NEST by Example: An Introduction to the Neural Simulation Tool NEST Version 2.6.0

Marc-Oliver Gewaltig[1], Abigail Morrison[2], and Hans Ekkehard Plesser[3, 2]

[1]Blue Brain Project, Ecole Polytechnique Federale de Lausanne, QI-J, Lausanne 1015, Switzerland
[2]Institute of Neuroscience and Medicine (INM-6) Functional Neural Circuits Group, Jülich Research Center, 52425 Jülich, Germany
[3]Dept of Mathematical Sciences and Technology, Norwegian University of Life Sciences, PO Box 5003, 1432 Aas, Norway

Abstract

The neural simulation tool NEST can simulate small to very large networks of point-neurons or neurons with a few compartments. In this chapter, we show by example how models are programmed and simulated in NEST.

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1 Introduction

NEST is a simulator for networks of point neurons, that is, neuron models that collapse the morphology (geometry) of dendrites, axons, and somata into either a single compartment or a small number of compartments (Gewaltig and Diesmann, 2007). This simplification is useful for questions about the dynamics of large neuronal networks with complex connectivity. In this text, we give a practical introduction to neural simulations with NEST. We describe how network models are defined and simulated, how simulations can be run in parallel, using multiple cores or computer clusters, and how parts of a model can be randomized.

The development of NEST started in 1994 under the name SYNOD to investigate the dynamics of a large cortex model, using integrate-and-fire neurons (Diesmann et al., 1995). At that time the only available simulators were NEURON (Hines and Carnevale, 1997) and GENESIS (Bower and Beeman, 1995), both focussing on morphologically detailed neuron models, often using data from microscopic reconstructions.

Since then, the simulator has been under constant development. In 2001, the Neural Simulation Technology Initiative was founded to disseminate our knowledge of neural simulation technology. The continuing research of the member institutions into algorithms for the simulation of large spiking networks has resulted in a number of influential publications. The algorithms and techniques developed are not only implemented in the NEST simulator, but have also found their way into other prominent simulation projects, most notably the NEURON simulator (for the Blue Brain Project: Migliore et al., 2006) and IBM's C2 simulator (Ananthanarayanan et al., 2009).

Today, in 2012, there are several simulators for large spiking networks to choose from (Brette et al., 2007), but NEST remains the best established simulator with the the largest developer community.

A NEST simulation consists of three main components:

Nodes Nodes are all neurons, devices, and also sub-networks. Nodes have a dynamic state that changes over time and that can be influenced by incoming *events*.

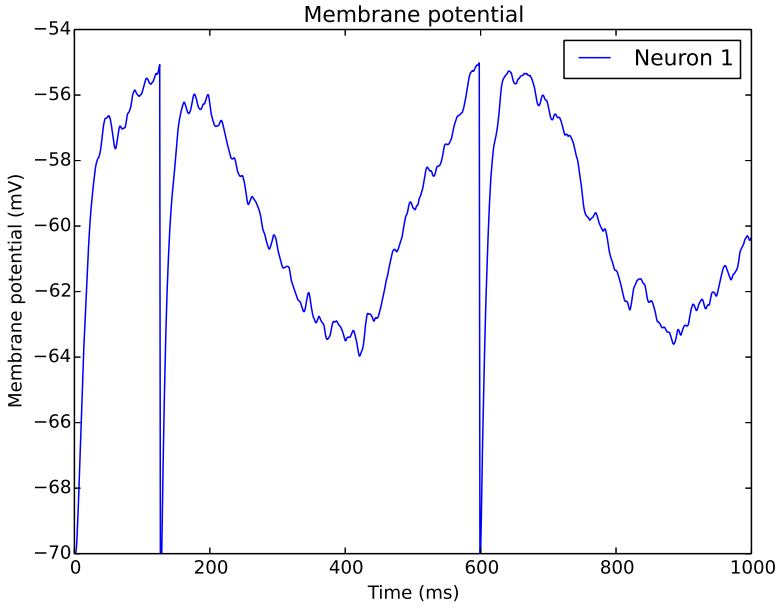

Figure 1: Membrane potential of a neuron in response to an alternating current as well as random excitatory and inhibitory spike events. The membrane potential roughly follows the injected sine current. The small deviations from the sine curve are caused by the excitatory and inhibitory spikes that arrive at random times. Whenever the membrane potential reaches the firing threshold at -55 mV, the neuron spikes and the membrane potential is reset to -70 mV. In this example this happens twice: once at around 110 ms and again at about 600 ms.

Events Events are pieces of information of a particular type. The most common event is the spike-event. Other event types are voltage events and current events.

Connections Connections are communication channels between nodes. Only if one node is connected to another node, can they exchange events. Connections are weighted, directed, and specific to one event type. Directed means that events can flow only in one direction. The node that sends the event is called *source* and the node that receives the event is called *target*. The weight determines how strongly an event will influence the target node. A second parameter, the *delay*, determines how long an event needs to travel from source to target.

In the next sections, we will illustrate how to use NEST, using examples with increasing complexity. Each of the examples is self-contained. We suggest that you try each example, by typing it into Python, line by line. Additionally, you can find all examples in your NEST distribution.

2 First steps

We begin by starting Python. For interactive sessions, we recommend the IPython shell (Pérez and Granger, 2007). It is convenient, because you can edit the command line and access previously typed commands using the up and down keys. However, all examples in this chapter work equally well without IPython. For data analysis and visualization, we also recommend the Python packages Matplotlib (Hunter, 2007) and NumPy (Oliphant, 2006).

Our first simulation investigates the response of one integrate-and-fire neuron to an alternating current and Poisson spike trains from an excitatory and an inhibitory source. We record the membrane potential of the neuron to observe how the stimuli influence the neuron (see Fig. 1).

In this model, we inject a sine current with a frequency of 2 Hz and an amplitude of 100 pA into a neuron. At the same time, the neuron receives random spiking input from two sources known as Poisson generators. One Poisson generator represents a large population of excitatory neurons and the other

a population of inhibitory neurons. The rate for each Poisson generator is set as the product of the assumed number of neurons in a population and their average firing rate.

The small network is simulated for 1000 milliseconds, after which the time course of the membrane potential during this period is plotted (see Fig. 1). For this, we use the pylab plotting routines of Python's Matplotlib package. The Python code for this small model is shown below.

```
1  import nest
2  import nest.voltage_trace
3  neuron = nest.Create('iaf_neuron')
4  sine = nest.Create('ac_generator', 1,
5                     {'amplitude': 100.0,
6                      'frequency': 2.0})
7  noise= nest.Create('poisson_generator', 2,
8                      [{'rate': 70000.0},
9                       {'rate': 20000.0}])
10 voltmeter = nest.Create('voltmeter',1,
11                         {'withgid': True})
12 nest.Connect(sine, neuron)
13 nest.Connect(voltmeter, neuron)
14 nest.Connect(noise[:1], neuron, syn_spec={'weight': 1.0, 'delay': 1.0})
15 nest.Connect(noise[1:], neuron, syn_spec={'weight': -1.0, 'delay': 1.0})
16 nest.Simulate(1000.0)
17 nest.voltage_trace.from_device(voltmeter)
```

We will now go through the simulation script and explain the individual steps. The first two lines **import** the modules nest and its sub-module **voltage_trace**. The nest module must be imported in every interactive session and in every Python script in which you wish to use NEST. NEST is a C++ library that provides a simulation kernel, many neuron and synapse models, and the simulation language interpreter SLI. The library which links the NEST simulation language interpreter to the Python interpreter is called PyNEST (Eppler et al., 2009).

Importing nest as shown above puts all NEST commands in the *namespace* nest. Consequently, all commands must be prefixed with the name of this namespace.

In line 3, we use the command **Create** to produce one node of the type iaf_neuron. As you see in lines 4, 7, and 10, **Create** is used for all node types. The first argument, 'iaf_neuron', is a string, denoting the type of node that you want to create. The second parameter of **Create** is an integer representing the number of nodes you want to create. Thus, whether you want one neuron or 100,000, you only need to call **Create** once. nest.Models() provides a list of all available node and connection models.

The third parameter is either a dictionary or a list of dictionaries, specifying the parameter settings for the created nodes. If only one dictionary is given, the same parameters are used for all created nodes. If an array of dictionaries is given, they are used in order and their number must match the number of created nodes. This variant of **Create** is used in lines 4, 7, and 10 to set the parameters for the Poisson noise generator, the sine generator (for the alternating current), and the voltmeter. All parameters of a model that are not set explicitly are initialized with default values. You can display them with nest.GetDefaults(*model_name*). Note that only the first parameter of **Create** is mandatory.

Create returns a list of integers, the global identifiers (or GID for short) of each node created. The GIDs are assigned in the order in which nodes are created. The first node is assigned GID 1, the second node GID 2, and so on.

In lines 12 to 15, the nodes are connected. First we connect the sine generator and the voltmeter to the neuron. The command **Connect** takes two or more arguments. The first argument is a list of source nodes. The second argument is a list of target nodes. **Connect** iterates these two lists and connects the corresponding pairs.

A node appears in the source position of **Connect** if it sends events to the target node. In our example, the sine generator is in the source position because it injects an alternating current into the neuron. The voltmeter is in the source position, because it polls the membrane potential of the neuron. Other devices may be in the target position, e.g., the spike detector which receives spike events from a neuron. If in doubt about the order, consult the documentation of the respective nodes using NEST's help system. For example, to read the documentation of the voltmeter you can type nest.**help**('voltmeter').

Next, we use the command **Connect** with the syn_spec parameter to connect the two Poisson generators to the neuron. In this example the synapse specification syn_spec provides only weight and delay values, in this case ±1 pA input current amplitude and 1 ms delay. We will see more advanced uses of syn_spec below.

After line 15, the network is ready. The following line calls the NEST function **Simulate** which runs the network for 1000 milliseconds. The function returns after the simulation is finished. Then, function **voltage_trace** is called to plot the membrane potential of the neuron. If you are running the script for the first time, you may have to tell Python to display the figure by typing pylab.show(). You should then see something similar to Fig. 1.

If you want to inspect how your network looks so far, you can print it using the command **PrintNetwork**():

```
>>>nest.PrintNetwork()
+-[0] root dim=[5]
    |
    +-[1] iaf_neuron
    +-[2] ac_generator
    +-[3]...[4] poisson_generator
    +-[5] voltmeter
```

If you run the example a second time, NEST will leave the existing nodes intact and will create a second instance for each node. To start a new NEST session without leaving Python, you can call nest.**ResetKernel**(). This function will erase the existing network so that you can start from scratch.

3 Example 1: A sparsely connected recurrent network

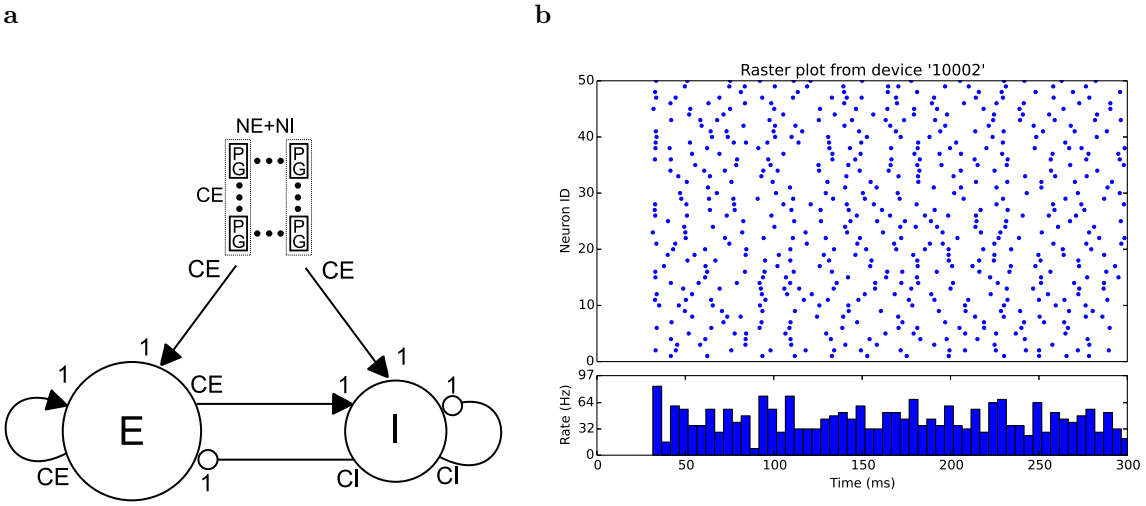

Figure 2: Sketch of the network model proposed by Brunel (2000). **a)** The network consists of three populations: N_E excitatory neurons (circle labeled E), N_I inhibitory neurons (circle labeled I), and a population of identical, independent Poisson processes (PGs) representing activity from outside the network. Arrows represent connections between the network nodes. Triangular arrow-heads represent excitatory and round arrow-heads represent inhibitory connections. The numbers at the start and end of each arrow indicate the multiplicity of the connection. See also table 1. **b)** Spiking activity of 50 neurons during the first 300 ms of simulated time as a raster plot. Time is shown on the x-axis, neuron id on the y-axis. Each dot corresponds to a spike of the respective neuron at the given time. The histogram below the raster plot shows the population rate of the network.

Next we discuss a model of activity dynamics in a local cortical network proposed by Brunel (2000). We only describe those parts of the model which are necessary to understand its NEST implementation. Please refer to the original paper for further details.

The local cortical network consists of two neuron populations: a population of N_E excitatory neurons and a population of N_I inhibitory neurons. To mimic the cortical ratio of 80% excitation and 20% inhibition, we assume that $N_E = 8000$ and $N_I = 2000$. Thus, our local network has a total of 10,000 neurons.

For both the excitatory and the inhibitory population, we use the same integrate-and-fire neuron model with current-based synapses. Incoming excitatory and inhibitory spikes displace the membrane potential V_m by J_E and J_I, respectively. If V_m reaches the threshold value V_{th}, the membrane potential is reset to V_{reset}, a spike is sent with delay $D = 1.5$ ms to all post-synaptic neurons, and the neuron remains refractory for $\tau_{\mathrm{rp}} = 2.0$ ms.

The neurons are mutually connected with a probability of 10%. Specifically, each neuron receives input from $C_E = 0.1 \cdot N_E$ excitatory and $C_I = 0.1 \cdot N_I$ inhibitory neurons (see Fig. 2a). The inhibitory synaptic weights J_I are chosen with respect to the excitatory synaptic weights J_E such that

$$J_I = -g \cdot J_E \tag{1}$$

with $g = 5.0$ in this example.

In addition to the sparse recurrent inputs from within the local network, each neuron receives excitatory input from a population of C_E randomly firing neurons, mimicking the input from the rest of cortex. The randomly firing population is modeled as C_E independent and identically distributed Poisson processes with rate ν_{ext}. Here, we set ν_{ext} to twice the rate ν_{th} that is needed to drive a neuron to threshold asymptotically. The details of the model are summarized in tables 1 and 2.

Fig. 2b shows a raster plot of 50 excitatory neurons during the first 300 ms of simulated time. Time is shown along the x-axis, neuron id along the y-axis. At $t = 0$, all neurons are in the same state $V_m = 0$ and hence there is no spiking activity. The external stimulus rapidly drives the membrane potentials towards the threshold. Due to the random nature of the external stimulus, not all the neurons reach the threshold at the same time. After a few milliseconds, the neurons start to spike irregularly at roughly 40 spikes/s. In the original paper, this network state is called the *asynchronous irregular state* (Brunel, 2000).

3.1 NEST Implementation

We now show how this model is implemented in NEST. Along the way, we explain the required steps and NEST commands in more detail so that you can apply them to your own models.

3.1.1 Preparations

The first three lines import NEST, a NEST module for raster plots, and the plotting package pylab. We then assign the various model parameters to variables.

```
1  import nest
2  import nest.raster_plot
3  import pylab
4  g       = 5.0
5  eta     = 2.0
6  delay   = 1.5
7  tau_m   = 20.0
8  V_th    = 20.0
9  N_E = 8000
10 N_I = 2000
11 N_neurons = N_E+N_I
12 C_E     = N_E/10
13 C_I     = N_I/10
14 J_E  = 0.1
15 J_I  = -g*J_E
16 nu_ex  = eta*V_th/(J_E*C_E*tau_m)
17 p_rate = 1000.0*nu_ex*C_E
```

Table 1: Summary of the network model, proposed by Brunel (2000).

A	**Model Summary**
Populations	Three: excitatory, inhibitory, external input
Topology	—
Connectivity	Random convergent connections with probability $P = 0.1$ and fixed in-degree of $C_E = PN_E$ and $C_I = PN_I$.
Neuron model	Leaky integrate-and-fire, fixed voltage threshold, fixed absolute refractory time (voltage clamp)
Channel models	—
Synapse model	δ-current inputs (discontinuous voltage jumps)
Plasticity	—
Input	Independent fixed-rate Poisson spike trains to all neurons
Measurements	Spike activity

B	**Populations**	
Name	**Elements**	**Size**
E	Iaf neuron	$N_{\mathrm{E}} = 4N_{\mathrm{I}}$
I	Iaf neuron	N_{I}
$\mathrm{E}_{\mathrm{ext}}$	Poisson generator	$C_E(N_{\mathrm{E}} + N_{\mathrm{I}})$

C	**Connectivity**		
Name	**Source**	**Target**	**Pattern**
EE	E	E	Random convergent $C_{\mathrm{E}} \to 1$, weight J, delay D
IE	E	I	Random convergent $C_{\mathrm{E}} \to 1$, weight J, delay D
EI	I	E	Random convergent $C_{\mathrm{I}} \to 1$, weight $-gJ$, delay D
II	I	I	Random convergent $C_{\mathrm{I}} \to 1$, weight $-gJ$, delay D
Ext	$\mathrm{E}_{\mathrm{ext}}$	E ∪ I	Non-overlapping $C_{\mathrm{E}} \to 1$, weight J, delay D

D	**Neuron and Synapse Model**
Name	Iaf neuron
Type	Leaky integrate-and-fire, δ-current input
Sub-threshold dynamics	$\tau_m \dot{V_m}(t) = -V_m(t) + R_m I(t)$ if not refractory ($t > t^* + \tau_{\mathrm{rp}}$) $V_m(t) = V_{\mathrm{r}}$ while refractory ($t^* < t \leq t^* + \tau_{\mathrm{rp}}$) $I(t) = \frac{\tau_m}{R_m} \sum_{\tilde{t}} w\delta(t - (\tilde{t} + D))$
Spiking	If $V_m(t-) < V_\theta \wedge V_m(t+) \geq V_\theta$ 1. set $t^* = t$ 2. emit spike with time-stamp t^*

E	**Input**
Type	**Description**
Poisson generators	Fixed rate ν_{ext}, C_{E} generators per neuron, each generator projects to one neuron

F	**Measurements**
Spike activity as raster plots, rates and "global frequencies", no details given	

Table 2: Summary of the network parameters for the model, proposed by Brunel (2000).

G	Network Parameters
Parameter	**Value**
Number of excitatory neurons N_E	8000
Number of inhibitory neurons N_I	2000
Excitatory synapses per neuron C_E	800
Inhibitory synapses per neuron C_E	200
H	**Neuron Parameters**
Parameter	**Value**
Membrane time constant τ_m	20 ms
Refractory period τ_{rp}	2 ms
Firing threshold V_{th}	20 mV
Membrane capatitance C_m	1pF
Resting potential V_E	0 mV
Reset potential V_{reset}	10 mV
Excitatory PSP amplitude J_E	0.1 mV
Inhibitory PSP amplitude J_I	-0.5 mV
Synaptic delay D	1.5 ms
Background rate η	2.0

In line 16, we compute the firing rate nu_ex (ν_{ext}) of a neuron in the external population. We define nu_ex as the product of a constant eta times the threshold rate ν_{th}, i.e. the steady state firing rate which is needed to bring a neuron to threshold. The value of the scaling constant eta is defined in line 5.

In line 17, we compute the population rate of the whole external population. With C_E neurons, the population rate is simply the product nu_ex∗C_E. The factor 1000.0 in the product changes the units from spikes per ms to spikes per second.

```
18 nest.SetKernelStatus({'print_time': True})
```

Next, we prepare the simulation kernel of NEST (line 18). The command **SetKernelStatus** modifies parameters of the simulation kernel. The argument is a Python dictionary with *key:value* pairs. Here, we set the NEST kernel to print the progress of the simulation time during simulation.

3.1.2 Creating neurons and devices

As a rule of thumb, we recommend that you create all elements in your network, i.e., neurons, stimulating devices and recording devices first, before creating any connections.

```
19 nest.SetDefaults('iaf_psc_delta',
20                  {'C_m': 1.0,
21                   'tau_m': tau_m,
22                   't_ref': 2.0,
23                   'E_L': 0.0,
24                   'V_th': V_th,
25                   'V_reset': 10.0})
```

In lines 19 to 25, we change the parameters of the neuron model we want to use from the built-in values to the defaults for our investigation. **SetDefaults** expects two parameters. The first is a string, naming the model for which the default parameters should be changed. Our neuron model for this simulation is the simplest integrate-and-fire model in NEST's repertoire: ' iaf_psc_delta '. The second parameter is a dictionary with parameters and their new values, entries separated by commas. All parameter values are taken from Brunel's paper (Brunel, 2000) and we insert them directly for brevity. Only the membrane

time constant tau_m and the threshold potential V_th are read from variables, because these values are needed in several places.

```
26 nodes   = nest.Create('iaf_psc_delta', N_neurons)
27 nodes_E = nodes[:N_E]
28 nodes_I = nodes[N_E:]
29
30 noise = nest.Create('poisson_generator',1,{'rate': p_rate})
31
32 spikes = nest.Create('spike_detector',2,
33                       [{'label': 'brunel-py-ex'},
34                        {'label': 'brunel-py-in'}])
35 spikes_E = spikes[:1]
36 spikes_I = spikes[1:]
```

In line 26 we create the neurons. **Create** returns a list of the global IDs which are consecutive numbers from 1 to N_neurons. We split this range into excitatory and inhibitory neurons. In line 27 we select the first N_E elements from the list nodes and assign them to the variable nodes_E. This list now holds the GIDs of the excitatory neurons.

Similarly, in line 28 we assign the range from position N_E to the end of the list to the variable nodes_I. This list now holds the GIDs of all inhibitory neurons. The selection is carried out using standard Python list commands. You may want to consult the Python documentation for more details.

Next, we create and connect the external population and some devices to measure the spiking activity in the network.

In line 30, we create a device known as a poisson_generator, which produces a spike train governed by a Poisson process at a given rate. We use the third parameter of **Create** to initialize the rate of the Poisson process to the population rate p_rate which we previously computed in line 17.

If a Poisson generator is connected to n targets, it generates n independent and identically distributed spike trains. Thus, we only need one generator to model an entire population of randomly firing neurons.

To observe how the neurons in the recurrent network respond to the random spikes from the external population, we create two spike detectors in line 32; one for the excitatory neurons and one for the inhibitory neurons. By default, each detector writes its spikes into a file whose name is automatically generated from the device type and its global id. We use the third argument of **Create** to give each spike detector a 'label', which will be part of the name of the output file written by the detector. Since two devices are created, we supply a list of dictionaries.

In line 35, we store the GID of the first spike detector in a one-element list and assign it to the variable spikes_E. In the next line, we do the same for the second spike detector that is dedicated to the inhibitory population.

3.1.3 Connecting the network

Once all network elements are in place, we connect them.

```
37 nest.CopyModel('static_synapse_hom_w',
38                 'excitatory',
39                 {'weight':J_E,
40                  'delay':delay})
41 nest.Connect(nodes_E, nodes,
42               {'rule': 'fixed_indegree',
43                'indegree': C_E},
44               'excitatory')
45 nest.CopyModel('static_synapse_hom_w',
46                 'inhibitory',
47                 {'weight':J_I,
48                  'delay':delay})
49 nest.Connect(nodes_I, nodes,
```

```
50                {'rule': 'fixed_indegree',
51                 'indegree': C_I},
52                'inhibitory')
```

On line 37, we create a new connection type 'excitatory' by copying the built-in connection type 'static_synapse_hom_w' while changing its default values for *weight* and *delay*. The command **CopyModel** expects either two or three arguments: the name of an existing neuron or synapse model, the name of the new model, and optionally a dictionary with the new default values of the new model.

The connection type 'static_synapse_hom_w' uses the same values of weight for all synapses. This saves memory for networks in which these values are identical for all connections. In Section 5 we use a different connection model to implement randomized weights and delays.

Having created and parameterized an appropriate synapse model, we draw the incoming excitatory connections for each neuron (line 41). The function **Connect** expects four arguments: a list of source nodes, a list of target nodes, a connection rule, and a synapse specification. Some connection rules, in particular 'one_to_one' and ' all_to_all ' require no parameters and can be specified as strings. All other connection rules must be specfied as a dictionary, while at least must contain the key 'rule' specifying a connection rule; nest.ConnectionRules() shows all connection rules. The remaining dictionary entries depend on the particular rule. We use the 'fixed_indegree' rule, which creates exactly indegree connections to each target neurons; in previous versions of NEST, this connectivity was provided by **RandomConvergentConnect**.

The final argument specifies the synapse model to be used, here the 'excitatory' model we defined previously.

In lines 45 to 52 we repeat the same steps for the inhibitory connections: we create a new connection type and draw the incoming inhibitory connections for all neurons.

```
53 nest.Connect(noise, nodes, syn_spec='excitatory')
54
55 N_rec    = 50
56 nest.Connect(nodes_E[:N_rec], spikes_E)
57 nest.Connect(nodes_I[:N_rec], spikes_I)
```

In the next line (53), we use **Connect** to connect the Poisson generator to all nodes of the local network. Since these connections are excitatory, we use the 'excitatory' connection type. Finally, we connect a subset of excitatory and inhibitory neurons to the spike detectors to record from them. If no connection rule is given, **Connect** connects all sources to all targets (all_to_all rule), i.e., on line 53 the noise generator is connected to all neurons (previously **DivergentConnect**), while on line 56, all recorded excitatory neurons are connected to the spikes_E spike detector (previously **ConvergentConnect**).

Our network consists of 10,000 neurons, all of which having the same activity statistics due to the random connectivity. Thus, it suffices to record from a representative sample of neurons, rather than from the entire network. Here, we choose to record from 50 neurons and assign this number to the variable N_rec. We then connect the first 50 excitatory neurons to their spike detector. Again, we use standard Python list operations to select N_rec neurons from the list of all excitatory nodes. Alternatively, we could select 50 neurons at random, but since the neuron order has no meaning in this model, the two approaches would yield qualitatively the same results. Finally, we repeat this step for the inhibitory neurons.

3.1.4 Simulating the network

Now everything is set up and we can run the simulation.

```
58 simtime=300
59 nest.Simulate(simtime)
60 events = nest.GetStatus(spikes,'n_events')
61 rate_ex= events[0]/simtime*1000.0/N_rec
62 print "Excitatory rate   : %.2f 1/s" % rate_ex
63 rate_in= events[1]/simtime*1000.0/N_rec
64 print "Inhibitory rate   : %.2f 1/s" % rate_in
65 nest.raster_plot.from_device(spikes_E, hist=True)
```

In line 58, we select a simulation time of 300 milliseconds and assign it to a variable. Next, we call the NEST command **Simulate** to run the simulation for 300 ms. During simulation, the Poisson generators send spikes into the network and cause the neurons to fire. The spike detectors receive spikes from the neurons and write them to a file, or to memory.

When the function returns, the simulation time has progressed by 300 ms. You can call **Simulate** as often as you like and with different arguments. NEST will resume the simulation at the point where it was last stopped. Thus, you can partition your simulation time into small epochs to regularly inspect the progress of your model.

After the simulation is finished, we compute the firing rate of the excitatory neurons (line 61) and the inhibitory neurons (line 63). Finally, we call the NEST function **raster_plot** to produce the raster plot shown in Fig. 2b. **raster_plot** has two modes. **raster_plot**.from_device expects the global ID of a spike detector. **raster_plot**.from_file expects the name of a data-file. This is useful to plot data without repeating a simulation.

4 Parallel simulation

Large network models often require too much time or computer memory to be conveniently simulated on a single computer. For example, if we increase the number of neurons in the previous model to 100,000, there will be a total of 10^9 connections, which won't fit into the memory of most computers. Similarly, if we use plastic synapses (see Section 7) and run the model for minutes or hours of simulated time, the execution times become uncomfortably long.

To address this issue, NEST has two modes of parallelization: multi-threading and distribution. Multi-threaded and distributed simulation can be used in isolation or in combination (Plesser et al., 2007), and both modes allow you to connect and run networks more quickly than in the serial case.

Multi-threading means that NEST uses all available processors or cores of the computer. Today, most desktop computers and even laptops have at least two processing cores. Thus, you can use NEST's multi-threaded mode to make your simulations execute more quickly whilst still maintaining the convenience of interactive sessions. Since a given computer has a fixed memory size, multi-threaded simulation can only reduce execution times. It cannot solve the problem that large models exhaust the computer's memory.

Distribution means that NEST uses many computers in a network or computer cluster. Since each computer contributes memory, distributed simulation allows you to simulate models that are too large for a single computer. However, in distributed mode it is not currently possible to use NEST interactively.

In most cases, writing a simulation script to be run in parallel is as easy as writing one to be executed on a single processor. Only minimal changes are required, as described below, and you can ignore the fact that the simulation is actually executed by more than one core or computer. However, in some cases your knowledge about the distributed nature of the simulation can help you improve efficiency even further. For example, in the distributed mode, all computers execute the same simulation script. We can improve performance if the script running on a specific computer only tries to execute commands relating to nodes that are represented on the same computer. An example of this technique is shown below in Section 6.

To switch NEST into multi-threaded mode, you only have to add one line to your simulation script:

```
nest.SetKernelStatus({'local_num_threads': n})
```

Here, n is the number of threads you want to use. It is important that you set the number of threads *before* you create any nodes. If you try to change the number of threads after nodes were created, NEST will issue an error.

A good choice for the number of threads is the number of cores or processors on your computer. If your processor supports hyperthreading, you can select an even higher number of threads.

The distributed mode of NEST is particularly useful for large simulations for which not only the processing speed, but also the memory of a single computer are insufficient. The distributed mode of NEST uses the Message Passing Interface (MPI, MPI Forum (2009)), a library that must be installed on your computer network when you install NEST. For details, please refer to NEST's website at `www.nest-initiative.org`.

The distributed mode of NEST is also easy to use. All you need to do is start NEST with the MPI command mpirun:

```
mpirun -np m python script.py
```

where m is the number of MPI processes that should be started. One sensible choice for m is the total number of cores available on the cluster. Another reasonable choice is the number of physically distinct machines, utilizing their cores through multithreading as described above. This can be useful on clusters of multi-core computers.

In NEST, processes and threads are both mapped to *virtual processes* (Plesser et al., 2007). If a simulation is started with m MPI processes and n threads on each process, then there are m×n virtual processes. You can obtain the number of virtual processes in a simulation with

```
nest.GetKernelStatus('total_num_virtual_procs')
```

The virtual process concept is reflected in the labeling of output files. For example, the data files for the excitatory spikes produced by the network discussed here follow the form brunel−py−ex−x−y.gdf, where x is the id of the data recording node and y is the id of the virtual process.

5 Randomness in NEST

NEST has built-in random number sources that can be used for tasks such as randomizing spike trains or network connectivity. In this section, we discuss some of the issues related to the use of random numbers in parallel simulations. In Section 6, we illustrate how to randomize parameters in a network.

Let us first consider the case that a simulation script does not explicitly generate random numbers. In this case, NEST produces identical simulation results for a given number of virtual processes, irrespective of how the virtual processes are partitioned into threads and MPI processes. The only difference between the output of two simulations with different configurations of threads and processes resulting in the same number of virtual processes is the result of query commands such as **GetStatus**. These commands gather data over threads on the local machine, but not over remote machines.

In the case that random numbers are explictly generated in the simulation script, more care must be taken to produce results that are independent of the parallel configuration. Consider, for example, a simulation where two threads have to draw a random number from a single random number generator. Since only one thread can access the random number generator at a time, the outcome of the simulation will depend on the access order.

Ideally, all random numbers in a simulation should come from a single source. In a serial simulation this is trivial to implement, but in parallel simulations this would require shipping a large number of random numbers from a central random number generator (RNG) to all processes. This is impractical. Therefore, NEST uses one independent random number generator on each virtual process. Not all random number generators can be used in parallel simulations, because many cannot reliably produce uncorrelated parallel streams. Fortunately, recent years have seen great progress in RNG research and there is a range of random number generators that can be used with great fidelity in parallel applications.

Based on this knowledge, each virtual process (VP) in NEST has its own RNG. Numbers from these RNGs are used to

- choose random convergent connections
- create random spike trains (e.g. poisson_generator) or random currents (e.g. noise_generator).

In order to randomize model parameters in a PyNEST script, it is convenient to use the random number generators provided by NumPy. To ensure consistent results for a given number of virtual processes, each virtual process should use a separate Python RNG. Thus, in a simulation running on N_{vp} virtual processes, there should be $2N_{\mathrm{vp}} + 1$ RNGs in total:

- the global NEST RNG;
- one RNG per VP in NEST;
- one RNG per VP in Python.

We need to provide separate seed values for each of these generators. Modern random number generators work equally well for all seed values. We thus suggest the following approach to choosing seeds: For each simulation run, choose a master seed msd and seed the RNGs with seeds msd, $msd + 1$, $\ldots msd + 2N_{\mathrm{vp}}$. Any two master seeds must differ by at least $2N_{\mathrm{vp}} + 1$ to avoid correlations between simulations.

By default, NEST uses Knuth's lagged Fibonacci RNG, which has the nice property that each seed value provides a different sequence of some 2^{70} random numbers (Knuth, 1998, Ch. 3.6). Python uses the Mersenne Twister MT19937 generator (Matsumoto and Nishimura, 1998), which provides no explicit guarantees, but given the enormous state space of this generator it appears astronomically unlikely that

neighboring integer seeds would yield overlapping number sequences. For a recent overview of RNGs, see L'Ecuyer and Simard (2007). For general introductions to random number generation, see Gentle (2003), Knuth (1998, Ch. 3), or Plesser (2010).

6 Example 2: Randomizing neurons and synapses

Let us now consider how to randomize some neuron and synapse parameters in the sparsely connected network model introduced in Section 3. We shall

- explicitly seed the random number generators;
- randomize the initial membrane potential of all neurons;
- randomize the weights of the recurrent excitatory connections.

We discuss here only those parts of the model script that differ from the script discussed in Section 3.1; the complete script brunel2000−rand.py is part of the NEST examples.

We begin by importing the NumPy package to get access to its random generator functions:

```
import numpy
```

After line 1 of the original script (cf. p. 10), we insert code to seed the random number generators:

```
r1  msd = 1000    # master seed
r2  msdrange1 = range(msd, msd+n_vp)
r3  n_vp = nest.GetKernelStatus('total_num_virtual_procs')
r4  pyrngs = [numpy.random.RandomState(s) for s in msdrange1]
r5  msdrange2 = range(msd+n_vp+1, msd+1+2*n_vp)
r6  nest.SetKernelStatus({'grng_seed': msd+n_vp,
r7                        'rng_seeds': msdrange2})
```

We first define the master seed msd and then obtain the number of virtual processes n_vp. On line r4 we then create a list of n_vp NumPy random number generators with seeds msd, msd+1, ... msd+n_vp−1. The next two lines set new seeds for the built-in NEST RNGs: the global RNG is seeded with msd+n_vp, the per-virtual-process RNGs with msd+n_vp+1, ..., msd+2*n_vp. Note that the seeds for the per-virtual-process RNGs must always be passed as a list, even in a serial simulation.

After creating the neurons as before, we insert the following code after line 28 to randomize the membrane potential of all neurons:

```
r8  node_info   = nest.GetStatus(nodes)
r9  local_nodes = [(ni['global_id'], ni['vp'])
r10                for ni in node_info if ni['local']]
r11 for gid,vp in local_nodes:
r12   nest.SetStatus([gid], {'V_m': pyrngs[vp].uniform(-V_th,V_th)})
```

In this code, we meet the concept of *local* nodes for the first time (Plesser et al., 2007). In serial and multi-threaded simulations, all nodes are local. In an MPI-based simulation with m MPI processes, each MPI process represents and is responsible for updating (approximately) $1/m$-th of all nodes—these are the local nodes for each process. In line r8 we obtain status information for each node; for local nodes, this will be full information, for non-local nodes this will only be minimal information. We then use a list comprehension to create a list of gid and vp tuples for all local nodes. The **for**-loop then iterates over this list and draws for each node a membrane potential value uniformly distributed in $[-V_{\mathrm{th}}, V_{\mathrm{th}})$, i.e., $[-20\mathrm{mV}, 20\mathrm{mV})$. We draw the inital membrane potential for each node from the NumPy RNG assigned to the virtual process vp responsible for updating that node.

As the next step, we create excitatory recurrent connections with the same connection rule as in the original script, but with randomized weights. To this end, we replace the code on lines 37–41 of the original script with

```
r13 nest.CopyModel('static_synapse', 'excitatory')
r14 nest.Connect(nodes_E, nodes,
r15              {'rule': 'fixed_indegree',
```

```
r16                 'indegree': C_E},
r17               {'model': 'excitatory',
r18                'delay': delay,
r19                'weight': {'distribution': 'uniform',
r20                           'low': 0.5 * J_E,
r21                           'high': 1.5 * J_E}})
```

The first difference to the original is that we base the excitatory synapse model on the built-in static_synapse model instead of static_synapse_hom_w, as the latter implies equal weights for all synapses. The second difference is that we randomize the initial weights. To this end, we have replaced the simple synapse specification 'excitatory' with a synapse specification dictionary on lines r17–r21. Such a dictionary must always contain the key 'model' providing the synapse model to use. In addition, we specify a fixed delay, and a distribution from which to draw the weights here a uniform distribution over $[J_E/2, 3J_E/2)$. NEST will automatically use the correct random number generator for each weight.

To see all available random distributions, please run nest.sli_run('rdevdict info'). To access documentation for an individual distribution, run, e.g., nest.**help**('rdevdict::binomial'). These distributions can be used for all parameters of a synapse.

Before starting our simulation, we want to visualize the randomized initial membrane potentials and weights. To this end, we insert the following code just before we start the simulation:

```
r22 pylab.figure()
r23 V_E = nest.GetStatus(nodes_E[:N_rec], 'V_m')
r24 pylab.hist(V_E, bins=10)
r25 pylab.figure()
r26 ex_conns = nest.GetConnections(nodes_E[:N_rec],
r27                               synapse_model='excitatory')
r28 w = nest.GetStatus(ex_conns, 'weight')
r29 pylab.hist(w, bins=100)
```

Line r23 retrieves the membrane potentials of all 50 recorded neurons. The data is then displayed as a histogram with 10 bins, see Fig. 3. Line r26 finds all connections that

- have one of the 50 recorded excitatory neurons as source;
- have any local node as target;
- and are of type excitatory.

In line r28, we then use **GetStatus**() to obtain the weights of these connections. Running the script in a single MPI process, we record approximately 50,000 weights, which we display in a histogram with 100 bins as shown in Fig. 3.

Note that the code on lines r23–r28 will return complete results only when run in a single MPI process. Otherwise, only data from local neurons or connections with local targets will be obtained. It is currently not possible to collect recorded data across MPI processes in NEST. In distributed simulations, you should thus let recording devices write data to files and collect the data after the simulation is complete.

The result of the simulation is displayed as before. Comparing the raster plot from the simulation with randomized initial membrane potentials in Fig. 3 with the same plot for the original network in Fig. 2 reveals that the membrane potential randomization has prevented the synchronous onset of activity in the network.

As a final point, we make a slight improvement to the rate computation on lines 61–64 of the original script. Spike detectors count only spikes from neurons on the local MPI process. Thus, the original computation is correct only for a single MPI process. To obtain meaningful results when simulating on several MPI processes, we count how many of the N_rec recorded nodes are local and use that number to compute the rates:

```
r30 N_rec_local_E = sum(nest.GetStatus(nodes_E[:N_rec], 'local'))
r31 rate_ex= events[0]/simtime*1000.0/N_rec_local_E
```

Each MPI process then reports the rate of activity of its locally recorded nodes.

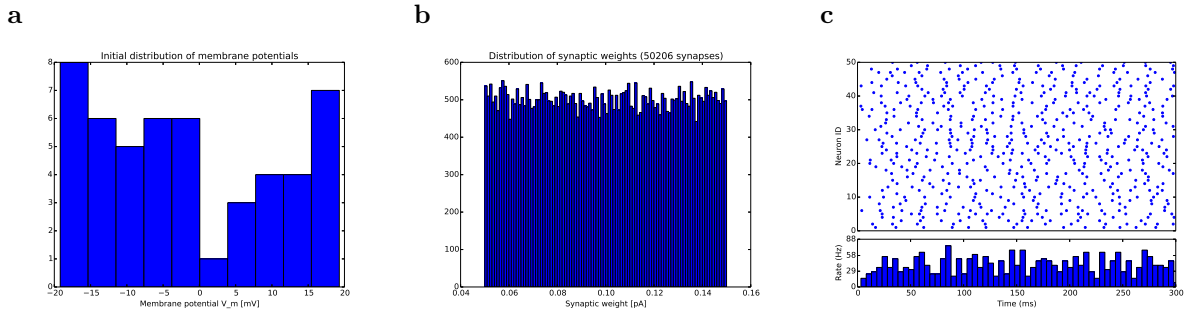

Figure 3: **a)** Distribution of membrane potentials V_m of 50 excitatory neurons after random initialization. **b)** Distribution of weights of randomized weights of approximately 50,000 recurrent connections originating from 50 excitatory neurons. **c)** Spiking activity of 50 excitatory neurons during the first 300 ms of network simulation; compare with the corresponding diagram for the same network without randomization of initial membrane potentials and weights in Fig. 2.

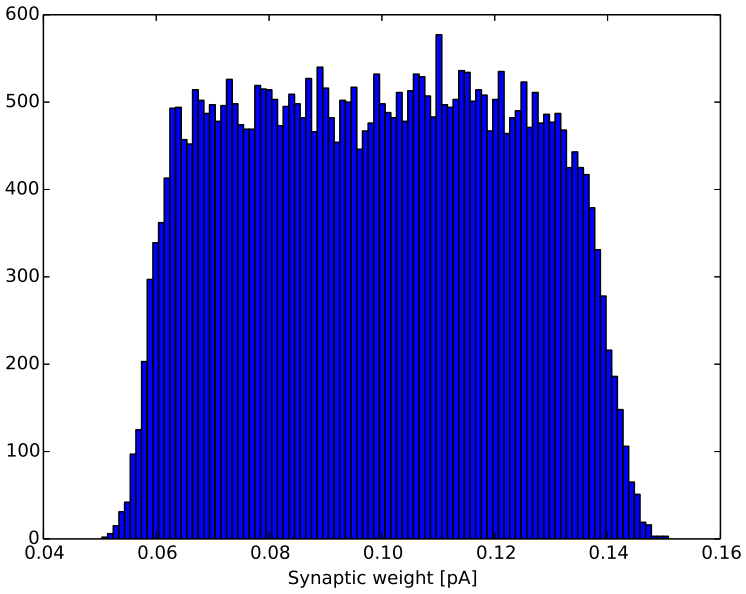

Figure 4: Distribution of synaptic weights in the plastic network simulation after 300 ms.

7 Example 3: Plastic Networks

NEST provides synapse models with a variety of short-term and long-term dynamics. To illustrate this, we extend the sparsely connected network introduced in section 3 with randomized synaptic weights as described in section 5 to incorporate spike-timing dependent plasticity (Bi and Poo, 1998) at its recurrent excitatory-excitatory synapses.

We create all nodes and randomize their initial membrane potentials as before. We then generate a plastic synapse model for the excitatory-excitatory connections and a static synapse model for the excitatory-inhibitory connections:

```
p1  nest.CopyModel('stdp_synapse_hom',
p2                 'excitatory-plastic',
p3                 {'alpha':STDP_alpha,
p4                  'Wmax':STDP_Wmax})
```

```
p5  nest.CopyModel('static_synapse', 'excitatory-static')
```

Here, we set the parameters alpha and Wmax of the synapse model but use the default settings for all its other parameters. The _hom suffix in the synapse model name indicates that all plasticity parameters such as alpha and Wmax are shared by all synapses of this model.

We again use nest.**Connect** to create connections with randomized weights:

```
p6  nest.Connect(nodes_E, nodes_E,
p7                {'rule': 'fixed_indegree',
p8                 'indegree': C_E},
p9                {'model': 'excitatory_plastic',
p10                'delay': delay,
p11                'weight': {'distribution': 'uniform',
p12                           'low': 0.5 * J_E,
p13                           'high': 1.5 * J_E}})
p14
p15 nest.Connect(nodes_E, nodes_I,
p16               {'rule': 'fixed_indegree',
p17                'indegree': C_E},
p18               {'model': 'excitatory_static',
p19                'delay': delay,
p20                'weight': {'distribution': 'uniform',
p21                           'low': 0.5 * J_E,
p22                           'high': 1.5 * J_E}})
```

After a period of simulation, we can access the plastic synaptic weights for analysis:

```
p1  w = nest.GetStatus(nest.GetConnections(nodes_E[:N_rec],
p2                                         synapse_model='excitatory-plastic'),
p3                                         'weight')
```

Plotting a histogram of the synaptic weights reveals that the initial uniform distribution has begun to soften (see Fig. 4). Simulation for a longer period results in an approximately Gaussian distribution of weights.

8 Example 4: Classes and Automatization Techniques

So far, we have encouraged you to try our examples line-by line. This is possible in interactive sessions, but if you want to run a simulation several times, possibly with different parameters, it is more practical to write a script that can be loaded from Python.

Python offers a number of mechanisms to structure and organize not only your simulations, but also your simulation data. The first step is to re-write a model as a *class*. In Python, and other object-oriented languages, a class is a data structure which groups data and functions into a single entity. In our case, data are the different parameters of a model and functions are what you can do with a model. Classes allow you to solve various common problems in simulations:

Parameter sets Classes are data structures and so are ideally suited to hold the parameter set for a model. Class inheritance allows you to modify one, few, or all parameters while maintaining the relation to the original model.

Model variations Often, we want to change minor aspects of a model. For example, in one version we have homogeneous connections and in another we want randomized weights. Again, we can use class inheritance to express both cases while maintaining the conceptual relation between the models.

Data management Often, we run simulations with different parameters, or other variations and forget to record which data file belonged to which simulation. Python's class mechanisms provide a simple solution.

We organize the model from Section 3 into a class, by realizing that each simulation has five steps which can be factored into separate functions:

1. Define all independent parameters of the model. Independent parameters are those that have concrete values which do not depend on any other parameter. For example, in the Brunel model, the parameter g is an independent parameter.
2. Compute all dependent parameters of the model. These are all parameters or variables that have to be computed from other quantities (e.g. the total number of neurons).
3. Create all nodes (neurons, devices, etc.)
4. Connect the nodes.
5. Simulate the model.

We translate these steps into a simple class layout that will fit most models:

```
c1  class Model(object):
c2      """Model description."""
c3      # Define all independent variables.
c4
c5      def __init__(self):
c6          """Initialize the simulation, setup data directory"""
c7      def calibrate(self):
c8          """Compute all dependent variables"""
c9      def build(self):
c10         """Create all nodes"""
c11     def connect(self):
c12         """Connect all nodes"""
c13     def run(self,simtime):
c14         """Build, connect and simulate the model"""
```

In the following, we illustrate how to fit the model from Section 3 into this scaffold. The complete and commented listing can be found in your NEST distribution.

```
c1  class Brunel2000(object):
c2      """
c3      Implementation of the sparsely connected random network,
c4      described by Brunel (2000) J. Comp. Neurosci.
c5      Parameters are chosen for the asynchronous irregular
c6      state (AI).
c7      """
c8      g      = 5.0
c9      eta    = 2.0
c10     delay  = 1.5
c11     tau_m  = 20.0
c12     V_th   = 20.0
c13     N_E    = 8000
c14     N_I    = 2000
c15     J_E    = 0.1
c16     N_rec   = 50
c17     threads=2       # Number of threads for parallel simulation
c18     built=False     # True, if build() was called
c19     connected=False# True, if connect() was called
c20     # more definitions follow...
```

A Python class is defined by the keyword **class** followed by the class name, Brunel2000 in this example. The parameter **object** indicates that our class is a subclass of a general Python Object. After the

colon, we can supply a documentation string, encased in triple quotes, which will be printed if we type **help**(Brunel2000). After the documentation string, we define all independent parameters of the model as well as some global variables for our simulation. We also introduce two Boolean variables built and connected to ensure that the functions build() and connect() are executed exactly once.

Next, we define the class functions. Each function has at least the parameter self, which is a reference to the current class object. It is used to access the functions and variables of the object.

The first function we look at is also the first one that is called for every class object. It has the somewhat cryptic name __init__():

```
c21     def __init__(self):
c22         """
c23         Initialize an object of this class.
c24         """
c25         self.name=self.__class__.__name__
c26         self.data_path=self.name+'/'
c27         nest.ResetKernel()
c28         if not os.path.exists(self.data_path):
c29             os.makedirs(self.data_path)
c30         print "Writing data to: "+self.data_path
c31         nest.SetKernelStatus({'data_path': self.data_path})
```

__init__() is automatically called by Python whenever a new object of a class is created and before any other class function is called. We use it to initialize the NEST simulation kernel and to set up a directory where the simulation data will be stored.

The general idea is this: each simulation with a specific parameter set gets its own Python class. We can then use the class name to define the name of a data directory where all simulation data are stored.

In Python it is possible to read out the name of a class from an object. This is done in line c25. Don't worry about the many underscores, they tell us that these names are provided by Python. In the next line, we assign the class name plus a trailing slash to the new object variable data_path. Note how all class variables are prefixed with self.

Next we reset the NEST simulation kernel to remove any leftovers from previous simulations.

The following two lines use functions from the Python library os which provides functions related to the operating system. In line c28 we check whether a directory with the same name as the class already exists. If not, we create a new directory with this name. Finally, we set the data path property of the simulation kernel. All recording devices use this location to store their data. This does not mean that this directory is automatically used for any other Python output functions. However, since we have stored the data path in an object variable, we can use it whenever we want to write data to file.

The other class functions are quite straightforward. Brunel2000.build() accumulates all commands that relate to creating nodes. The only addition is a piece of code that checks whether the nodes were already created:

```
c32     def build(self):
c33         """
c34         Create all nodes, used in the model.
c35         """
c36         if self.built: return
c37         self.calibrate()
c38         # remaining code to create nodes
c39         self.built=True
```

The last line in this function sets the variable self.built to True so that other functions know that all nodes were created.

In function Brunel2000.connect() we first ensure that all nodes are created before we attempt to draw any connection:

```
c40     def connect(self):
c41         """
```

```
c42         Connect all nodes in the model.
c43         """
c44         if self.connected: return
c45         if not self.built:
c46             self.build()
c47         # remaining connection code
c48         self.connected=True
```

Again, the last line sets a variable, telling other functions that the connections were drawn successfully.

Brunel2000.built and Brunel2000.connected are state variables that help you to make dependencies between functions explicit and to enforce an order in which certain functions are called. The main function Brunel2000.run() uses both state variables to build and connect the network:

```
c49     def run(self, simtime=300):
c50         """
c51         Simulate the model for simtime milliseconds and print the
c52         firing rates of the network during this period.
c53         """
c54         if not self.connected:
c55             self.connect()
c56         nest.Simulate(simtime)
c57         # more code, e.g. to compute and print rates
```

In order to use the class, we have to load the file with the class definition and then create an object of the class:

```
from brunel2000_classes import *
net=Brunel2000()
net.run(500)
```

Finally, we demonstrate how to use Python's class inheritance to express different parameter configurations and versions of a model. In the following listing, we derive a new class that simulates a network where excitation and inhibition are exactly balanced, i.e. $g = 4$:

```
c58 class Brunel_balanced(Brunel2000):
c59     """
c60     Exact balance of excitation and inhibition
c61     """
c62     g=4
```

Class Brunel_balanced is defined with class Brunel2000 as parameter. This means the new class inherits all parameters and functions from class Brunel2000. Then, we redefine the value of the parameter g. When we create an object of this class, it will create its new data directory.

We can use the same mechanism to implement alternative version of the model. For example, instead of re-implementing the model with randomized connection weights, we can use inheritance to change just the way nodes are connected:

```
c63 class Brunel_randomized(Brunel2000):
c64     """
c65     Like Brunel2000, but with randomized connection weights.
c66     """
c67     def connect(self):
c68         """
c69         Connect nodes with randomized weights.
c70         """
c71         # Code for randomized connections follows
```

Thus, using inheritance, we can easily keep track of different parameter sets and model versions and their associated simulation data. Moreover, since we keep all alternative versions, we also have a simple versioning system that only depends on Python features, rather than on third party tools or libraries. The full implementation of the model using classes can be found in the examples directory of your NEST distribution.

9 How to continue from here

In this chapter we have presented a step-by-step introduction to NEST, using concrete examples. The simulation scripts and more examples are part of the examples included in the NEST distribution. Information about individual PyNEST functions can be obtained with Python's **help**() function. For example:

```
>>>help(nest.Connect)

Connect(*args, **kwargs)
    Connect pre neurons to post neurons.

    Neurons in pre and post are connected using the specified connectivity
    (one-to-one by default) and synapse type (static_synapse by default).
    Details depend on the connectivity rule.

    ...
```

To learn more about NEST's node and synapse types, you can access NEST's help system, using the PyNEST command NEST's online help still uses a lot of SLI syntax, NEST's native simulation language. However the general information is also valid for PyNEST.

Help and advice can also be found on NEST's user mailing list where developers and users exchange their experience, problems and ideas. And finally, we encourage you to visit the web site of the NEST Initiative at `www.nest-initiative.org`.

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Version information

The examples in this chapter were tested with the following versions.
NEST: pre-2.6.0 (r11744), Python: 2.7.8, Matplotlib: 1.3.1, NumPy: 1.8.1.

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