

What's new with



*Andrew Davison
UNIC, CNRS*

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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

Goal

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

* *or hardware device*



A common scripting language for neuroscience simulators

Simulator

PCSIM

MOOSE

MVASpike

NEST

NEURON

SPLIT

Brian

FACETS hardware

Language

C++ or Python

SLI or Python

C++ or Python

sli or Python

hoc or Python

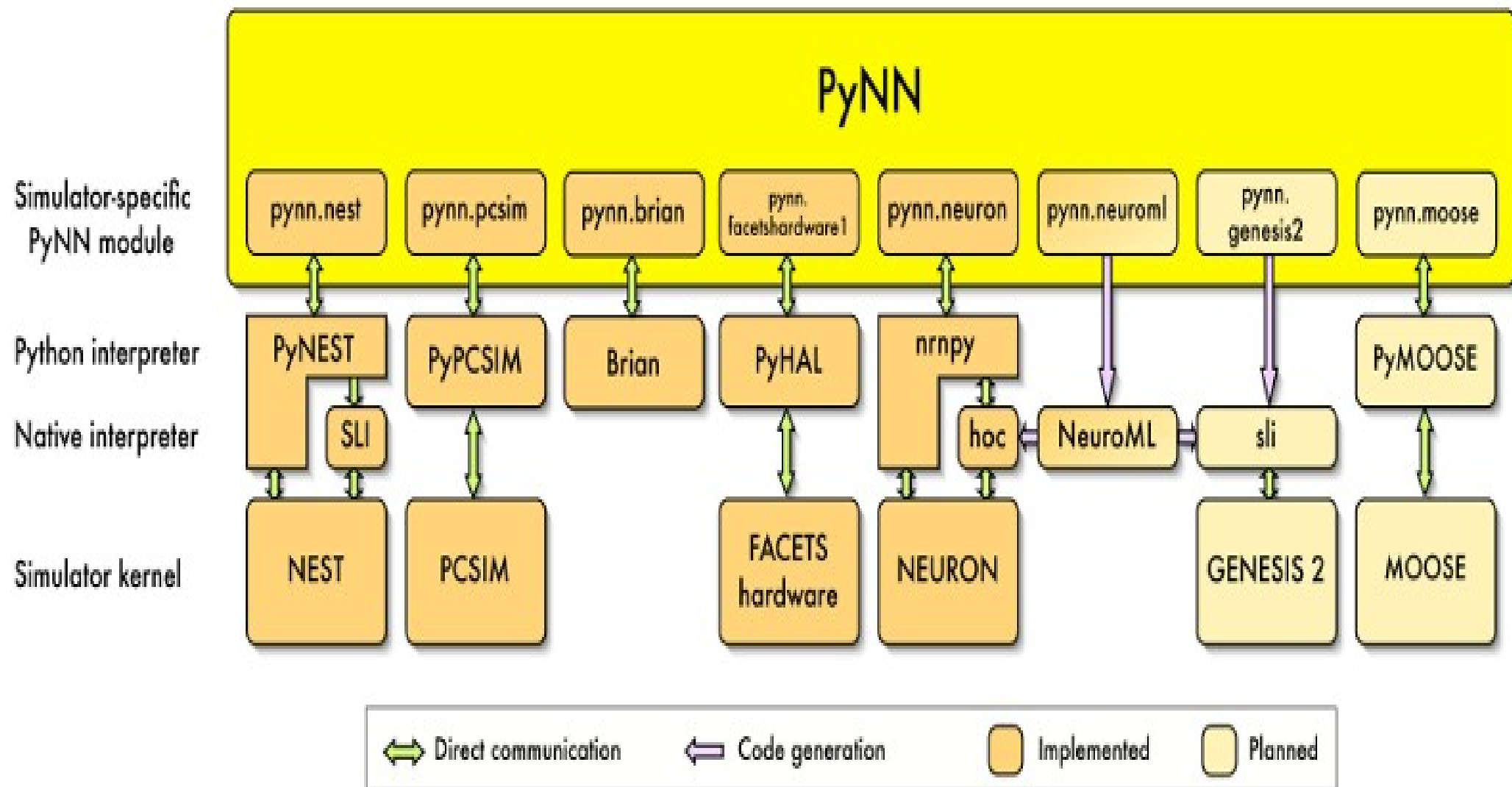
C++ (*Python interface planned*)

Python

Python



PyNN Approach: A standardized API



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
```



Overview:

PyNN low-level API

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]
```



Overview:

PyNN high-level API

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)
```



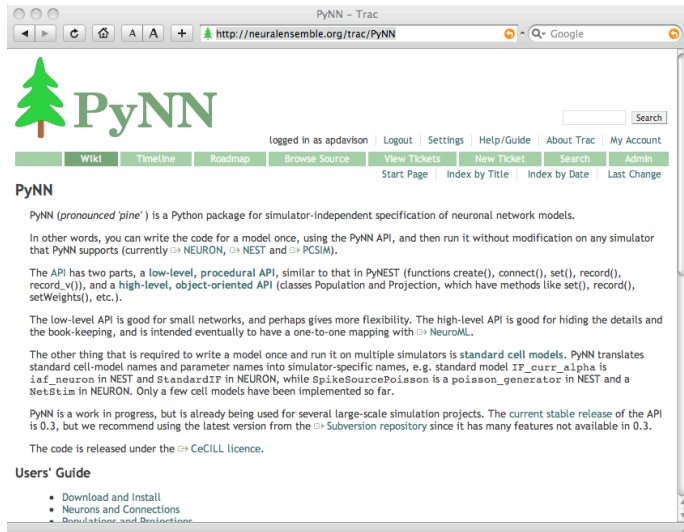
Synaptic plasticity

```
# 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))
```



How to participate in PyNN development



The screenshot shows a web browser window with the address bar displaying `http://neuralensemble.org/trac/PyNN`. The page features the PyNN logo, which consists of a green pine tree icon and the text "PyNN". Below the logo, there is a navigation bar with links: "Wiki", "Timeline", "Roadmap", "Browse Source", "View Tickets", "New Ticket", "Search", and "Admin". A search bar is also present. The main content area is titled "PyNN" and contains the following text:

PyNN (*pronounced 'pine'*) is a Python package for simulator-independent specification of neuronal network models.

In other words, you can write the code for a model once, using the PyNN API, and then run it without modification on any simulator that PyNN supports (currently [NEURON](#), [NEST](#) and [PCSIM](#)).

The API has two parts, a **low-level, procedural API**, similar to that in PyNEST (functions `create()`, `connect()`, `set()`, `record()`, `record_v()`), and a **high-level, object-oriented API** (classes `Population` and `Projection`, which have methods like `set()`, `record()`, `setWeights()`, etc.).

The low-level API is good for small networks, and perhaps gives more flexibility. The high-level API is good for hiding the details and the book-keeping, and is intended eventually to have a one-to-one mapping with [NeuroML](#).

The other thing that is required to write a model once and run it on multiple simulators is **standard cell models**. PyNN translates standard cell-model names and parameter names into simulator-specific names, e.g. standard model `IF_curr_alpha` is `iaf_neuron` in NEST and `StandardIF` in NEURON, while `SpikeSourcePoisson` is a `poisson_generator` in NEST and a `NetStim` in NEURON. Only a few cell models have been implemented so far.

PyNN is a work in progress, but is already being used for several large-scale simulation projects. The [current stable release](#) of the API is 0.3, but we recommend using the latest version from the [Subversion repository](#) since it has many features not available in 0.3.

The code is released under the [CeCILL licence](#).

Users' Guide

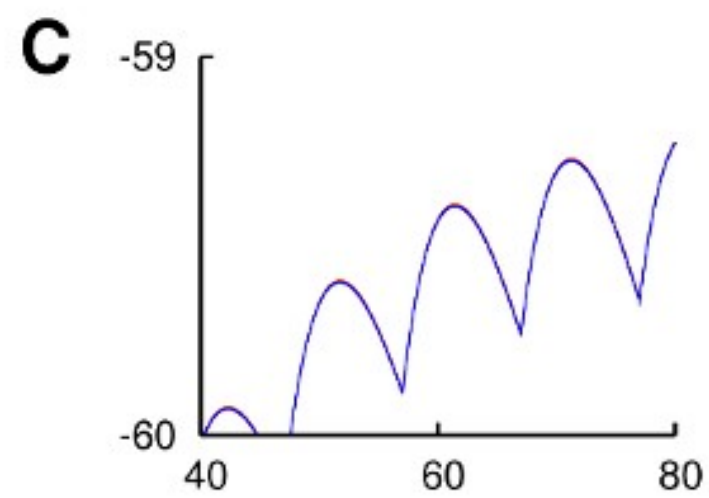
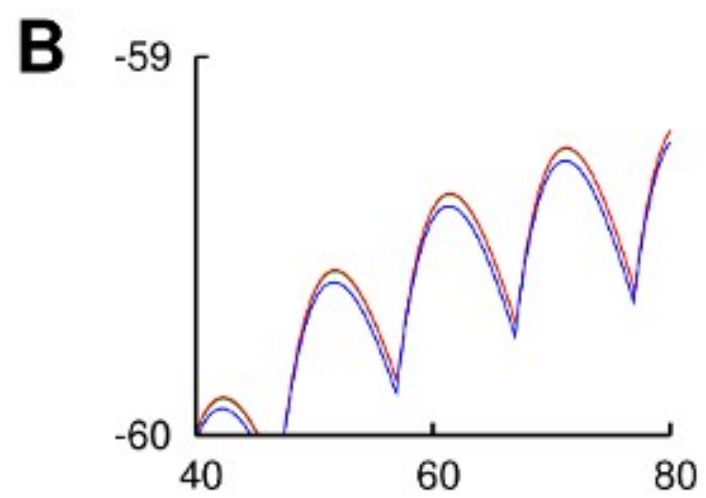
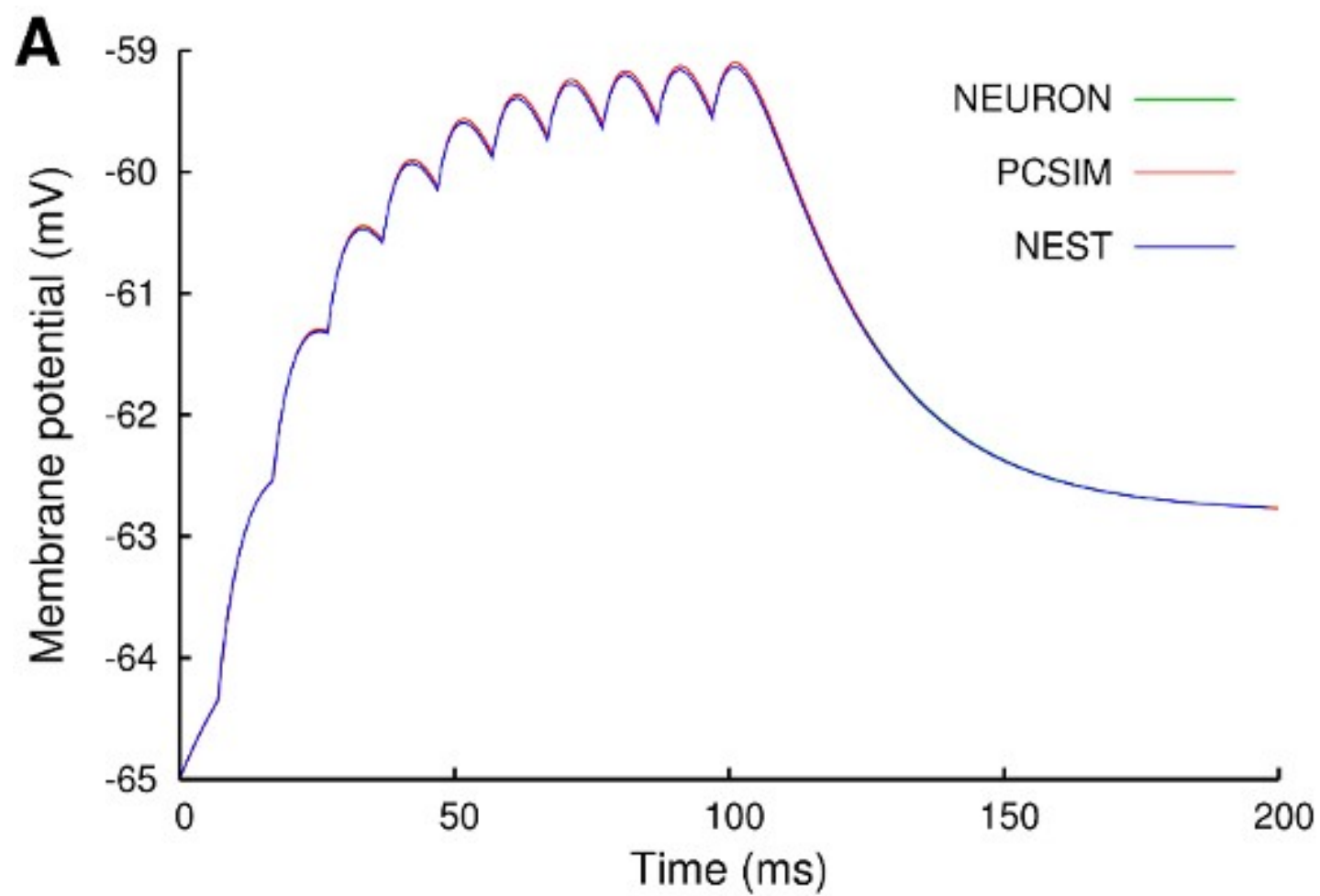
- Download and Install
- Neurons and Connections
- Populations and Projections

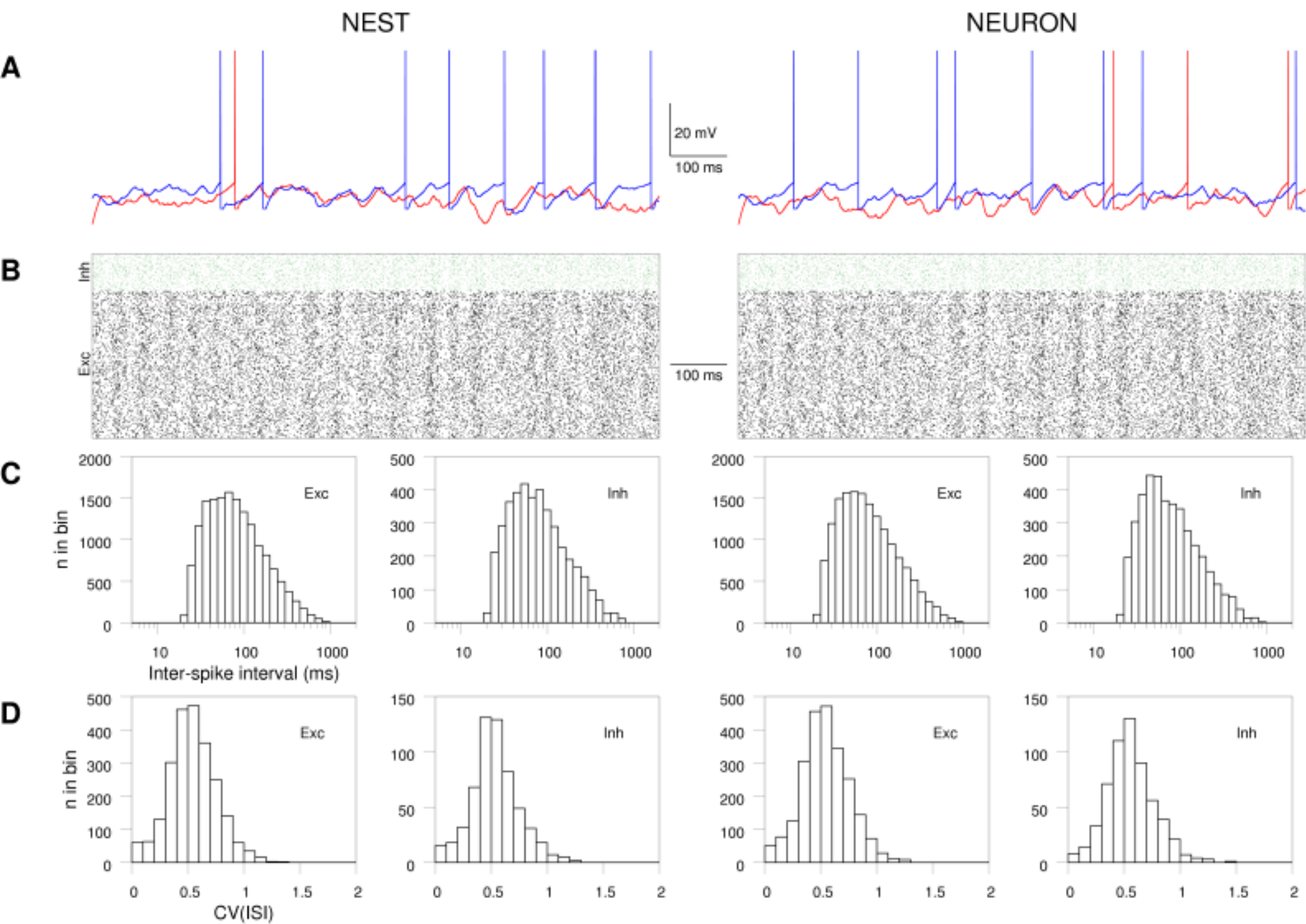
`http://neuralensemble.org/PyNN`



Why might PyNN be important for this INCF initiative?

- Declarative XML
 - Not generally human generatable or even readable
 - PyNN is human generatable and can generate NeuroML
- Standards compliance verification
 - A test-suite for compliance
 - Write once in PyNN for all
 - No testing of the various test suites, no bash|perl





- Implement XML importer/parser for PyNN
 - Writing and maintaining Python+PyNN support for a given simulator is orders of magnitude more appealing than writing and maintaining a compliant XML parser. PyNN can provide this.
- PyNN API user extensions in terms of the API
 - Such extensions supported by all simulators implementing the API
 - Maintain existing isomorphism between PyNN API Object Model and NeuroML for I&F networks
 - Avoid re-inventing a general modeling language in XML with associated difficulties to parse and support downstream.

1 API (PyNN low-level)

- create, connect

2 Object model (PyNN high-level)

- Population, Projection

3 Object Declarative Mapping (à la ORM for DBs)

- PyNN \Leftrightarrow NeuroML

Main message:

- Unification of simulator object models (hard)
- Declarative model format through ODM (easy)

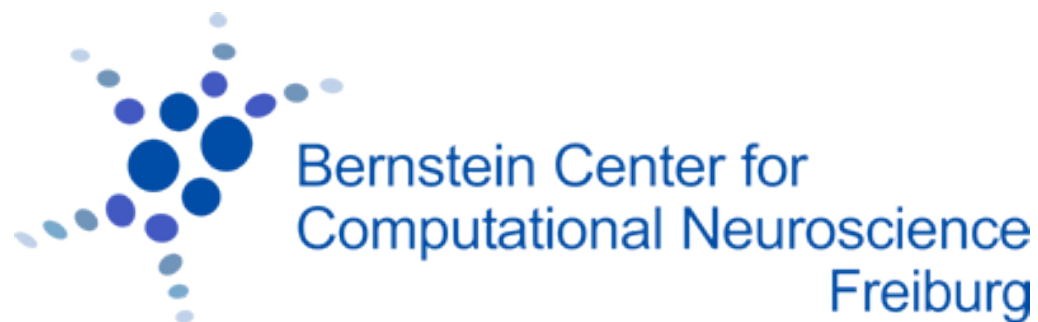


The FACETS Project

CodeJam Workshop #3

When: ~7-10.10.2009

Where:



Bernstein Center for
Computational Neuroscience
Freiburg

Contact: Abigail Morrison (abigail@brain.riken.jp)

CodeJam #1 (2007)

Heidelberg



CodeJam #2 (2008)

Gif-sur-Yvette

