What's new with

PyNN

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Outline

Simulator diversity
Problem and opportunity

Cons

- Considerable difficulty in translating models from one simulator to another...
- ...or even in understanding someone else's code.
- This:
  - impedes communication between investigators,
  - makes it harder to reproduce other people's work,
  - makes it harder to build on other people's work.

Pros

- Each simulator has a different balance between efficiency, flexibility, scalability and user-friendliness $\longrightarrow$ can choose the most appropriate for a given problem.
- Any given simulator is likely to have bugs and hidden assumptions, which will be revealed by cross-checking results between different simulators $\longrightarrow$ greater confidence in correctness of results.

Simulator-independent model specification
("Meta-simulators")

Simulator-independent environments for developing neuroscience models:

- keep the advantages of having multiple simulators
- but remove the translation barrier.

Three *(complementary)* approaches:

- GUI (e.g. neuroConstruct)
- XML-based language (e.g. NeuroML)
- interpreted language (e.g. Python)

A common scripting language for neuroscience simulators

Simulator	Language
PCSIM	C++ or Python
MOOSE	SLI or Python
MVASpike	C++ or Python
NEST	sli or Python
NEURON	hoc or Python
SPLIT	C++ *(Python interface planned)*
Brian	Python
FACETS hardware	Python

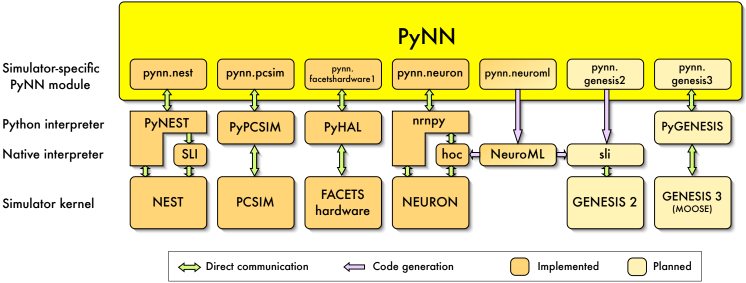
A common scripting language for neuroscience simulators

Goal

Write the code for a model simulation *once*, run it on any supported simulator* *without modification*.

* *or hardware device*

Architecture



How to get PyNN

Latest stable version

`http://neuralensemble.org/PyNN/wiki/Download`

Latest development version

```
svn co https://neuralensemble.org/svn/PyNN/trunk pyNN
```

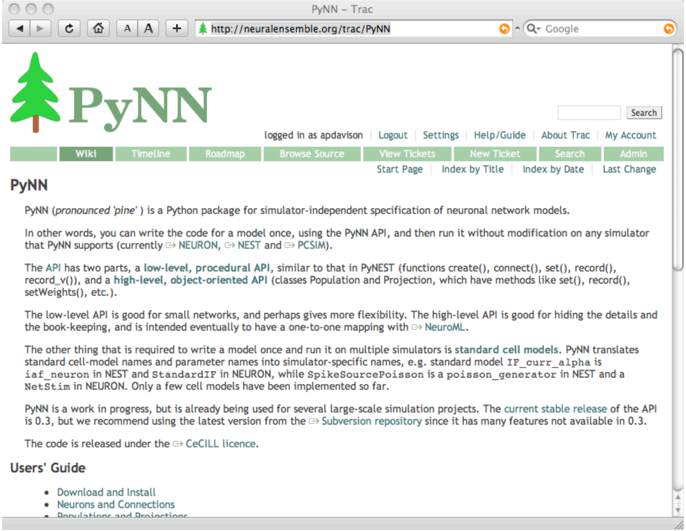
Full documentation

`http://neuralensemble.org/PyNN`

Installing PyNN

via svn or distutils

How to participate in PyNN development



http://neuralensemble.org/PyNN

How to participate in PyNN development

Google groups screenshot

Google groups URL

Outline

Selecting the simulator

```
from pyNN.neuron import *
from pyNN.nest1 import *
from pyNN.nest2 import *
from pyNN.pcsim import *
from pyNN.moose import *
from pyNN.brian import *

import pyNN.neuron as sim
```

setup() and end()

```
setup(timestep=0.1, min_delay=0.1, debug=False)

setup(timestep=0.1, min_delay=0.1, debug='pyNN.log',
      threads=2, shark_teeth=999)

end()
```

create()

```
create(IF_curr_alpha)

create(IF_curr_alpha, n=10)

create(IF_curr_alpha, {’tau_m’: 15.0, ’cm’: 0.9}, n=10)

>>> IF_curr_alpha.default_parameters
{’tau_refrac’: 0.0, ’tau_m’: 20.0, ’i_offset’: 0.0,
 ’cm’: 1.0, ’v_init’: -65.0,’v_thresh’: -50.0,
 ’tau_syn_E’: 0.5, ’v_rest’: -65.0, ’tau_syn_I’: 0.5,
 ’v_reset’: -65.0}
```

create()

```
>>> create(IF_curr_alpha, param_dict=’foo’: 15.0)
    Traceback (most recent call last):
      .
      .
      .
    NonExistentParameterError: foo

    >>> create(IF_curr_alpha, param_dict=’tau_m’: ’bar’)
    Traceback (most recent call last):
      .
      .
      .
    InvalidParameterValueError:
        (<type ’str’>, should be <type ’float’>)
```

create()

```
create(IF_curr_alpha, 'v_thresh': -50, 'cm': 0.9)

create('iaf_neuron', 'V_th': -50, 'C_m': 900.0)
```

Standard cell models

```
IF_curr_alpha
IF_curr_exp
IF_cond_alpha
IF_cond_exp,
IF_cond_exp_gsfa_grr
IF_facets_hardware1
HH_cond_exp,
EIF_cond_alpha_isfa_ista
SpikeSourcePoisson
SpikeSourceInhGamma
SpikeSourceArray
```

Standard cell models

Example: Leaky integrate-and-fire model with fixed firing threshold, and current-based, alpha-function synapses.

Name	Units	NEST	NEURON
v_rest	mV	U0	v_rest
v_reset	mV	Vreset	v_reset
cm	nF	C†	CM
tau_m	ms	Tau	tau_m
tau_refrac	ms	TauR	t_refrac
tau_syn	ms	TauSyn	tau_syn
v_thresh	mV	Theta	v_thresh
i_offset	nA	I0†	i_offset

†Unit differences: C is in pF, I0 in pA.

ID objects

```
>>> my_cell = create(IF_cond_exp)
>>> print my_cell
1
>>> type(my_cell)
<class 'pyNN.nest2.ID'>
>>> my_cell.tau_m
20.0
>>> my_cell.position
(1.0, 0.0, 0.0)
>>> my_cell.position = (0.76, 0.54, 0.32)
```

connect()

```
spike_source = create(SpikeSourceArray,
                      {'spike_times': [10.0, 20.0, 30.0]})
cell_list = create(IF_curr_exp, n=10)

connect(spike_source, cell_list)
```

```
connect(sources, targets, weight=1.5, delay=0.5,
        p=0.2, synapse_type='inhibitory')
```

record()

```
record(cell, "spikes.dat")

record_v(cell_list, "Vm.dat")
```

Writing occurs on `end()`

run()

```
run(100.0)
```

Simulation status

```
get_current_time()

get_time_step()

get_min_delay()

num_processes()

rank()
```

Random numbers

```
>>> from pyNN.random import NumpyRNG, GSLRNG, NativeRNG

>>> rng = NumpyRNG(seed=12345)
>>> rng.next()
0.6754034
>>> rng.next(3, 'uniform', (-70,-65))
[-67.4326, -69.9223, -65.4566]
```

- Use `NativeRNG` or `GSLRNG` to ensure different simulators get the same random numbers
- Use `NativeRNG` to use a simulator's built-in RNG

Random numbers

```
>>> from pyNN.random import RandomDistribution

>>> distr = RandomDistribution('uniform', (-70, -65),
...                            rng=rng)
>>> distr.next(3)
[-67.4326, -69.9223, -65.4566]
```

Populations

```
p1 = Population((10,10), IF_curr_exp)

p2 = Population(100, SpikeSourceArray,
                label="Input Population")

p3 = Population(dims=(3,4,5), cellclass=IF_cond_alpha,
                cellparams={'v_thresh': -55.0},
                label="Column 1")

p4 = Population(20, 'iaf_neuron', {'Tau': 15.0,
                                   'C': 100.0})
```

Populations

Accessing individual members

```
>>> p1[0,0]
    1
    >>> p1[9,9]
    100
    >>> p3[2,1,0]
    246

    >>> p3.locate(246)
    (2, 1, 0)

>>> p1.index(99)
100

>>> p1[0,0].tau_m = 12.3
```

Populations

Iterators

```
>>> for id in p1:
...     print id, id.tau_m
...
0 12.3
1 20.0
2 20.0
...

>>> for addr in p1.addresses():
...     print addr
...
(0, 0)
(0, 1)
(0, 2)
...
(0, 9)
(1, 0)
```

set(), tset(), rset()

```
>>> p1.set("tau_m", 20.0)

>>> p1.set('tau_m':20, 'v_rest':-65)

>>> distr = RandomDistribution('uniform', [-70,-55])
>>> p1.rset('v_init', distr)

>>> import numpy
>>> current_input = numpy.zeros(p1.dim)
>>> current_input[:,0] = 0.1
>>> p1.tset('i_offset', current_input)
```

Recording

```
# record from all neurons in the population
>>> p1.record()

# record from 10 neurons chosen at random
>>> p1.record(10)

# record from specific neurons
>>> p1.record([p1[0,0], p1[0,1], p1[0,2]])


>>> p1.printSpikes("spikefile.dat")

>>> p1.getSpikes()
array([])
```

Position in space

```
>>> p1[1,0].position = (0.0, 0.1, 0.2)
>>> p1[1,0].position
array([ 0. ,  0.1,  0.2])

>>> p1.positions
array([[...]])

>>> p1.nearest((4.5, 7.8, 3.3))
48
>>> p1[p1.locate(48)].position
array([ 4.,  8.,  0.])
```

Projections

```
prj2_1 = Projection(p2, p1, AllToAllConnector())

prj1_2 = Projection(p1, p2, FixedProbabilityConnector(0.02),
                    target='inhibitory', label='foo',
                    rng=NumpyRNG())
```

Connectors

`AllToAllConnector`

`OneToOneConnector`

`FixedProbabilityConnector`

`DistanceDependentProbabilityConnector`

`FixedNumberPostConnector`

`FixedNumberPostConnector`

`FromFileConnector*`

`FromListConnector`

(* cf `Projection.saveConnections(filename)`)

Connectors

```
c = DistanceDependentProbabilityConnector(
        "exp(-abs(d))",
        axes='xy',
        periodic_boundaries=(500, 500, 0),
        weights=0.7,
        delays=RandomDistribution('gamma', [1,0.1])
    )
```

Weights and delays

```
>>> prj1_1.setWeights(0.2)

>>> weight_list = 0.1*numpy.ones(len(prj2_1))
>>> weight_list[0:5] = 0.2
>>> prj2_1.setWeights(weight_list)

>>> prj1_1.randomizeWeights(weight_distr)

>>> prj1_2.setDelays('exp(-d/50.0)+0.1')
```

[Note: synaptic weights are in nA for current-based synapses and μS for conductance-based synapses]

Weights and delays

```
w_array = prj.getWeights()

prj.printWeights(filename)
```

Synaptic plasticity

```
# Facilitating/depressing synapses
depressing_syn = SynapseDynamics(
                    fast=TsodyksMarkramMechanism(**params))
prj = Projection(pre, post, AllToAllConnector(),
                 synapse_dynamics=depressing_syn)

# STDP
stdp_model = STDPMechanism(
               timing_dependence=SpikePairRule(
                                   tau_plus=20.0,
                                   tau_minus=20.0),
               weight_dependence=AdditiveWeightDependence(
                                   w_min=0, w_max=0.02,
                                   A_plus=0.01, A_minus=0.012)
             )
prj2 = Projection(pre, post, FixedProbabilityConnector(p=0.1),
                  synapse_dynamics=SynapseDynamics(slow=stdp_model))
```

Outline

mpirun

png from NEURON on different numbers of processors?

Outline

Use cases

Testing a model on multiple simulators

Cross-checking gives greater confidence in correctness of results.

Porting a model between simulators

Gradually replace simulator-specific code with Python code, checking results are unchanged at each step.

Hardware interface

Neuromorphic VLSI hardware can also use PyNN, allowing direct comparison of numerical simulations and emulations in silicon.

Collaborating between different groups

Each group can use their preferred simulator, while working on a common code base.

Outline

1. A brief introduction to PyNN
2. A tour of the API
3. Parallel simulations
4. Use cases
5. **Future directions**

Future directions

- Extend range of simulators supported (full NeuroML support, MOOSE, Brian,...)
- Support non-spiking (firing-rate based) neuron models?
- Support explicit units (cf Brian)
- Optimisation, so PyNN is only a little slower than native code
- Improved parallelisation
- Extensions of the API:
  - current highest level of organisation is Population, Projection.
  - extend to Column, Layer, Meta-column, Map, ...
  - extend stimuli, e.g., DriftingGrating, DenseNoise,...
  - extend recording, e.g. recordActivityMap(), ...