in the following example:

```
eqs=Equations('''dx/dt=-x/tau + sigma*xi/tau**.5 : volt
                 sigma : volt''')
group = NeuronGroup(1, eqs, threshold='x>vt')
```

However, the problem can usually be solved by some rewriting:

```
eqs=Equations('''dy/dt=-y/tau + xi/tau**.5 : 1
                  x=sigma*y : volt
                  sigma : volt''')
group = NeuronGroup(1, eqs, threshold = 'x>vt')
```

4.13.6 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.

4.13.7 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.

4.13.8 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.

4.13.9 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.

4.14 File management

A few functions are provided to read files with common formats.

The function `read_neuron_dat()` reads a Neuron .dat text file and returns a vector of times and a vector of values. This is the format used by the Neuron simulator when saving the time-varying value of a variable from the GUI. For example:

```
t, v = read_neuron_dat('myfile.dat')
```

The function `read_atf()` reads an Axon .atf text file and returns a vector of times and a vector of values. This is a format used to store data recorded with Axon amplifiers. Note that metadata stored in the file are not extracted. Binary .abf files are currently not supported.

See also *Input/output*.

For more detailed information, see the reference chapter.

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 Compartmental modelling

Compartmental neuron models can be created by merging several `MembraneEquation` objects, with the `compartments` module. If `soma` and `dendrite` are two compartments defined as `MembraneEquation` objects, then a neuron with those 2 compartments can be created as follows:

```
neuron_eqs=Compartments({'soma':soma,'dendrite':dendrite})
neuron_eqs.connect('soma','dendrite',Ra)
neuron=NeuronGroup(1,model=neuron_eqs)
```

The `Compartments` object is initialised with a dictionary of `MembraneEquation` objects. The returned object `neuron_eqs` is also a `MembraneEquation` object, where the name of each compartment has been appended to variable names (with a leading underscore). For example, `neuron.vm_soma` refers to variable `vm` of the somatic compartment. The `connect` method adds a coupling current between the two named compartments, with the given resistance `Ra`.

5.1.3 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)
```

5.1.4 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
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))
```

5.1.5 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.

5.1.6 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

The electrophysiology library contains a number of models of electrodes, amplifiers and recording protocols to simulate intracellular electrophysiological recordings. To import the electrophysiology library:

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

There is a series of example scripts in the examples/electrophysiology folder.

5.3.1 Electrodes

Electrodes are defined as resistor/capacitor (RC) circuits, or multiple RC circuits in series. Define a simple RC electrode with resistance Re and capacitance Ce (possibly 0 pF) as follows:

```
el=electrode(Re,Ce)
```

The `electrode` function returns an `Equations` object containing the electrode model, where the electrode potential is `v_el` (the recording), the membrane potential is `vm`, the electrode current entering the membrane is `i_inj` and command current is `i_cmd`. These names can be overriden using the corresponding keywords. For example, a membrane equation with a .5 nA current injected through an electrode is defined as follows:

```
eqs=Equations('dv/dt=(-gl*v+i_inj)/Cm : volt')+electrode(50*Mohm,10*pF,vm='v',i_cmd=.5*nA)
```

Specify `i_cmd=None` if the electrode is only used to record (no current injection). More complex electrodes can be defined by passing lists of resistances and capacitances, e.g.:

```
el=electrode([50*Mohm,20*Mohm],[5*pF,3*pF])
```

5.3.2 Amplifiers

Current-clamp amplifier

A current-clamp amplifier injects a current through an intracellular electrode and records the membrane potential. Two standard circuits are included to compensate for the electrode voltage: bridge compensation and capacitance neutralization (see e.g. the Axon guide). The following command:

```
amp=current_clamp(Re=80*Mohm,Ce=10*pF)
```

defines a current-clamp amplifier with an electrode modelled as a RC circuit. The function returns an `Equations` object, where the recording potential is `v_rec`, the membrane potential is `vm`, the electrode current entering the membrane is `i_inj` and command current is `i_cmd`. These names can be overriden using the corresponding keywords. For implementation reasons, the amplifier always includes an electrode. Optionally, bridge compensation, can be used with the `bridge` keyword and capacitance neutralization with the `capa_comp` keyword. For example, the following instruction defines a partially compensated recording:

```
amp=current_clamp(Re=80*Mohm,Ce=10*pF,bridge=78*Mohm,capa_comp=8*pF)
```

The capacitance neutralization is a feedback circuit, so that it becomes unstable if the feedback capacitance is larger than the actual capacitance of the electrode. The bridge compensation is an input-dependent voltage offset (`bridge*i_cmd`), and thus is always stable (unless an additional feedback, such as dynamic clamp, is provided). Note that the bridge and capacitance neutralization parameters can be variable names, e.g.:

```
amp=current_clamp(Re=80*Mohm,Ce=10*pF,bridge='Rbridge',capa_comp=8*pF)
```

and then the bridge compensation can be changed dynamically during the simulation.

Voltage-clamp amplifier

The library includes a single-electrode voltage-clamp amplifier, which clamps the potential at a given value and records the current going through the electrode. The following command:

```
amp=voltage_clamp(Re=20*Mohm)
```

defines a voltage-clamp amplifier with an electrode modelled as a pure resistance. The function returns an `Equations` object, where the recording current is `i_rec`, the membrane potential is `vm`, the electrode current entering the membrane is `i_inj` and command voltage is `v_cmd` (note that `i_rec` = - `i_inj`). These names can be overriden using the corresponding keywords. For implementation reasons, the amplifier always includes an electrode. Electrode capacitance is not included, meaning that the capacitance neutralization circuit is always set at the maximum value. The quality of the clamp is limited by the electrode or ''series" resistance, which can be compensated in a similar way as bridge compensation in current-clamp recordings. Series resistance compensation consists in adding a current-dependent voltage offset to the voltage command. Because of the feedback, that compensation needs to be slightly delayed (with a low-pass circuit). The following example defines a voltage-clamp amplifier with half-compensated series resistance and compensation delay 1 ms:

```
amp=voltage_clamp(Re=20*Mohm,Rs=10*Mohm,tau_u=1*ms)
```

The `tau_u` keyword is optional and defaults to 1 ms.

Acquisition board

An acquisition board samples a recording and sends a command (e.g. injected current) at regular times. It is defined as a `NeuronGroup`. Use:

```
board=AcquisitionBoard(P=neuron,V='V',I='I',clock)
```

where `P` = neuron group (possibly containing amplifier and electrode), `V` = potential variable name, `I` = current variable name, `clock` = acquisition clock. The recording variable is then stored in `board.record` and a command is sent with the instruction `board.command=I`.

Discontinuous current clamp

The discontinuous current clamp (DCC) consists in alternatively injecting current and measuring the potential, in order to measure the potential when the voltage across the electrode has vanished. The sampling clock is mainly determined by the electrode time constant (the sampling period should be two orders of magnitude larger than the electrode time constant). It is defined and used in the same way as an acquisition board (above):

```
board=DCC(P=neuron,V='V',I='I',frequency=2*kHz)
```

where `frequency` is the sampling frequency. The duty cycle is 1/3 (meaning current is injected during 1/3 of each sampling step).

Discontinuous voltage clamp

The discontinuous voltage clamp or single-electrode voltage clamp (SEVC) is an implementation of the voltage clamp using a feedback current with a DCC amplifier. It is defined as the DCC:

```
board=SEVC(P=neuron,V='V',I='I',frequency=2*kHz,gain=10*nS)
```

except that a gain parameter is included. The SEVC injects a negative feedback current I=gain*(Vcommand-V). The quality of the clamp improves with higher gains, but there is a maximum value above which the system is unstable, because of the finite temporal resolution. The recorded current is stored in `board.record` and the command voltage is

sent with the instruction `board.command=-20*mV`. With this implementation of the SEVC, the membrane is never perfectly clamped. A better clamp is obtained by adding an integral controller with the keyword `gain2=10*nS/ms`. The additional current J(t) is governed by the differential equation dJ/dt=gain2*(Vcommand-V), so that it ensures perfect clamping in the stationary state. However, this controller does not improve the settling time of the clamp, but only the final voltage value.

5.3.3 Active Electrode Compensation (AEC)

The electrophysiology library includes the Active Electrode Compensation (AEC) technique described in Brette et al (2008), High-resolution intracellular recordings using a real-time computational model of the electrode, Neuron 59(3):379-91.

Offline AEC

Given a digital current-clamp recording of the (uncompensated) potential `v` (vector of values) and injected current `i`, the following instructions calculate the full kernel of the system and the electrode kernel:

```
K=full_kernel(v,i,ksize)
Ke=electrode_kernel_soma(K,start_tail)
```

`ksize` is the size of the full kernel (number of sampling steps; typical size is about 15 ms) and `start_tail` is the size of the electrode kernel (start point of the ''tail" of the full kernel; typical size if about 4 ms). The electrode should be compensated for capacitance (capacitance neutralization) but not resistance (bridge compensation). The best choice for the input current is a series of independent random values, and the last `ksize` steps of `v` should be null (i.e., the injection should stop before the end). Here it was assumed that the recording was done at the soma; if it is done in a thin process such as a dendrite or axon, the function `electrode_kernel_dendrite` should be used instead. The full kernel can also be obtained from a step current injection:

```
K=full_kernel_from_step(v,i,ksize)
Ke=electrode_kernel_soma(K,start_tail)
```

where `i` is a constant value in this case (note that this is not the best choice for real recordings).

Once the electrode kernel has been found, any recording can be compensated as follows:

```
vcomp=AEC_compensate(v,i,ke)
```

where `v` is the raw voltage recording, `i` is the injected current and `ke` is the electrode kernel.

Online AEC

For dynamic-clamp or voltage-clamp recordings, the electrode compensation must be done online. An AEC board is initialized in the same way as an acquisition board:

```
board=AEC(neuron,'V','I',clock)
```

where `clock` is the acquisition clock. The estimation phase typically looks like:

```
board.start_injection()
run(2*second)
board.start_injection()
run(100*ms)
board.estimate()
```

where white noise is injected for 2 seconds (default amplitude .5 nA). You can change the default amplitude and DC current as follows: `board.start_injection(amp=.5*nA,DC=1*nA)`. After estimation, the kernel is stored in `board.Ke`. The following options can be passed to the function `estimate`: `ksize` (default 150 sampling steps), `ktail` (default 50 sampling steps) and `dendritic` (default `False`, use `True` is the recording is a thin process, i.e., axon or dendrite). Online compensation is then switched on with `board.switch_on()` and off with `board.switch_off()`. For example, to inject a .5 nA current pulse for 200 ms, use the following instructions:

```
board.switch_on()
board.command=.5*nA
run(200*ms)
board.command=0*nA
run(150*ms)
board.switch_off()
```

During the simulation, the variable `board.record` stores the compensated potential.

Voltage-clamp with AEC

To be documented!

5.4 Model fitting

The modelfitting library is used for fitting a neuron model to data.

The library provides a single function `modelfitting()`, which accepts the model and the data as arguments and returns the model parameters that fit best the data. The model is a spiking neuron model, whereas the data consists of both an input (time-varying signal, for example an injected current) and a set of spike trains. Only spikes are considered for the fitness. Several target spike trains can be specified in order to fit independently several data sets. In this case, the `modelfitting()` function returns as many parameters sets as there are target spike trains.

The model is defined as any spiking neuron model in Brian, by giving the equations as mathematical equations, and the reset and threshold values. The free parameters of the model that shall be fitted by the library are also specified. The data is specified by the input (a vector containing the time-varying injected current), the timestep of the input, and the data as a list of spike times.

5.4.1 How it works

Fitting a spiking neuron model to electrophysiological data is performed by maximizing a fitness function measuring the adequacy of the model to the data. This function is defined as the gamma factor, which is based on the number of coincidences between the model spikes and the experimentally-recorded spikes, defined as the number of spikes in the experimental train such that there is at least one spike in the model train within plus or minus `delta`, where `delta` is the size of the temporal window (typically a few milliseconds). For more details on the gamma factor, see Jolivet et al. 2008, "A benchmark test for a quantitative assessment of simple neuron models", J. Neurosci. Methods (available in PDF here).

The optimization procedure is performed by an optimization algorithm. The optimization toolbox used by modelfitting is implemented in the external Python package Playdoh. It also supports distributed and parallel optimization across CPUs and machines. Different optimization algorithms are supported, the default one is `CMAES`. All those algorithms require the evaluation of the fitness function for a large number of parameter sets. Each iteration of the algorithm involves the simulation of a large number of neurons (one neuron corresponding to one parameter set) as well as the computation of the gamma factor for each neuron. The quality of the result depends on the number of neurons used, which is specified in the `modelfitting()` function.

Playdoh supports the use of graphical processing units (GPUs) in order to accelerate the speed of convergence of the algorithm. If multiple cores are detected, the library will use all of them by default. Also, if a CUDA-enabled GPU is present on the system, and if PyCUDA is installed, the library will automatically use the GPU by default. In addition, several computers can be networked over IP, see *Clusters*.

5.4.2 Usage example

To import the library, use

```
from brian.library.modelfitting import *
```

To fit the parameters of a neuron model with respect to some data, use the `modelfitting()` function

```
results = modelfitting(model = equations, reset = 0, threshold = 1,
                       data = spikes,
                       input = input, dt = .1*ms,
                       popsize = 1000, maxiter = 10,
                       R = [1.0e9, 1.0e10], tau = [1*ms, 50*ms])

print_table(results)
```

Warning: Windows users should read the section *Important note for Windows users*.

The model is defined by `equations` (an `Equations` object), `reset` (a scalar value or a set of equations as a string) and `threshold` (a scalar value or a set of equations as a string).

The target spike trains are defined by `data` (a list of pairs `(neuron index, spike time)` or a list of spike times if there is only one target spike train).

The input is specified with `input` (a vector containing the time-varying signal) and `dt` (the time step of the signal). The input variable should be `I` in the equations, although the input variable name can be specified with `input_var`.

The number of particles per target train used in the optimization algorithm is specified with `popsize`. The total number of neurons is `popsize` multiplied by the number of target spike trains. The number of iterations in the algorithm is specified with `maxiter`.

Each free parameter of the model that shall be fitted is defined by two values

```
param_name = [min, max]
```

`param_name` should correspond to the parameter name in the model equations. `min` and `max` specify the initial interval from which the parameter values will be uniformly sampled at the beginning of the optimization algorithm. A boundary interval can also be specified by giving four values

```
param_name = [bound_min, min, max, bound_max]
```

The parameter values will be forced to stay inside the interval [bound_min, bound_max] during the optimization.

The complete list of arguments can be found in the reference section of the `modelfitting()` function.

The best parameters and the corresponding best fitness values found by the optimization procedure are returned in the `OptimizationResult` object `result`.

5.4.3 Important note for Windows users

The model fitting library uses the Python multiprocessing package to distribute fitting across processors in a single computer or across multiple computers. However, there is a limitation of the Windows version of multiprocessing which you can read about here. The end result is that a script like this:

```
from brian.library.modelfitting import *
...
results = modelfitting(...)
```

will crash, going into an endless loop and creating hundreds of Python processes that have to be shut down by hand. Instead, you have to do this:

```
from brian.library.modelfitting import *
...
if __name__=='__main__':
        results = modelfitting(...)
```

5.4.4 Clusters

The model fitting package can be used with a cluster of computers connected over IP. Every computer must have Brian and Playdoh installed, and they must run the Playdoh server: see the Playdoh documentation. Then, you can launch the `modelfitting` function with the `machines` keyword, which is the list of the IP addresses of the machines to use in parallel for the fitting procedure. You must also specify the `unit_type` keyword, which is `CPU` or `GPU`, to indicate whether you want to use CPUs or GPUs on these computers. You can't mix CPUs and GPUs for the same optimization.

IP

To connect several machines via IP, pass a list of host names or IP addresses as strings to the `machines` keyword of the `modelfitting()` function. To specify a specific port, use a tuple `(IP, port)` instead of a string. You can also specify a default port in the Playdoh user preferences, see the Playdoh documentation.

Authentication

You can specify an authentication string on all the computers running the Playdoh server to secure communications. See the Playdoh documentation.

Example

The following script launches a fitting procedure in parallel on two machines:

```
from brian import loadtxt, ms, Equations
from brian.library.modelfitting import *

if __name__ == '__main__':
    # List of machines IP addresses
    machines = ['bobs-machine.university.com',
                'jims-machine.university.com']

    equations = Equations('''
        dV/dt=(R*I-V)/tau : 1
        I : 1
        R : 1
        tau : second
    ''')
    input = loadtxt('current.txt')
    spikes = loadtxt('spikes.txt')
    results = modelfitting( model = equations,
```

```
                                reset = 0,
                                threshold = 1,
                                data = spikes,
                                input = input,
                                dt = .1*ms,
                                popsize = 1000,
                                maxiter = 3,
                                delta = 4*ms,
                                unit_type = 'CPU',
                                machines = machines,
                                R = [1.0e9, 9.0e9],
                                tau = [10*ms, 40*ms],
                                refractory = [0*ms, 10*ms])
    print_table(results)
```

The two remote machines would run the Playdoh server.

5.5 Brian hears

Brian hears is an auditory modelling library for Python. It is part of the neural network simulator package Brian, but can also be used on its own. To download Brian hears, simply *download Brian*: Brian hears is included as part of the package.

Brian hears is primarily designed for generating and manipulating sounds, and applying large banks of filters. We import the package by writing:

```
from brian import *
from brian.hears import *
```

Then, for example, to generate a tone or a whitenoise we would write:

```
sound1 = tone(1*kHz, .1*second)
sound2 = whitenoise(.1*second)
```

These sounds can then be manipulated in various ways, for example:

```
sound = sound1+sound2
sound = sound.ramp()
```

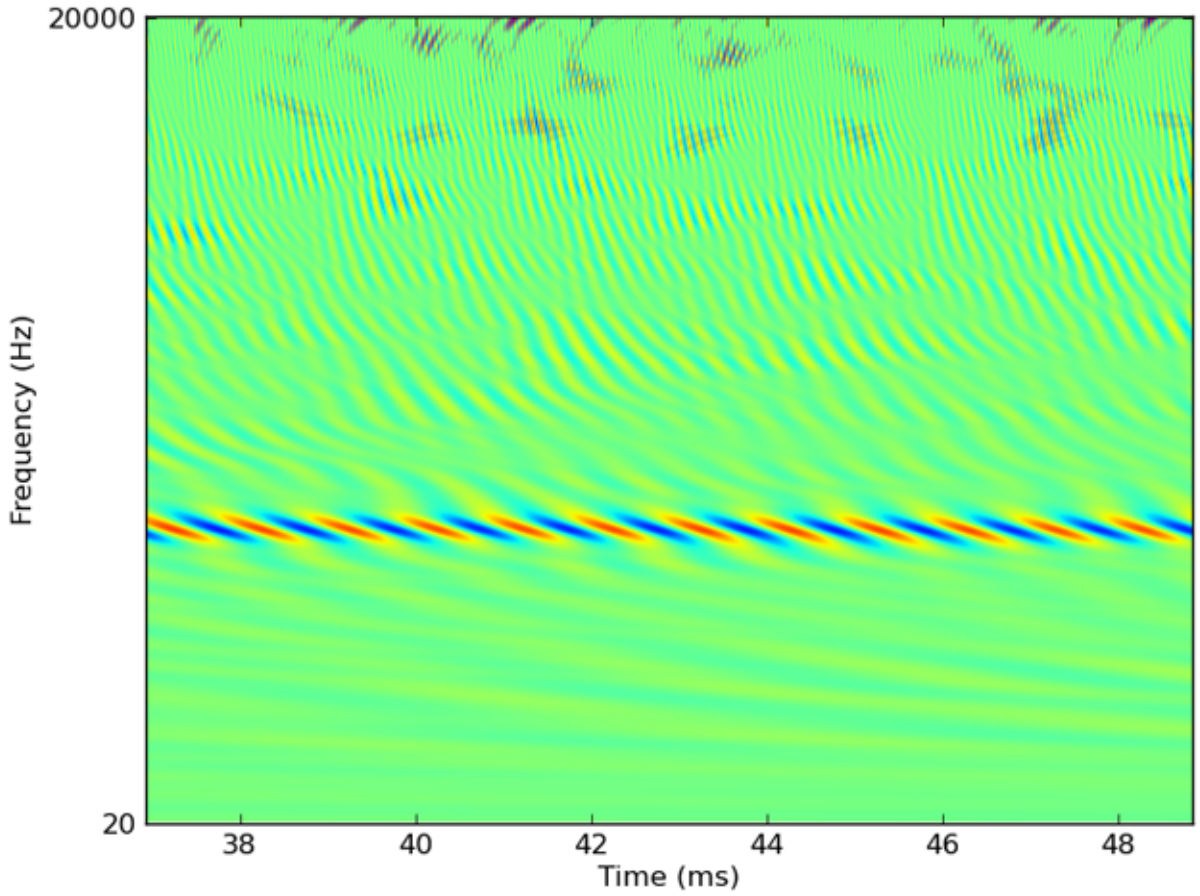
If you have the pygame package installed, you can also play these sounds:

```
sound.play()
```

We can filter these sounds through a bank of 3000 gammatone filters covering the human auditory range as follows:

```
cf = erbspace(20*Hz, 20*kHz, 3000)
fb = Gammatone(sound, cf)
output = fb.process()
```

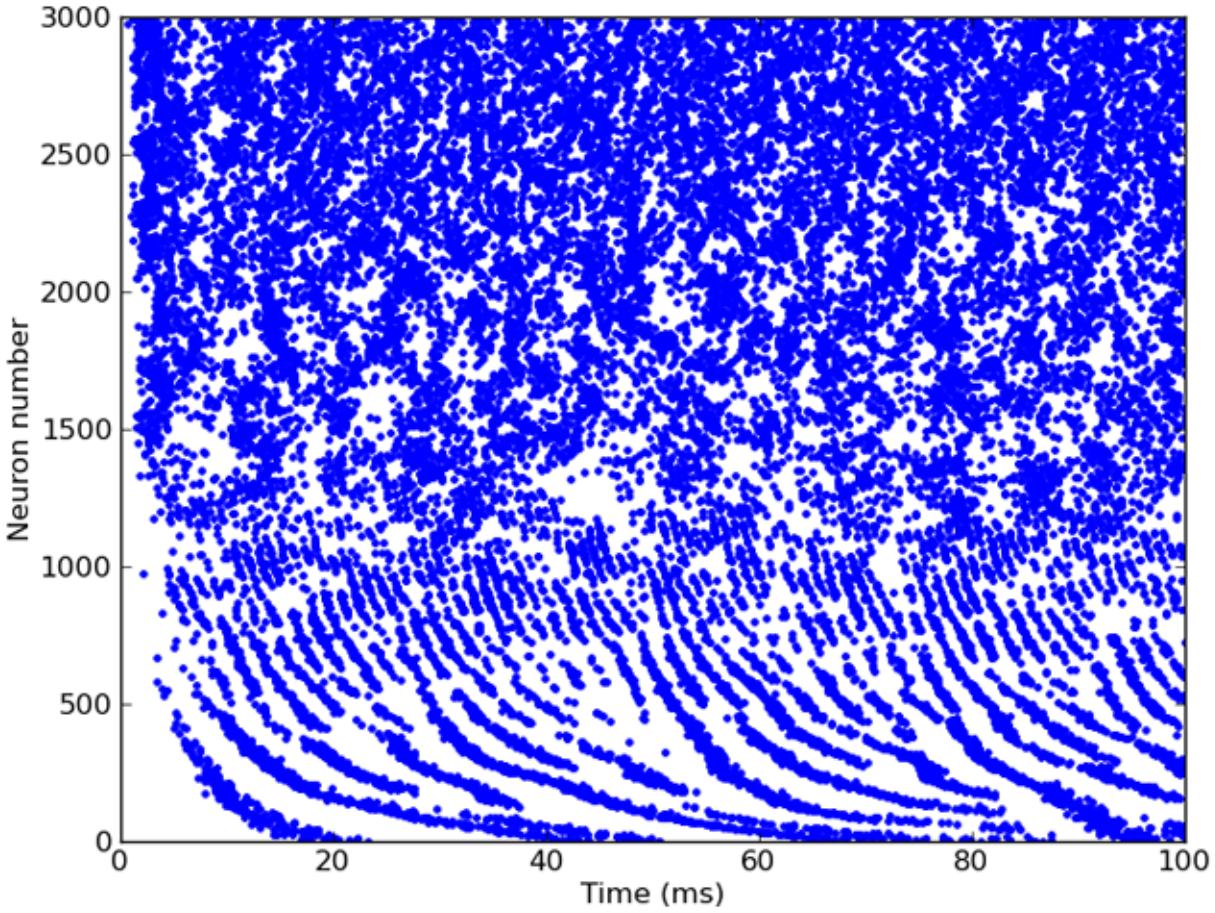
The output of this would look something like this (zoomed into one region):



Alternatively, if we're interested in modelling auditory nerve fibres, we could feed the output of this filterbank directly into a group of neurons defined with Brian:

```
# Half-wave rectification and compression [x]^(1/3)
ihc = FunctionFilterbank(fb, lambda x: 3*clip(x, 0, Inf)**(1.0/3.0))
# Leaky integrate-and-fire model with noise and refractoriness
eqs = '''
dv/dt = (I-v)/(1*ms)+0.2*xi*(2/(1*ms))**.5 : 1
I : 1
'''
anf = FilterbankGroup(ihc, 'I', eqs, reset=0, threshold=1, refractory=5*ms)
```

This model would give output something like this:



The human cochlea applies the equivalent of 3000 auditory filters, which causes a technical problem for modellers which this package is designed to address. At a typical sample rate, the output of 3000 filters would saturate the computer's RAM in a few seconds. To deal with this, we use online computation, that is we only ever keep in memory the output of the filters for a relatively short duration (say, the most recent 20ms), do our modelling with these values, and then discard them. Although this requires that some models be rewritten for online rather than offline computation, it allows us to easily handle models with very large numbers of channels. 3000 or 6000 for human monaural or binaural processing is straightforward, and even much larger banks of filters can be used (for example, around 30,000 in Goodman DFM, Brette R (2010). Spike-timing-based computation in sound localization. PLoS Comput. Biol. 6(11): e1000993. doi:10.1371/journal.pcbi.1000993). Techniques for online computation are discussed below in the section Online computation.

Brian hears consists of classes and functions for defining sounds, filter chains, cochlear models, neuron models and head-related transfer functions. These classes are designed to be modular and easily extendable. Typically, a model will consist of a chain starting with a sound which is plugged into a chain of filter banks, which are then plugged into a neuron model.

The two main classes in Brian hears are `Sound` and `Filterbank`, which function very similarly. Each consists of multiple channels (typically just 1 or 2 in the case of sounds, and many in the case of filterbanks, but in principle any number of channels is possible for either). The difference is that a filterbank has an input source, which can be either a sound or another filterbank.

All scripts using Brian hears should start by importing the Brian and Brian hears packages as follows:

```
from brian import *
from brian.hears import *
```

To download Brian hears, simply *download Brian*: Brian hears is included as part of the package.

See Also:

Reference documentation for *Brian hears*, which covers everything in this overview in detail, and more. List of *examples of using Brian hears*.

5.5.1 Sounds

Sounds can be loaded from a WAV or AIFF file with the `loadsound()` function (and saved with the `savesound()` function or `Sound.save()` method), or by initialising with a filename:

```
sound = loadsound('test.wav')
sound = Sound('test.aif')
sound.save('test.wav')
```

Various standard types of sounds can also be constructed, e.g. pure tones, white noise, clicks and silence:

```
sound = tone(1*kHz, 1*second)
sound = whitenoise(1*second)
sound = click(1*ms)
sound = silence(1*second)
```

You can pass a function of time or an array to initialise a sound:

```
# Equivalent to Sound.tone
sound = Sound(lambda t:sin(50*Hz*2*pi*t), duration=1*second)

# Equivalent to Sound.whitenoise
sound = Sound(randn(int(1*second*44.1*kHz)), samplerate=44.1*kHz)
```

Multiple channel sounds can be passed as a list or tuple of filenames, arrays or `Sound` objects:

```
sound = Sound(('left.wav', 'right.wav'))
sound = Sound((randn(44100), randn(44100)), samplerate=44.1*kHz)
sound = Sound((Sound.tone(1*kHz, 1*second),
               Sound.tone(2*kHz, 1*second)))
```

A multi-channel sound is also a numpy array of shape `(nsamples, nchannels)`, and can be initialised as this (or converted to a standard numpy array):

```
sound = Sound(randn(44100, 2), samplerate=44.1*kHz)
arr = array(sound)
```

Sounds can be added and multiplied:

```
sound = Sound.tone(1*kHz, 1*second)+0.1*Sound.whitenoise(1*second)
```

For more details on combining and operating on sounds, including shifting them in time, repeating them, resampling them, ramping them, finding and setting intensities, plotting spectrograms, etc., see `Sound`.

Sounds can be played using the `play()` function or `Sound.play()` method:

```
play(sound)
sound.play()
```

Sequences of sounds can be played as:

```
play(sound1, sound2, sound3)
```

The number of channels in a sound can be found using the `nchannels` attribute, and individual channels can be extracted using the `Sound.channel()` method, or using the `left` and `right` attributes in the case of stereo sounds:

```
print sound.nchannels
print amax(abs(sound.left-sound.channel(0)))
```

As an example of using this, the following swaps the channels in a stereo sound:

```
sound = Sound('test_stereo.wav')
swappedsound = Sound((sound.right, sound.left))
swappedsound.play()
```

The level of the sound can be computed and changed with the `sound.level` attribute. Levels are returned in dB which is a special unit in Brian hears. For example, `10*dB+10` will raise an error because `10` does not have units of dB. The multiplicative gain of a value in dB can be computed with the function `gain(level)`. All dB values are measured as RMS dB SPL assuming that the values of the sound object are measured in Pascals. Some examples:

```
sound = whitenoise(100*ms)
print sound.level
sound.level = 60*dB
sound.level += 10*dB
sound *= gain(-10*dB)
```

5.5.2 Filter chains

The standard way to set up a model based on filterbanks is to start with a sound and then construct a chain of filterbanks that modify it, for example a common model of cochlear filtering is to apply a bank of gammatone filters, and then half wave rectify and compress it (for example, with a 1/3 power law). This can be achieved in Brian hears as follows (for 3000 channels in the human hearing range from 20 Hz to 20 kHz):

```
cfmin, cfmax, cfN = 20*Hz, 20*kHz, 3000
cf = erbspace(cfmin, cfmax, cfN)
sound = Sound('test.wav')
gfb = GammatoneFilterbank(sound, cf)
ihc = FunctionFilterbank(gfb, lambda x: clip(x, 0, Inf)**(1.0/3.0))
```

The `erbspace()` function constructs an array of centre frequencies on the ERB scale. The `GammatoneFilterbank(source, cf)` class creates a bank of gammatone filters with inputs coming from `source` and the centre frequencies in the array `cf`. The `FunctionFilterbank(source, func)` creates a bank of filters that applies the given function `func` to the inputs in `source`.

Filterbanks can be added and multiplied, for example for creating a linear and nonlinear path, e.g.:

```
sum_path_fb = 0.1*linear_path_fb+0.2*nonlinear_path_fb
```

A filterbank must have an input with either a single channel or an equal number of channels. In the former case, the single channel is duplicated for each of the output channels. However, you might want to apply gammatone filters to a stereo sound, for example, but in this case it's not clear how to duplicate the channels and you have to specify it explicitly. You can do this using the `Repeat`, `Tile`, `Join` and `Interleave` filterbanks. For example, if the input is a stereo sound with channels LR then you can get an output with channels LLLRRR or LRLRLR by writing (respectively):

```
fb = Repeat(sound, 3)
fb = Tile(sound, 3)
```

To combine multiple filterbanks into one, you can either join them in series or interleave them, as follows:

```
fb = Join(source1, source2)
fb = Interleave(source1, source2)
```

For a more general (but more complicated) approach, see RestructureFilterbank.

Two of the most important generic filterbanks (upon which many of the others are based) are LinearFilterbank and FIRFilterbank. The former is a generic digital filter for FIR and IIR filters. The latter is specifically for FIR filters. These can be implemented with the former, but the implementation is optimised using FFTs with the latter (which can often be hundreds of times faster, particularly for long impulse responses). IIR filter banks can be designed using IIRFilterbank which is based on the syntax of the iirdesign scipy function.

You can change the input source to a Filterbank by modifying its source attribute, e.g. to change the input sound of a filterbank fb you might do:

```
fb.source = newsound
```

Note that the new source should have the same number of channels.

You can implement control paths (using the output of one filter chain path to modify the parameters of another filter chain path) using ControlFilterbank (see reference documentation for more details). For examples of this in action, see the following:

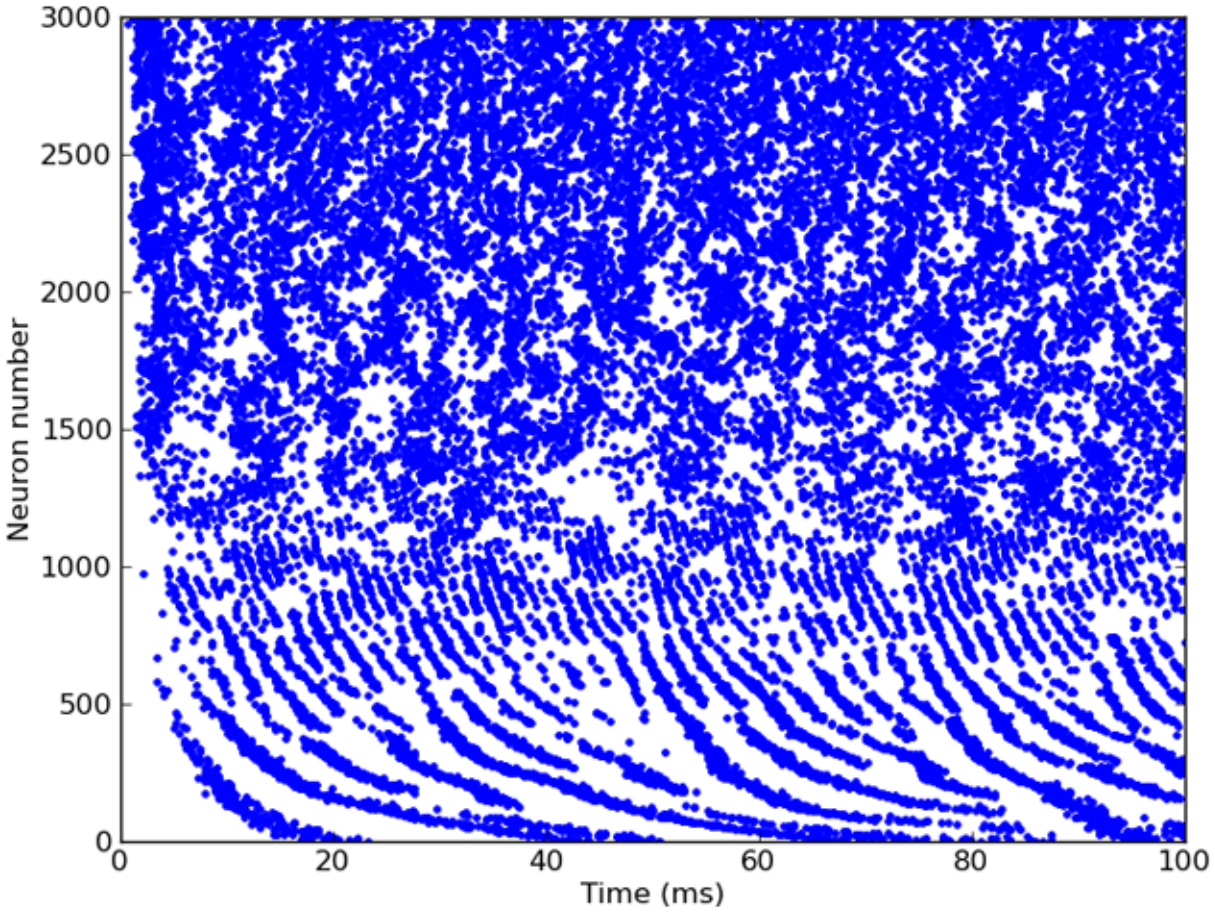
- *Example: time_varying_filter1 (hears)*.
- *Example: time_varying_filter2 (hears)*.
- *Example: dcgc (hears)*.

5.5.3 Connecting with Brian

To create spiking neuron models based on filter chains, you use the FilterbankGroup class. This acts exactly like a standard Brian NeuronGroup except that you give a source filterbank and choose a state variable in the target equations for the output of the filterbank. A simple auditory nerve fibre model would take the inner hair cell model from earlier, and feed it into a noisy leaky integrate-and-fire model as follows:

```
# Inner hair cell model as before
cfmin, cfmax, cfN = 20*Hz, 20*kHz, 3000
cf = erbspace(cfmin, cfmax, cfN)
sound = Sound.whitenoise(100*ms)
gfb = GammatoneFilterbank(sound, cf)
ihc = FunctionFilterbank(gfb, lambda x: 3*clip(x, 0, Inf)**(1.0/3.0))
# Leaky integrate-and-fire model with noise and refractoriness
eqs = '''
dv/dt = (I-v)/(1*ms)+0.2*xi*(2/(1*ms))**.5 : 1
I : 1
'''
G = FilterbankGroup(ihc, 'I', eqs, reset=0, threshold=1, refractory=5*ms)
# Run, and raster plot of the spikes
M = SpikeMonitor(G)
run(sound.duration)
raster_plot(M)
show()
```

And here's the output (after 6 seconds of computation on a 2GHz laptop):



5.5.4 Online computation

Typically in auditory modelling, we precompute the entire output of each channel of the filterbank ("offline computation"), and then work with that. This is straightforward, but puts a severe limit on the number of channels we can use or the length of time we can work with (otherwise the RAM would be quickly exhausted). Brian hears allows us to use a very large number of channels in filterbanks, but at the cost of only storing the output of the filterbanks for a relatively short period of time ("online computation"). This requires a slight change in the way we use the output of the filterbanks, but is actually not too difficult. For example, suppose we wanted to compute the vector of RMS values for each channel of the output of the filterbank. Traditionally, or if we just use the syntax `output = fb.process()` in Brian hears, we have an array `output` of shape `(nsamples, nchannels)`. We could compute the vector of RMS values as:

```
rms = sqrt(mean(output**2, axis=0))
```

To do the same thing with online computation, we simply store a vector of the running sum of squares, and update it for each buffered segment as it is computed. At the end of the processing, we divide the sum of squares by the number of samples and take the square root.

The `Filterbank.process()` method allows us to pass an optional function `f(output, running)` of two arguments. In this case, `process()` will first call `running = f(output, 0)` for the first buffered segment `output`. It will then call `running = f(output, running)` for each subsequent segment. In other words, it will "accumulate" the output of `f`, passing the output of each call to the subsequent call. To compute the vector of RMS values then, we simply do:

```
def sum_of_squares(input, running):
    return running+sum(input**2, axis=0)

rms = sqrt(fb.process(sum_of_squares)/nsamples)
```

If the computation you wish to perform is more complicated than can be achieved with the `process()` method, you can derive a class from `Filterbank` (see that class' reference documentation for more details on this).

5.5.5 Buffering interface

The `Sound`, `OnlineSound` and `Filterbank` classes (and all classes derived from them) all implement the same buffering mechanism. The purpose of this is to allow for efficient processing of multiple channels in buffers. Rather than precomputing the application of filters to all channels (which for large numbers of channels or long sounds would not fit in memory), we process small chunks at a time. The entire design of these classes is based on the idea of buffering, as defined by the base class `Bufferable` (see section *Options*). Each class has two methods, `buffer_init()` to initialise the buffer, and `buffer_fetch(start, end)` to fetch the portion of the buffer from samples with indices from `start` to `end` (not including `end` as standard for Python). The `buffer_fetch(start, end)` method should return a 2D array of shape `(end-start, nchannels)` with the buffered values.

From the user point of view, all you need to do, having set up a chain of `Sound` and `Filterbank` objects, is to call `buffer_fetch(start, end)` repeatedly. If the output of a `Filterbank` is being plugged into a `FilterbankGroup` object, everything is handled automatically. For cases where the number of channels is small or the length of the input source is short, you can use the `Filterbank.fetch(duration)()` method to automatically handle the initialisation and repeated application of `buffer_fetch`.

To extend `Filterbank`, it is often sufficient just to implement the `buffer_apply(input)` method. See the documentation for `Filterbank` for more details.

5.5.6 Library

Brian hears comes with a package of predefined filter classes to be used as basic blocks by the user. All of them are implemented as filterbanks.

First, a series of standard filters widely used in audio processing are available:

Class	Descripition	Example
`IIRFilterbank`	Bank of low, high, bandpass or bandstop filter of type Chebyshef, Elliptic, etc...	*Example: IIRfilterbank (hears)*
`Butterworth`	Bank of low, high, bandpass or bandstop Butterworth filters	*Example: butterworth (hears)*
`LowPass`	Bank of lowpass filters of order 1	*Example: cochleagram (hears)*

Second, the library provides linear auditory filters developed to model the frequency analysis of the cochlea:

Class	Description	Example
Gammatone	Bank of IIR gammatone filters (based on Slaney implementation)	*Example: gammatone (hears)*
ApproximateGammatone	Bank of IIR gammatone filters (based on Hohmann implementation)	*Example: approximate_gammatone (hears)*
LogGammachirp	Bank of IIR gammachirp filters with logarithmic sweep (based on Irino implementation)	*Example: log_gammachirp (hears)*
LinearGammachirp	Bank of FIR chirp filters with linear sweep and gamma envelope	*Example: linear_gammachirp (hears)*
LinearGaborchirp	Bank of FIR chirp filters with linear sweep and gaussian envelope	

Finally, Brian hears comes with a series of complex nonlinear cochlear models developed to model nonlinear effects such as filter bandwith level dependency, two-tones suppression, peak position level dependency, etc.

Class	Description	Example
DRNL	Dual resonance nonlinear filter as described in Lopez-Paveda and Meddis, JASA 2001	*Example: drnl (hears)*
DCGC	Compressive gammachirp auditory filter as described in Irino and Patterson, JASA 2001	*Example: dcgc (hears)*

5.5.7 Head-related transfer functions

You can work with head-related transfer functions (HRTFs) using the three classes `HRTF` (a single pair of left/right ear HRTFs), `HRTFSet` (a set of HRTFs, typically for a single individual), and `HRTFDatabase` (for working with databases of individuals). At the moment, we have included only one HRTF database, the `IRCAM_LISTEN` public HRTF database. However, we will add support for the CIPIC and MIT-KEMAR databases in a subsequent release. There is also one artificial HRTF database, `HeadlessDatabase` used for generating HRTFs of artifically introduced ITDs.

An example of loading the IRCAM database, selecting a subject and plotting the pair of impulse responses for a particular direction:

```
hrtfdb = IRCAM_LISTEN(r'F:\HRTF\IRCAM')
hrtfset = hrtfdb.load_subject(1002)
hrtf = hrtfset(azim=30, elev=15)
plot(hrtf.left)
plot(hrtf.right)
show()
```

`HRTFSet` has a set of coordinates, which can be accessed via the `coordinates` attribute, e.g.:

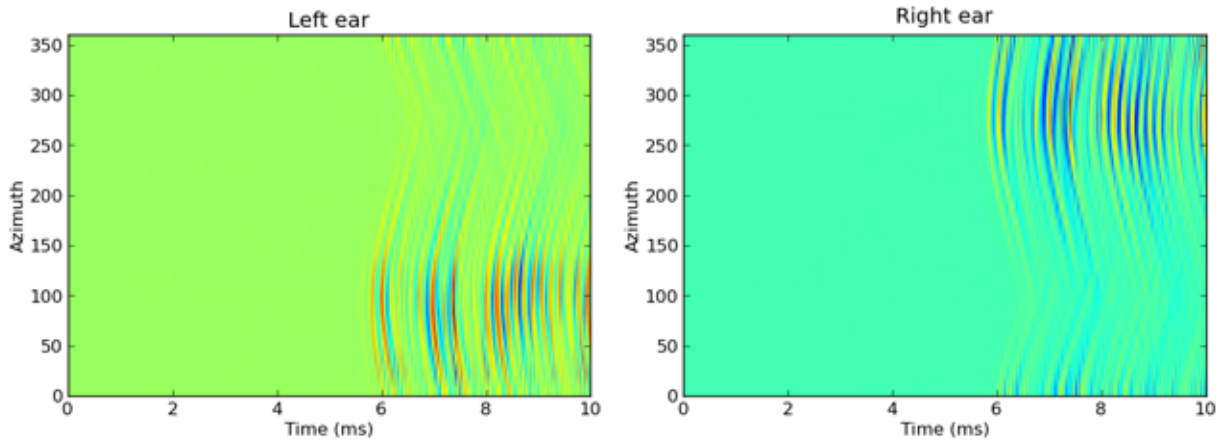
```
print hrtfset.coordinates['azim']
print hrtfset.coordinates['elev']
```

You can also generated filterbanks associated either to an `HRTF` or an entire `HRTFSet`. Here is an example of doing this with the IRCAM database, and applying this filterbank to some white noise and plotting the response as an image:

```
# Load database
hrtfdb = IRCAM_LISTEN(r'D:\HRTF\IRCAM')
hrtfset = hrtfdb.load_subject(1002)
# Select only the horizontal plane
hrtfset = hrtfset.subset(lambda elev: elev==0)
# Set up a filterbank
sound = whitenoise(10*ms)
fb = hrtfset.filterbank(sound)
```

```
# Extract the filtered response and plot
img = fb.process().T
img_left = img[:img.shape[0]/2, :]
img_right = img[img.shape[0]/2:, :]
subplot(121)
imshow(img_left, origin='lower left', aspect='auto',
       extent=(0, sound.duration/ms, 0, 360))
xlabel('Time (ms)')
ylabel('Azimuth')
title('Left ear')
subplot(122)
imshow(img_right, origin='lower left', aspect='auto',
       extent=(0, sound.duration/ms, 0, 360))
xlabel('Time (ms)')
ylabel('Azimuth')
title('Right ear')
show()
```

This generates the following output:



For more details, see the reference documentation for HRTF, HRTFSet, HRTFDatabase, IRCAM_LISTEN and HeadlessDatabase.

CHAPTER

SIX

ADVANCED CONCEPTS

6.1 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. For more performance tips, see also *Compiled code*.

6.1.1 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.

6.1.2 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.

6.2 Compiled code

Compiled C code can be used in several places in Brian to get speed improvements in cases where performance is the most important factor.

6.2.1 Weave

Weave is a SciPy module that allows the use of inlined C++ code. Brian by default doesn't use any C++ optimisations for maximum compatibility across platforms, but you can enable several optimised versions of Brian objects and functions by enabling weave compilation. See *Preferences* for more information.

See also *Vectorisation* for some information on writing your own inlined C++ code using Weave.

6.2.2 Circular arrays

For maximum compatibility, Brian works with pure Python only. However, as well as the optional weave optimisations, there is also an object used in the spike propagation code that can run with a pure C++ version for a considerable speedup (1.5-3x). You need a copy of the `gcc` compiler installed (either on linux or through cygwin on Windows) to build it.

Installation:

In a command prompt or shell window, go to the directory where Brian is installed. On Windows this will probably be `C:\Python25\lib\site-packages\brian`. Now go to the Brian/brian/utils/ccircular folder. If you're on Linux (and this may also work for Mac) run the command "python setup.py build_ext –inplace". If you're on windows you'll need to have cygwin with gcc installed, and then you run "setup.py build_ext –inplace -c mingw32" instead. You should see some compilation, possibly with some warnings but no errors.

6.2.3 Automatically generated C code

There is an experimental module for automatic generation of C code, see *Code generation*.

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 Connection matrices

A `Connection` object has an attribute `W` which is its connection matrix.

Brian's system for connection matrices can be slightly confusing. The way it works is roughly as follows. There are two types of connection matrix data structures, `ConstructionMatrix` and `ConnectionMatrix`. The construction matrix types are used for building connectivity, and are optimised for insertion and deletion of elements, but access is slow. The connection matrix types are used when the simulation is running, and are optimised for fast access, but not for adding/removing or modifying elements. When a `Connection` object is created, it is given a construction matrix data type, and when the network is run, this matrix is converted to its corresponding connection matrix type. As

well as this construction/connection matrix type distinction, there is also the distinction between dense/sparse/dynamic matrices, each of which have their own construction and connection versions.

The dense matrix structure is very simple, both the construction and connection types are basically just 2D numpy arrays.

The sparse and dynamic matrix structures are very different for construction and connection. Both the sparse and dynamic construction matrices are essentially just the `scipy.lil_matrix` sparse matrix type, however we add some slight improvements to scipy's matrix data type to make it more efficient for our case.

The sparse and dynamic connection matrix structures are documented in more detail in the reference pages for `SparseConnectionMatrix` and `DynamicConnectionMatrix`.

For customised run-time modifications to sparse and dense connection matrices you have two options. You can modify the data structures directly using the information in the reference pages linked to in the paragraph above, or you can use the methods defined in the `ConnectionMatrix` class, which work for dense, sparse and dynamic matrix structures, and do not depend on implementation specific details. These methods provide element, row and column access. The row and column access methods use either `DenseConnectionVector` or `SparseConnectionVector` objects. The dense connection vector is just a 1D numpy array of length the size of the row/column. The sparse connection vector is slightly more complicated (but not much), see its documentation for details. The idea is that in most cases, both dense and sparse connection vectors can be operated on without having to know how they work, so for example if `v` is a `ConnectionVector` then `2*v` is of the same type. So for a `ConnectionMatrix` `W`, this should work, whatever the structure of `W`:

```
W.set_row(i, 2*W.get_row(i))
```

Or equivalently:

```
W[i,:] = 2*W[i,:]
```

The syntax `W[i,:]`, `W[:,i]` and `W[i,j]` is supported for integers `i` and `j` for (respectively) row, column and element access.

6.5 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 `brian.`**`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).

6.6 Precalculated tables

One way to speed up simulations is to use precalculated tables for complicated functions. The `Tabulate` class defines a table of values of the given function at regularly sampled points. The `TabulateInterp` class defines a table with linear interpolation, which is much more precise. Both work with scalar and vector arguments.

class `brian.`**`Tabulate`**(*f*, *xmin*, *xmax*, *n*)
An object to tabulate a numerical function.

Sample use:

```
g=Tabulate(f,0.,1.,1000)
y=g(.5)
v=g([.1,.3])
v=g(array([.1,.3]))
```

Arguments of g must lie in [xmin,xmax). An IndexError is raised is arguments are above xmax, but not always when they are below xmin (it can give weird results).

class `brian.`**`TabulateInterp`**(*f*, *xmin*, *xmax*, *n*)
An object to tabulate a numerical function with linear interpolation.

Sample use:

```
g=TabulateInterp(f,0.,1.,1000)
y=g(.5)
v=g([.1,.3])
v=g(array([.1,.3]))
```

Arguments of g must lie in [xmin,xmax). An IndexError is raised is arguments are above xmax, but not always when they are below xmin (it can give weird results).

6.7 Preferences

6.7.1 Functions

Setting and getting global preferences is done with the following functions:

brian.**set_global_preferences**(***kwds*)
Set global preferences for Brian

Usage:

```
``set_global_preferences(...)``
```

where ... is a list of keyword assignments.

brian.**get_global_preference**(*k*)
Get the value of the named global preference

6.7.2 Global configuration file

If you have a module named `brian_global_config` anywhere on your Python path, Brian will attempt to import it to define global preferences. For example, to automatically enable weave compilation for all your Brian projects, create a file `brian_global_config.py` somewhere in the Python path with the following contents:

```
from brian.globalprefs import *
set_global_preferences(useweave=True)
```

6.7.3 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.

gcc_options = ['-ffast-math'] Defines the compiler switches passed to the gcc compiler. For gcc versions 4.2+ we recommend using `-march=native`. By default, the `-ffast-math` optimisations are turned on - if you need IEEE guaranteed results, turn this switch off.

usecodegen = False Whether or not to use experimental code generation support.

usecodegenweave = False Whether or not to use C with experimental code generation support.

usecodegenstateupdate = True Whether or not to use experimental code generation support on state updaters.

usecodegenreset = False Whether or not to use experimental code generation support on resets. Typically slower due to weave overheads, so usually leave this off.

usecodegenthreshold = True Whether or not to use experimental code generation support on thresholds.

usenewpropagate = False Whether or not to use experimental new C propagation functions.

usecstdp = False Whether or not to use experimental new C STDP.

brianhears_usegpu = False Whether or not to use the GPU (if available) in Brian.hears. Support is experimental at the moment, and requires the PyCUDA package to be installed.

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`.

6.8 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.

`brian.`**`log_level_error`**`()`
Shows log messages only of level ERROR or higher.

`brian.`**`log_level_warn`**`()`
Shows log messages only of level WARNING or higher (including ERROR level).

`brian.`**`log_level_info`**`()`
Shows log messages only of level INFO or higher (including WARNING and ERROR levels).

`brian.`**`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 SciPy, NumPy and PyLab

See the following web sites:

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

8.2 Units system

brian.**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.

brian.**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 brian.**DimensionMismatchError**(*description*, **dims*)
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
    ...
```

brian.**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 brian.**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 brian.**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`.

8.3 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.

8.3.1 The `Clock` class

class `brian.`**`Clock`**(**args*, ***kwds*)

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.

`order` If two clocks have the same time, the order of the clock is used to resolve which clock is processed first, lower orders first.

`makedefaultclock` Set to `True` to make this clock the default clock.

The times returned by this clock are always off the form `n*dt+offset` for integer `n` and float `dt` and `offset`. For example, for a clock with `dt=10*ms`, setting `t=25*ms` will set `n=2` and `offset=5*ms`. For a clock that uses true float values for `t` rather than underlying integers, use `FloatClock` (although see the caveats there).

In order to make sure that certain operations happen in the correct sequence, you can use the `order` attribute, clocks with a lower order will be processed first if the time is the same. The condition for two clocks to be considered as having the same time is `abs(t1-t2)<epsilon*abs(t1)`, a standard test for equality of floating point values. For ordinary clocks based on integer times, the value of `epsilon` is `1e-14`, and for float based clocks it is `1e-8`.

The behaviour of clocks was changed in version 1.3 of Brian, if this is causing problems you might try using `FloatClock` or if that doesn't solve the problem, `NaiveClock`.

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).

class `brian.`**EventClock**(**args*, ***kwds*)
Clock that is used for events.

Works the same as a `Clock` except that it is never guessed as a clock to use by `NeuronGroup`, etc. These clocks can be used to make multiple clock simulations without causing ambiguous clock problems.

class `brian.`**FloatClock**(**args*, ***kwds*)
Similar to a `Clock` except that it uses a float value of `t` rather than an integer based underlying value. This means that over time the values of `t` can drift slightly off the grid, and sometimes `t/dt` will be slightly less than an integer value, sometimes slightly more. This can cause problems in cases where the computation `int(t/dt)` is performed to extract an index value, as sometimes an index will be repeated or skipped. However, this form of clock can be used for backwards compatibility with versions of Brian before the new integer based clock was introduced, and for more flexibility than the new version allows for. Note also that the equality condition for this clock uses an `epsilon` of `1e-8` rather than `1e-14`. See `Clock` for more details on this. For full backwards compatibility with older versions of Brian, use `NaiveClock`.

class `brian.`**NaiveClock**(**args*, ***kwds*)
Provided for backwards compatibility with older versions of Brian. Does not perform any approximate equality tests for clocks, meaning that clock processing sequence is undpredictable. Typically, users should use `Clock` or `FloatClock`.

class `brian.`**RegularClock**(**args*, ***kwds*)
Deprecated. Now the same as `Clock`. The old `Clock` class is now `FloatClock`.

8.3.2 The default clock

`brian.`**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
...
```

brian.**define_default_clock**(***kwds*)
Create a new default clock

Uses the keywords of the `Clock` initialiser.

Sample usage:

```
define_default_clock(dt=1*ms)
```

brian.**reinit_default_clock**(*t=0.0 s*)
Reinitialise the default clock (to zero or a specified time)

brian.**get_default_clock**()
Returns the default clock object.

8.4 Neuron models and groups

8.4.1 The `Equations` object

class brian.**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
''')
```

Details

For more details, see *More on equations* in the user manual.

For information on integration methods, and the `StateUpdater` class, see *Integration*.

8.4.2 The `NeuronGroup` object

class `brian.`**`NeuronGroup`**(**args*, ***kwds*)

Group of neurons

Initialised with arguments:

`N` The number of neurons in the group.

`model` 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, a scalar quantity or a string. 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. If `threshold` is a string then the appropriate threshold type will be chosen, for example you could do `threshold='V>10*mV'`. The string must be a one line string.

`reset=None` A `Reset` object, a function, a scalar quantity or a string. 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. If `reset` is a string it should be a series of expressions which

are evaluated for each neuron that is resetting. The series of expressions can be multiline or separated by a semicolon. For example, `reset='Vt+=5*mV; V=Vt'`. Statements involving `if` constructions will often not work because the code is automatically vectorised. For such constructions, use a function instead of a string.

refractory=0*ms, min_refractory, max_refractory A refractory period, used in combination with the `reset` value if it is a scalar. For constant resets only, you can specify refractory as an array of length the number of elements in the group, or as a string, giving the name of a state variable in the group. In the case of these variable refractory periods, you should specify `min_refractory` (optional) and `max_refractory` (required).

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). This doesn't usually need to be specified because Connections will update it.

compile=False Whether or not to attempt to compile the differential equation solvers (into Python code). Typically, for best performance, both `compile` and `freeze` should be set to `True` for nonlinear differential equations.

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).

unit_checking=True Set to `False` to bypass unit-checking.

Methods

subgroup(*N*)
Returns the next sequential subgroup of `N` neurons. See the section on subgroups below.

state(*var*)
Returns the array of values for state variable `var`, with length the number of neurons in the group.

rest()
Sets the neuron state values at rest for their differential equations.

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 For any valid Python variable name `x` corresponding to a state variable of the the `NeuronGroup`, this returns the array of values for the state variable `x`, as for the `state()` method above. Writing `G.x = arr` for `arr` a `TimedArray` will set the values of variable x to be `arr(t)` at time t. See `TimedArraySetter` for details.

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?

8.4.3 Resets

Reset objects are called each network update step to reset specified state variables of neurons that have fired.

class `brian.`**`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 `brian.`**`StringReset`**(*expr*, *level=0*)
Reset defined by a string

Initialised with arguments:

`expr` The string expression used to reset. This can include multiple lines or statements separated by a semicolon. For example, `'V=-70*mV'` or `'V=-70*mV; Vt+=10*mV'`. Some standard functions are provided, see below.

`level` How many levels up in the calling sequence to look for names in the namespace. Usually 0 for user code.

Standard functions for expressions:

`rand()` A uniform random number between 0 and 1.

`randn()` A Gaussian random number with mean 0 and standard deviation 1.

For example, these could be used to implement an adaptive model with random reset noise with the following string:

```
E -= 1*mV
V = Vr+rand()*5*mV
```

class `brian.`**`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 `brian.`**`Refractoriness`**(**args*, ***kwds*)
Holds the state variable at the reset value for a fixed time after a spike.

Initialised with arguments:

`resetvalue` The value to reset and hold to.

period The length of time to hold at the reset value. If using variable refractoriness, this is the maximum period.

state The name or number of the state variable to reset and hold.

class brian.**SimpleCustomRefractoriness**(**args*, ***kwds*)
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 brian.**CustomRefractoriness**(**args*, ***kwds*)
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 brian.**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 brian.**NoReset**
Absence of reset mechanism.

Initialised as:

```
NoReset()
```

8.4.4 Thresholds

A threshold mechanism checks which neurons have fired a spike.

class `brian.`**`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 `brian.`**`StringThreshold`**(*expr*, *level=0*)
A threshold specified by a string expression.

Initialised with arguments:

`expr` The expression used to test whether a neuron has fired a spike. Should be a single statement that returns a value. For example, `'V>50*mV'` or `'V>Vt'`.

`level` How many levels up in the calling sequence to look for names in the namespace. Usually 0 for user code.

class `brian.`**`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 `brian.`**`EmpiricalThreshold`**(**args*, ***kwds*)
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 brian.**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 brian.**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 brian.**NoThreshold**
No thresholding mechanism.

Initialised as:

```
NoThreshold()
```

8.5 Integration

See *Numerical integration* for an overview.

8.5.1 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 `brian.`**`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 `brian.`**`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

8.6 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 `brian.`**`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 brian.**PulsePacket**(**args*, ***kwds*)

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 brian.**SpikeGeneratorGroup**(*N*, *spiketimes*, *clock=None*, *period=None*, *gather=False*, *sort=True*)

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). `i` can be an integer or an array (list of neurons that spike at the same time). 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.

gather=False Set to True if you want to gather spike events that fall in the same timestep (makes the simulation faster if you have many events).

sort=True Set to False if your spike events are already sorted.

Has an attribute:

spiketimes This can be used to reset the list of spike times, however the values of `N`, `clock` and `period` cannot be changed.

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 `brian.`**`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)
```

8.7 Connections

The best way to understand the concept of a `Connection` in Brian is to work through Tutorial 2: Connections.

class `brian.`**`Connection`**(*source*, *target*, *state=0*, *delay=0.0 s*, *modulation=None*, *structure='sparse'*, *weight=None*, *sparseness=None*, *max_delay=5.0 ms*, ***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.

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. Depending on the type of `delay` it has different effects. If `delay` is a scalar value, then the connection will be initialised with all neurons having that delay. For very long delays, this may raise an error. If `delay=True` then the connection will be initialised as a `DelayConnection`, allowing heterogeneous delays (a different delay for each synapse). `delay` can also be a pair `(min,max)` or a function of one or two variables, in both cases it will be initialised as a `DelayConnection`, see the documentation for that class for details. Note that in these cases, initialisation of delays will only have the intended effect if used with the `weight` and `sparseness` arguments below.

`max_delay` If you are using a connection with heterogeneous delays, specify this to set the maximum allowed delay (smaller values use less memory). The default is 5ms.

`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 `dynamic`. See below for more information on structures.

`weight` If specified, the connection matrix will be initialised with values specified by `weight`, which can be any of the values allowed in the methods *connect*‘* below.

`sparseness` If `weight` is specified and `sparseness` is not, a full connection is assumed, otherwise random connectivity with this level of sparseness is assumed.

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.

Connection matrix structures

Brian currently features three types of connection matrix structures, each of which is suited for different situations. Brian has two stages of connection matrix. The first is the construction stage, used for building a weight matrix. This stage is optimised for the construction of matrices, with lots of features, but would be slow for runtime behaviour. Consequently, the second stage is the connection stage, used when Brian is being run. The connection stage is optimised for run time behaviour, but many features which are useful for construction are absent (e.g. the ability to add or remove synapses). Conversion between construction and connection stages is done by the `compress()` method of `Connection` which is called automatically when it is used for the first time.

The structures are:

`dense` A dense matrix. Allows runtime modification of all values. If connectivity is close to being dense this is probably the most efficient, but in most cases it is less efficient. In addition, a dense connection matrix will often do the wrong thing if using STDP. Because a synapse will be considered to exist but with weight 0, STDP will be able to create new synapses where there were previously none. Memory requirements are `8NM` bytes where `(N,M)` are the dimensions. (A `double` float value uses 8 bytes.)

`sparse` A sparse matrix. See `SparseConnectionMatrix` for details on implementation. This class features very fast row access, and slower column access if the `column_access=True` keyword is specified (making it suitable for learning algorithms such as STDP which require this). Memory requirements are 12 bytes per nonzero entry for row access only, or 20 bytes per nonzero entry if column access is specified. Synapses cannot be created or deleted at runtime with this class (although weights can be set to zero).

`dynamic` A sparse matrix which allows runtime insertion and removal of synapses. See `DynamicConnectionMatrix` for implementation details. This class features row and column access. The row access is slower than for `sparse` so this class should only be used when insertion and removal of synapses is crucial. Memory requirements are 24 bytes per nonzero entry. However, note that more memory than this may be required because memory is allocated using a dynamic array which grows by doubling its size when it runs out. If you know the maximum number of nonzero entries you will have in advance, specify the `nnzmax` keyword to set the initial size of the array.

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`.

class `brian.`**`DelayConnection`**(*source*, *target*, *state=0*, *modulation=None*, *structure='sparse'*, *weight=None*, *sparseness=None*, *delay=None*, *max_delay=5.0 ms*, ***kwds*)

Connection which implements heterogeneous postsynaptic delays

Initialised as for a `Connection`, but with the additional keyword:

max_delay Specifies the maximum delay time for any neuron. Note, the smaller you make this the less memory will be used.

Overrides the following attribute of Connection:

delay
A matrix of delays. This array can be changed during a run, but at no point should it be greater than max_delay.

In addition, the methods connect, connect_random, connect_full, and connect_one_to_one have a new keyword delay=... for setting the initial values of the delays, where delay can be one of:

- A float, all delays will be set to this value
- A pair (min, max), delays will be uniform between these two values.
- A function of no arguments, will be called for each nonzero entry in the weight matrix.
- A function of two argument (i,j) will be called for each nonzero entry in the weight matrix.
- A matrix of an appropriate type (e.g. ndarray or lil_matrix).

Finally, there is a method:

set_delays(source, target, delay) Where delay must be of one of the types above.

Notes

This class implements post-synaptic delays. This means that the spike is propagated immediately from the presynaptic neuron with the synaptic weight at the time of the spike, but arrives at the postsynaptic neuron with the given delay. At the moment, Brian only provides support for presynaptic delays if they are homogeneous, using the delay keyword of a standard Connection.

Implementation

DelayConnection stores an array of size (n,m) where n is max_delay/dt for dt of the target NeuronGroup's clock, and m is the number of neurons in the target. This array can potentially be quite large. Each row in this array represents the array that should be added to the target state variable at some particular future time. Which row corresponds to which time is tracked using a circular indexing scheme.

When a spike from neuron i in the source is encountered, the delay time of neuron i is looked up, the row corresponding to the current time plus that delay time is found using the circular indexing scheme, and then the spike is propagated to that row as for a standard connection (although this won't be propagated to the target until a later time).

Warning

If you are using a dynamic connection matrix, it is your responsibility to ensure that the nonzero entries of the weight matrix and the delay matrix exactly coincide. This is not an issue for sparse or dense matrices.

class brian.**IdentityConnection**(**args*, ***kwds*)
A Connection between two groups of the same size, where neuron i in the source group is connected to neuron i in the target group.

Initialised with arguments:

source, target The source and target NeuronGroup objects.

state The target state variable.

weight The weight of the synapse, must be a scalar.

delay Only homogeneous delays are allowed.

The benefit of this class is that it has no storage requirements and is optimised for this special case.

8.7.1 Connection matrix types

class brian.**ConnectionMatrix**
Base class for connection matrix objects

Connection matrix objects support a subset of the following methods:

get_row(i),get_col(i) Returns row/col i as a DenseConnectionVector or SparseConnectionVector as appropriate for the class.

set_row(i, val),set_col(i, val) Sets row/col with an array, DenseConnectionVector or SparseConnectionVector (if supported).

get_element(i, j),set_element(i, j, val) Gets or sets a single value.

get_rows(rows) Returns a list of rows, should be implemented without Python function calls for efficiency if possible.

get_cols(cols) Returns a list of cols, should be implemented without Python function calls for efficiency if possible.

insert(i,j,x),remove(i,j) For sparse connection matrices which support it, insert a new entry or remove an existing one.

getnnz() Return the number of nonzero entries.

todense() Return the matrix as a dense array.

The __getitem__ and __setitem__ methods are implemented by default, and automatically select the appropriate methods from the above in the cases where the item to be got or set is of the form :, i,:, :,j or i,j.

class brian.**DenseConnectionMatrix**(*val*, ***kwds*)
Dense connection matrix

See documentation for ConnectionMatrix for details on connection matrix types.

This matrix implements a dense connection matrix. It is just a numpy array. The get_row and get_col methods return DenseConnectionVector ` objects.

class brian.**SparseConnectionMatrix**(*val*, *column_access=True*, ***kwds*)
Sparse connection matrix

See documentation for ConnectionMatrix for details on connection matrix types.

This class implements a sparse matrix with a fixed number of nonzero entries. Row access is very fast, and if the column_access keyword is True then column access is also supported (but is not as fast as row access).

The matrix should be initialised with a scipy sparse matrix.

The get_row and get_col methods return SparseConnectionVector objects. In addition to the usual slicing operations supported, M[:]=val is supported, where val must be a scalar or an array of length nnz.

Implementation details:

The values are stored in an array alldata of length nnz (number of nonzero entries). The slice alldata[rowind[i]:rowind[i+1]] gives the values for row i. These slices are stored in the list rowdata so that rowdata[i] is the data for row i. The array rowj[i] gives the corresponding column j indices. For row access, the memory requirements are 12 bytes per entry (8 bytes for the float value, and 4 bytes for the column indices). The array allj of length nnz gives the column j coordinates for each element in alldata (the elements of rowj are slices of this array so no extra memory is used).

If column access is being used, then in addition to the above there are lists coli and coldataindices. For column j, the array coli[j] gives the row indices for the data values in column j, while

`coldataindices[j]` gives the indices in the array `alldata` for the values in column `j`. Column access therefore involves a copy operation rather than a slice operation. Column access increases the memory requirements to 20 bytes per entry (4 extra bytes for the row indices and 4 extra bytes for the data indices).

class `brian.`**`DynamicConnectionMatrix`**(*val*, *nnzmax=None*, *dynamic_array_const=2*, ***kwds*)
Dynamic (sparse) connection matrix

See documentation for `ConnectionMatrix` for details on connection matrix types.

This class implements a sparse matrix with a variable number of nonzero entries. Row access and column access are provided, but are not as fast as for `SparseConnectionMatrix`.

The matrix should be initialised with a scipy sparse matrix.

The `get_row` and `get_col` methods return `SparseConnectionVector` objects. In addition to the usual slicing operations supported, `M[:]=val` is supported, where `val` must be a scalar or an array of length `nnz`.

Implementation details

The values are stored in an array `alldata` of length `nnzmax` (maximum number of nonzero entries). This is a dynamic array, see:

http://en.wikipedia.org/wiki/Dynamic_array

You can set the resizing constant with the argument `dynamic_array_const`. Normally the default value 2 is fine but if memory is a worry it could be made smaller.

Rows and column point in to this data array, and the list `rowj` consists of an array of column indices for each row, with `coli` containing arrays of row indices for each column. Similarly, `rowdataind` and `coldataind` consist of arrays of pointers to the indices in the `alldata` array.

8.7.2 Construction matrix types

class `brian.`**`ConstructionMatrix`**
Base class for construction matrices

A construction matrix is used to initialise and build connection matrices. A `ConstructionMatrix` class has to implement a method `connection_matrix(*args, **kwds)` which returns a `ConnectionMatrix` object of the appropriate type.

class `brian.`**`DenseConstructionMatrix`**(*val*, ***kwds*)
Dense construction matrix. Essentially just numpy.ndarray.

The `connection_matrix` method returns a `DenseConnectionMatrix` object.

The `__setitem__` method is overloaded so that you can set values with a sparse matrix.

class `brian.`**`SparseConstructionMatrix`**(*arg*, ***kwds*)
SparseConstructionMatrix is converted to SparseConnectionMatrix.

class `brian.`**`DynamicConstructionMatrix`**(*arg*, ***kwds*)
DynamicConstructionMatrix is converted to DynamicConnectionMatrix.

8.7.3 Connection vector types

class `brian.`**`ConnectionVector`**
Base class for connection vectors, just used for defining the interface

ConnectionVector objects are returned by ConnectionMatrix objects when they retrieve rows or columns. At the moment, there are two choices, sparse or dense.

This class has no real function at the moment.

class brian.**DenseConnectionVector**
Just a numpy array.

class brian.**SparseConnectionVector**
Sparse vector class

A sparse vector is typically a row or column of a sparse matrix. This class can be treated in many cases as if it were just a vector without worrying about the fact that it is sparse. For example, if you write `2*v` it will evaluate to a new sparse vector. There is one aspect of the semantics which is potentially confusing. In a binary operation with a dense vector such as `sv+dv` where `sv` is sparse and `dv` is dense, the result will be a sparse vector with zeros where `sv` has zeros, the potentially nonzero elements of `dv` where `sv` has no entry will be simply ignored. It is for this reason that it is a `SparseConnectionVector` and not a general `SparseVector`, because these semantics make sense for rows and columns of connection matrices but not in general.

Implementation details:

The underlying numpy array contains the values, the attribute `n` is the length of the sparse vector, and `ind` is an array of the indices of the nonzero elements.

8.8 Plasticity

8.8.1 Spike timing dependent plasticity (STDP)

class brian.**STDP**(*C*, *eqs*, *pre*, *post*, *wmin=0*, *wmax=inf*, *level=0*, *clock=None*, *delay_pre=None*, *delay_post=None*)
Spike-timing-dependent plasticity

Initialised with arguments:

C Connection object to apply STDP to.

eqs Differential equations (with units)

pre Python code for presynaptic spikes, use the reserved symbol `w` to refer to the synaptic weight.

post Python code for postsynaptic spikes, use the reserved symbol `w` to refer to the synaptic weight.

wmin Minimum weight (default 0), weights are restricted to be within this value and wmax.

wmax Maximum weight (default unlimited), weights are restricted to be within wmin and this value.

delay_pre Presynaptic delay

delay_post Postsynaptic delay (backward propagating spike)

The STDP object works by specifying a set of differential equations associated to each synapse (`eqs`) and two rules to specify what should happen when a presynaptic neuron fires (`pre`) and when a postsynaptic neuron fires (`post`). The equations should be standard set of equations in the usual string format. The `pre` and `post` rules should be a sequence of statements to be executed triggered on pre- and post-synaptic spikes. The sequence of statements can be separated by a `;` or by using a multiline string. The reserved symbol `w` can be used to refer to the synaptic weight of the associated synapse.

This framework allows you to implement most STDP rules. Specifying differential equations and pre- and post-synaptic event code allows for a much more efficient implementation than specifying, for example, the spike pair weight modification function, but does unfortunately require transforming the definition into this form.

There is one restriction on the equations that can be implemented in this system, they need to be separable into independent pre- and post-synaptic systems (this is done automatically). In this way, synaptic variables and updates can be stored per neuron rather than per synapse.

Example

```
eqs_stdp = """
dA_pre/dt  = -A_pre/tau_pre   : 1
dA_post/dt = -A_post/tau_post : 1
"""
stdp = STDP(synapses, eqs=eqs_stdp, pre='A_pre+=delta_A_pre; w+=A_post',
            post='A_post+=delta_A_post; w+=A_pre', wmax=gmax)
```

STDP variables

You can access the pre- and post-synaptic variables as follows:

```
stdp = STDP(...)
print stdp.A_pre
```

Alternatively, you can access the group of pre/post-synaptic variables as:

```
stdp.pre_group
stdp.post_group
```

These latter attributes can be passed to a `StateMonitor` to record their activity, for example. However, note that in the case of STDP acting on a connection with heterogeneous delays, the recent values of these variables are automatically monitored and these can be accesses as follows:

```
stdp.G_pre_monitors['A_pre']
stdp.G_post_monitors['A_post']
```

Technical details

The equations are split into two groups, pre and post. Two groups are created to carry these variables and to update them (these are implemented as `NeuronGroup` objects). As well as propagating spikes from the source and target of `C` via `C`, spikes are also propagated to the respective groups created. At spike propagation time the weight values are updated.

class `brian.`**`ExponentialSTDP`**(*C*, *taup*, *taum*, *Ap*, *Am*, *interactions='all'*, *wmin=0*, *wmax=None*, *update='additive'*, *delay_pre=None*, *delay_post=None*, *clock=None*)

Exponential STDP.

Initialised with the following arguments:

`taup`, `taum`, `Ap`, `Am` Synaptic weight change (relative to the maximum weight wmax):

```
f(s) = Ap*exp(-s/taup) if s >0
f(s) = Am*exp(s/taum) if s <0
```

`interactions`

- 'all': contributions from all pre-post pairs are added
- 'nearest': only nearest-neighbour pairs are considered
- 'nearest_pre': nearest presynaptic spike, all postsynaptic spikes
- 'nearest_post': nearest postsynaptic spike, all presynaptic spikes

`wmin=0` minimum synaptic weight

`wmax` maximum synaptic weight

`update`

- 'additive': modifications are additive (independent of synaptic weight) (or "hard bounds")
- 'multiplicative': modifications are multiplicative (proportional to w) (or "soft bounds")

- 'mixed': depression is multiplicative, potentiation is additive

See documentation for STDP for more details.

8.8.2 Short term plasticity (STP)

class brian.**STP**(*C*, *taud*, *tauf*, *U*)

Short-term synaptic plasticity, following the Tsodyks-Markram model.

Implements the short-term plasticity model described in Markram et al (1998). Differential signaling via the same axon of neocortical pyramidal neurons, PNAS. Synaptic dynamics is described by two variables x and u, which follow the following differential equations:

```
dx/dt=(1-x)/taud   (depression)
du/dt=(U-u)/tauf   (facilitation)
```

where taud, tauf are time constants and U is a parameter in 0..1. Each presynaptic spike triggers modifications of the variables:

```
u<-u+U*(1-u)
x<-x*(1-u)
```

Synaptic weights are modulated by the product `u*x` (in 0..1) (before update).

Reference:

•Markram et al (1998). "Differential signaling via the same axon of neocortical pyramidal neurons", PNAS.

8.9 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 brian.**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[, report[, report_period]]) Runs the network for the given duration. See below for details about what happens when you do this. See documentation for `run()` for an explanation of the `report` and `report_period` keywords.

reinit(states=True) Reinitialises the network, runs each object's `reinit()` and each clock's `reinit()` method (resetting them to 0). If `states=False` then it will not reinitialise the `NeuronGroup` state variables.

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.

brian.**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 brian.**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.

brian.**run**(*duration*, *threads=1*, *report=None*, *report_period=10.0 s*)
Run a network created from any suitable objects that can be found

Arguments:

duration the length of time to run the network for.

report How to report progress, the default None doesn't report the progress. Some standard values for report:

text, stdout Prints progress to the standard output.

stderr Prints progress to the standard error output stderr.

graphical, tkinter Uses the Tkinter module to show a graphical progress bar, this may interfere with any other GUI code you have.

Alternatively, you can provide your own callback function by setting report to be a function report(elapsed, complete) of two variables elapsed, the amount of time elapsed in seconds, and complete the proportion of the run duration simulated (between 0 and 1). The report function is guaranteed to be called at the end of the run with complete=1.0 so this can be used as a condition for reporting that the computation is finished.

report_period How often the progress is reported (by default, every 10s).

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.

brian.**reinit**(*states=True*)
Reinitialises any suitable objects that can be found

Usage:

```
reinit(states=True)
```

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.

If states=False then NeuronGroup state variables will not be reinitialised.

brian.**stop**()
Globally stops any running network, this is reset the next time a network is run

brian.**clear**(*erase=True*, *all=False*)
Clears all Brian objects.

Specifically, it stops all existing Brian objects from being collected by MagicNetwork (objects created after clearing will still be collected). If erase is True then it will also delete all data from these objects. This is useful in, for example, ipython which stores persistent references to objects in any given session, stopping the data and memory from being freed up. If all=True then all Brian objects will be cleared. See also forget().

brian.**forget**(**objs*)
Forgets the list of objects passed

Forgetting means that MagicNetwork will not pick up these objects, but all data is retained. You can pass objects or lists of objects. Forgotten objects can be recalled with recall(). See also clear().

brian.**recall**(**objs*)
Recalls previously forgotten objects

See forget() and clear().

class brian.**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.

8.10 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 `brian.`**`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 three attributes:

`nspikes` The number of recorded spikes

`spikes` A time ordered list of pairs `(i,t)` where neuron `i` fired at time `t`.

`spiketimes` A dictionary with keys the indices of the neurons, and values an array of the spike times of that neuron. For example, `t=M.spiketimes[3]` gives the spike times for neuron 3.

For `M` a `SpikeMonitor`, you can also write:

`M[i]` An array 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 `brian.`**`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 brian.**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 brian.**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 an array of the spike times for the whole monitored group, or just for neuron i if specified.

values(*var*, *i=None*)
Returns an array of the values of variable var for the whole monitored group, or just for neuron i if specified.

class brian.**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:

times The times at which recordings were made

mean The mean value of the state variable for every neuron in the group (not just the ones specified in the `record` keyword)

var The unbiased estimate of the variances, as in `mean`

std The square root of `var`, as in `mean`

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 numpy array.

Methods:

plot(*[indices=None[, cmap=None[, refresh=None[, showlast=None[, redraw=True]]]]]*)
Plots the recorded values using pylab. You can specify an index or list of indices, otherwise all the recorded values will be plotted. The graph plotted will have legends of the form `name[i]` for `name` the variable name, and `i` the neuron index. If cmap is specified then the colours will be set according to the matplotlib colormap cmap. `refresh` specifies how often (in simulation time) you would like the plot to refresh. Note that this will only work if pylab is in interactive mode, to ensure this call the pylab `ion()` command. If you are using the `refresh` option, `showlast` specifies a fixed time window to display (e.g. the last 100ms). If you are using more than one realtime monitor, only one of them needs to issue a redraw command, therefore set `redraw=False` for all but one of them.

Note that with some IDEs, interactive plotting will not work with the default matplotlib backend, try doing something like this at the beginning of your script (before importing brian):

```
import matplotlib
matplotlib.use('WXAgg')
```

You may need to experiment, try WXAgg, GTKAgg, QTAgg, TkAgg.

insert_spikes(*spikemonitor[, value=0]*)
Inserts spikes into recorded traces (for plotting). State values at spike times are replaced with the given value (peak value of spike).

class brian.**MultiStateMonitor**(*G*, *vars=None*, *clock=None*, ***kwds*)

Monitors multiple state variables of a group

This class is a container for multiple StateMonitor objects, one for each variable in the group. You can retrieve individual StateMonitor objects using M[name] or retrieve the recorded values using M[name, i] for neuron i.

Initialised with a group G and a list of variables vars. If vars is omitted then all the variables of G will be recorded. Any additional keyword argument used to initialise the object will be passed to the individual StateMonitor objects (e.g. the when keyword).

Methods:

vars() Returns the variables

items(),iteritems() Returns the pairs (var, mon)

plot([indices[, cmap]]) Plots all the monitors (note that real-time plotting is not supported for this class).

Attributes:

times The times at which recordings were made.

monitors The dictionary of monitors indexed by variable name.

Usage:

```
G = NeuronGroup(N, eqs, ...)
M = MultiStateMonitor(G, record=True)
...
run(...)
...
plot(M['V'].times, M['V'][0])
figure()
for name, m in M.iteritems():
    plot(m.times, m[0], label=name)
legend()
show()
```

class brian.**RecentStateMonitor**(*P*, *varname*, *duration=5.0 ms*, *clock=None*, *record=True*, *timestep=1*, *when='end'*)

StateMonitor that records only the most recent fixed amount of time.

Works in the same way as a StateMonitor except that it has one additional initialiser keyword duration which gives the length of time to record values for, the record keyword defaults to True instead of False, and there are some different or additional attributes:

values, values_, times, times_ These will now return at most the most recent values over an interval of maximum time duration. These arrays are copies, so for faster access use unsorted_values, etc.

unsorted_values, unsorted_values_, unsorted_times, unsorted_times_ The raw versions of the data, the associated times may not be in sorted order and if duration hasn't passed, not all the values will be meaningful.

current_time_index Says which time index the next values to be recorded will be stored in, varies from 0 to M-1.

has_looped Whether or not the current_time_index has looped from M back to 0 - can be used to tell whether or not every value in the unsorted_values array is meaningful or not (they will only all be meaningful when has_looped==True, i.e. after time duration).

The __getitem__ method also returns values in sorted order.

To plot, do something like:

```
plot(M.times, M.values[:, i])
```

class brian.**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 brian.**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 brian.**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_ An array of the rates in Hz.

times, times_ The times of the bins.

bin The duration of a bin (in second).

class brian.**VanRossumMetric**(*source*, *tau=2.0 ms*)
van Rossum spike train metric. From M. van Rossum (2001): A novel spike distance (Neural Computation).

Compute the van Rossum distance between every spike train from the source population.

Arguments:

source The group to compute the distances for.

tau Time constant of the kernel (low pass filter).

Has one attribute:

distance A square symmetric matrix containing the distances.

class brian.**CoincidenceCounter**(*source*, *data=None*, *spiketimes_offset=None*, *spikedelays=None*, *coincidence_count_algorithm='exclusive'*, *onset=None*, *delta=4.0 ms*)

Coincidence counter class.

Counts the number of coincidences between the spikes of the neurons in the network (model spikes), and some user-specified data spike trains (target spikes). This number is defined as the number of target spikes such that there is at least one model spike within +- `delta`, where `delta` is the half-width of the time window.

Initialised as:

```
cc = CoincidenceCounter(source, data, delta = 4*ms)
```

with the following arguments:

source A `NeuronGroup` object which neurons are being monitored.

data The list of spike times. Several spike trains can be passed in the following way. Define a single 1D array `data` which contains all the target spike times one after the other. Now define an array `spiketimes_offset` of integers so that neuron `i` should be linked to target train: `data[spiketimes_offset[i]], data[spiketimes_offset[i]+1]`, etc.

It is essential that each spike train with the spiketimes array should begin with a spike at a large negative time (e.g. -1*second) and end with a spike that is a long time after the duration of the run (e.g. duration+1*second).

delta=4*ms The half-width of the time window for the coincidence counting algorithm.

spiketimes_offset A 1D array, `spiketimes_offset[i]` is the index of the first spike of the target train associated to neuron i.

spikedelays A 1D array with spike delays for each neuron. All spikes from the target train associated to neuron i are shifted by `spikedelays[i]`.

coincidence_count_algorithm If set to `'exclusive'`, the algorithm cannot count more than one coincidence for each model spike. If set to `'inclusive'`, the algorithm can count several coincidences for a single model spike.

onset A scalar value in seconds giving the start of the counting: no coincidences are counted before `onset`.

Has three attributes:

coincidences The number of coincidences for each neuron of the `NeuronGroup`. `coincidences[i]` is the number of coincidences for neuron i.

model_length The number of spikes for each neuron. `model_length[i]` is the spike count for neuron i.

target_length The number of spikes in the target spike train associated to each neuron.

class brian.**StateHistogramMonitor**(*group*, *varname*, *range*, *period=1.0 ms*, *nbins=20*)

Records the histogram of a state variable from a `NeuronGroup`.

Initialise as:

```
StateHistogramMonitor(P,varname,range(,period=1*ms)(,nbins=20))
```

Where:

P The group to be recorded from

varname The state variable name or number to be recorded

range The minimum and maximum values for the state variable. A 2-tuple of floats.

period When to record.

nbins Number of bins for the histogram.

The `StateHistogramMonitor` object has the following properties:

mean The mean value of the state variable for every neuron in the group

var The unbiased estimate of the variances, as in `mean`

std The square root of `var`, as in `mean`

hist A 2D array of the histogram values of all the neurons, each row is a single neuron's histogram.

bins A 1D array of the bin centers used to compute the histogram

bin_edges A 1D array of the bin edges used to compute the histogram

In addition, if `M` is a `StateHistogramMonitor` object, you write:

```
M[i]
```

for the histogram of neuron `i`.

8.11 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()`.

brian.**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=False set to `True` 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

refresh Specify how often (in simulation time) you would like the plot to refresh. Note that this will only work if pylab is in interactive mode, to ensure this call the pylab `ion()` command.

showlast If you are using the `refresh` option above, plots are much quicker if you specify a fixed time window to display (e.g. the last 100ms).

redraw If you are using more than one realtime monitor, only one of them needs to issue a redraw command, therefore set this to `False` for all but one of them.

Note that with some IDEs, interactive plotting will not work with the default matplotlib backend, try doing something like this at the beginning of your script (before importing brian):

```
import matplotlib
matplotlib.use('WXAgg')
```

You may need to experiment, try WXAgg, GTKAgg, QTAgg, TkAgg.

brian.**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

8.12 Variable updating

8.12.1 Timed Arrays

class brian.**TimedArray**(*arr*, *times=None*, *clock=None*, *start=None*, *dt=None*)

An array where each value has an associated time.

Initialisation arguments:

arr The values of the array. The first index is the time index. Any array shape works in principle, but only 1D/2D arrays are supported (other shapes may work, but may not). The idea is to, have the shapes (T,) or (T, N) for T the number of time steps and N the number of neurons.

times A 1D array of times whose length should be the same as the first dimension of `arr`. Usually it is preferable to specify a clock rather than an array of times, but this doesn't work in the case where the time intervals are not fixed.

clock Specify the times corresponding to array values by a clock. The `t` attribute of the clock is the time of the first value in the array, and the time interval is the `dt` attribute of the clock. If neither `times` nor `clock` is specified, a clock will be guessed in the usual way (see `Clock`).

start, dt Rather than specifying a clock, you can specify the start time and time interval explicitly. Technically, this is useful because it doesn't create a `Clock` object which can lead to ambiguity about which clock is the default. If dt is specified and start is not, start is assumed to be 0.

Note that if the clock, or start time and dt, of the array should be the default clock values, then you should not specify clock, start or dt (see Technical notes below).

Arbitrary slicing of the array is supported, but the clock will only be preserved where the intervals can be guaranteed to be fixed, that is except for the case where lists or numpy arrays are used on the time index.

Timed arrays can be called as if they were a function of time if the array times are based on a clock (but not if the array times are arbitrary as the look up costs would be excessive). If `x(t)` is called where `times[i]<=t<times[i]+dt` for some index i then `x(t)` will have the value `x[i]`. You can also call `x(t)` with `t` a 1D array. If x is 1D then `x(t)[i]=x(t[i])`, if x is 2D then `x(t)[i]=x(t[i])[i]`.

Has one method:

See also `TimedArraySetter`, `set_group_var_by_array()` and `NeuronGroup`.

Technical notes

Note that specifying a new clock, or values of start and dt, will mean that if you use this `TimedArray` to set the value of a `NeuronGroup` variable, it will be updated on the schedule of this clock, which can (due to floating point errors) induce some timing problems. This rarely happens, but if an occasional inaccuracy of order dt might conceivably be critical for your simulation, you should use `RegularClock` objects instead of `Clock` objects.

class `brian.`**`TimedArraySetter`**(*group*, *var*, *arr*, *times=None*, *clock=None*, *start=None*, *dt=None*, *when='start'*)

Sets NeuronGroup values with a TimedArray.

At the beginning of each update step, this object will set the values of a given state variable of a group with the value from the array corresponding to the current simulation time.

Initialisation arguments:

group The `NeuronGroup` to which the variable belongs.

var The name or index of the state variable in the group.

arr The array of values used to set the variable in the group. Can be an array or a `TimedArray`. If it is an array, you should specify the `times` or `clock` arguments, or leave them blank to use the default clock.

times Times corresponding to the array values, see `TimedArray` for more details.

clock The clock for the `NetworkOperation`. If none is specified, use the group's clock. If `arr` is not a `TimedArray` then this clock will be used to initialise it too.

start, dt Can specify these instead of a clock (see `TimedArray` for details).

when The standard `NetworkOperation` `when` keyword, although note that the default value is 'start'.

brian.**set_group_var_by_array**(*group*, *var*, *arr*, *times=None*, *clock=None*, *start=None*, *dt=None*)
Sets NeuronGroup values with a TimedArray.

Creates a TimedArraySetter, see that class for details.

8.12.2 Linked variables

brian.**linked_var**(*source*, *var=0*, *func=None*, *when='start'*, *clock=None*)
Used for linking one NeuronGroup variable to another.

Sample usage:

```
G = NeuronGroup(...)
H = NeuronGroup(...)
G.V = linked_var(H, 'W')
```

In this scenario, the variable V in group G will always be updated with the values from variable W in group H. The groups G and H must be the same size (although subgroups can be used if they are not the same size).

Arguments:

source The group from which values will be taken.

var The state variable of the source group to take values from.

func An additional function of one argument to pass the source variable values through, e.g. `func=lambda x:clip(x,0,Inf)` to half rectify the values.

when The time in the main Brian loop at which the copy operation is performed, as explained in Network.

clock The update clock for the copy operation, by default it will use the clock of the target group.

8.13 Analysis

8.13.1 Statistics of spike trains

brian.**firing_rate**(*spikes*)
Rate of the spike train.

brian.**CV**(*spikes*)
Coefficient of variation.

brian.**correlogram**(*T1*, *T2*, *width=20.0 ms*, *bin=1.0 ms*, *T=None*)
Returns a cross-correlogram with lag in [-width,width] and given bin size. T is the total duration (optional) and should be greater than the duration of T1 and T2. The result is in Hz (rate of coincidences in each bin).

N.B.: units are discarded. TODO: optimise?

brian.**autocorrelogram**(*T0*, *width=20.0 ms*, *bin=1.0 ms*, *T=None*)
Returns an autocorrelogram with lag in [-width,width] and given bin size. T is the total duration (optional) and should be greater than the duration of T1 and T2. The result is in Hz (rate of coincidences in each bin).

N.B.: units are discarded.

brian.**CCF**(*T1*, *T2*, *width=20.0 ms*, *bin=1.0 ms*, *T=None*)
Returns the cross-correlation function with lag in [-width,width] and given bin size. T is the total duration (optional). The result is in Hz**2: CCF(T1,T2)=<T1(t)T2(t+s)>

N.B.: units are discarded.

brian.**ACF**(*T0*, *width=20.0 ms*, *bin=1.0 ms*, *T=None*)
Returns the autocorrelation function with lag in [-width,width] and given bin size. T is the total duration (optional). The result is in Hz**2: ACF(T0)=<T0(t)T0(t+s)>

N.B.: units are discarded.

brian.**CCVF**(*T1*, *T2*, *width=20.0 ms*, *bin=1.0 ms*, *T=None*)
Returns the cross-covariance function with lag in [-width,width] and given bin size. T is the total duration (optional). The result is in Hz**2: CCVF(T1,T2)=<T1(t)T2(t+s)>-<T1><T2>

N.B.: units are discarded.

brian.**ACVF**(*T0*, *width=20.0 ms*, *bin=1.0 ms*, *T=None*)
Returns the autocovariance function with lag in [-width,width] and given bin size. T is the total duration (optional). The result is in Hz**2: ACVF(T0)=<T0(t)T0(t+s)>-<T0>**2

N.B.: units are discarded.

brian.**total_correlation**(*T1*, *T2*, *width=20.0 ms*, *T=None*)
Returns the total correlation coefficient with lag in [-width,width]. T is the total duration (optional). The result is a real (typically in [0,1]): total_correlation(T1,T2)=int(CCVF(T1,T2))/rate(T1)

8.14 Input/output

class brian.tools.datamanager.**DataManager**(*name*, *datapath=''*)
DataManager is a simple class for managing data produced by multiple runs of a simulation carried out in separate processes or machines. Each process is assigned a unique ID and Python Shelf object to write its data to. Each shelf is a dictionary whose keys must be strings. The DataManager can collate information across multiple shelves using the get(key) method, which returns a dictionary with keys the unique session names, and values the value written in that session (typically only the values will be of interest). If each value is a tuple or list then you can use the get_merged(key) to get a concatenated list. If the data type is more complicated you can use the get(key) method and merge by hand. The idea is each process generates files with names that do not interfere with each other so that there are no file concurrency issues, and then in the data analysis phase, the data generated separately by each process is merged together.

Methods:

get(key) Return dictionary with keys the session names, and values the values stored in that session for the given key.

get_merged(key) Return a single list of the merged lists or tuples if each value for every session is a list or tuple.

get_matching(match) Returns a dictionary with keys the keys matching match and values get(key). If match is a string, a matching key has to start with that string. If match is a function, a key matches if match(key).

get_merged_matching(match) Like get_merged(key) but across all keys that match.

get_flat_matching(match) Returns a straight list of every value session[key] for all sessions and all keys matching match.

iteritems() Returns all `(key, value)` pairs, for each Shelf file, as an iterator (useful for large files with too much data to be loaded into memory).

itemcount() Returns the total number of items across all the Shelf files.

keys() A list of all the keys across all sessions.

session() Returns a randomly named session Shelf, multiple processes can write to these without worrying about concurrency issues.

computer_session() Returns a consistently named Shelf specific to that user and computer, only one process can write to it without worrying about concurrency issues.

locking_session(),locking_computer_session() Returns a LockingSession object, a limited proxy to the underlying Shelf which acquires and releases a lock before and after every operation, making it safe for concurrent access.

session_filenames() A list of all the shelf filenames for all sessions.

make_unique_key() Generates a unique key for inserting an element into a session without overwriting data, uses uuid4.

Attributes:

basepath The base path for data files.

computer_name A (hopefully) unique identifier for the user and computer, consists of the username and the computer network name.

computer_session_filename The filename of the computer-specific session file. This file should only be accessed by one process at a time, there's no way to protect against concurrent write accesses causing it to be corrupted.

brian.**read_neuron_dat**(*name*)
Reads a Neuron vector file (.dat).

Returns vector of times, vector of values

brian.**read_atf**(*name*)
Reads an Axon ATF file (.atf).

Returns vector of times, vector of values

8.15 Remote control

class brian.**RemoteControlServer**(*server=None*, *authkey='brian'*, *clock=None*, *global_ns=None*, *local_ns=None*, *level=0*)
Allows remote control (via IP) of a running Brian script

Initialisation arguments:

server The IP server details, a pair (host, port). If you want to allow control only on the one machine (for example, by an IPython shell), leave this as `None` (which defaults to host='localhost', port=2719). To allow remote control, use ('', portnumber).

authkey The authentication key to allow access, change it from 'brian' if you are allowing access from outside (otherwise you allow others to run arbitrary code on your machine).

clock The clock specifying how often to poll for incoming commands.

global_ns, local_ns, level Namespaces in which incoming commands will be executed or evaluated, if you leave them blank it will be the local and global namespace of the frame from which this function was called (if level=1, or from a higher level if you specify a different level here).

Once this object has been created, use a `RemoteControlClient` to issue commands.

Example usage

Main simulation code includes a line like this:

```
server = RemoteControlServer()
```

In an IPython shell you can do something like this:

```
client = RemoteControlClient()
spikes = client.evaluate('M.spikes')
i, t = zip(*spikes)
plot(t, i, '.')
client.execute('stop()')
```

class brian.**RemoteControlClient**(*server=None*, *authkey='brian'*)
Used to remotely control (via IP) a running Brian script

Initialisation arguments:

server The IP server details, a pair (host, port). If you want to allow control only on the one machine (for example, by an IPython shell), leave this as `None` (which defaults to host='localhost', port=2719). To allow remote control, use ('', portnumber).

authkey The authentication key to allow access, change it from 'brian' if you are allowing access from outside (otherwise you allow others to run arbitrary code on your machine).

Use a `RemoteControlServer` on the simulation you want to control.

Has the following methods:

execute(*code*)
Executes the specified code in the server process. If it raises an exception, the server process will catch it and reraise it in the client process.

evaluate(*code*)
Evaluate the code in the server process and return the result. If it raises an exception, the server process will catch it and reraise it in the client process.

pause()
Temporarily stop the simulation in the server process, continue simulation with the :meth:'go' method.

go()
Continue a simulation that was paused.

stop()
Stop a simulation, equivalent to `execute('stop()')`.

Example usage

Main simulation code includes a line like this:

```
server = RemoteControlServer()
```

In an IPython shell you can do something like this:

```
client = RemoteControlClient()
spikes = client.evaluate('M.spikes')
i, t = zip(*spikes)
plot(t, i, '.')
client.execute('stop()')
```

8.16 Progress reporting

class brian.utils.progressreporting.**ProgressReporter**(*report*, *period=10.0*)
Standard text and graphical progress reports

Initialised with arguments:

`report`

Can be one of the following strings:

'print','text','stdout' Reports progress to standard console.

'stderr' Reports progress to error console.

'graphical','tkinter' A simple graphical progress bar using Tkinter.

Alternatively, it can be any output stream in which case text reports will be sent to it, or a custom callback function `report(elapsed, complete)` taking arguments `elapsed` the amount of time that has passed and `complete` the fraction of the computation finished.

period How often reports should be generated in seconds.

Methods:

start()
Call at the beginning of a task to start timing it.

finish()
Call at the end of a task to finish timing it. Note that with the Tkinter class, if you do not call this it will stop the Python script from finishing, stopping memory from being freed up.

update(*complete*)
Call with the fraction of the task (or subtask if `subtask()` has been called) completed, between 0 and 1.

subtask(*complete*, *tasksize*)
After calling `subtask(complete, tasksize)`, subsequent calls to update will report progress between a fraction `complete` and `complete+tasksize` of the total task. `complete` represents the amount of the total task completed at the beginning of the task, and `tasksize` the size of the subtask as a proportion of the whole task.

equal_subtask(*tasknum*, *numtasks*)
If a task can be divided into `numtasks` equally sized subtasks, you can use this method instead of `subtask`, where `tasknum` is the number of the subtask about to start.

8.17 Model fitting toolbox

The model fitting toolbox uses the package Playdoh, you can see the documentation here.

brian.library.modelfitting.**modelfitting**(***kwds*)
Model fitting function.

Fits a spiking neuron model to electrophysiological data (injected current and spikes).

See also the section *Model fitting* in the user manual.

Arguments

model An `Equations` object containing the equations defining the model.

reset A reset value for the membrane potential, or a string containing the reset equations.

threshold A threshold value for the membrane potential, or a string containing the threshold equations.

refractory The refractory period in second. If it's a single value, the same refractory will be used in all the simulations. If it's a list or a tuple, the fitting will also optimize the refractory period (see `**params` below).

Warning: when using a refractory period, you can't use a custom reset, only a fixed one.

data A list of spike times, or a list of several spike trains as a list of pairs (index, spike time) if the fit must be performed in parallel over several target spike trains. In this case, the modelfitting function returns as many parameters sets as target spike trains.

input_var='I' The variable name used in the equations for the input current.

input A vector of values containing the time-varying signal the neuron responds to (generally an injected current).

dt The time step of the input (the inverse of the sampling frequency).

****params** The list of parameters to fit the model with. Each parameter must be set as follows: `param_name=[bound_min, min, max, bound_max]` where `bound_min` and `bound_max` are the boundaries, and `min` and `max` specify the interval from which the parameter values are uniformly sampled at the beginning of the optimization algorithm. If not using boundaries, set `param_name=[min, max]`.

Also, you can add a fit parameter which is a spike delay for all spikes : add the special parameter `delays` in `**params`, for example `modelfitting(..., delays=[-10*ms, 10*ms])`.

You can also add fit the refractory period by specifying `modelfitting(..., refractory=[-10*ms, 10*ms])`.

popsize Size of the population (number of particles) per target train used by the optimization algorithm.

maxiter Number of iterations in the optimization algorithm.

optparams Optimization algorithm parameters. It is a dictionary: keys are parameter names, values are parameter values or lists of parameters (one value per group). This argument is specific to the optimization algorithm used. See `PSO`, `GA`, `CMAES`.

delta=4*ms The precision factor delta (a scalar value in second).

slices=1 The number of time slices to use.

overlap=0*ms When using several time slices, the overlap between consecutive slices, in seconds.

initial_values A dictionary containing the initial values for the state variables.

cpu The number of CPUs to use in parallel. It is set to the number of CPUs in the machine by default.

gpu The number of GPUs to use in parallel. It is set to the number of GPUs in the machine by default.

precision GPU only: a string set to either `float` or `double` to specify whether to use single or double precision on the GPU. If it is not specified, it will use the best precision available.

returninfo=False Boolean indicating whether the modelfitting function should return technical information about the optimization.

scaling=None Specify the scaling used for the parameters during the optimization. It can be `None` or `'mapminmax'`. It is `None` by default (no scaling), and `mapminmax` by default for the CMAES algorithm.

algorithm=CMAES The optimization algorithm. It can be `PSO`, `GA` or `CMAES`.

optparams={} Optimization parameters. See

method='Euler' Integration scheme used on the CPU and GPU: `'Euler'` (default), `RK`, or `exponential_Euler`. See also *Numerical integration*.

machines=[] A list of machine names to use in parallel. See *Clusters*.

Return values

Return an `OptimizationResult` object with the following attributes:

best_pos Minimizing position found by the algorithm. For array-like fitness functions, it is a single vector if there is one group, or a list of vectors. For keyword-like fitness functions, it is a dictionary where keys are parameter names and values are numeric values. If there are several groups, it is a list of dictionaries.

best_fit The value of the fitness function for the best positions. It is a single value if there is one group, or it is a list if there are several groups.

info A dictionary containing various information about the optimization.

Also, the following syntax is possible with an `OptimizationResult` instance `or`. The `key` is either an optimizing parameter name for keyword-like fitness functions, or a dimension index for array-like fitness functions.

or[key] it is the best `key` parameter found (single value), or the list of the best parameters `key` found for all groups.

or[i] where `i` is a group index. This object has attributes `best_pos`, `best_fit`, `info` but only for group `i`.

or[i][key] where `i` is a group index, is the same as `or[i].best_pos[key]`.

For more details on the gamma factor, see Jolivet et al. 2008, "A benchmark test for a quantitative assessment of simple neuron models", J. Neurosci. Methods (available in PDF here).

`brian.library.modelfitting.`**print_table**(*results*, *precision=4*, *colwidth=16*)

Displays the results of an optimization in a table.

Arguments:

results The results returned by the `minimize` of `maximize` function.

precision = 4 The number of decimals to print for the parameter values.

colwidth = 16 The width of the columns in the table.

`brian.library.modelfitting.`**open_server**(*port=None*, *maxcpu=None*, *maxgpu=None*, *local=None*)

Start the Playdoh server.

Arguments:

port=DEFAULT_PORT The port (integer) of the Playdoh server. The default is DEFAULT_PORT, which is 2718.

maxcpu=MAXCPU The total number of CPUs the Playdoh server can use. `MAXCPU` is the total number of CPUs on the computer.

maxgpu=MAXGPU The total number of GPUs the Playdoh server can use. `MAXGPU` is the total number of GPUs on the computer, if PyCUDA is installed.

`brian.library.modelfitting.`**get_spikes**(*model=None*, *reset=None*, *threshold=None*, *input=None*, *input_var='I'*, *dt=None*, ***params*)

Retrieves the spike times corresponding to the best parameters found by the modelfitting function.

Arguments

model, reset, threshold, input, input_var, dt Same parameters as for the `modelfitting` function.

****params** The best parameters returned by the `modelfitting` function.

Returns

spiketimes The spike times of the model with the given input and parameters.

`brian.library.modelfitting.`**predict**(*model=None*, *reset=None*, *threshold=None*, *data=None*, *delta=4.0 ms*, *input=None*, *input_var='I'*, *dt=None*, ***params*)

Predicts the gamma factor of a fitted model with respect to the data with a different input current.

Arguments

model, reset, threshold, input_var, dt Same parameters as for the `modelfitting` function.

input The input current, that can be different from the current used for the fitting procedure.

data The experimental spike times to compute the gamma factor against. They have been obtained with the current `input`.

****params** The best parameters returned by the `modelfitting` function.

Returns

gamma The gamma factor of the model spike trains against the data. If there were several groups in the fitting procedure, it is a vector containing the gamma factor for each group.

class `brian.library.modelfitting.`**PSO**

Particle Swarm Optimization algorithm. See the wikipedia entry on PSO.

Optimization parameters:

omega The parameter `omega` is the "inertial constant"

cl `cl` is the "local best" constant affecting how much the particle's personal best position influences its movement.

cg `cg` is the "global best" constant affecting how much the global best position influences each particle's movement.

See the wikipedia entry on PSO for more details (note that they use `c_1` and `c_2` instead of `cl` and `cg`). Reasonable values are (.9, .5, 1.5), but experimentation with other values is a good idea.

class `brian.library.modelfitting.`**GA**

Standard genetic algorithm. See the wikipedia entry on GA

If more than one worker is used, it works in an island topology, i.e. as a coarse-grained parallel genetic algorithms which assumes a population on each of the computer nodes and migration of individuals among the nodes.

Optimization parameters:

proportion_parents=1 proportion (out of 1) of the entire population taken as potential parents.

migration_time_interval=20 whenever more than one worker is used, it is the number of iteration at which a migration happens . (note for different groups case: this parameter can only have one value, i.e. every group will have the same value (the first of the list))

proportion_migration=0.2 proportion (out of 1) of the island population that will migrate to the next island (the best one) and also the worst that will be replaced by the best of the previous island. (note for different groups case: this parameter can only have one value, i.e. every group will have the same value (the first of the list))

proportion_xover=0.65 proportion (out of 1) of the entire population which will undergo a cross over.

proportion_elite=0.05 proportion (out of 1) of the entire population which will be kept for the next generation based on their best fitness.

The proportion of mutation is automatically set to `1-proportion_xover-proportion_elite`.

func_selection='stoch_uniform' This function define the way the parents are chosen (it is the only one available). It lays out a line in which each parent corresponds to a section of the line of length proportional to its scaled value. The algorithm moves along the line in steps of equal size. At each step, the algorithm allocates a parent from the section it lands on. The first step is a uniform random number less than the step size.

`func_xover='intermediate'`

`func_xover` specifies the function that performs the crossover. The following ones are available:

- *intermediate*: creates children by taking a random weighted average of the parents. You can specify the weights by a single parameter,''ratio_xover'' (which is 0.5 by default). The function creates the child from parent1 and parent2 using the following formula:

```
child = parent1 + rand * Ratio * ( parent2 - parent1)
```

- *discrete_random*: creates a random binary vector and selects the genes where the vector is a 1 from the first parent, and the genes where the vector is a 0 from the second parent, and combines the genes to form the child.
- *one_point*: chooses a random integer n between 1 and ndimensions and then selects vector entries numbered less than or equal to n from the first parent. It then Selects vector entries numbered greater than n from the second parent. Finally,it concatenates these entries to form a child vector.
- *two_points*: it selects two random integers m and n between 1 and ndimensions. The function selects vector entries numbered less than or equal to m from the first parent. Then it selects vector entries numbered from m+1 to n, inclusive, from the second parent. Then it selects vector entries numbered greater than n from the first parent. The algorithm then concatenates these genes to form a single gene.
- *heuristic*: returns a child that lies on the line containing the two parents, a small distance away from the parent with the better fitness value in the direction away from the parent with the worse fitness value. You can specify how far the child is from the better parent by the parameter `ratio_xover` (which is 0.5 by default)
- *linear_combination*: creates children that are linear combinations of the two parents with the parameter `ratio_xover` (which is 0.5 by default and should be between 0 and 1):

```
child = parent1 + Ratio * ( parent2 - parent1)
```

For `ratio_xover=0.5` every child is an arithmetic mean of two parents.

`func_mutation='gaussian'`

This function define how the genetic algorithm makes small random changes in the individuals in the population to create mutation children. Mutation provides genetic diversity and enable the genetic algorithm to search a broader space. Different options are available:

- *gaussian*: adds a random number taken from a Gaussian distribution with mean 0 to each entry of the parent vector.

The 'scale_mutation' parameter (0.8 by default) determines the standard deviation at the first generation by `scale_mutation*(Xmax-Xmin)` where Xmax and Xmin are the boundaries.

The 'shrink_mutation' parameter (0.2 by default) controls how the standard deviation shrinks as generations go by:

`:math:'\sigma_{i}=\sigma_{i-1}(1-shrink_{mutation}*i/maxiter)' at iteration i.`

- *uniform*: The algorithm selects a fraction of the vector entries of an individual for mutation, where each entry has a probability `mutation_rate` (default is 0.1) of being mutated. In the second step, the algorithm replaces each selected entry by a random number selected uniformly from the range for that entry.

class `brian.library.modelfitting.`**CMAES**

Covariance Matrix Adaptation Evolution Strategy algorithm See the wikipedia entry on CMAES and also the author's website <http://www.lri.fr/~hansen/cmaesintro.html>'

Optimization parameters:

proportion_selective=0.5 This parameter (refered to as mu in the CMAES algorithm) is the proportion (out of 1) of the entire population that is selected and used to update the generative distribution. (note for different groups case: this parameter can only have one value, i.e. every group will have the same value (the first of the list))

bound_strategy=1: In the case of a bounded problem, there are two ways to handle the new generated points which fall outside the boundaries. (note for different groups case: this parameter can only have one value, i.e. every group will have the same value (the first of the list))

`bound_strategy=1`. With this strategy, every point outside the domain is repaired, i.e. it is projected to its nearset possible value $x_{repaired}$. In other words, components that are infeasible in x are set to the (closest) boundary value in $x_{repaired}$. The fitness function on the repaired search points is evaluated and a penalty which depends on the distance to the repaired solution is added $f_{fitness}(x) = f(x_{repaired}) + \gamma\|x - x_{repaired}\|^2$

The repaired solution is disregarded afterwards.

`bound_strategy=2` With this strategy any infeasible solution x is resampled until it become feasible. It should be used only if the optimal solution is not close to the infeasible domain.

See p.28 of <http://www.lri.fr/~hansen/cmatutorial.pdf> for more details

gamma `gamma` is the weight γ in the previously introduced penalty function. (note for different groups case: this parameter can only have one value, i.e. every group will have the same value (the first of the list))

8.18 Brian hears

See Also:

User guide for *Brian hears*.

`brian.hears.`**set_default_samplerate**(*samplerate*)

Sets the default samplerate for Brian hears objects, by default 44.1 kHz.

8.18.1 Sounds

class `brian.hears.`**Sound**

Class for working with sounds, including loading/saving, manipulating and playing.

For an overview, see *Sounds*.

Initialisation

The following arguments are used to initialise a sound object

data Can be a filename, an array, a function or a sequence (list or tuple). If its a filename, the sound file (WAV or AIFF) will be loaded. If its an array, it should have shape `(nsamples, nchannels)`. If its a function, it should be a function f(t). If its a sequence, the items in the sequence can be filenames, functions, arrays or Sound objects. The output will be a multi-channel sound with channels the corresponding sound for each element of the sequence.

samplerate=None The samplerate, if necessary, will use the default (for an array or function) or the samplerate of the data (for a filename).

duration=None The duration of the sound, if initialising with a function.

Loading, saving and playing

static load(*filename*)
Load the file given by filename and returns a Sound object. Sound file can be either a .wav or a .aif file.

save(*filename*, *normalise=False*, *samplewidth=2*)
Save the sound as a WAV.

If the normalise keyword is set to True, the amplitude of the sound will be normalised to 1. The samplewidth keyword can be 1 or 2 to save the data as 8 or 16 bit samples.

play(*normalise=False*, *sleep=False*)
Plays the sound (normalised to avoid clipping if required). If sleep=True then the function will wait until the sound has finished playing before returning.

Properties

duration
The length of the sound in seconds.

nsamples
The number of samples in the sound.

nchannels
The number of channels in the sound.

times
An array of times (in seconds) corresponding to each sample.

left
The left channel for a stereo sound.

right
The right channel for a stereo sound.

channel(*n*)
Returns the nth channel of the sound.

Generating sounds

All sound generating methods can be used with durations arguments in samples (int) or units (e.g. 500*ms). One can also set the number of channels by setting the keyword argument nchannels to the desired value. Notice that for noise the channels will be generated independantly.

static tone(*frequency*, *duration*, *phase=0*, *samplerate=None*, *nchannels=1*)
Returns a pure tone at frequency for duration, using the default samplerate or the given one. The

`frequency` and `phase` parameters can be single values, in which case multiple channels can be specified with the `nchannels` argument, or they can be sequences (lists/tuples/arrays) in which case there is one frequency or phase for each channel.

static whitenoise(*duration*, *samplerate=None*, *nchannels=1*)
Returns a white noise. If the samplerate is not specified, the global default value will be used.

static powerlawnoise(*duration*, *alpha*, *samplerate=None*, *nchannels=1*, *normalise=False*)
Returns a power-law noise for the given duration. Spectral density per unit of bandwidth scales as 1/(f**alpha).

Sample usage:

```
noise = powerlawnoise(200*ms, 1, samplerate=44100*Hz)
```

Arguments:

duration Duration of the desired output.

alpha Power law exponent.

samplerate Desired output samplerate

static brownnoise(*duration*, *samplerate=None*, *nchannels=1*, *normalise=False*)
Returns brown noise, i.e `powerlawnoise()` with alpha=2

static pinknoise(*duration*, *samplerate=None*, *nchannels=1*, *normalise=False*)
Returns pink noise, i.e `powerlawnoise()` with alpha=1

static silence(*duration*, *samplerate=None*, *nchannels=1*)
Returns a silent, zero sound for the given duration. Set nchannels to set the number of channels.

static click(*duration*, *peak=None*, *samplerate=None*, *nchannels=1*)
Returns a click of the given duration.

If `peak` is not specified, the amplitude will be 1, otherwise `peak` refers to the peak dB SPL of the click, according to the formula `28e-6*10**(peak/20.)`.

static clicks(*duration*, *n*, *interval*, *peak=None*, *samplerate=None*, *nchannels=1*)
Returns a series of n clicks (see `click()`) separated by interval.

static harmoniccomplex(*f0*, *duration*, *amplitude=1*, *phase=0*, *samplerate=None*, *nchannels=1*)
Returns a harmonic complex composed of pure tones at integer multiples of the fundamental frequency `f0`. The `amplitude` and `phase` keywords can be set to either a single value or an array of values. In the former case the value is set for all harmonics, and harmonics up the the sampling frequency are generated. In the latter each harmonic parameter is set separately, and the number of harmonics generated corresponds to the length of the array.

Timing and sequencing

static sequence(**sounds*, *samplerate=None*)
Returns the sequence of sounds in the list sounds joined together

repeat(*n*)
Repeats the sound n times

extended(*duration*)
Returns the Sound with length extended by the given duration, which can be the number of samples or a length of time in seconds.

shifted(*duration*)
Returns the sound delayed by duration, which can be the number of samples or a length of time in seconds.

resized(*L*)
Returns the Sound with length extended (or contracted) to have L samples.

Slicing

One can slice sound objects in various ways, for example `sound[100*ms:200*ms]` returns the part of the sound between 100 ms and 200 ms (not including the right hand end point). If the sound is less than 200 ms long it will be zero padded. You can also set values using slicing, e.g. `sound[:50*ms] = 0` will silence the first 50 ms of the sound. The syntax is the same as usual for Python slicing. In addition, you can select a subset of the channels by doing, for example, `sound[:, -5:]` would be the last 5 channels. For time indices, either times or samples can be given, e.g. `sound[:100]` gives the first 100 samples. In addition, steps can be used for example to reverse a sound as `sound[::-1]`.

Arithmetic operations

Standard arithemetical operations and numpy functions work as you would expect with sounds, e.g. `sound1+sound2`, `3*sound` or `abs(sound)`.

Level

level
Can be used to get or set the level of a sound, which should be in dB. For single channel sounds a value in dB is used, for multiple channel sounds a value in dB can be used for setting the level (all channels will be set to the same level), or a list/tuple/array of levels. It is assumed that the unit of the sound is Pascals.

atlevel(*level*)
Returns the sound at the given level in dB SPL (RMS) assuming array is in Pascals. `level` should be a value in dB, or a tuple of levels, one for each channel.

Ramping

ramp(*when='onset'*, *duration=10.0 ms*, *envelope=None*, *inplace=True*)
Adds a ramp on/off to the sound

when='onset' Can take values 'onset', 'offset' or 'both'

duration=10*ms The time over which the ramping happens

envelope A ramping function, if not specified uses `sin(pi*t/2)**2`. The function should be a function of one variable `t` ranging from 0 to 1, and should increase from `f(0)=0` to `f(0)=1`. The reverse is applied for the offset ramp.

inplace Whether to apply ramping to current sound or return a new array.

ramped(*when='onset'*, *duration=10.0 ms*, *envelope=None*)
Returns a ramped version of the sound (see `Sound.ramp()`).

Plotting

spectrogram(*low=None*, *high=None*, *log_power=True*, *other=None*, ***kwds*)
Plots a spectrogram of the sound

Arguments:

low=None, high=None If these are left unspecified, it shows the full spectrogram, otherwise it shows only between `low` and `high` in Hz.

log_power=True If True the colour represents the log of the power.

****kwds** Are passed to Pylab's `specgram` command.

Returns the values returned by pylab's `specgram`, namely `(pxx, freqs, bins, im)` where `pxx` is a 2D array of powers, `freqs` is the corresponding frequencies, `bins` are the time bins, and `im` is the image axis.

spectrum(*low=None*, *high=None*, *log_power=True*, *display=False*)
Returns the spectrum of the sound and optionally plots it.

Arguments:

low, high If these are left unspecified, it shows the full spectrum, otherwise it shows only between `low` and `high` in Hz.

log_power=True If True it returns the log of the power.

display=False Whether to plot the output.

Returns `(Z, freqs, phase)` where `Z` is a 1D array of powers, `freqs` is the corresponding frequencies, `phase` is the unwrapped phase of spectrum.

brian.hears.**savesound**(*sound*, *filename*, *normalise=False*, *samplewidth=2*)
Save the sound as a WAV.

If the normalise keyword is set to True, the amplitude of the sound will be normalised to 1. The samplewidth keyword can be 1 or 2 to save the data as 8 or 16 bit samples.

brian.hears.**loadsound**(*filename*)
Load the file given by filename and returns a Sound object. Sound file can be either a .wav or a .aif file.

brian.hears.**play**(**sounds*, *normalise=False*, *sleep=False*)
Plays the sound (normalised to avoid clipping if required). If sleep=True then the function will wait until the sound has finished playing before returning.

brian.hears.**whitenoise**(*duration*, *samplerate=None*, *nchannels=1*)
Returns a white noise. If the samplerate is not specified, the global default value will be used.

brian.hears.**powerlawnoise**(*duration*, *alpha*, *samplerate=None*, *nchannels=1*, *normalise=False*)
Returns a power-law noise for the given duration. Spectral density per unit of bandwidth scales as 1/(f**alpha).

Sample usage:

```
noise = powerlawnoise(200*ms, 1, samplerate=44100*Hz)
```

Arguments:

duration Duration of the desired output.

alpha Power law exponent.

samplerate Desired output samplerate

brian.hears.**brownnoise**(*duration*, *samplerate=None*, *nchannels=1*, *normalise=False*)
Returns brown noise, i.e `powerlawnoise()` with alpha=2

brian.hears.**pinknoise**(*duration*, *samplerate=None*, *nchannels=1*, *normalise=False*)
Returns pink noise, i.e `powerlawnoise()` with alpha=1

brian.hears.**tone**(*frequency*, *duration*, *phase=0*, *samplerate=None*, *nchannels=1*)
Returns a pure tone at frequency for duration, using the default samplerate or the given one. The `frequency` and `phase` parameters can be single values, in which case multiple channels can be specified with the `nchannels` argument, or they can be sequences (lists/tuples/arrays) in which case there is one frequency or phase for each channel.

brian.hears.**click**(*duration*, *peak=None*, *samplerate=None*, *nchannels=1*)
Returns a click of the given duration.

If `peak` is not specified, the amplitude will be 1, otherwise `peak` refers to the peak dB SPL of the click, according to the formula `28e-6*10**(peak/20.)`.

brian.hears.**clicks**(*duration*, *n*, *interval*, *peak=None*, *samplerate=None*, *nchannels=1*)
Returns a series of n clicks (see `click()`) separated by interval.

brian.hears.**harmoniccomplex**(*f0*, *duration*, *amplitude=1*, *phase=0*, *samplerate=None*, *nchannels=1*)
Returns a harmonic complex composed of pure tones at integer multiples of the fundamental frequency `f0`. The `amplitude` and `phase` keywords can be set to either a single value or an array of values. In the former case the value is set for all harmonics, and harmonics up the the sampling frequency are generated. In the latter each harmonic parameter is set separately, and the number of harmonics generated corresponds to the length of the array.

brian.hears.**silence**(*duration*, *samplerate=None*, *nchannels=1*)
Returns a silent, zero sound for the given duration. Set nchannels to set the number of channels.

brian.hears.**sequence**(**sounds*, *samplerate=None*)
Returns the sequence of sounds in the list sounds joined together

dB

class brian.hears.**dB_type**
The type of values in dB.

dB values are assumed to be RMS dB SPL assuming that the sound source is measured in Pascals.

class brian.hears.**dB_error**
Error raised when values in dB are used inconsistently with other units.

8.18.2 Filterbanks

class brian.hears.**LinearFilterbank**(*source*, *b*, *a*)
Generalised linear filterbank

Initialisation arguments:

source The input to the filterbank, must have the same number of channels or just a single channel. In the latter case, the channels will be replicated.

b, a The coeffs b, a must be of shape `(nchannels, m)` or `(nchannels, m, p)`. Here `m` is the order of the filters, and `p` is the number of filters in a chain (first you apply `[:, :, 0]`, then `[:, :, 1]`, etc.).

The filter parameters are stored in the modifiable attributes `filt_b`, `filt_a` and `filt_state` (the variable `z` in the section below).

Notes

These notes adapted from scipy's `lfilter()` function.

The filterbank is implemented as a direct II transposed structure. This means that for a single channel and element of the filter cascade, the output y for an input x is defined by:

```
a[0]*y[m] = b[0]*x[m] + b[1]*x[m-1] + ... + b[m]*x[0]
                      - a[1]*y[m-1] - ... - a[m]*y[0]
```

using the following difference equations:

```
y[i] = b[0]*x[i] + z[0,i-1]
z[0,i] = b[1]*x[i] + z[1,i-1] - a[1]*y[i]
...
z[m-3,i] = b[m-2]*x[i] + z[m-2,i-1] - a[m-2]*y[i]
z[m-2,i] = b[m-1]*x[i] - a[m-1]*y[i]
```

where i is the output sample number.

The rational transfer function describing this filter in the z-transform domain is:

```
                    -1              -nb
        b[0] + b[1]z  + ... + b[m] z
Y(z) = --------------------------------- X(z)
                    -1              -na
        a[0] + a[1]z  + ... + a[m] z
```

class brian.hears.**FIRFilterbank**(*source*, *impulse_response*, *use_linearfilterbank=False*, *minimum_buffer_size=None*)

Finite impulse response filterbank

Initialisation parameters:

source Source sound or filterbank.

impulse_response Either a 1D array providing a single impulse response applied to every input channel, or a 2D array of shape `(nchannels, ir_length)` for `ir_length` the number of samples in the impulse response. Note that if you are using a multichannel sound `x` as a set of impulse responses, the array should be `impulse_response=array(x.T)`.

minimum_buffer_size=None If specified, gives a minimum size to the buffer. By default, for the FFT convolution based implementation of `FIRFilterbank`, the minimum buffer size will be `3*ir_length`. For maximum efficiency with FFTs, `buffer_size+ir_length` should be a power of 2 (otherwise there will be some zero padding), and `buffer_size` should be as large as possible.

class brian.hears.**RestructureFilterbank**(*source*, *numrepeat=1*, *type='serial'*, *numtile=1*, *indexmapping=None*)

Filterbank used to restructure channels, including repeating and interleaving.

Standard forms of usage:

Repeat mono source N times:

```
RestructureFilterbank(source, N)
```

For a stereo source, N copies of the left channel followed by N copies of the right channel:

```
RestructureFilterbank(source, N)
```

For a stereo source, N copies of the channels tiled as LRLRLR...LR:

```
RestructureFilterbank(source, numtile=N)
```

For two stereo sources AB and CD, join them together in serial to form the output channels in order ABCD:

```
RestructureFilterbank((AB, CD))
```

For two stereo sources AB and CD, join them together interleaved to form the output channels in order ACBD:

```
RestructureFilterbank((AB, CD), type='interleave')
```

These arguments can also be combined together, for example to AB and CD into output channels AABBCCDDAABBCCDDAABBCCDD:

```
RestructureFilterbank((AB, CD), 2, 'serial', 3)
```

The three arguments are the number of repeats before joining, the joining type ('serial' or 'interleave') and the number of tilings after joining. See below for details.

Initialise arguments:

source Input source or list of sources.

numrepeat=1 Number of times each channel in each of the input sources is repeated before mixing the source channels. For example, with repeat=2 an input source with channels `AB` will be repeated to form `AABB`

type='serial' The method for joining the source channels, the options are `'serial'` to join the channels in series, or `'interleave'` to interleave them. In the case of `'interleave'`, each source must have the same number of channels. An example of serial, if the input sources are `abc` and `def` the output would be `abcdef`. For interleave, the output would be `adbecf`.

numtile=1 The number of times the joined channels are tiled, so if the joined channels are `ABC` and `numtile=3` the output will be `ABCABCABC`.

indexmapping=None Instead of specifying the restructuring via `numrepeat, type, numtile` you can directly give the mapping of input indices to output indices. So for a single stereo source input, `indexmapping=[1,0]` would reverse left and right. Similarly, with two mono sources, `indexmapping=[1,0]` would have channel 0 of the output correspond to source 1 and channel 1 of the output corresponding to source 0. This is because the indices are counted in order of channels starting from the first source and continuing to the last. For example, suppose you had two sources, each consisting of a stereo sound, say source 0 was `AB` and source 1 was `CD` then `indexmapping=[1, 0, 3, 2]` would swap the left and right of each source, but leave the order of the sources the same, i.e. the output would be `BADC`.

class `brian.hears.`**Join**(**sources*)
Filterbank that joins the channels of its inputs in series, e.g. with two input sources with channels AB and CD respectively, the output would have channels ABCD. You can initialise with multiple sources separated by commas, or by passing a list of sources.

class `brian.hears.`**Interleave**(**sources*)
Filterbank that interleaves the channels of its inputs, e.g. with two input sources with channels AB and CD respectively, the output would have channels ACBD. You can initialise with multiple sources separated by commas, or by passing a list of sources.

class `brian.hears.`**Repeat**(*source*, *numrepeat*)
Filterbank that repeats each channel from its input, e.g. with 3 repeats channels ABC would map to AAABBBCCC.

class `brian.hears.`**Tile**(*source*, *numtile*)
Filterbank that tiles the channels from its input, e.g. with 3 tiles channels ABC would map to ABCABCABC.

class `brian.hears.`**FunctionFilterbank**(*source*, *func*, *nchannels=None*)
Filterbank that just applies a given function. The function should take as many arguments as there are sources.

For example, to half-wave rectify inputs:

```
FunctionFilterbank(source, lambda x: clip(x, 0, Inf))
```

The syntax `lambda x: clip(x, 0, Inf)` defines a function object that takes a single argument `x` and returns `clip(x, 0, Inf)`. The numpy function `clip(x, low, high)` returns the values of `x` clipped between `low` and `high` (so if `x<low` it returns `low`, if `x>high` it returns `high`, otherwise it returns `x`). The symbol `Inf` means infinity, i.e. no clipping of positive values.

Technical details

Note that functions should operate on arrays, in particular on 2D buffered segments, which are arrays of shape `(bufsize, nchannels)`. Typically, most standard functions from numpy will work element-wise.

If you want a filterbank that changes the shape of the input (e.g. changes the number of channels), set the `nchannels` keyword argument to the number of output channels.

class `brian.hears.`**SumFilterbank**(*source*, *weights=None*)
Sum filterbanks together with given weight vectors.

For example, to take the sum of two filterbanks:

```
SumFilterbank((fb1, fb2))
```

To take the difference:

```
SumFilterbank((fb1, fb2), (1, -1))
```

class brian.hears.**DoNothingFilterbank**(*source*)
Filterbank that does nothing to its input.

Useful for removing a set of filters without having to rewrite your code. Can also be used for simply writing compound derived classes. For example, if you want a compound Filterbank that does AFilterbank and then BFilterbank, but you want to encapsulate that into a single class, you could do:

```
class ABFilterbank(DoNothingFilterbank):
    def __init__(self, source):
        a = AFilterbank(source)
        b = BFilterbank(a)
        DoNothingFilterbank.__init__(self, b)
```

However, a more general way of writing compound filterbanks is to use CombinedFilterbank.

class brian.hears.**ControlFilterbank**(*source*, *inputs*, *targets*, *updater*, *max_interval=None*)
Filterbank that can be used for controlling behaviour at runtime

Typically, this class is used to implement a control path in an auditory model, modifying some filterbank parameters based on the output of other filterbanks (or the same ones).

The controller has a set of input filterbanks whose output values are used to modify a set of output filterbanks. The update is done by a user specified function or class which is passed these output values. The controller should be inserted as the last bank in a chain.

Initialisation arguments:

source The source filterbank, the values from this are used unmodified as the output of this filterbank.

inputs Either a single filterbank, or sequence of filterbanks which are used as inputs to the updater.

targets The filterbank or sequence of filterbanks that are modified by the updater.

updater The function or class which does the updating, see below.

max_interval If specified, ensures that the updater is called at least as often as this interval (but it may be called more often). Can be specified as a time or a number of samples.

The updater

The updater argument can be either a function or class instance. If it is a function, it should have a form like:

```
# A single input
def updater(input):
    ...

# Two inputs
def updater(input1, input2):
    ...

# Arbitrary number of inputs
def updater(*inputs):
    ...
```

Each argument `input` to the function is a numpy array of shape `(numsamples, numchannels)` where `numsamples` is the number of samples just computed, and `numchannels` is the number of channels in the corresponding filterbank. The function is not restricted in what it can do with these inputs.

Functions can be used to implement relatively simple controllers, but for more complicated situations you may want to maintain some state variables for example, and in this case you can use a class. The object `updater` should be an instance of a class that defines the `__call__` method (with the same syntax as above for functions). In addition, you can define a reinitialisation method `reinit()` which will be called when the `buffer_init()` method is called on the filterbank, although this is entirely optional.

Example

The following will do a simple form of gain control, where the gain parameter will drift exponentially towards target_rms/rms with a given time constant:

```
# This class implements the gain (see Filterbank for details)
class GainFilterbank(Filterbank):
    def __init__(self, source, gain=1.0):
        Filterbank.__init__(self, source)
        self.gain = gain
    def buffer_apply(self, input):
        return self.gain*input

# This is the class for the updater object
class GainController(object):
    def __init__(self, target, target_rms, time_constant):
        self.target = target
        self.target_rms = target_rms
        self.time_constant = time_constant
    def reinit(self):
        self.sumsquare = 0
        self.numsamples = 0
    def __call__(self, input):
        T = input.shape[0]/self.target.samplerate
        self.sumsquare += sum(input**2)
        self.numsamples += input.size
        rms = sqrt(self.sumsquare/self.numsamples)
        g = self.target.gain
        g_tgt = self.target_rms/rms
        tau = self.time_constant
        self.target.gain = g_tgt+exp(-T/tau)*(g-g_tgt)
```

And an example of using this with an input `source`, a target RMS of 0.2 and a time constant of 50 ms, updating every 10 ms:

```
gain_fb = GainFilterbank(source)
updater = GainController(gain_fb, 0.2, 50*ms)
control = ControlFilterbank(gain_fb, source, gain_fb, updater, 10*ms)
```

class `brian.hears.`**`CombinedFilterbank`**(*source*)

Filterbank that encapsulates a chain of filterbanks internally.

This class should mostly be used by people writing extensions to Brian hears rather than by users directly. The purpose is to take an existing chain of filterbanks and wrap them up so they appear to the user as a single filterbank which can be used exactly as any other filterbank.

In order to do this, derive from this class and in your initialisation follow this pattern:

```
class RectifiedGammatone(CombinedFilterbank):
    def __init__(self, source, cf):
```

```
        CombinedFilterbank.__init__(self, source)
        source = self.get_modified_source()
        # At this point, insert your chain of filterbanks acting on
        # the modified source object
        gfb = Gammatone(source, cf)
        rectified = FunctionFilterbank(gfb,
                        lambda input: clip(input, 0, Inf))
        # Finally, set the output filterbank to be the last in your chain
        self.set_output(fb)
```

This combination of a `Gammatone` and a rectification via a `FunctionFilterbank` can now be used as a single filterbank, for example:

```
x = whitenoise(100*ms)
fb = RectifiedGammatone(x, [1*kHz, 1.5*kHz])
y = fb.process()
```

Details

The reason for the `get_modified_source()` call is that the source attribute of a filterbank can be changed after creation. The modified source provides a buffer (in fact, a `DoNothingFilterbank`) so that the input to the chain of filters defined by the derived class doesn't need to be changed.

8.18.3 Filterbank library

class `brian.hears.`**`Gammatone`**(*source*, *cf*, *b=1.019*, *erb_order=1*, *ear_Q=9.26449*, *min_bw=24.7*)
Bank of gammatone filters.

They are implemented as cascades of four 2nd-order IIR filters (this 8th-order digital filter corresponds to a 4th-order gammatone filter).

The approximated impulse response IR is defined as follow $\mathrm{IR}(t) = t^3 \exp(-2\pi b \mathrm{ERB}(f)t)\cos(2\pi f t)$ where $\mathrm{ERB}(f) = 24.7 + 0.108f$ [Hz] is the equivalent rectangular bandwidth of the filter centered at f.

It comes from Slaney's exact gammatone implementation (Slaney, M., 1993, "An Efficient Implementation of the Patterson-Holdsworth Auditory Filter Bank". Apple Computer Technical Report #35). The code is based on Slaney's Matlab implementation.

Initialised with arguments:

`source` Source of the filterbank.

`cf` List or array of center frequencies.

`b=1.019` parameter which determines the bandwidth of the filters (and reciprocally the duration of its impulse response). In particular, the bandwidth = b.ERB(cf), where ERB(cf) is the equivalent bandwidth at frequency `cf`. The default value of `b` to a best fit (Patterson et al., 1992). `b` can either be a scalar and will be the same for every channel or an array of the same length as `cf`.

`erb_order=1, ear_Q=9.26449, min_bw=24.7` Parameters used to compute the ERB bandwidth. $\mathrm{ERB} = ((\mathrm{cf}/\mathrm{ear\_Q})^{\mathrm{erb\_order}} + \mathrm{min\_bw}^{\mathrm{erb\_order}})^{(1/\mathrm{erb\_order})}$. Their default values are the ones recommended in Glasberg and Moore, 1990.

class `brian.hears.`**`ApproximateGammatone`**(*source*, *cf*, *bandwidth*, *order=4*)
Bank of approximate gammatone filters implemented as a cascade of `order` IIR gammatone filters.

The filter is derived from the sampled version of the complex analog gammatone impulse response $g_\gamma(t) = t^{\gamma-1}\lambda e^{i\eta t}$ where γ corresponds to `order`, η defines the oscillation frequency `cf`, and λ defines the bandwidth parameter.

The design is based on the Hohmann implementation as described in Hohmann, V., 2002, "Frequency analysis and synthesis using a Gammatone filterbank", Acta Acustica United with Acustica. The code is based on the Matlab gammatone implementation from Meddis' toolbox.

Initialised with arguments:

source Source of the filterbank.

cf List or array of center frequencies.

bandwidth List or array of filters bandwidth corresponding, one for each cf.

order=4 The number of 1st-order gammatone filters put in cascade, and therefore the order the resulting gammatone filters.

class `brian.hears.`**LogGammachirp**(*source*, *f*, *b=1.019*, *c=1*, *ncascades=4*)
Bank of gammachirp filters with a logarithmic frequency sweep.

The approximated impulse response IR is defined as follows: $\mathrm{IR}(t) = t^3 e^{-2\pi b \mathrm{ERB}(f)t} \cos(2\pi(ft + c \cdot \ln(t))$ where $\mathrm{ERB}(f) = 24.7 + 0.108f$ [Hz] is the equivalent rectangular bandwidth of the filter centered at f.

The implementation is a cascade of 4 2nd-order IIR gammatone filters followed by a cascade of ncascades 2nd-order asymmetric compensation filters as introduced in Unoki et al. 2001, "Improvement of an IIR asymmetric compensation gammachirp filter".

Initialisation parameters:

source Source sound or filterbank.

f List or array of the sweep ending frequencies ($f_{\mathrm{instantaneous}} = f + c/t$).

b=1.019 Parameters which determine the duration of the impulse response. `b` can either be a scalar and will be the same for every channel or an array with the same length as `f`.

c=1 The glide slope (or sweep rate) given in Hz/second. The trajectory of the instantaneous frequency towards f is an upchirp when c<0 and a downchirp when c>0. `c` can either be a scalar and will be the same for every channel or an array with the same length as `f`.

ncascades=4 Number of times the asymmetric compensation filter is put in cascade. The default value comes from Unoki et al. 2001.

class `brian.hears.`**LinearGammachirp**(*source*, *f*, *time_constant*, *c*, *phase=0*)
Bank of gammachirp filters with linear frequency sweeps and gamma envelope as described in Wagner et al. 2009, "Auditory responses in the barn owl's nucleus laminaris to clicks: impulse response and signal analysis of neurophonic potential", J. Neurophysiol.

The impulse response IR is defined as follow $\mathrm{IR}(t) = t^3 e^{-t/\sigma} \cos(2\pi(ft + c/2t^2) + \phi)$ where σ corresponds to `time_constant` and ϕ to `phase` (see definition of parameters).

Those filters are implemented as FIR filters using truncated time representations of gammachirp functions as the impulse response. The impulse responses, which need to have the same length for every channel, have a duration of 15 times the biggest time constant. The length of the impulse response is therefore `15*max(time_constant)*sampling_rate`. The impulse responses are normalized with respect to the transmitted power, i.e. the rms of the filter taps is 1.

Initialisation parameters:

source Source sound or filterbank.

f List or array of the sweep starting frequencies ($f_{\mathrm{instantaneous}} = f + ct$).

time_constant Determines the duration of the envelope and consequently the length of the impulse response.

c=1 The glide slope (or sweep rate) given in Hz/second. The time-dependent instantaneous frequency is `f+c*t` and is therefore going upward when c>0 and downward when c<0. `c` can either be a scalar and will be the same for every channel or an array with the same length as `f`.

phase=0 Phase shift of the carrier.

Has attributes:

length_impulse_response Number of samples in the impulse responses.

impulse_response Array of shape `(nchannels, length_impulse_response)` with each row being an impulse response for the corresponding channel.

class `brian.hears.`**LinearGaborchirp**(*source*, *f*, *time_constant*, *c*, *phase=0*)

Bank of gammachirp filters with linear frequency sweeps and gaussian envelope as described in Wagner et al. 2009, "Auditory responses in the barn owl's nucleus laminaris to clicks: impulse response and signal analysis of neurophonic potential", J. Neurophysiol.

The impulse response IR is defined as follows: $\mathrm{IR}(t) = e^{-t/2\sigma^2}\cos(2\pi(ft + c/2t^2) + \phi)$, where σ corresponds to `time_constant` and ϕ to `phase` (see definition of parameters).

These filters are implemented as FIR filters using truncated time representations of gammachirp functions as the impulse response. The impulse responses, which need to have the same length for every channel, have a duration of 12 times the biggest time constant. The length of the impulse response is therefore `12*max(time_constant)*sampling_rate`. The envelope is a gaussian function (Gabor filter). The impulse responses are normalized with respect to the transmitted power, i.e. the rms of the filter taps is 1.

Initialisation parameters:

source Source sound or filterbank.

f List or array of the sweep starting frequencies ($f_{\mathrm{instantaneous}} = f + c * t$).

time_constant Determines the duration of the envelope and consequently the length of the impluse response.

c=1 The glide slope (or sweep rate) given ins Hz/second. The time-dependent instantaneous frequency is `f+c*t` and is therefore going upward when c>0 and downward when c<0. `c` can either be a scalar and will be the same for every channel or an array with the same length as `f`.

phase=0 Phase shift of the carrier.

Has attributes:

length_impulse_response Number of sample in the impulse responses.

impulse_response Array of shape `(nchannels, length_impulse_response)` with each row being an impulse response for the corresponding channel.

class `brian.hears.`**IIRFilterbank**(*source*, *nchannels*, *passband*, *stopband*, *gpass*, *gstop*, *btype*, *ftype*)

Filterbank of IIR filters. The filters can be low, high, bandstop or bandpass and be of type Elliptic, Butterworth, Chebyshev etc. The `passband` and `stopband` can be scalars (for low or high pass) or pairs of parameters (for stopband and passband) yielding similar filters for every channel. They can also be arrays of shape `(1, nchannels)` for low and high pass or `(2, nchannels)` for stopband and passband yielding different filters along channels. This class uses the scipy iirdesign function to generate filter coefficients for every channel.

See the documentation for scipy.signal.iirdesign for more details.

Initialisation parameters:

samplerate The sample rate in Hz.

nchannels The number of channels in the bank

passband, stopband The edges of the pass and stop bands in Hz. For lowpass and highpass filters, in the case of similar filters for each channel, they are scalars and passband<stopband for low pass or stopband>passband for a highpass. For a bandpass or bandstop filter, in the case of similar filters for each channel, make passband and stopband a list with two elements, e.g. for a bandpass have `passband=[200*Hz, 500*Hz]` and `stopband=[100*Hz, 600*Hz]`. `passband` and `stopband` can also be arrays of shape `(1, nchannels)` for low and high pass or `(2, nchannels)` for stopband and passband yielding different filters along channels.

gpass The maximum loss in the passband in dB. Can be a scalar or an array of length `nchannels`.

gstop The minimum attenuation in the stopband in dB. Can be a scalar or an array of length `nchannels`.

btype One of 'low', 'high', 'bandpass' or 'bandstop'.

ftype The type of IIR filter to design: 'ellip' (elliptic), 'butter' (Butterworth), 'cheby1' (Chebyshev I), 'cheby2' (Chebyshev II), 'bessel' (Bessel).

class `brian.hears.`**Butterworth**(*source*, *nchannels*, *order*, *fc*, *btype='low'*)
Filterbank of low, high, bandstop or bandpass Butterworth filters. The cut-off frequencies or the band frequencies can either be the same for each channel or different along channels.

Initialisation parameters:

samplerate Sample rate.

nchannels Number of filters in the bank.

order Order of the filters.

fc Cutoff parameter(s) in Hz. For the case of a lowpass or highpass filterbank, `fc` is either a scalar (thus the same value for all of the channels) or an array of length `nchannels`. For the case of a bandpass or bandstop, `fc` is either a pair of scalar defining the bandpass or bandstop (thus the same values for all of the channels) or an array of shape `(2, nchannels)` to define a pair for every channel.

btype One of 'low', 'high', 'bandpass' or 'bandstop'.

class `brian.hears.`**Cascade**(*source*, *filterbank*, *n*)
Cascade of `n` times a linear filterbank.

Initialised with arguments:

source Source of the new filterbank.

filterbank Filterbank object to be put in cascade

n Number of cascades

class `brian.hears.`**LowPass**(*source*, *fc*)
Bank of 1st-order lowpass filters

The code is based on the code found in the Meddis toolbox. It was implemented here to be used in the DRNL cochlear model implementation.

Initialised with arguments:

source Source of the filterbank.

fc Value, list or array (with length = number of channels) of cutoff frequencies.

class `brian.hears.`**AsymmetricCompensation**(*source*, *f*, *b=1.0189999999999999*, *c=1*, *ncascades=4*)
Bank of asymmetric compensation filters.

Those filters are meant to be used in cascade with gammatone filters to approximate gammachirp filters (Unoki et al., 2001, Improvement of an IIR asymmetric compensation gammachirp filter, Acoust. Sci. & Tech.). They are

implemented a a cascade of low order filters. The code is based on the implementation found in the AIM-MAT toolbox.

Initialised with arguments:

source Source of the filterbank.

f List or array of the cut off frequencies.

b=1.019 Determines the duration of the impulse response. Can either be a scalar and will be the same for every channel or an array with the same length as `cf`.

c=1 The glide slope when this filter is used to implement a gammachirp. Can either be a scalar and will be the same for every channel or an array with the same length as `cf`.

ncascades=4 The number of time the basic filter is put in cascade.

8.18.4 Cochlear model library

class `brian.hears.`**DRNL**(*source*, *cf*, *type='human'*, *param={}*)

Implementation of the dual resonance nonlinear (DRNL) filter as described in Lopez-Paveda, E. and Meddis, R., "A human nonlinear cochlear filterbank", JASA 2001.

The entire pathway consists of the sum of a linear and a nonlinear pathway.

The linear path consists of a bank of bandpass filters (second order gammatone), a low pass function, and a gain/attenuation factor, g, in a cascade.

The nonlinear path is a cascade consisting of a bank of gammatone filters, a compression function, a second bank of gammatone filters, and a low pass function, in that order.

Initialised with arguments:

source Source of the cochlear model.

cf List or array of center frequencies.

type defines the parameters set corresponding to a certain fit. It can be either:

type='human' The parameters come from Lopez-Paveda, E. and Meddis, R.., "A human nonlinear cochlear filterbank", JASA 2001.

type ='guinea pig' The parameters come from Summer et al., "A nonlinear filter-bank model of the guinea-pig cochlear nerve: Rate responses", JASA 2003.

param Dictionary used to overwrite the default parameters given in the original papers.

The possible parameters to change and their default values for humans (see Lopez-Paveda, E. and Meddis, R.,"A human nonlinear cochlear filterbank", JASA 2001. for notation) are:

```
param['stape_scale']=0.00014
param['order_linear']=3
param['order_nonlinear']=3
```

from there on the parameters are given in the form $x = 10^{\mathrm{p0}+m\log_{10}(\mathrm{cf})}$ where `cf` is the center frequency:

```
param['cf_lin_p0']=-0.067
param['cf_lin_m']=1.016
param['bw_lin_p0']=0.037
param['bw_lin_m']=0.785
param['cf_nl_p0']=-0.052
param['cf_nl_m']=1.016
param['bw_nl_p0']=-0.031
```

```
param['bw_nl_m']=0.774
param['a_p0']=1.402
param['a_m']=0.819
param['b_p0']=1.619
param['b_m']=-0.818
param['c_p0']=-0.602
param['c_m']=0
param['g_p0']=4.2
param['g_m']=0.48
param['lp_lin_cutoff_p0']=-0.067
param['lp_lin_cutoff_m']=1.016
param['lp_nl_cutoff_p0']=-0.052
param['lp_nl_cutoff_m']=1.016
```

class brian.hears.**DCGC**(*source*, *cf*, *update_interval*, *param={}*)

The compressive gammachirp auditory filter as described in Irino, T. and Patterson R., "A compressive gammachirp auditory filter for both physiological and psychophysical data", JASA 2001.

Technical implementation details and notation can be found in Irino, T. and Patterson R., "A Dynamic Compressive Gammachirp Auditory Filterbank", IEEE Trans Audio Speech Lang Processing.

The model consists of a control pathway and a signal pathway in parallel.

The control pathway consists of a bank of bandpass filters followed by a bank of highpass filters (this chain yields a bank of gammachirp filters).

The signal pathway consist of a bank of fix bandpass filters followed by a bank of highpass filters with variable cutoff frequencies (this chain yields a bank of gammachirp filters with a level-dependent bandwidth). The highpass filters of the signal pathway are controlled by the output levels of the two stages of the control pathway.

Initialised with arguments:

source Source of the cochlear model.

cf List or array of center frequencies.

update_interval Interval in samples controlling how often the band pass filter of the signal pathway is updated. Smaller values are more accurate, but give longer computation times.

param Dictionary used to overwrite the default parameters given in the original paper.

The possible parameters to change and their default values (see Irino, T. and Patterson R., "A Dynamic Compressive Gammachirp Auditory Filterbank", IEEE Trans Audio Speech Lang Processing) are:

```
param['b1'] = 1.81
param['c1'] = -2.96
param['b2'] = 2.17
param['c2'] = 2.2
param['decay_tcst'] = .5*ms
param['lev_weight'] = .5
param['level_ref'] = 50.
param['level_pwr1'] = 1.5
param['level_pwr2'] = .5
param['RMStoSPL'] = 30.
param['frat0'] = .2330
param['frat1'] = .005
param['lct_ERB'] = 1.5  #value of the shift in ERB frequencies
param['frat_control'] = 1.08
param['order_gc']=4
param['ERBrate']= 21.4*log10(4.37*cf/1000+1) # cf is the center frequency
param['ERBwidth']= 24.7*(4.37*cf/1000 + 1)
```

class brian.hears.**PMFR**(*source*, *cf*, *update_interval*, *param={}*)
Class implementing the nonlinear auditory filterbank model as described in Tan, G. and Carney, L., "A phenomenological model for the responses of auditory-nerve fibers. II. Nonlinear tuning with a frequency glide", JASA 2003.

The model consists of a control path and a signal path. The control path controls both its own bandwidth via a feedback loop and also the bandwidth of the signal path.

Initialised with arguments:

source Source of the cochlear model.

cf List or array of center frequencies.

update_interval Interval in samples controlling how often the band pass filter of the signal pathway is updated. Smaller values are more accurate but increase the computation time.

param Dictionary used to overwrite the default parameters given in the original paper.

8.18.5 Filterbank group

class brian.hears.**FilterbankGroup**(*filterbank*, *targetvar*, **args*, ***kwds*)
Allows a Filterbank object to be used as a NeuronGroup

Initialised as a standard `NeuronGroup` object, but with two additional arguments at the beginning, and no `N` (number of neurons) argument. The number of neurons in the group will be the number of channels in the filterbank. (TODO: add reference to interleave/serial channel stuff here.)

filterbank The Filterbank object to be used by the group. In fact, any Bufferable object can be used.

targetvar The target variable to put the filterbank output into.

One additional keyword is available beyond that of `NeuronGroup`:

buffersize=32 The size of the buffered segments to fetch each time. The efficiency depends on this in an unpredictable way, larger values mean more time spent in optimised code, but are worse for the cache. In many cases, the default value is a good tradeoff. Values can be given as a number of samples, or a length of time in seconds.

Note that if you specify your own `Clock`, it should have 1/dt=samplerate.

8.18.6 Functions

brian.hears.**erbspace**(**args*, ***kwds*)
Returns the centre frequencies on an ERB scale.

low, high Lower and upper frequencies

N Number of channels

earQ=9.26449, minBW=24.7, order=1 Default Glasberg and Moore parameters.

brian.hears.**asymmetric_compensation_coeffs**(*samplerate*, *fr*, *filt_b*, *filt_a*, *b*, *c*, *p0*, *p1*, *p2*, *p3*, *p4*)
This function is used to generated the coefficient of the asymmetric compensation filter used for the gammachirp implementation.

8.18.7 HRTFs

class brian.hears.**HRTF**(*hrir_l*, *hrir_r=None*)
Head related transfer function.

Attributes

impulse_response The pair of impulse responses (as stereo Sound objects)

fir The impulse responses in a format suitable for using with FIRFilterbank (the transpose of impulse_response).

left, right The two HRTFs (mono Sound objects)

samplerate The sample rate of the HRTFs.

Methods

apply(*sound*)
Returns a stereo Sound object formed by applying the pair of HRTFs to the mono sound input. Equivalently, you can write hrtf(sound) for hrtf an HRTF object.

filterbank(*source*, ***kwds*)
Returns an FIRFilterbank object that can be used to apply the HRTF as part of a chain of filterbanks.

You can get the number of samples in the impulse response with len(hrtf).

class brian.hears.**HRTFSet**(*data*, *samplerate*, *coordinates*)
A collection of HRTFs, typically for a single individual.

Normally this object is created automatically by an HRTFDatabase.

Attributes

hrtf A list of HRTF objects for each index.

num_indices The number of HRTF locations. You can also use len(hrtfset).

num_samples The sample length of each HRTF.

fir_serial, fir_interleaved The impulse responses in a format suitable for using with FIRFilterbank, in serial (LLLLL...RRRRR....) or interleaved (LRLRLR...).

Methods

subset(*condition*)
Generates the subset of the set of HRTFs whose coordinates satisfy the condition. This should be one of: a boolean array of length the number of HRTFs in the set, with values of True/False to indicate if the corresponding HRTF should be included or not; an integer array with the indices of the HRTFs to keep; or a function whose argument names are names of the parameters of the coordinate system, e.g. condition=lambda azim:azim<pi/2.

filterbank(*source*, *interleaved=False*, ***kwds*)
Returns an FIRFilterbank object which applies all of the HRTFs in the set. If interleaved=False then the channels are arranged in the order LLLL...RRRR..., otherwise they are arranged in the order LRLRLR....

You can access an HRTF by index via hrtfset[index], or by its coordinates via hrtfset(coord1=val1, coord2=val2).

Initialisation

data An array of shape (2, num_indices, num_samples) where data[0,:,:] is the left ear and data[1,:,:] is the right ear, num_indices is the number of HRTFs for each ear, and num_samples is the length of the HRTF.

samplerate The sample rate for the HRTFs (should have units of Hz).

coordinates A record array of length `num_indices` giving the coordinates of each HRTF. You can use `make_coordinates()` to help with this.

class `brian.hears.`**`HRTFDatabase`**(*samplerate=None*)
Base class for databases of HRTFs

Should have an attribute 'subjects' giving a list of available subjects, and a method `load_subject(subject)` which returns an `HRTFSet` for that subject.

The initialiser should take (optional) keywords:

samplerate The intended samplerate (resampling will be used if it is wrong). If left unset, the natural samplerate of the data set will be used.

`brian.hears.`**`make_coordinates`**(***kwds*)
Creates a numpy record array from the keywords passed to the function. Each keyword/value pair should be the name of the coordinate the array of values of that coordinate for each location. Returns a numpy record array. For example:

```
coords = make_coordinates(azimuth=[0, 30, 60, 0, 30, 60],
                          elevation=[0, 0, 0, 30, 30, 30])
print coords['azimuth']
```

class `brian.hears.`**`IRCAM_LISTEN`**(*basedir*, *compensated=False*, *samplerate=None*)
`HRTFDatabase` for the IRCAM LISTEN public HRTF database.

For details on the database, see the website.

The database object can be initialised with the following arguments:

basedir The directory where the database has been downloaded and extracted, e.g. `r'D:\HRTF\IRCAM'`.

compensated=False Whether to use the raw or compensated impulse responses.

samplerate=None If specified, you can resample the impulse responses to a different samplerate, otherwise uses the default 44.1 kHz.

The coordinates are pairs `(azim, elev)` where `azim` ranges from 0 to 345 degrees in steps of 15 degrees, and elev ranges from -45 to 90 in steps of 15 degrees.

Obtaining the database

The database can be downloaded here. Each subject archive should be extracted to a folder (e.g. IRCAM) with the names of the subject, e.g. IRCAM/IRC_1002, etc.

class `brian.hears.`**`HeadlessDatabase`**(*n=None*, *azim_max=1.5707963267948966*, *diameter=0.22308 m*, *itd=None*, *samplerate=None*)
Database for creating HRTFSet with artificial interaural time-differences

Initialisation keywords:

n, azim_max, diameter Specify the ITDs for two ears separated by distance `diameter` with no head. ITDs corresponding to `n` angles equally spaced between `-azim_max` and `azim_max` are used. The default diameter is that which gives the maximum ITD as 650 microseconds. The ITDs are computed with the formula `diameter*sin(azim)/speed_of_sound_in_air`. In this case, the generated `HRTFSet` will have coordinates of `azim` and `itd`.

itd Instead of specifying the keywords above, just give the ITDs directly. In this case, the generated `HRTFSet` will have coordinates of `itd` only.

To get the HRTFSet, the simplest thing to do is just:

```
hrtfset = HeadlessDatabase(13).load_subject()
```

The generated ITDs can be returned using the `itd` attribute of the `HeadlessDatabase` object.

Note that the delays induced in the left and right channels are not symmetric as making them so wastes half the samplerate (if the delay to the left channel is itd/2 and the delay to the right channel is -itd/2). Instead, for each channel either the left channel delay is 0 and the right channel delay is -itd (if itd<0) or the left channel delay is itd and the right channel delay is 0 (if itd>0).

8.18.8 Base classes

Useful for understanding more about the internals.

class `brian.hears.`**`Bufferable`**
Base class for Brian.hears classes

Defines a buffering interface of two methods:

`buffer_init()` Initialise the buffer, should set the time pointer to zero and do any other initialisation that the object needs.

`buffer_fetch(start, end)` Fetch the next samples `start:end` from the buffer. Value returned should be an array of shape `(end-start, nchannels)`. Can throw an `IndexError` exception if it is outside the possible range.

In addition, bufferable objects should define attributes:

`nchannels` The number of channels in the buffer.

`samplerate` The sample rate in Hz.

By default, the class will define a default buffering mechanism which can easily be extended. To extend the default buffering mechanism, simply implement the method:

`buffer_fetch_next(samples)` Returns the next `samples` from the buffer.

The default methods for `buffer_init()` and `buffer_fetch()` will define a buffer cache which will get larger if it needs to to accommodate a `buffer_fetch(start, end)` where `end-start` is larger than the current cache. If the filterbank has a `minimum_buffer_size` attribute, the internal cache will always have at least this size, and the `buffer_fetch_next(samples)` method will always get called with `samples>=minimum_buffer_size`. This can be useful to ensure that the buffering is done efficiently internally, even if the user request buffered chunks that are too small. If the filterbank has a `maximum_buffer_size` attribute then `buffer_fetch_next(samples)` will always be called with `samples<=maximum_buffer_size` - this can be useful for either memory consumption reasons or for implementing time varying filters that need to update on a shorter time window than the overall buffer size.

The following attributes will automatically be maintained:

`self.cached_buffer_start`, `self.cached_buffer_end` The start and end of the cached segment of the buffer

`self.cached_buffer_output` An array of shape `((cached_buffer_end-cached_buffer_start, nchannels)` with the current cached segment of the buffer. Note that this array can change size.

class `brian.hears.`**`Filterbank`**(*source*)
Generalised filterbank object

Documentation common to all filterbanks

Filterbanks all share a few basic attributes:

source
The source of the filterbank, a `Bufferable` object, e.g. another `Filterbank` or a `Sound`. It can also be a tuple of sources. Can be changed after the object is created, although note that for some filterbanks this may cause problems if they do make assumptions about the input based on the first source object they were passed. If this is causing problems, you can insert a dummy filterbank (`DoNothingFilterbank`) which is guaranteed to work if you change the source.

nchannels
The number of channels.

samplerate
The sample rate.

duration
The duration of the filterbank. If it is not specified by the user, it is computed by finding the maximum of its source durations. If these are not specified a `KeyError` will be raised (for example, using `OnlineSound` as a source).

To process the output of a filterbank, the following method can be used:

process(*func=None*, *duration=None*, *buffersize=32*)
Returns the output of the filterbank for the given duration.

func If a function is specified, it should be a function of one or two arguments that will be called on each filtered buffered segment (of shape `(buffersize, nchannels)` in order. If the function has one argument, the argument should be buffered segment. If it has two arguments, the second argument is the value returned by the previous application of the function (or 0 for the first application). In this case, the method will return the final value returned by the function. See example below.

duration=None The length of time (in seconds) or number of samples to process. If no `func` is specified, the method will return an array of shape `(duration, nchannels)` with the filtered outputs. Note that in many cases, this will be too large to fit in memory, in which you will want to process the filtered outputs online, by providing a function `func` (see example below). If no duration is specified, the maximum duration of the inputs to the filterbank will be used, or an error raised if they do not have durations (e.g. in the case of `OnlineSound`).

buffersize=32 The size of the buffered segments to fetch, as a length of time or number of samples. 32 samples typically gives reasonably good performance.

For example, to compute the RMS of each channel in a filterbank, you would do:

```
def sum_of_squares(input, running_sum_of_squares):
    return running_sum_of_squares+sum(input**2, axis=0)
rms = sqrt(fb.process(sum_of_squares)/nsamples)
```

Alternatively, the buffer interface can be used, which is described in more detail below.

Filterbank also defines arithmetical operations for +, -, *, / where the other operand can be a filterbank or scalar.

Details on the class

This class is a base class not designed to be instantiated. A Filterbank object should define the interface of `Bufferable`, as well as defining a `source` attribute. This is normally a `Bufferable` object, but could be an iterable of sources (for example, for filterbanks that mix or add multiple inputs).

The `buffer_fetch_next(samples)` method has a default implementation that fetches the next input, and calls the `buffer_apply(input)` method on it, which can be overridden by a derived class. This is typically the easiest way to implement a new filterbank. Filterbanks with multiple sources will need to override this default implementation.

There is a default `__init__` method that can be called by a derived class that sets the `source`, `nchannels` and `samplerate` from that of the `source` object. For multiple sources, the default implementation will check that each source has the same number of channels and samplerate and will raise an error if not.

There is a default `buffer_init()` method that calls `buffer_init()` on the `source` (or list of sources).

Example of deriving a class

The following class takes N input channels and sums them to a single output channel:

```
class AccumulateFilterbank(Filterbank):
    def __init__(self, source):
        Filterbank.__init__(self, source)
        self.nchannels = 1
    def buffer_apply(self, input):
        return reshape(sum(input, axis=1), (input.shape[0], 1))
```

Note that the default `Filterbank.__init__` will set the number of channels equal to the number of source channels, but we want to change it to have a single output channel. We use the `buffer_apply` method which automatically handles the efficient cacheing of the buffer for us. The method receives the array `input` which has shape `(bufsize, nchannels)` and sums over the channels (`axis=1`). It's important to reshape the output so that it has shape `(bufsize, outputnchannels)` so that it can be used as the input to subsequent filterbanks.

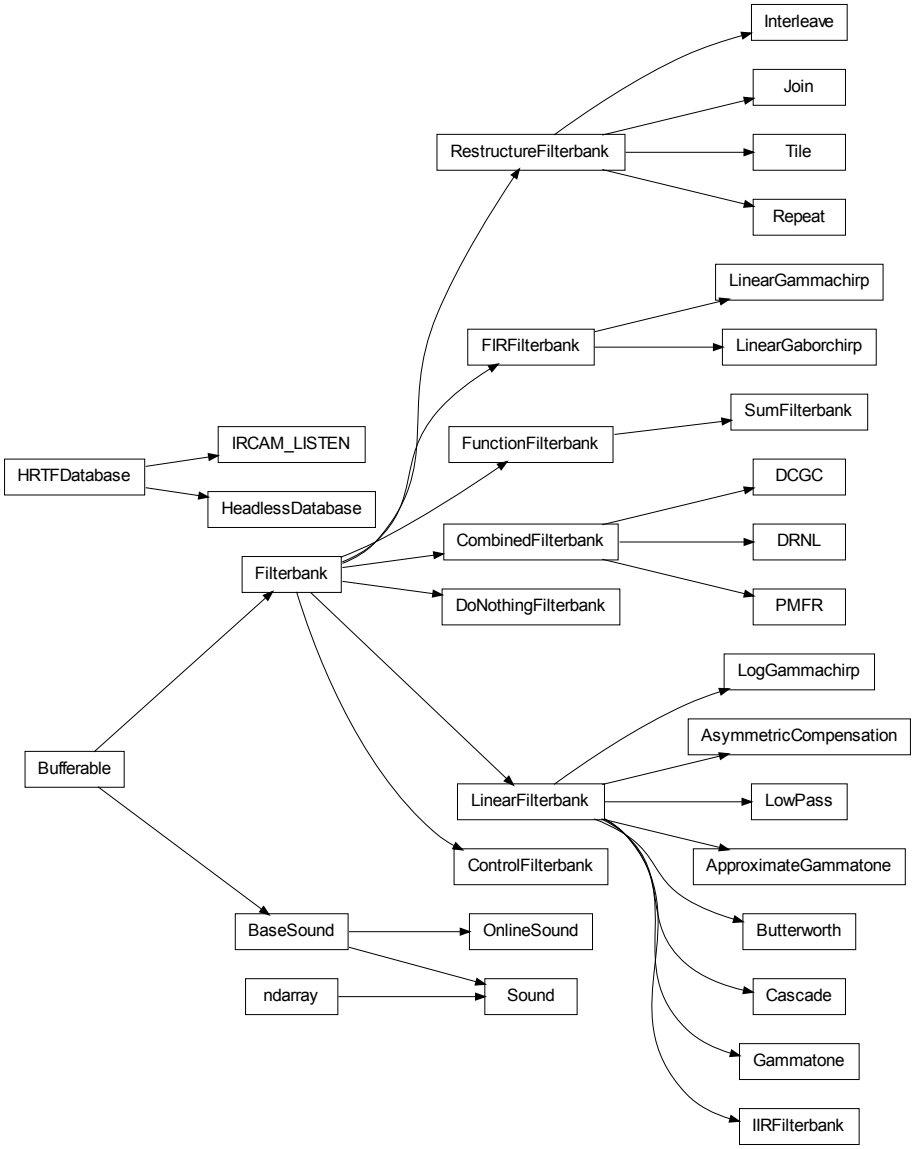
class `brian.hears.`**BaseSound**
Base class for Sound and OnlineSound

class `brian.hears.`**OnlineSound**

8.18.9 Options

There are several relevant global options for Brian hears. In particular, activating scipy Weave support with the `useweave=True` will give considerably faster linear filtering. See *Preferences* and *Compiled code* for more details.

8.18.10 Class diagram



8.19 Magic in Brian

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()`.

brian.**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.

8.20 Tests

brian.**run_all_tests**()

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.

CHAPTER

TEN

EXPERIMENTAL FEATURES

The following features are located in the `experimental` package inside Brian, and are subject to change without notice. The most likely changes are ones of syntax and naming, although functionality may also be subject to change.

10.1 Code generation

Brian has support for automatic generation of C code, detailed in *Compiled code*. We also have experimental support for C code generation more widely, implementing the algorithms described in Goodman (2010). This support can be activated using the `usecodegen*`, `usenewpropagate` and `usecstdp` global preferences (see *Preferences*).

Note that not all code will run without problems using code generation yet, but in most cases it will and speed improvements can be very substantial, especially for STDP.

10.1.1 References

- Goodman DFM (2010). Code Generation: A Strategy for Neural Network Simulators. Neuroinformatics 8, no. 3 (9). doi:10.1007/s12021-010-9082-x. [pdf]

10.2 GPU/CUDA

Brian has some experimental support for doing numerical integration only using GPUs, using the PyCUDA package.

Note that only numerical integration is done on the GPU, which means that variables that can be altered on the CPU (via synapses or user operations) need to be copied to and from the GPU each time step, as well as variables that are used for thresholding and reset operations. This creates a memory bandwidth bottleneck, which means that for the moment the GPU code is only useful for complicated neuron models such as Hodgkin-Huxley type neurons (although in this case it can lead to very substantial speed improvements).

class `brian.experimental.cuda.`**`GPUNeuronGroup`**(*N*, *model*, *threshold=None*, *reset=No reset*, *init=None*, *refractory=0.0 s*, *level=0*, *clock=None*, *order=1*, *implicit=False*, *unit_checking=True*, *max_delay=0.0 s*, *compile=False*, *freeze=False*, *method=None*, *precision='double'*, *maxblocksize=512*, *forcesync=False*, *pagelocked_mem=True*, *gpu_to_cpu_vars=None*, *cpu_to_gpu_vars=None*)

Neuron group which performs numerical integration on the GPU.

Warning: This class is still experimental, not supported and subject to change in future versions of Brian.

Initialised with arguments as for `NeuronGroup` and additionally:

precision='double' The GPU scalar precision to use, older models can only use `precision='float'`.

maxblocksize=512 If GPU compilation fails, reduce this value.

forcesync=False Whether or not to force copying of state variables to and from the GPU each time step. This is slow, so it is better to specify precisely which variables should be copied to and from using `gpu_to_cpu_vars` and `cpu_to_gpu_vars`.

pagelocked_mem=True Whether to store state variables in pagelocked memory on the CPU, which makes copying data to/from the GPU twice as fast.

cpu_to_gpu_vars=None, gpu_to_cpu_vars=None Which variables should be copied each time step from the CPU to the GPU (before state update) and from the GPU to the CPU (after state update).

The point of the copying of variables to and from the GPU is that the GPU maintains a separate memory from the CPU, and so changes made on either the CPU or GPU won't automatically be reflected in the other. Since only numerical integration is done on the GPU, any state variable that is modified by incoming synapses, for example, should be copied to and from the GPU each time step. In addition, any variables used for thresholding or resetting need to be appropriately copied (GPU->CPU for thresholding, and both for resetting).

10.3 Multilinear state updater

class `brian.experimental.multilinearstateupdater.`**MultiLinearNeuronGroup**(*eqs*, *subs*, *clock=None*, *level=0*, ***kwds*)

Make a NeuronGroup with a linear differential equation for each neuron

You give a single set of differential equations with parameters, the variables you want substituted should be defined as parameters in the equations, but they will not be treated as parameters, instead they will be substituted. You also pass a list of variables to have their values substituted, and these names should exist in the namespace initialising the MultiLinearNeuronGroup.

Arguments:

eqs should be the equations, and must be a string not an `Equations` object.

subs A list of variables to be substituted with values.

level How many levels up to look for the equations' namespace.

clock If you want.

kwds Any additonal arguments to pass to `NeuronGroup` init.

Example:

```
eqs = '''
dv/dt = k*v/(1*second) : 1
dw/dt = k*w/(1*second) : 1
k : 1
'''
k = array([-1,-2,-3])
```

```
subs = ['k']
G = MultiLinearNeuronGroup(eqs, subs)
G.v = 1
G.w = 0
M = StateMonitor(G, 'v', record=True)
run(1*second)
for i in range(len(G)):
    plot(M.times, M[i])
show()
```

10.4 Realtime Connection Monitor

You can visual weight matrices in realtime, using the PyGame package with the following class.

class `brian.experimental.realtime_monitor.`**`RealtimeConnectionMonitor`**(*C*, *size=None*, *scaling='fast'*, *wmin=None*, *wmax=None*, *clock=None*, *cmap=<matplotlib.colors.LinearSeg instance at 0x03A82C10>*)

Realtime monitoring of weight matrix

Short docs:

`C` Connection to monitor

`size` Dimensions (width, height) of output window, leave as `None` to use `C.W.shape`.

`scaling` If output window dimensions are different to connection matrix, scaling is used, options are `'fast'` for no interpolation, or `'smooth'` for (slower) smooth interpolation.

`wmin, wmax` Minimum and maximum weight matrix values, if left to `None` then the min/max of the weight matrix at each moment is used (and this scaling can change over time).

`clock` Leave to `None` for an update every 100ms.

`cmap` Colour map to use, black and white by default. Get other values from `matplotlib.cm.*`.

Note that this class uses PyGame and due to a limitation with pygame, there can be only one window using it. Other options are being considered.

CHAPTER

ELEVEN

DEVELOPER'S GUIDE

This section is intended as a guide to how Brian functions internally for people developing Brian itself, or extensions to Brian. It may also be of some interest to others wishing to better understand how Brian works internally.

11.1 Guidelines

The basic principles of developing Brian are:

1. For the user, the emphasis is on making the package flexible, readable and easy to use. See the paper "The Brian simulator" in Frontiers in Neuroscience for more details.
2. For the developer, the emphasis is on keeping the package maintainable by a small number of people. To this end, we use stable, well maintained, existing open source packages whenever possible, rather than writing our own code.

Coding conventions. We use the PEP-8 coding conventions for our code. Syntax is chosen as much as possible from the user point of view, to reflect the concepts as directly as possible. Ideally, a Brian script should be readable by someone who doesn't know Python or Brian, although this isn't always possible. Function and class names should be explicit rather than abbreviated.

Documentation. It is very important to maintain documentation. We use the Sphinx documentation generator tools. The documentation is all hand written. Sphinx source files are stored in the `docs_sphinx` folder in the repository, and compiled HTML files are stored in the `docs` folder. Most of the documentation is stored directly in the Sphinx source text files, but reference documentation for important Brian classes and functions are kept in the documentation strings of those classes themselves. This is automatically pulled from these classes for the reference manual section of the documentation. The idea is to keep the definitive reference documentation near the code that it documents, serving as both a comment for the code itself, and to keep the documentation up to date with the code.

In the code, every class or function should start with an explanation of what it does, unless it is trivial. A good idea is to use explicit names rather than abbreviations, so that you instantly understand what it is about. Inside a function, important chunks should also be commented.

Testing. Brian uses the nose package for its testing framework. Tests are stored in the `brian/tests` directory. Tests associated to a Brian module are stored in `brian/tests/testinterface` and tests of the mathematical correctness of Brian's algorithms are stored in `brian/tests/testcorrectness`.

Errors. It is a good idea to start an important function (e.g. object initialisation) with a check of the arguments, and possibly issue errors. This way errors are more understandable by the user.

Enhancements. Brian uses a system parallel to the Python Enhancement Proposals (PEPs) system for Python, called *Brian Enhancement Proposals* (BEPs). These are stored in `dev/BEPs`. Ideas for new functionality for Brian are put in here for comment and discussion. A BEP typically includes:

- How the feature will look from user point of view, with example scripts.

- Detailed implementation ideas and options.

We also use the Brian development mailing list.

11.1.1 Contributing code

First of all, you should register to the developers mailing list. If you want to modify existing modules, you should make sure that you work on the latest SVN version. We use the Eclipse IDE because it has a nice Python plugin (Pydev) and SVN plugin, but of course you can use your preferred IDE. The next step is to carefully read the guidelines in this guide.

Now that you wrote your code:

- Write a test for it in `brian/tests/testinterface`. If it is a new module, create a new file `test_mymodule.py`;
- Write documentation, both in the file (see how it's done in existing modules) and, if appropriate, in the relevant file in `docs_sphinx`. We use the Sphinx documentation generator tools. If you want to see how it looks, generate the html docs by executing `dev/tools/docs/build_html.py`. The html files will then be in `docs`.
- If it is a significant feature, write an example script in `examples` and insert a line in `examples/examples_guide.txt`.
- Create a patch file. For example with Eclipse, right-click on the Brian project, then Team > Create Patch > Save in filesystem, then Next > Project.
- Send your patch as an attachment to the developers mailing list and make sure the subject of your message starts with [PATCH]. Then describe your patch in your message.

From that point, your patch will either be directly included in the svn or (more likely) will be first discussed in the mailing list.

New modules. New Brian modules typically start in the `dev/ideas` folder, then go to `brian/experimental` when they starting looking like modules. They move to the main folder when they are stable (especially the user syntax).

11.2 Simulation principles

The following paper outlines the principles of Brian simulation: Goodman, D and Brette R (2008), Brian: a simulator for spiking neural networks in Python, Front. Neuroinform. doi:10.3389/neuro.11.005.2008.

This one describes the simulation algorithms, which are based on vectorisation: Brette R and Goodman, DF, Vectorised algorithms for spiking neural network simulation, Neural Computation (in press).

11.2.1 Sample script

Below we present a Brian script, and a translation into pure Python to illustrate the basic principles of Brian simulations.

Original Brian script

A script in Brian:

```
'''
Very short example program.
'''
from brian import *
from time import time

N=10000        # number of neurons
Ne=int(N*0.8) # excitatory neurons
Ni=N-Ne       # inhibitory neurons
p=80./N
duration=1000*ms

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(N,model=eqs,
              threshold=-50*mV,reset=-60*mV)
P.v=-60*mV+10*mV*rand(len(P))
Pe=P.subgroup(Ne)
Pi=P.subgroup(Ni)

Ce=Connection(Pe,P,'ge',weight=1.62*mV,sparseness=p)
Ci=Connection(Pi,P,'gi',weight=-9*mV,sparseness=p)

M=SpikeMonitor(P)
trace=StateMonitor(P,'v',record=0)

t1=time()
run(1*second)
t2=time()
print "Simulated in",t2-t1,"s"
print len(M.spikes),"spikes"

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

Equivalent in pure Python

The script above translated into pure Python (no Brian):

```
'''
A pure Python version of the CUBA example, that reproduces basic Brian principles.
'''
from pylab import *
from time import time
from random import sample
from scipy import random as scirandom

"""
Parameters
"""
```

```
N=10000         # number of neurons
Ne=int(N*0.8) # excitatory neurons
Ni=N-Ne       # inhibitory neurons
mV=ms=1e-3    # units
dt=0.1*ms     # timestep
taum=20*ms    # membrane time constant
taue=5*ms
taui=10*ms
p=80.0/N # connection probability (80 synapses per neuron)
Vt=-1*mV      # threshold = -50+49
Vr=-11*mV     # reset = -60+49
we=60*0.27/10 # excitatory weight
wi=-20*4.5/10 # inhibitory weight
duration=1000*ms

"""
Equations
---------
eqs='''
dv/dt = (ge+gi-(v+49*mV))/(20*ms) : volt
dge/dt = -ge/(5*ms) : volt
dgi/dt = -gi/(10*ms) : volt
'''

This is a linear system, so each update corresponds to
multiplying the state matrix by a (3,3) 'update matrix'
"""

# Update matrix
A=array([[exp(-dt/taum),0,0],
         [taue/(taum-taue)*(exp(-dt/taum)-exp(-dt/taue)),exp(-dt/taue),0],
         [taui/(taum-taui)*(exp(-dt/taum)-exp(-dt/taui)),0,exp(-dt/taui)]]).T

"""
State variables
---------------
P=NeuronGroup(4000,model=eqs,
              threshold=-50*mV,reset=-60*mV)
"""
S=zeros((3,N))

"""
Initialisation
--------------
P.v=-60*mV+10*mV*rand(len(P))
"""
S[0,:]=rand(N)*(Vt-Vr)+Vr # Potential: uniform between reset and threshold

"""
Connectivity matrices
---------------------
Pe=P.subgroup(3200) # excitatory group
Pi=P.subgroup(800)  # inhibitory group
Ce=Connection(Pe,P,'ge',weight=1.62*mV,sparseness=p)
Ci=Connection(Pi,P,'gi',weight=-9*mV,sparseness=p)
"""
We_target=[]
We_weight=[]
```

```
for _ in range(Ne):
    k=scirandom.binomial(N,p,1)[0]
    target=sample(xrange(N),k)
    target.sort()
    We_target.append(target)
    We_weight.append([1.62*mV]*k)
Wi_target=[]
Wi_weight=[]
for _ in range(Ni):
    k=scirandom.binomial(N,p,1)[0]
    target=sample(xrange(N),k)
    target.sort()
    Wi_target.append(target)
    Wi_weight.append([-9*mV]*k)

"""
Spike monitor
-------------
M=SpikeMonitor(P)

will contain a list of (i,t), where neuron i spiked at time t.
"""
spike_monitor=[] # Empty list of spikes

"""
State monitor
-------------
trace=StateMonitor(P,'v',record=0) # record only neuron 0
"""
trace=[] # Will contain v(t) for each t (for neuron 0)

"""
Simulation
----------
run(duration)
"""
t1=time()
t=0*ms
while t<duration:
    # STATE UPDATES
    S[:]=dot(A,S)

    # Threshold
    all_spikes=(S[0,:]>Vt).nonzero()[0]      # List of neurons that meet threshold condition

    # PROPAGATION OF SPIKES
    # Excitatory neurons
    spikes=(S[0,:Ne]>Vt).nonzero()[0]        # In Brian we actually use bisection to speed it up
    for i in spikes:
        S[1,We_target[i]]+=We_weight[i]

    # Inhibitory neurons
    spikes=(S[0,Ne:N]>Vt).nonzero()[0]
    for i in spikes:
        S[2,Wi_target[i]]+=Wi_weight[i]

    # Reset neurons after spiking
    S[0,all_spikes]=Vr                        # Reset membrane potential
```

```
    # Spike monitor
    spike_monitor+=[(i,t) for i in all_spikes]

    # State monitor
    trace.append(S[0,0])

    t+=dt

t2=time()
print "Simulated in",t2-t1,"s"
print len(spike_monitor),"spikes"

"""
Plot
----
subplot(211)
raster_plot(M)
subplot(212)
plot(trace.times/ms,trace[0]/mV)
show()

Here we cheat a little.
"""
from brian import raster_plot
class M:
    pass
M.spikes=spike_monitor
subplot(211)
raster_plot(M)
subplot(212)
plot(arange(len(trace))*dt/ms,array(trace)/mV)
show()
```

11.3 Main code structure

11.3.1 Overview

Brian features can be broadly categorised into *construction* of the network, and *running* the network.

Constructing the network

The following objects need to be specified by the user explicitly or implicitly:

- `NeuronGroup`
- `Connection`
- Monitors
- `Network`

After that, the network needs to be *prepared*. Preparation of the network involves initialising objects' data structures appropriately, in particular compressing the `Connection` matrices. Connection matrices are initially stored as instances of a `ConstructionMatrix` class (sparse, dense, etc.), and then later *compressed* into an instance of a `ConnectionMatrix` class. Two levels are necessary, because at construction time, all matrices have to be editable,

whereas at runtime, for efficiency reasons, some matrix types are read-only or partially read-only. Data structures appropriate to the construction of a matrix, particularly sparse matrices, are not the most efficient for runtime access.

Constructing the `NeuronGroup` object is a rather complicated operation, involving the construction of many subsidiary objects. The most complicated aspect is the creation, manipulation and analysis of an `Equations` object.

Running the network

The network is run by repeatedly evaluating the 'update schedule' and updating the clock or clocks. The 'update schedule' is user specifiable, but usually consists of the following sequence of operations (interspersed with optional user network operation calls):

- Update state variables of `NeuronGroup`
- Call thresholding function
- Push spikes into `SpikeContainer`
- Propagate spikes (possibly with delays) via `Connection`
- Call reset function on neurons which have spiked

11.3.2 Details of network construction

Construction of `NeuronGroup`

The `NeuronGroup` object is responsible for storing the state variables of each of its neurons, for updating them each time step, generating spikes via a thresholding mechanism, storing spikes so that they can be accessed with a delay, and resetting state variables after spiking. State variable update is done by a `StateUpdater` class defined in `brian/stateupdater.py`. Thresholding is done by a `Threshold` class defined in `brian/threshold.py` and resetting is done by a `Reset` class defined in `brian/reset.py`. The `__init__` method of `NeuronGroup` takes these objects as arguments, but it also has various additional keywords which can be used more intuitively. In this case, the appropriate object is selected automatically. For example, if you specify `reset=0*mV` in the keyword arguments, Brian generates a `Reset(0*mV)` object. The `NeuronGroup.__init__()` method code is rather complicated and deals with many special cases.

The most complicated aspect of this is the definition of the state variables and the update procedure. Typically, the user simply gives a list of differential equations, and Brian attempts to automatically extract the appropriate state variable definitions, and creates a differential equation solver appropriate to them (it needs some help in this at the moment, e.g. specifying the order or type of the solver). The main work in this is done by the `magic_state_updater()` function, which uses the `Equations` object (see next section).

Once the state variables are defined, various internal objects are created. The state variables are stored in the `_S` attribute of a `NeuronGroup`. This is an MxN matrix where M is the number of variables and N is the number of neurons.

The other major data structure generated is the `LS` attribute (last spikes). This is a `SpikeContainer` instance, a circular array used to contain spikes. See `brian/utils/circular.py`.

Finally note that the construction of many of these objects requires a `Clock` object, which can either be specified explicitly, or is guessed by the `guess_clock()` function which searches for clocks using the magic module (see below). `EventClock` objects are excluded from this guessing.

The `magic_state_updater()` function and the `Equations` object

This function returns an appropriate `StateUpdater` object and a list of the dynamic variables of an `Equations` object. It uses methods of the `Equations` object to do this (such as `Equations.is_linear()`).

The `Equations` object can be constructed in various ways. It can be constructed from a multi-line string or by adding (concatenating) other `Equations` objects. Construction by multi-line string is done by pattern matching. The four forms are:

1. `dx/dt = f : unit` (differential equation)
2. `x = f : unit` (equation)
3. `x = y` (alias)
4. `x : unit` (parameter)

Differential equations and parameters are dynamic variables, equations and aliases are just computed and substituted when necessary. The `f` patterns in the forms above are stored for differential equations and parameters. For the solution of nonlinear equations, these `f` patterns are executed as Python code in the evaluation of the state update. For example, the equations `dV/dt = -V*V/(10*ms) : 1` and `dW/dt = cos(W)/(20*ms) : 1` are numerically evaluated with an Euler method as the following code (generated from the list of dynamic variables and their defining strings):

```
V, W = P._S
V__tmp, W__tmp = P._dS
V__tmp[:] = -V*V/(10*ms)
W__tmp[:] = cos(W)/(20*ms)
P._S += dt*P._dS
```

This code generation is done by the `Equations.forward_euler()` family of methods.

In the case where the equations are linear, they are solved by a matrix exponential using the code in `get_linear_equations()` defined in `brian/stateupdater.py`.

Finally, note that equations strings can contain references to names of objects that are defined in the namespace of the string, and the `Equations` object can pick these out. It does this by inspecting the call stack, extracting the namespace for the appropriate level (which has to be kept track of), and plucking out the appropriate name. The `level=...` keywords you see dotted around Brian's code are there to keep track of these levels for this reason.

Construction of `Connection`

`Connection` objects provide methods for storing weight matrices and propagating spikes. Spike propagation is done via the `Connection.do_propagate()` and `Connection.propagate()` methods. Weight matrices are stored in the `W` attribute. Initially, weight matrices are `ConstructionMatrix` objects and are converted by the `Connection.compress()` method, via the matrices' `connection_matrix()` methods to `ConnectionMatrix` objects. The idea is to have two data structures, one appropriate to the construction of a matrix, supporting adding and removing new synapses, and one appropriate to runtime behaviour, focussing on fast row access above all else. There are three matrix structures, 'dense', 'sparse' and 'dynamic' (and 'computed' may be added later). The 'dense' matrix is just a full 2D array, and the matrix objects just reproduce the functionality of numpy arrays. The 'sparse' and 'dynamic' structures are sparse matrices. The first doesn't allow you to add or remove elements at runtime and is very optimised, the second does allow you to and is less optimised. Both are more optimised than scipy's sparse matrices, which are used as the basis for the construction phase.

`Connection` objects can handle homogeneous delays (all synapses with the same delay) by pulling spikes from `NeuronGroup`'s `LS` object with a delay. Heterogeneous delays (each synapse with a different delay) are done by the `DelayConnection` object, which stores a `_delayvec` attribute alongside the `W` attribute. The delay matrix is of the same type as the weight matrix and in the case of sparse matrices must have nonzero elements at the same places. The `Connection` object automatically turns itself into a `DelayConnection` object if heterogeneous delays are requested, so that the user doesn't even need to know of the existence of `DelayConnection`.

The `Connection` object also provides methods for initialising the weight matrices either fully, randomly, etc. (See the user docs.)

Construction of monitors

The `SpikeMonitor` class of monitors derive from `Connection`. Rather than propagating spikes to another group, they store them in a list. The work is done in the `SpikeMonitor.propagate()` method.

The `StateMonitor` class of monitors derive from `NetworkOperation`. Network operations are called once every time step and execute arbitrary Python code. The `StateMonitor` class of monitors record state variables each time step to a list.

Construction of `Network`

When the user calls the function `run()`, a `MagicNetwork` object is created, and the `Network.run()` method is called. `MagicNetwork` gathers, using the magic module, a list of all appropriate objects and runs them together. Alternatively, the user can specify their own list of objects using a `Network` object. Each time an object is added to a `Network` either via the initialiser or the `Network.add()` method, it checks to see if it has an attribute `contained_objects`, and if so it adds all the objects in that to the network too. This allows, for example, the `STDP` object to contained `NeuronGroup` and `Connection` objects which the user doesn't see, but are used to implement the STDP functionality.

The `Network.run()` method calls the `Connection.compress()` method on every `Connection` object to convert construction matrices to connection matrices. It also builds an update schedule (see below).

The magic module

The magic module is used for tracking instances of objects. A class that derives from the `magic.InstanceTracker` class can be tracked in this way, including `NeuronGroup`, `Connection`, `NetworkOperation` and `Clock`. The `find_instances()` function can be used to search for instances. Note that `find_instances()` will only return instances which were instantiated in the same execution frame as the `find_instances()` calling frame, or (if the `level` keyword is used) one of the frames higher up in the call stack. The idea is that you may have modular code with objects defined in different places, but that you don't want to use all objects that exist at all in the network. This system causes a bit of trouble, but seems unavoidable. See the user manual section *Projects with multiple files or functions* for details on getting around this.

11.3.3 Details of network running

Update schedules

An update schedule gives the sequence of operations to be carried out each time step of the simulation. Typically this is: state update and threshold; propagation; reset, although an option is available for switching propagation and reset around. Network operations can be weaved in anywhere amongst these basic steps. See the reference documentation for the `Network` object for more details.

Simulation proceeds by choosing the clock with the lowest current time, selecting all objects which have that clock as their clock, and performing the update schedule on those objects, before applying the `Clock.tick()` method to increment the clock time by `dt`.

Network operations

A `NetworkOperation` object is called as if it were a function, i.e. the `__call__()` method is called with no arguments. The `network_operation()` decorator exists to convert a function into a suitable `NetworkOperation` object. This technique is used for the internal functioning of many of Brian's features (such as `StateMonitor`).

NeuronGroup update

The NeuronGroup.update() method does the following three things. First of all it calls the StateUpdater to update the state variables. Then it calls its Threshold object if one exists to extract the indices of the spiking neurons. Finally it pushes these into the LS attribute for extraction by any Connection objects.

NeuronGroup reset

The Reset.__call__() method pulls spike from the NeuronGroup's LS attribute and then resets the state variables for those.

Spike propagation

The Connection.do_propagate() method does two things, it gets the spike indices to propagate (with homogeneous delays if chosen) from the LS attribute of the NeuronGroup and then passes these to its Connection.propagate() method. This method extracts a list of connection matrix rows using the ConnectionMatrix.get_rows() method. This method returns a list of ConnectionVector instances. There are two types of ConnectionVector, dense and sparse. Dense ones are simply numpy arrays, sparse ones consist of two numpy arrays, an array of values and an array of corresponding column indices. The SparseConnectionVector class has some methods which make this distinction seamless to the user in most instances, although developers need to be aware of it. Finally, the Connection.propagate() method goes through this list applying the row vectors one by one. The pure Python version of this is straightforward, but there is also a C++ accelerated version which uses the scipy Weave package if the user has a suitable compiler on their system. This version is much more efficient, but the code is rather dense and difficult to understand.

11.4 Equations

An Equation is a set of single lines in a string:

1. dx/dt = f : unit (differential equation)
2. x = f : unit (equation)
3. x = y (alias)
4. x : unit (parameter)

The equations may be defined on multiple lines with the character . Comments using # may also be included.

Two special variables are defined: t (time) and xi (white noise). Ultimately, it should be possible (using Sympy) to define equations implicitly, e.g.: 'tau*dv/dt=-v : unit' (although it makes unit specification ambiguous).

An equation can be seen as a set of functions or code and a namespace to evaluate them. A key part of object construction is the construction of the namespace (after parsing).

11.4.1 Namespace construction

The namespaces are stored in eq._namespace. Each equation (string) has a specific namespace.

Proposition for a simplification: there could be just one namespace per Equation object rather than per string. Possible conflicts would be dealt with when equations are added (with prefix as when inserting static variables, see below).

Variable substitution

These are simply string substitutions.

- Equation('dv/dt=-v/tau:volt',tau='taum')

The name of the variable (tau) is changed in the string to taum.

- Equation('dv/dt=-v/tau:volt',tau=None)

The name of the variable (tau) is changed in the string to a unique identifier.

Explicit namespace

- Equation('dv/dt=-v/tau:volt',tau=2*ms)

The namespace is explicitly given: {'tau':2*ms}. In this case, Brian does not try to build a namespace "magically", so the namespace must be exhaustive. Units need not be passed.

Implicit namespace

- Equation('dv/dt=-v/tau:volt')

The namespace is built from the globals and locals in the caller's frame. For each identifier in the string, the name is looked up in: 1) locals of caller, 2) globals of caller, 3) globals of equations.py module (typically units). Identifiers can be any Python object (for example functions).

Issues

- Special variables (xi and t) are not taken into account at this stage, i.e., they are integrated in the namespace if present. This should probably be fixed and a warning should be raised. A warning is raised for t at the preparation stage (see below).
- If identifiers are not found, then no error is raised. This is to allow equations to be built in several pieces, which is useful in particular for library objects.
- If an identifier is found whose name is the same as the name of a variable, then no error is raised here and it is included in the namespace. This is difficult to avoid in the case when equations are built in several pieces (e.g. the conflict appears only when the pieces are put together). A warning is issued at the preparation stage (see below).

11.4.2 Attributes after initialisation

After initialisation, an Equation object contains:

- a namespace (_namespace)
- a dictionary of units for all variables (_units)
- a dictionary of strings corresponding to each variable (right hand side of each equation), including parameters and aliases (_string). Parameters are defined as differential equations with RHS 0*unit/second. All comments are removed and multiline strings are concatenated.
- a list of variables of non-differential equations (_eq_names)
- a list of variables of differential equations, including parameters (_diffeq_names)
- a list of variables of differential equations, excluding parameters (_diffeq_names_nonzero)

- a dictionary of aliases (_alias), mapping a variable name to its alias

There is no explicit list of parameters, maybe it should be added. Nothing more is done at initialisation time (no units checking, etc). The reason is that the equation set might not be complete at this time, in the case when equations are built in several pieces. Various checks are done using the prepare() method.

11.4.3 Finalisation (prepare())

The Equation object is finalised by an explicit call to the prepare() method.

Finding Vm

The first step is to find the name of the membrane potential variable (getVm()). This is useful when the variable name for threshold or reset is not given (e.g. threshold=10*mV). The method looks for one these names: 'v','V','vm','Vm'. If one is present, it is the membrane potential variable. If none or more than one is present, no variable is found. If it is found, the corresponding variable is swapped with the first variable in the _diffeq_names list (note: not in the _diffeq_names_nonzero list). Otherwise, nothing happens. This way, the first variable in the list is the membrane potential. Possibly, a warning could be issued if it is not found. The problem it might issue warnings too often. A better way would be to issue warnings only when threshold and reset are used ambiguously (i.e., no Vm found and more than 1 variable).

Cleaning the namespace

Then variables and t are removed from the namespace if present (N.B.: xi does not appear to be removed), and warnings are issued using log_warn (method clean_namespace()).

Compiling functions

This is done by the compile_functions() method. Python functions are created from the string definition of equations. For each equation/differential equation, the list of identifiers is obtained from the string definition, then only those referring to variables are kept. A Python lambda function of these remaining identifiers is then compiled (using eval) and put in the _function dictionary.

Compiled functions are used for:

- checking units
- obtaining the list of arguments (this could be done independently)
- state updates

This step might be avoided and replaced by eval calls. It might actually be a little simpler because arguments would be replaced by namespace. It seems to be faster with the current implementation, but the string could be compiled with compile() (then evaluated in the relevant namespace). Besides, with the way it is currently evaluated in the Euler update: `f(*[S[var] for var in f.func_code.co_varnames])`, it is not faster than direct evaluation in the namespace.

Checking units

This is done by the check_units() method. First, the static equations are ordered (see next section).

To check the units of a static equation, one calls the associated function (giving the RHS) where the arguments are units (e.g., 1*volt for v, etc.) and adds the units of the LHS. A dimension error is raised if it is not homogeneous. Currently, the message states "The differential equation is not homogeneous" but it should be adapted to non-differential

equations. One problem with this way of checking units is that the RHS function may not be defined at the point it is checked.

Differential equations are checked in the same way, with two specificities: the units of RHS should be the units of the variable divided by second (dx/dt), and noise (xi) has units of second**-.5 (this is put in the globals of the function, which might not be a very clean way to do it).

Ordering static variables

It seems that this method (set_eq_order()) is already called by check_units() and therefore it is probably not necessary to call it here. This method computes the dependency graph of (static) equations on other static variables, which must have no cycle (otherwise an error is raised). From that graph, an update list is built and put in _eq_names. Then for each variable (static or differential), the list of dependent static variables is built and sorted in update order. The result is put in the _dependencies dictionary.

This is a necessary step to calculate the RHS of any equation: it gives the ordered list of static variables to calculate first before calculating the RHS.

Inserting static variables into differential equations

The value of static variables are then replaced by their string value (RHS) in all differential equations (substitute_eq()). The previous step (ordering) ensures that the result if correct and does not depend on static variables anymore. To avoid namespace conflicts, all identifiers in the namespace of a static variable is augmented by a prefix: name+'_' (e.g. 'x_y' for identifier y in equation 'x=2*y'). Then namespaces are merged.

It might not be optimal to do it in this way, because some of calculations will be done several times in an update step. It might be better to keep the static variables separate.

Recompiling functions

Functions are then recompiled so that differential equations are now independent of static variables.

Checking free variables

Finally, the list of undefined identifiers is checked (free_variables()) and a warning is issued if any is found.

11.4.4 Freezing

Freezing is done by calling compile_functions(freeze=True). Each string expression is then frozen with optimiser.freeze(), which replaces identifiers by their float value. This step does not necessarily succeed, in which case a warning (not an error) is issued.

11.4.5 Adding Equation objects

Adding equations consists simply in merging the lists/dictionaries of variables, namespaces, strings, units and functions. Conflicts raise an error. This step must precede preparation of the object.

11.5 Brian package structure

List of modules with descriptions of contents:

Root package

base Shared base classes for some Brian clases. At the moment, just the `ObjectContainer` class used to implement the `contained_objects` protocol.

clock The `Clock` object, `guess_clock()` function, and other clock manipulation functions.

compartments A class used in compartmental modelling (see user documentation).

connection Everything to do with connections, including the `Connection` and `DelayConnection` classes, but also construction/connection matrices and connection vector code. One of the longest and most technical parts of Brian.

correlatedspikes A tool for producing correlated spike trains.

directcontrol Classes for producing groups which fire spikes at user specified times.

equations Everything to do with the `Equations` class.

globalprefs Global preferences for Brian, a few routines for getting and setting.

group A base class for `NeuronGroup` which creates an `_S` attribute from an `Equations` object with the appropriate dynamical variables, and allows these variables to be accessed by e.g. `grp.V` by overriding the `__getattr__` and `__setattr__` methods.

inspection Utility functions for inspecting namespaces, checking consistency of equations, some code manipulation, etc.

log Brian's somewhat under-developed logging capabilities.

magic Classes and functions for tracking and finding instances of classes.

membrane_equations More code for compartmental modelling (see user docs).

monitor All the monitors, including `SpikeMonitor` and `StateMonitor`.

network The `Network` and `MagicNetwork` classes as well as the `NetworkOperation` class. Also includes the `run()`, etc. functions.

neurongroup The `NeuronGroup` definition and some related stuff, including linked variables (the `LinkedVar` class) and `PoissonGroup`.

optimiser Some tools for freezing expressions (converting e.g. `3*ms` into 0.003) and simplifying some equations (e.g. `a/(10*ms)` converted to `a*100`).

plotting Plotting tools, mostly `raster_plot`.

quantityarray A leftover from the day when Brian had support for arrays with units, will be removed when practical.

reset Reset classes.

stateupdater State update classes and the `magic_state_updater()` function.

stdp STDP features.

stdunits Standard unit names such as `mV` for `mvolt`, etc.

stp Short term plasticity features.

threshold Threshold classes.

timedarray The `TimedArray` class and related functions.

units The Brian units package, including the `Quantity` class.

unitsafefunctions Some functions which override the numpy ones which are safe to use with units, e.g. `sin(3*volt)` raises a dimensionality error.

‘‘library‘‘ subpackage

electrophysiology Electrophysiology library with electrode and amplifier models.

IF Integrate-and-fire models (leaky, quadratic, exponential...).

ionic_currents Ionic current models (K+, Na+...).

random_processes Currently only Ornstein-Uhlenbeck.

synapses Synaptic models (exponential, alpha and biexponential models).

‘‘utils‘‘ subpackage

approximatecomparisons Some tools for doing approximate comparisons with floating point numbers (because they are inexact).

autodiff Automatic differentiation routines (for single-valued functions).

circular and the ccircular subpackage The important `SpikeContainer` and related classes. The `C` version uses SWIG and is much faster but requires the user to compile themselves at the moment (this will be addressed at some point in the future).

documentation Some utility functions related to documentation.

information_theory Entropy and mutual information estimators. Requires the ANN wrapper in scikits.

parallelpython A utility function for using the Parallel Python module.

parameters The `Parameters` class, basically independent of Brian but potentially useful.

progressreporting A progress reporting framework which `Network.run()` can use to report how long it is taking to run, with text or graphical options.

statistics Statistics of spike trains (CV, vector strength, correlograms...).

tabulate Tabulation of numerical functions (precalculation).

11.6 Repository structure

The Brian source code repository is broken into the following directories:

brian The main package, documented above, with the following additional directories:

- **deprecated** For code that is no longer up to date, but that we keep for backwards compatibility.
- **experimental** Package for storing experimental code that can be used but whose syntax and functionality may change.
- **library** Modules where specific models are defined (e.g. neuron and synaptic models).
- **tests** Package for storing tests, composed of:
  - **testcorrectness** Package for tests of mathematical correctness of algorithms, etc.
  - **testinterface** Package for tests of individual Brian modules. Module names are the names of the module being tested prepended by ‘test’.
- **unused** Old stuff

utils Modules that are not Brian-specific, for example circular.py defines circular arrays used for storing spiking events.

dev The main development folder, for works in progress, debugging stuff, tools, etc. Consists of:

benchmarking Code for benchmarking performance against other languages and simulators.

BEPs The Brian Enhancement Proposals.

debugging Dumping ground for files used for debugging a problem.

troubleshooting Used for debugging problems from the `brian-support` mailing list.

ideas For ideas for new features, incomplete implementations, etc. This is where new things go before going into the main Brian package or the `experimental` package.

logo The Brian logo in various sizes.

optimising Ideas for making Brian faster.

speedtracking A sort of testing framework which tracks, over time, the speed of various Brian features.

tests A few scripts to run Brian's tests.

tools The main folder for developer tools.

docs Scripts for invoking Sphinx and building the documentation. Includes script to automatically generate documentation for examples and tutorials, and to build index entries for these.

newrelease Tools for creating a new public release of Brian.

searchreplace Some tools for doing global changes to the code (e.g. syntax changes).

dist Automatically generated distribution files.

docs Automatically generated documentation files in HTML/PDF format.

docs_sphinx Sources for Sphinx documentation.

examples Examples of Brian's use. Documentation is automatically generated from all of these examples.

tutorials Source files for the tutorials, documentation is automatically generated from these. Each tutorial has a directory, possibly containing an `introduction.txt` Sphinx source, followed by a series of files in alphabetical order (e.g. 1a, 1b, 1c, etc.). Multi-line strings are treated as Sphinx source code (take a look at a few examples to get the idea).

See also the reference sheet. You can download a PDF version of the documentation here.

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