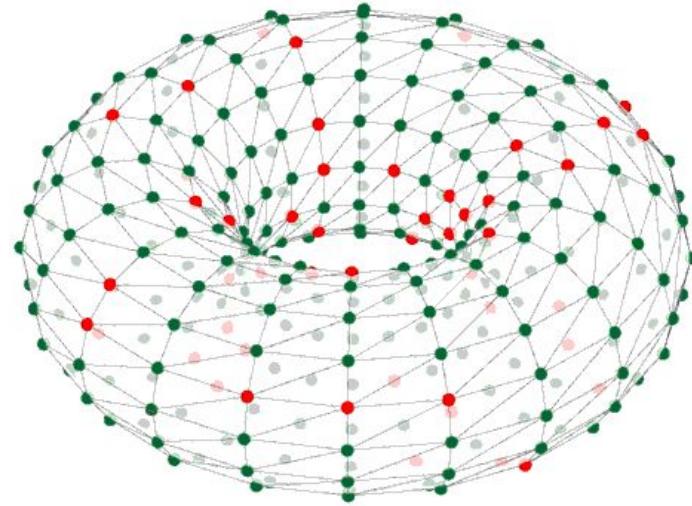


SpiNNaker Tutorial



Accessing SpiNNaker

Accessing SpiNNaker via Jupyter - Create a Collaboratory

<https://wiki.ebrains.eu/>

Log in to Wiki

The screenshot shows a web browser window with the URL <https://wiki.ebrains.eu/bin/view/Main/>. The page is titled "Collaborate on reproducible sci" and features the EBRAINS Collaboratory logo. The navigation bar includes links for Collabs, Documentation, Support, Chat, Community, and Log-in. A red oval highlights the "Log-in" button. The main content area contains text about collaborating, creating reproducible science, and discovering services, along with a "Getting started" button. To the right, there is an illustration of people working together on a large screen displaying a graph. Below this is a section titled "Highlighted collabs" with a "View all" link.

Collaborate.
Create reproducible science.
Discover EBRAINS services at work.
From anywhere.

Getting started

Highlighted collabs

View all

<https://wiki.ebrains.eu/bin/view/Collabs/>

Create a Collaboratory

The screenshot shows a web browser window with the title bar "JupyterLab" and "Collaborate on reproducible sci". The address bar shows the URL "wiki.ebrains.eu/bin/view/Main/". The main content area is the EBRAINS Collaboratory homepage. At the top left is the logo "EBRAINS Collaboratory". To its right is a navigation bar with links: "Collabs" (which is circled in red), "Documentation", "Support", "Chat", "Community", a search icon, a bell icon, a user profile icon, and a "Log-out" link. Below the navigation bar, there is a section with the text: "Collaborate. Create reproducible science. Discover EBRAINS services at work. From anywhere." A green button labeled "Getting started" is visible. To the right of this text is a stylized illustration of four people working together on a large document or board, with one person climbing a ladder. At the bottom of the page is a search bar with the placeholder "Search word in all wiki pages" and a magnifying glass icon.

Create a Collaboratory

Screenshot of the EBRAINS Collaboratory website showing the 'Collab Search' page.

The browser tabs show 'JupyterHub' and 'Collabs - HBP Wiki'. The URL is 'wiki.ebrains.eu/bin/view/Collabs/'.

The page header includes the EBRAINS Collaboratory logo, navigation links for 'Collabs', 'Documentation', 'Support', 'Chat', 'Community', and 'Log-out'.

A red circle highlights the green 'Create a collab' button in the top right corner.

Collab Search

Find available collabs searching for words in title and description.
You can refine the results using the filters.

Search bar: Search word in collab titles & descriptions. You can use AND, OR and - operators.

Search button: Search

Filter Collabs button: FILTER COLLABS

Filter options: Your favourites

Your Role button: YOUR ROLE

Filter options: Admin Editor

Showing highlighted collabs
Do you want to [promote your collab?](#)

INPUT: A stack of brain sections. Process: NIfTI QuickAlign and Registration → Registration of images to reference brain atlas space. OUTPUT: Customized atlas image and coordinate files.

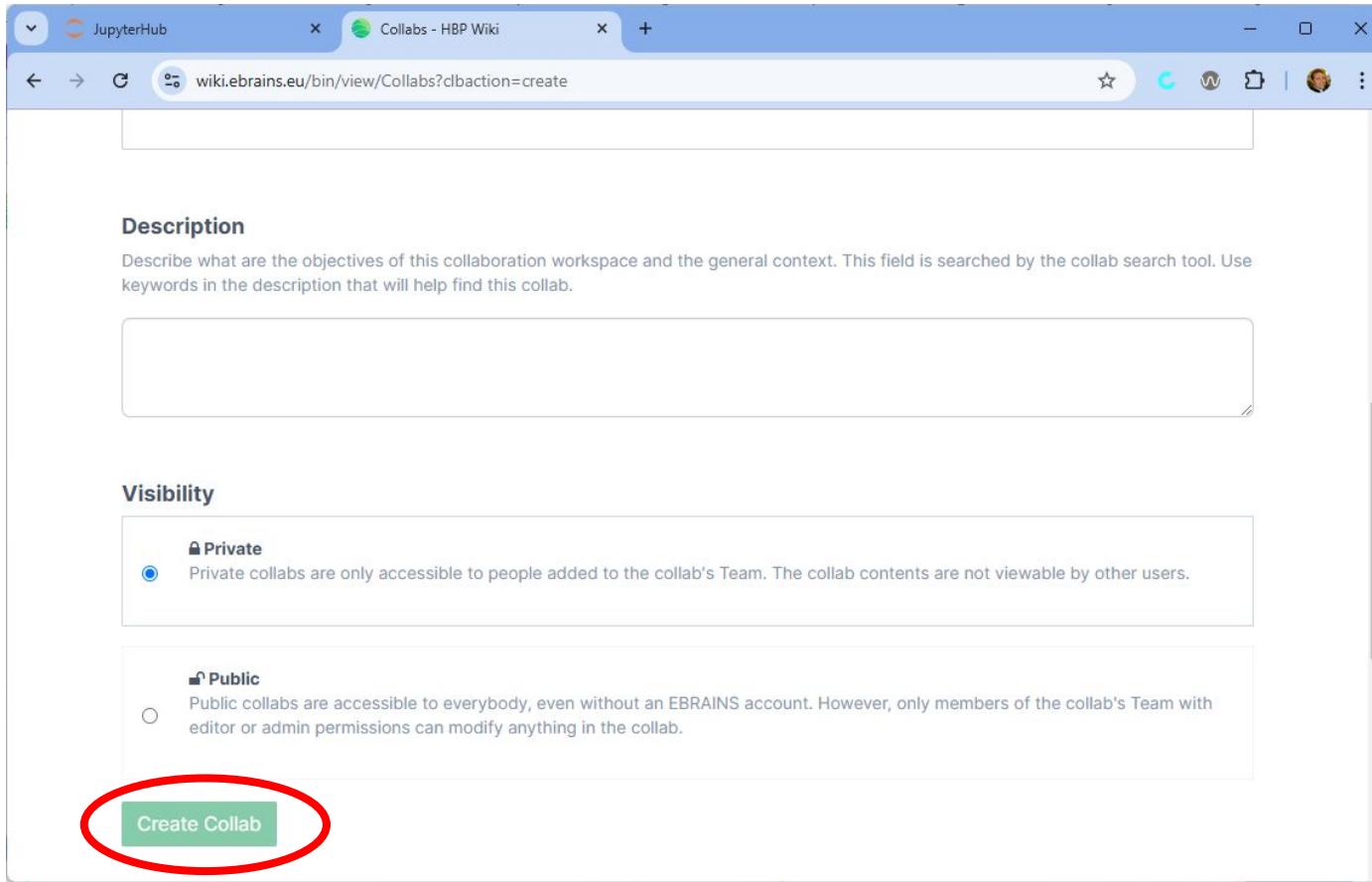
INPUT: A stack of brain sections. Process: **Kotiki** Image registration to extract the labeling. OUTPUT: Same brain sections.

INPUT: A stack of brain sections. Process: **AutoQuantifier** Orientation of segmented objects per brain atlas region. OUTPUT: Quantification results. Boxed text: Quantification results. Boxed text: Quantification results.

EBRAINS Curation Services
How to share your data

Drivers

Create a Collaboratory



The screenshot shows a web browser window with the title "Collabs - HBP Wiki". The URL in the address bar is "wiki.ebrains.eu/bin/view/Collabs?clbaction=create". The page content is a form for creating a new collaboratory workspace.

Description
Describe what are the objectives of this collaboration workspace and the general context. This field is searched by the collab search tool. Use keywords in the description that will help find this collab.

Visibility

Private Private collabs are only accessible to people added to the collab's Team. The collab contents are not viewable by other users.

Public Public collabs are accessible to everybody, even without an EBRAINS account. However, only members of the collab's Team with editor or admin permissions can modify anything in the collab.

Create Collab

Accessing SpiNNaker via Jupyter - Go to EBRAINS Lab

<https://lab.ebrains.eu/>

EBRAINS Lab - Choose a Site

The screenshot shows a web browser window titled "Jupyterlab - Execution Site" with the URL "lab.ebrains.eu". The page features the Jupyter logo (orange and grey dots) at the top. Below it is the heading "Select Lab Execution Site" with a help icon. A list of five execution sites is provided, each with a radio button:

- Fenix CH - Swiss National Supercomputing Center (CSCS)
- Fenix DE - Jülich Supercomputing Center (JSC)
- Fenix ES - Barcelona Supercomputing Center (BSC)
- Fenix FR - French Alternative Energies and Atomic Energy Commission (CEA)
- Fenix IT - Cineca

A large orange "Select" button is located below the site list. At the bottom, there are two logos: EBRAINS (green globe) and Human Brain Project (blue and red globe).

EBRAINS Lab - Choose a Site

Jupyterlab - Execution Site

lab.ebrains.eu

jupyter

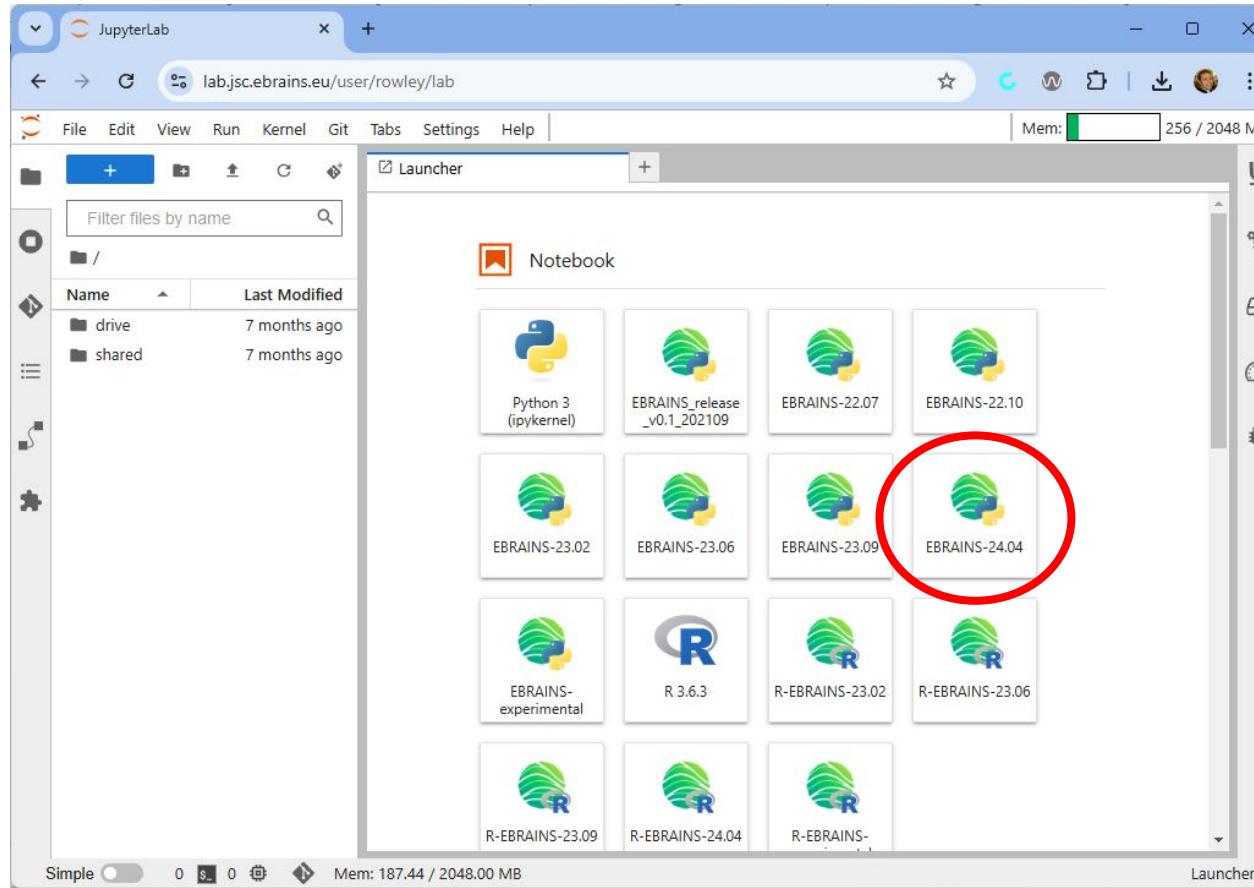
Select Lab Execution Site ?

- Fenix CH - Swiss National Supercomputing Center (CSCS)
- Fenix DE - Jülich Supercomputing Center (JSC)
- Fenix ES - Barcelona Supercomputing Center (BSC)
- Fenix FR - French Alternative Energies and Atomic Energy Commission (CEA)
- Fenix IT - Cineca

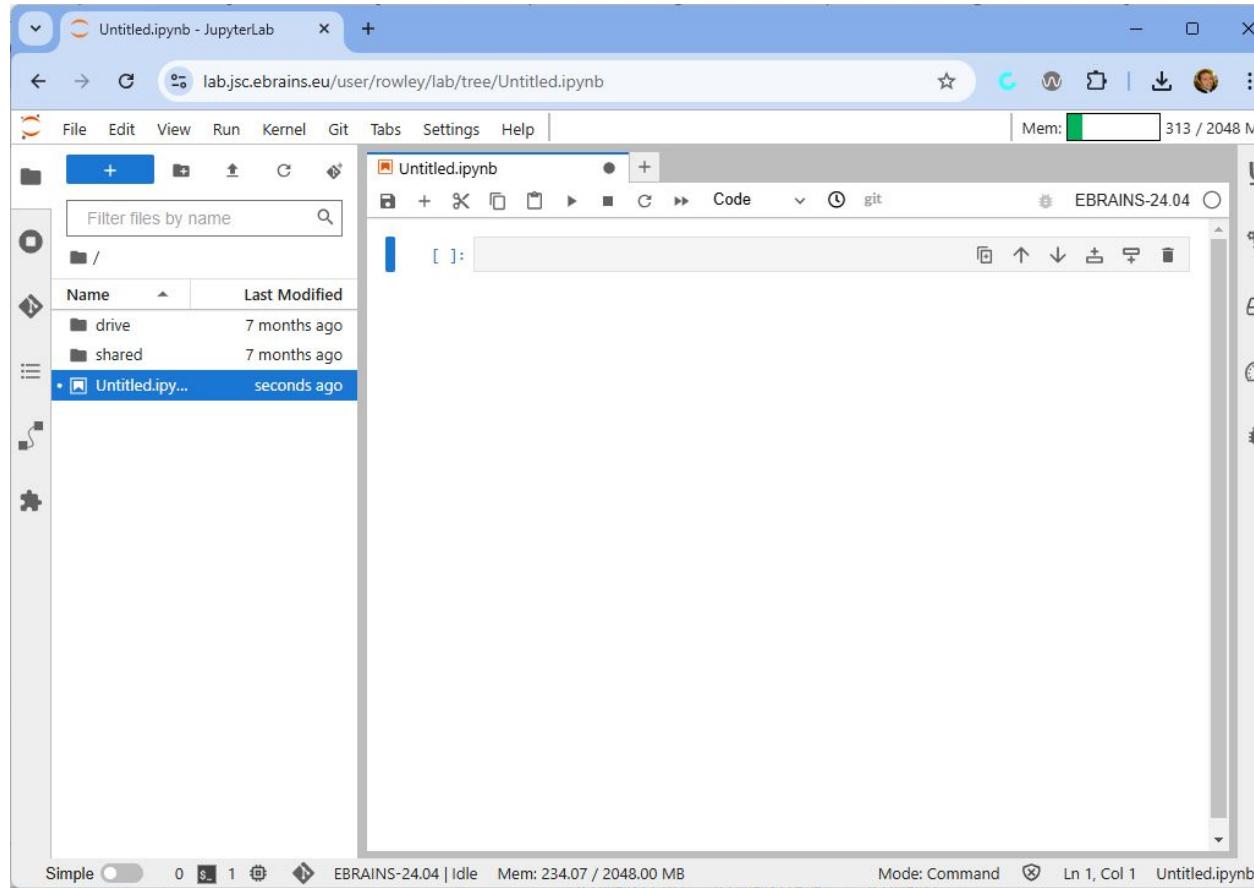
Select

E BRAINS Human Brain Project

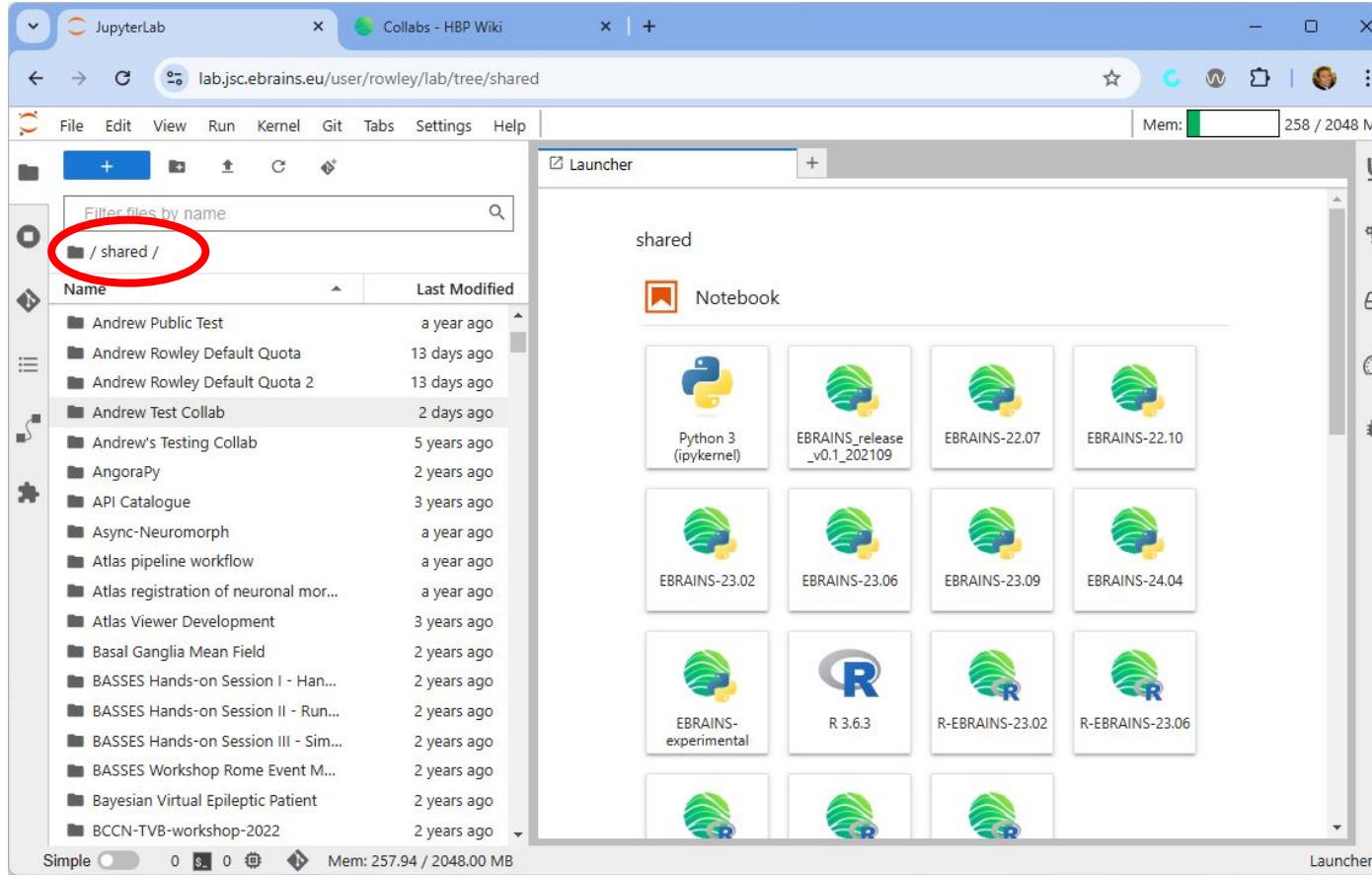
EBRAINS Lab - Choose a Kernel



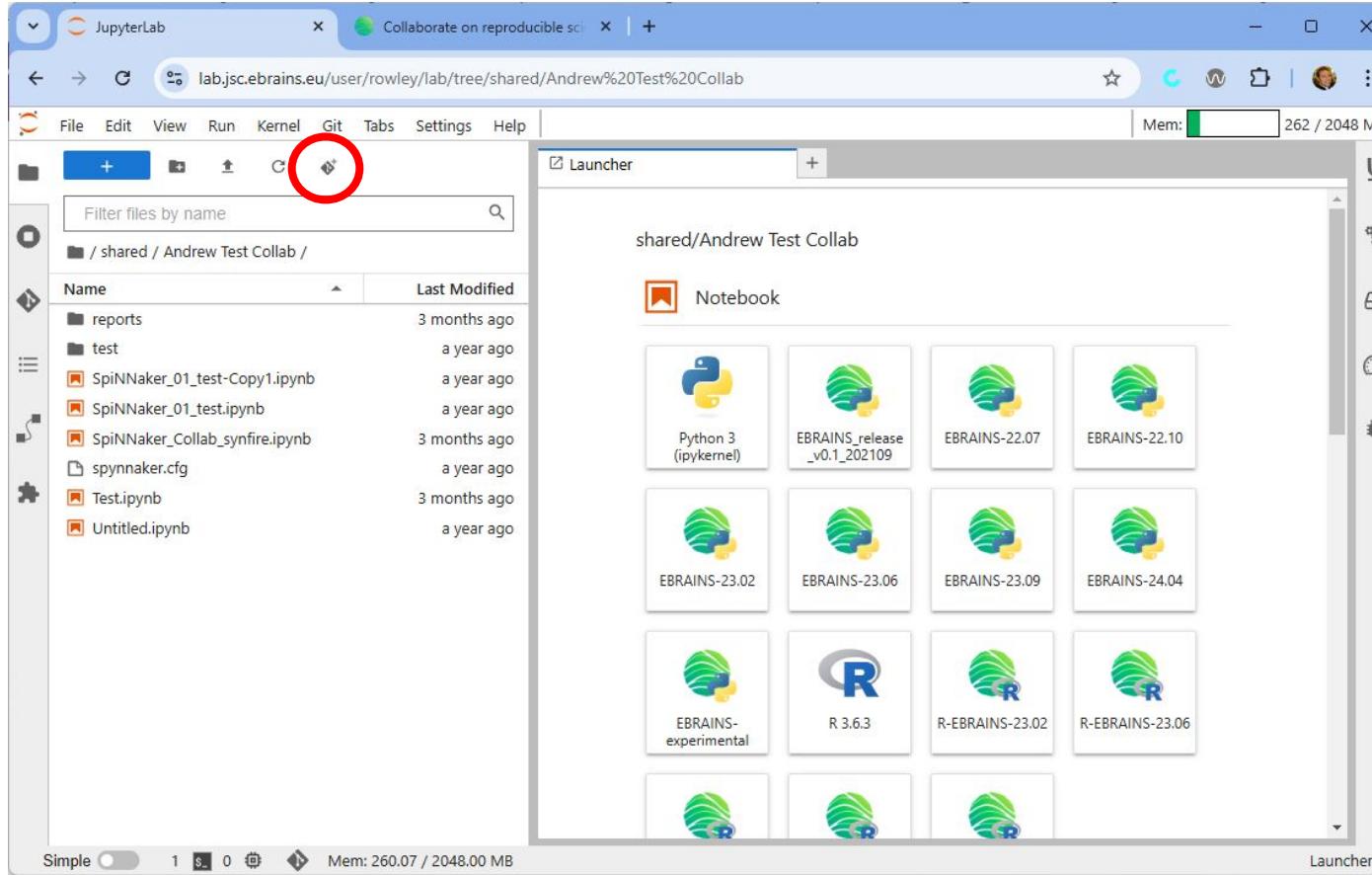
EBRAINS Lab - Choose a Kernel



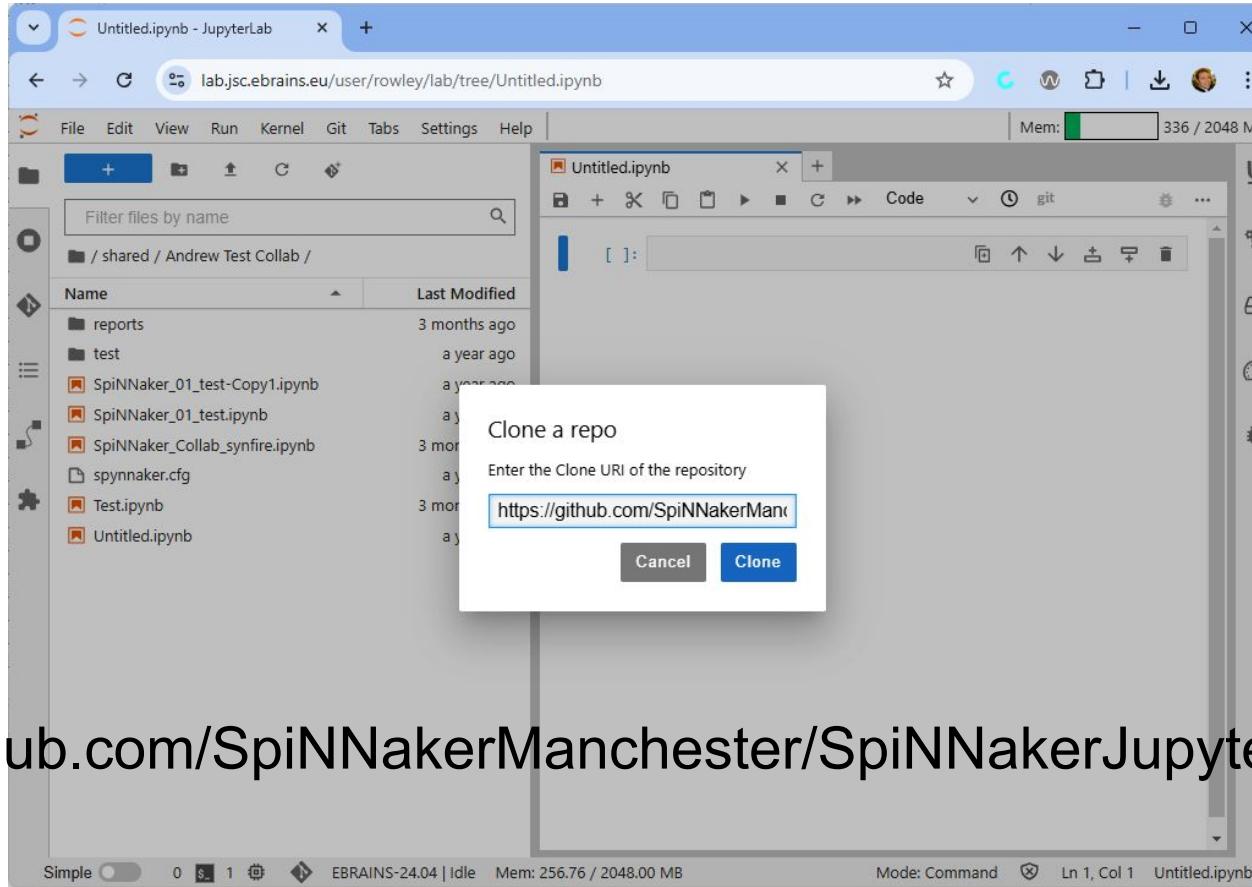
Find your Collab: /shared/...



Clone SpiNNaker Repository

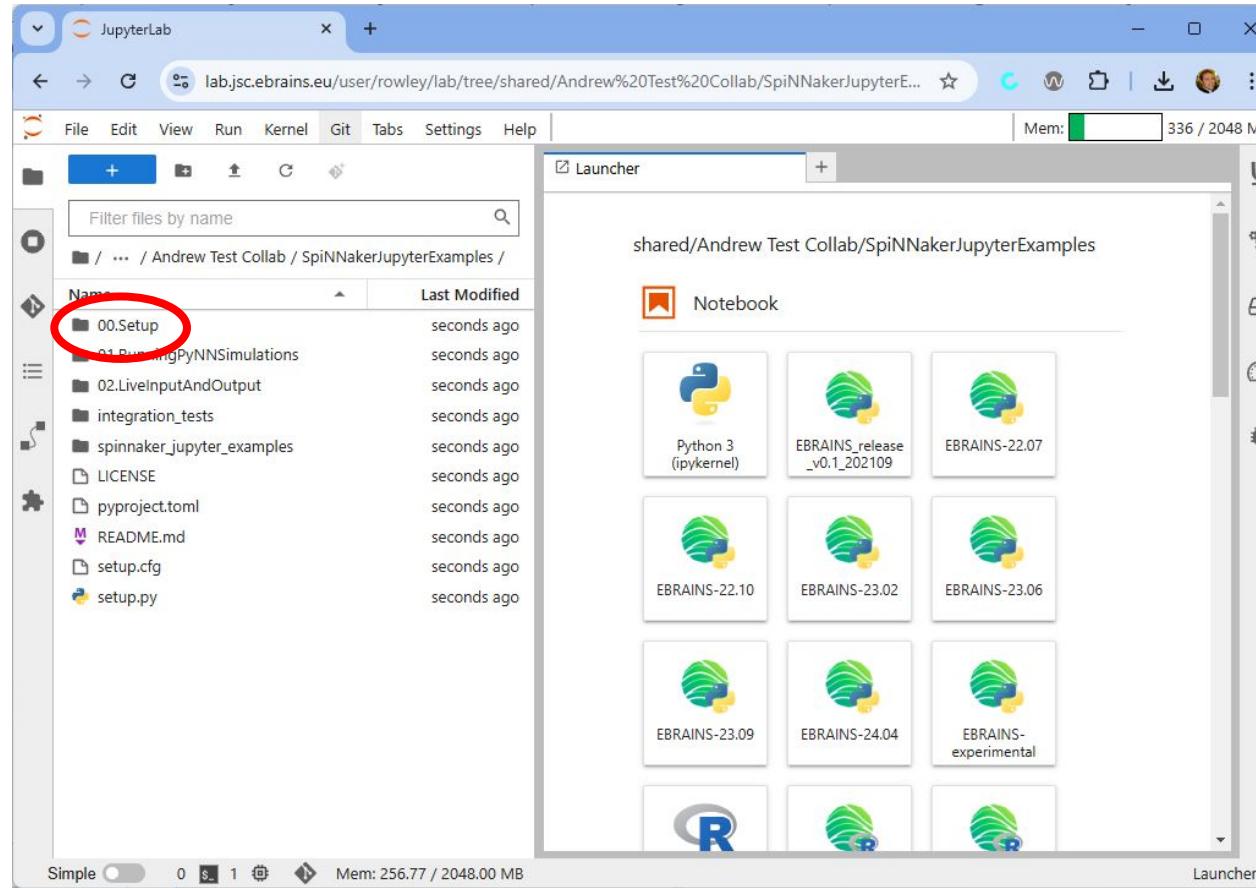


Clone SpiNNaker Repository

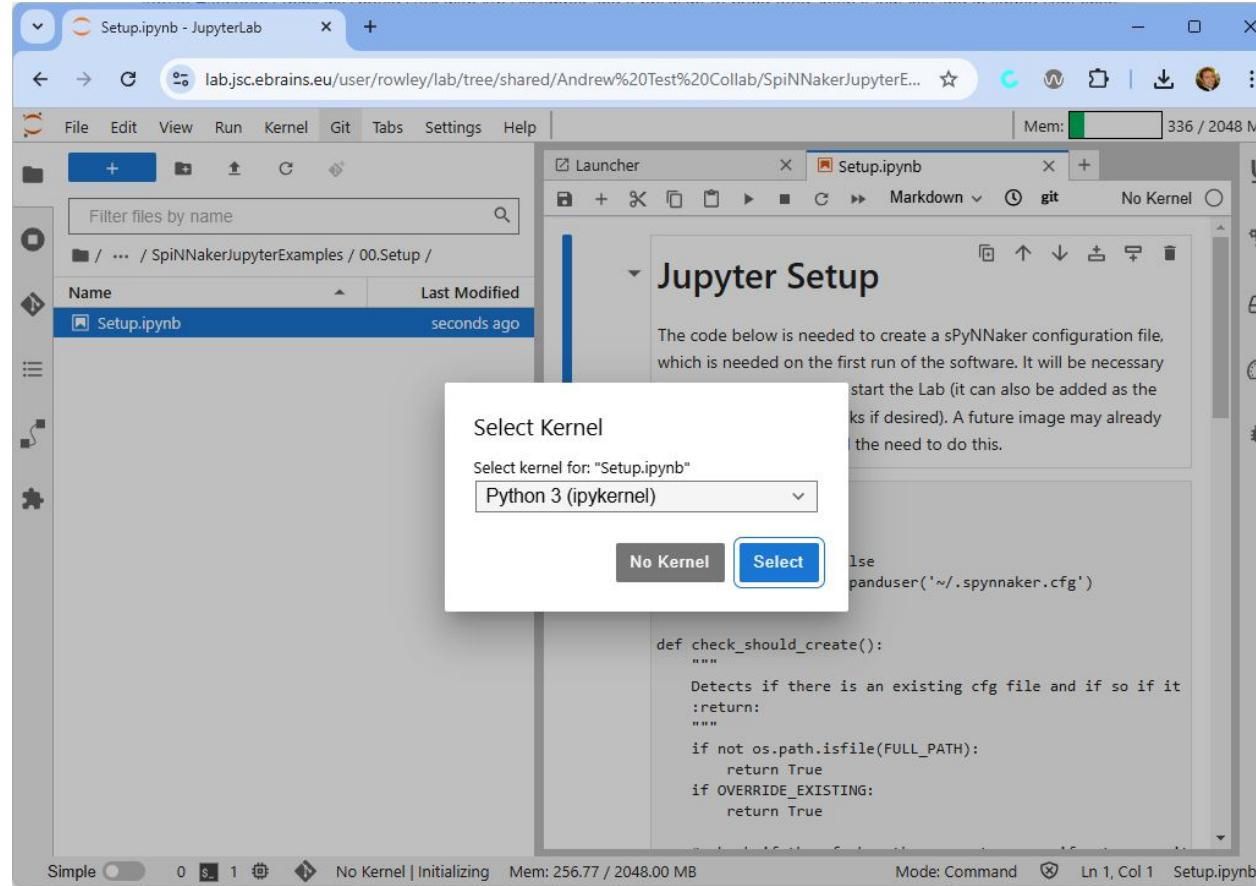


<https://github.com/SpiNNakerManchester/SpiNNakerJupyterExamples>

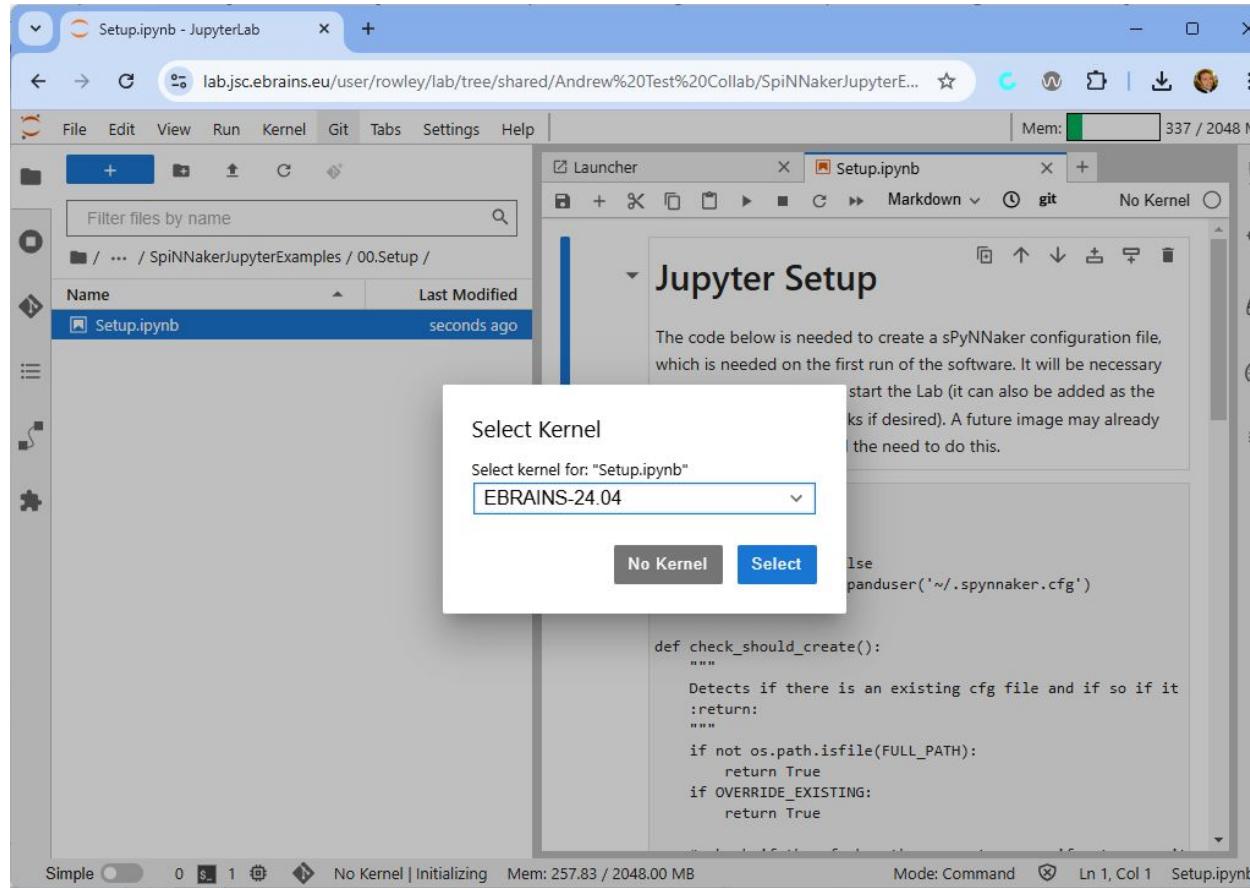
Clone SpiNNaker Repository



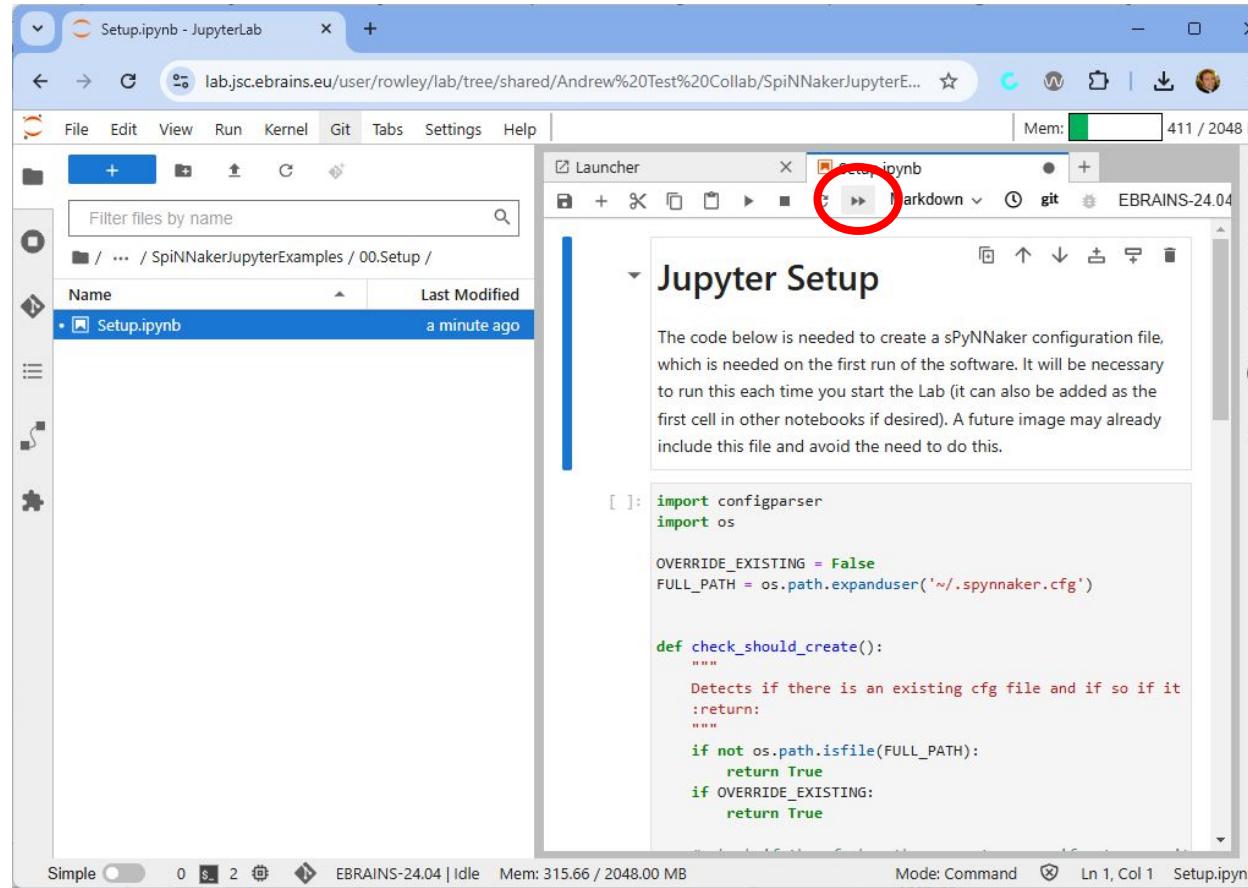
Open Setup Notebook



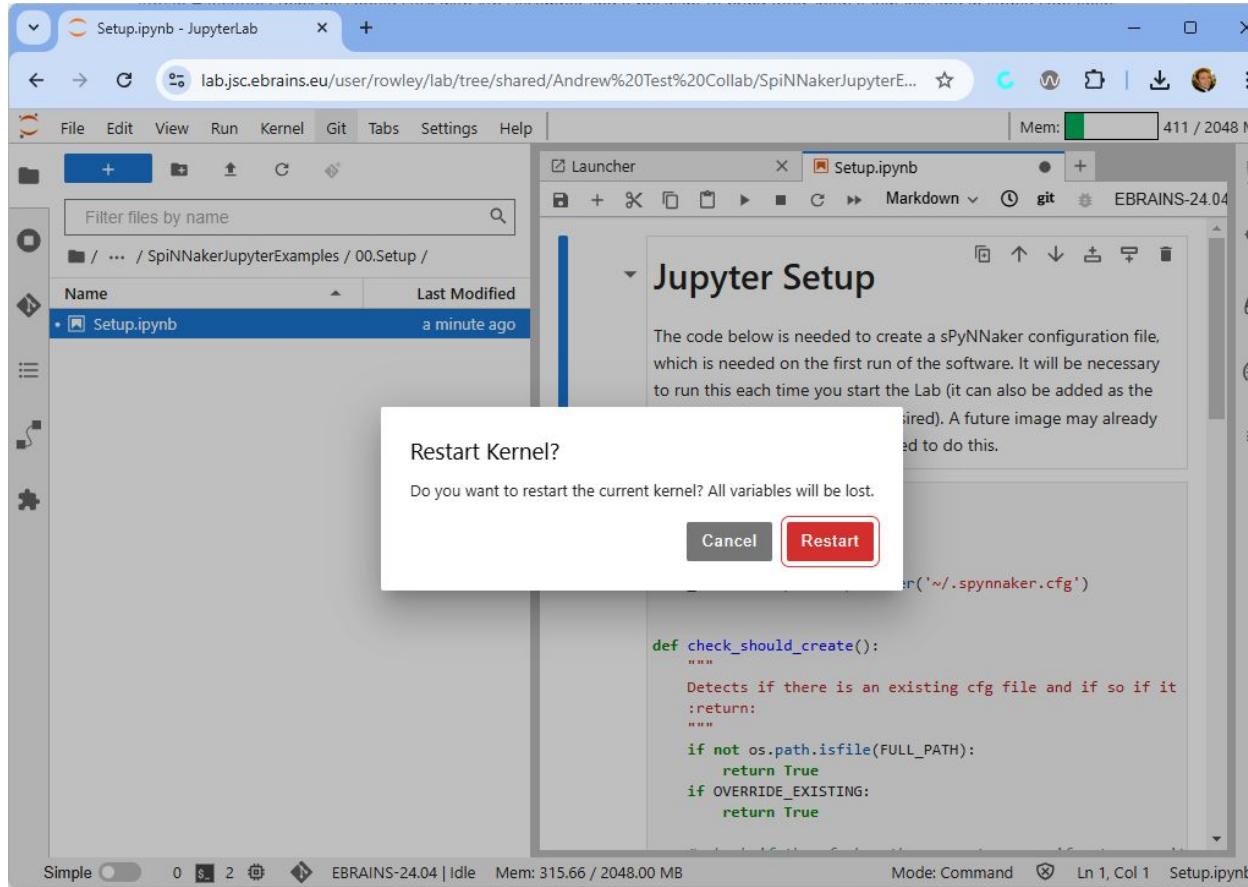
Open Setup Notebook



Open Setup Notebook - Run



Open Setup Notebook - Run



Open Setup Notebook - Run

The screenshot shows a JupyterLab interface with the title bar "Setup.ipynb - JupyterLab". The left sidebar displays a file tree under "/ ... / SpiNNakerJupyterExamples / 00.Setup /" with "Setup.ipynb" selected. The main content area shows Python code for creating a configuration file:

```
# Make sure there is a spynnaker.cfg file
if check_should_create():
    with open(FULL_PATH, 'w') as cfg:
        cfg.write("[Machine]\n")
        cfg.write("spalloc_server = https://spinnaker.cs.man.ac.uk\n")
        cfg.write("\n")
        cfg.write("[Java]\n")
        cfg.write("use_java=True\n")
        cfg.write("\n")
        cfg.write("[Reports]\n")
        cfg.write("read_provenance_data = False\n")
    print(f"New {FULL_PATH} created")
```

A red circle highlights a warning message at the bottom of the code cell:

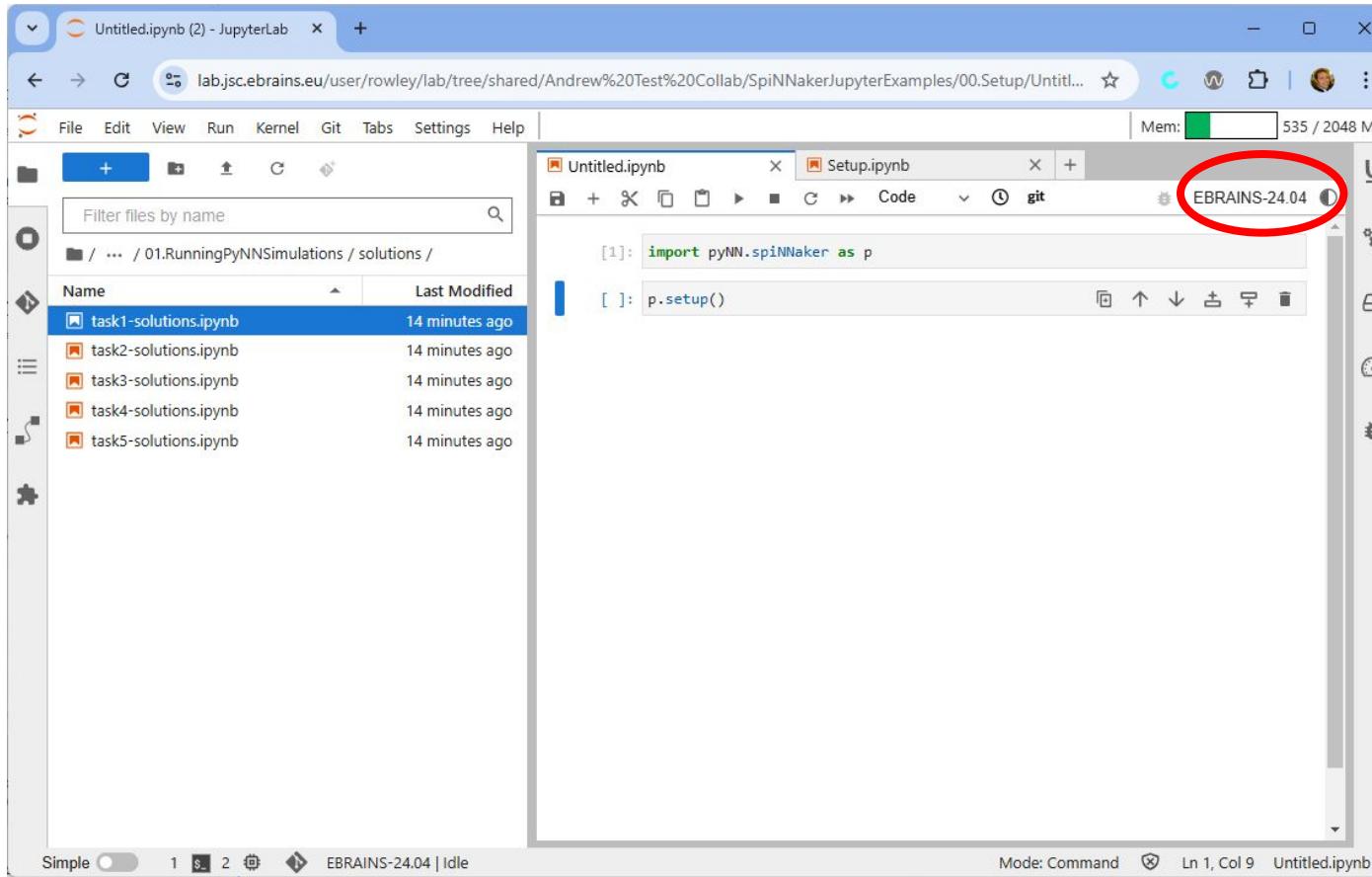
/opt/app-root/src/.spynnaker.cfg already exists.
To replace it change OVERRIDE_EXISTING to True

The bottom right corner shows a "Contents" section with two items:

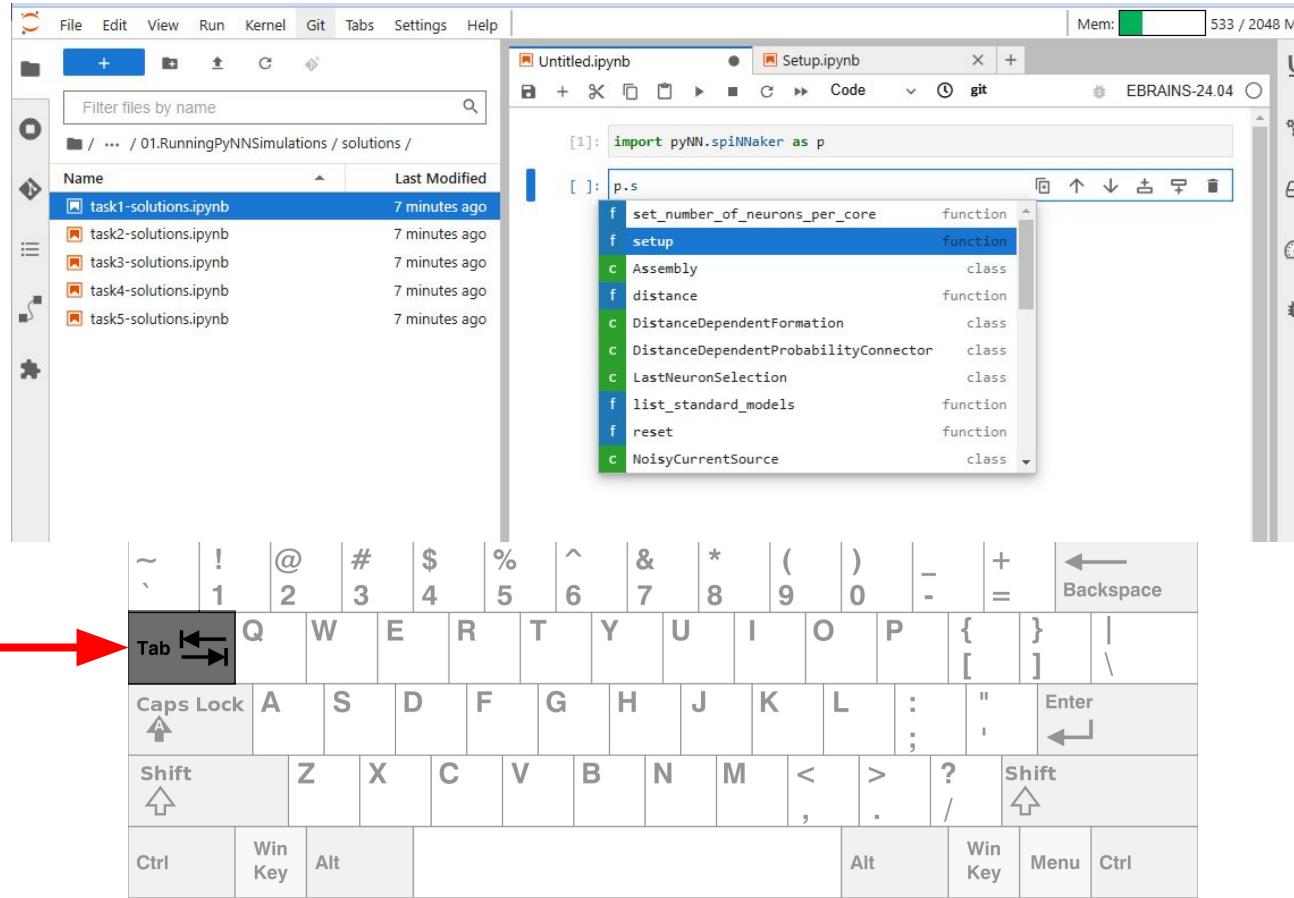
- 1. Running PyNN Simulations on SpiNNaker
- 2. Live Input and Output

At the bottom of the window, status bars show "Simple" mode, "Idle", "Mem: 315.93 / 2048.00 MB", "Mode: Command", "Ln 1, Col 1", and "Setup.ipynb".

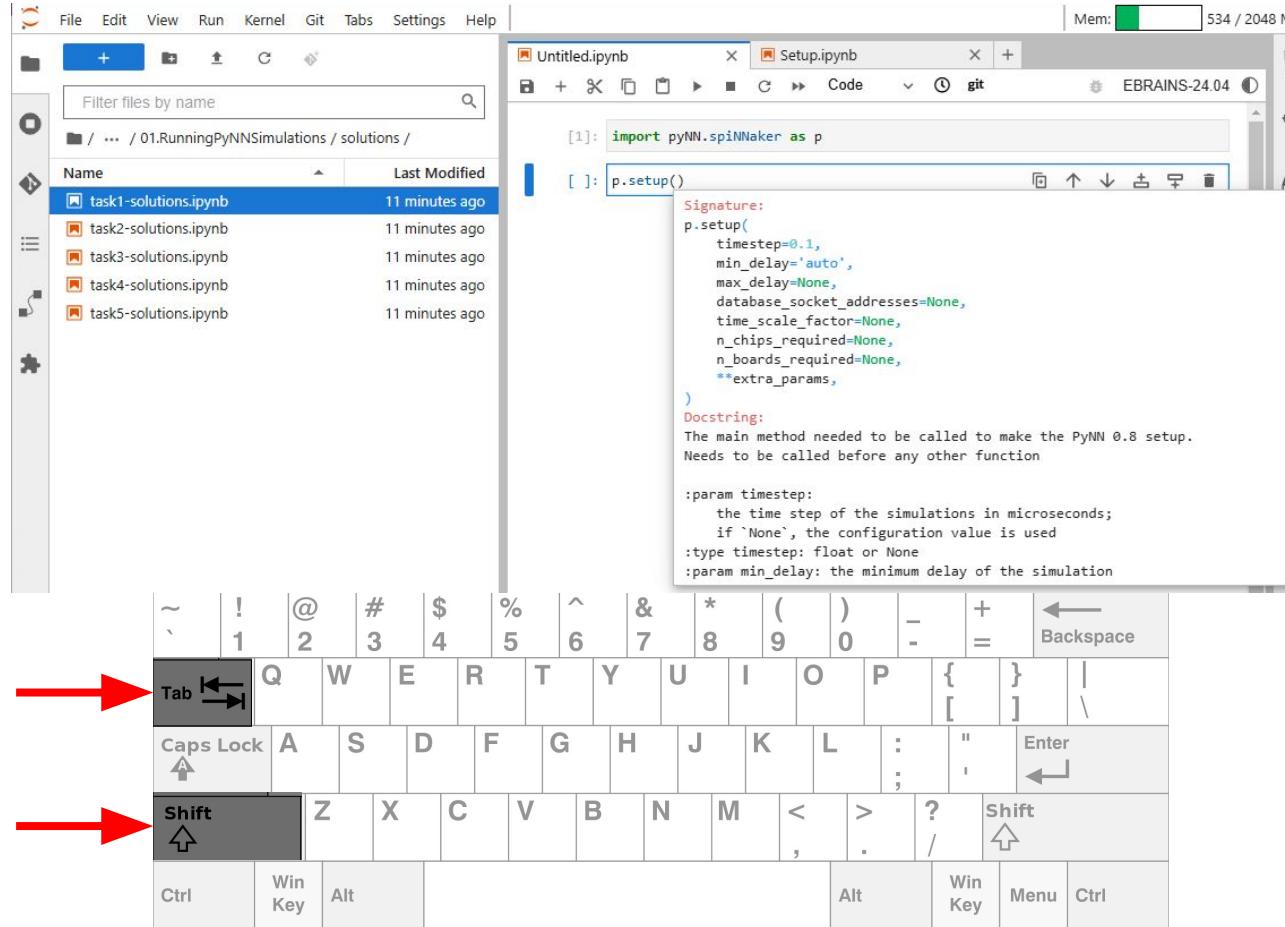
Changing Kernel



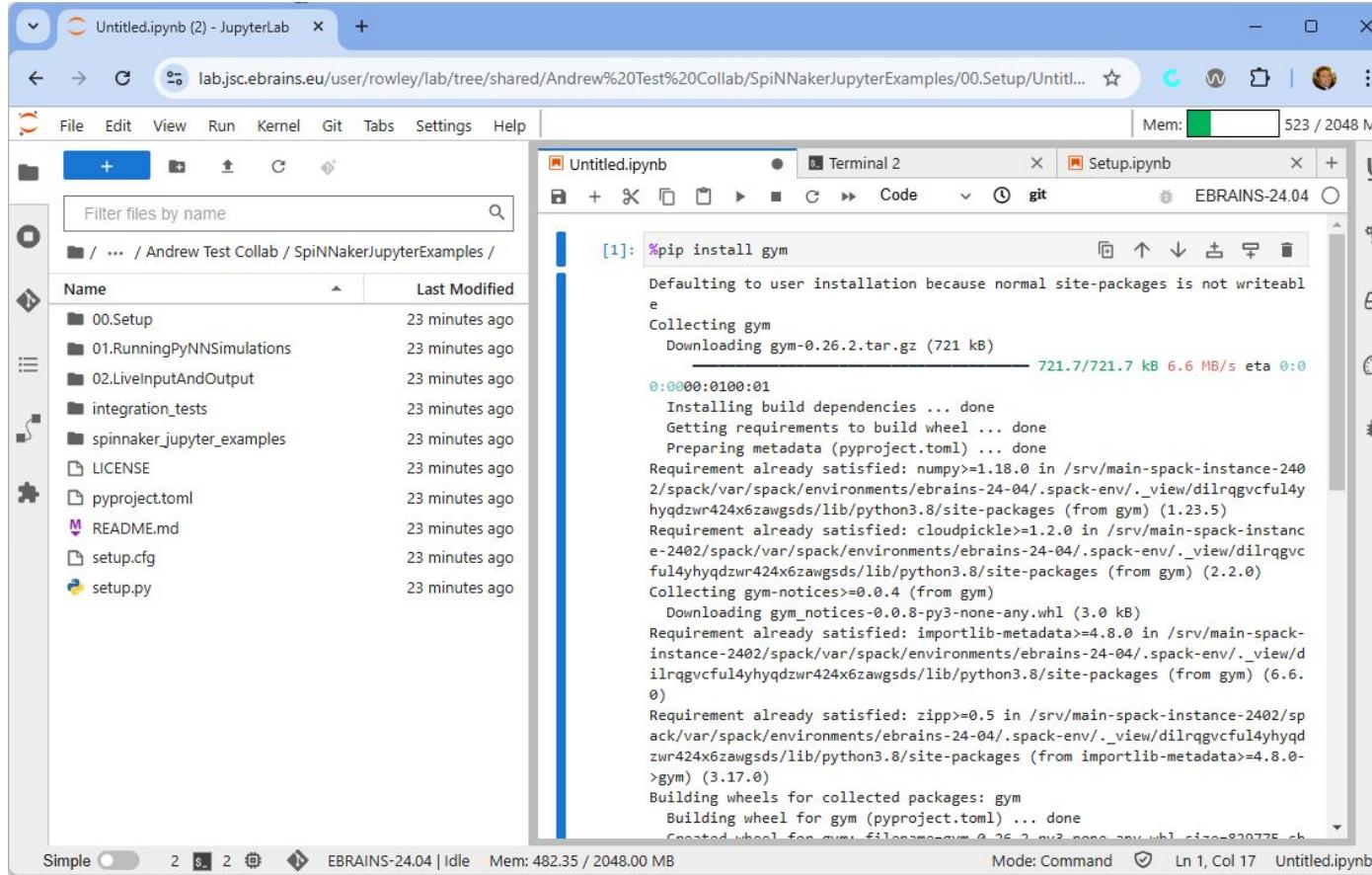
Jupyter Autocomplete



Jupyter Function Help



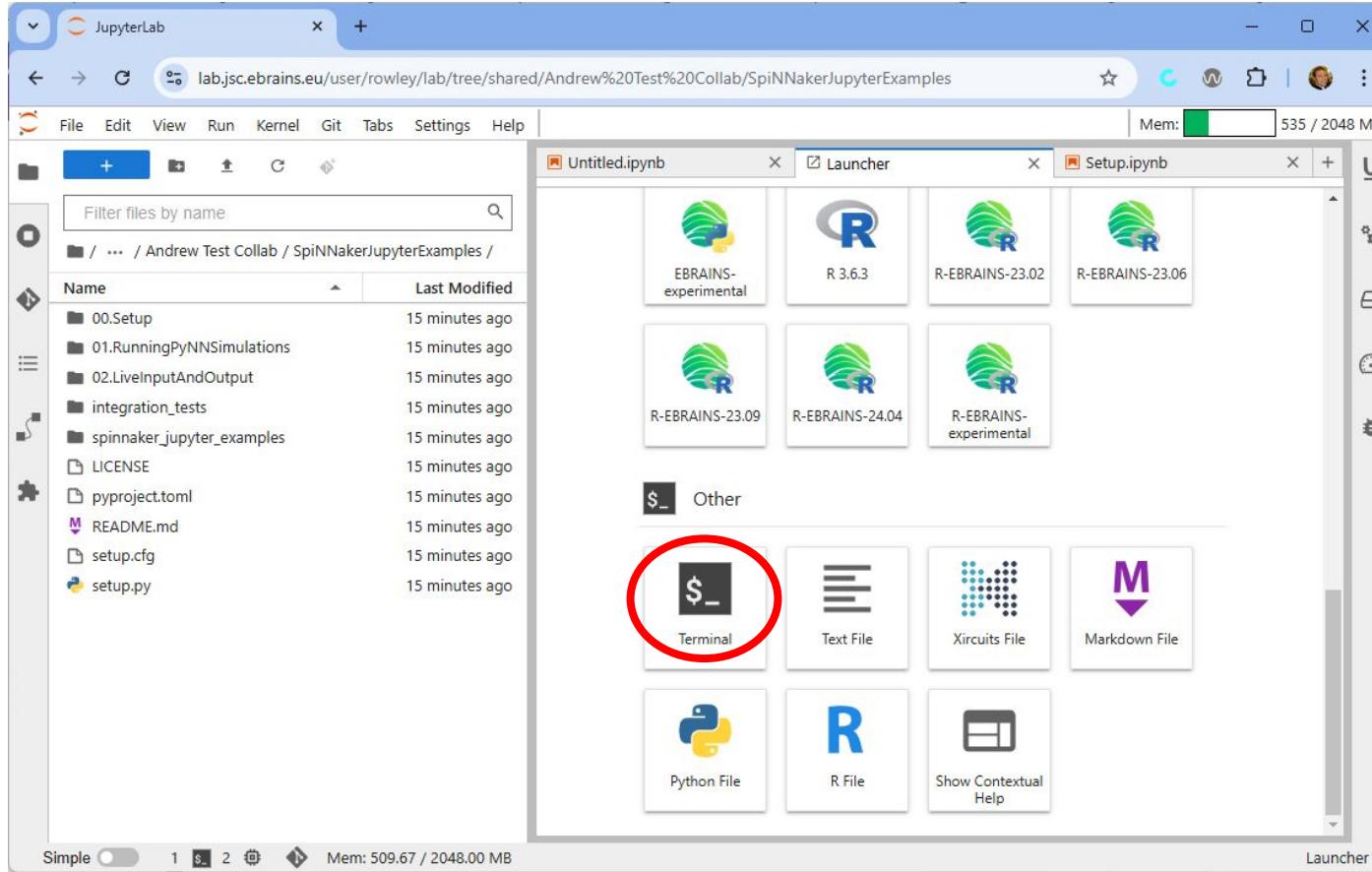
Install Libraries



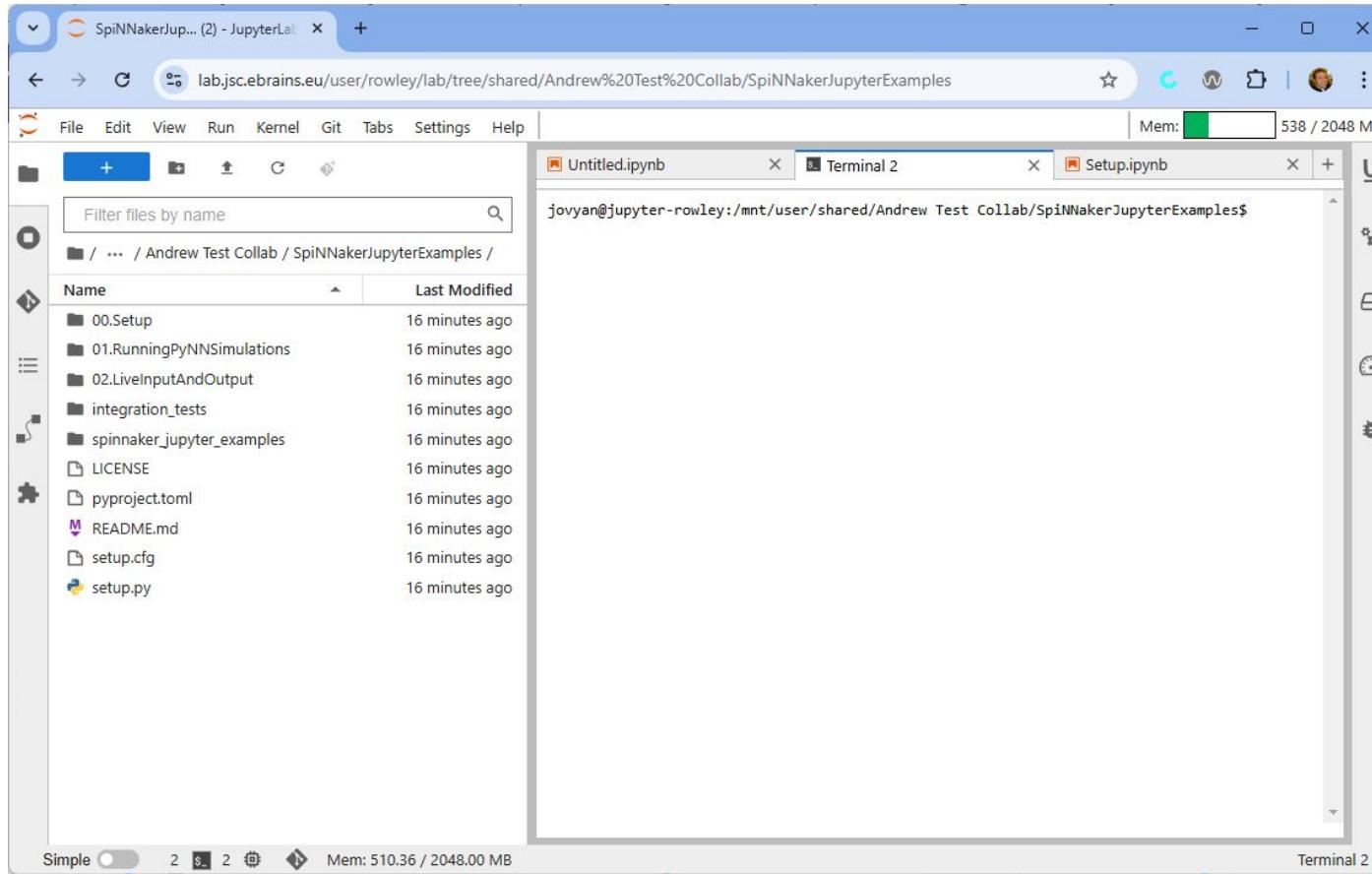
The screenshot shows a JupyterLab interface with the following components:

- File Browser:** On the left, it displays a file tree under the path `/ ... / Andrew Test Collab / SpiNNakerJupyterExamples /`. The visible files and their last modified times are:
 - 00.Setup (23 minutes ago)
 - 01.RunningPyNNSimulations (23 minutes ago)
 - 02.LiveInputAndOutput (23 minutes ago)
 - integration_tests (23 minutes ago)
 - spinnaker_jupyter_examples (23 minutes ago)
 - LICENSE (23 minutes ago)
 - pyproject.toml (23 minutes ago)
 - README.md (23 minutes ago)
 - setup.cfg (23 minutes ago)
 - setup.py (23 minutes ago)
- Terminal:** In the center, a terminal window titled "Untitled.ipynb" is running the command `%pip install gym`. The output shows the process of downloading and installing the gym library version 0.26.2. The terminal also indicates that user installation is being used because site-packages are not writeable.
- Status Bar:** At the bottom, the status bar shows "Simple" mode, two tabs open, and the system memory usage as "Mem: 482.35 / 2048.00 MB". It also shows the kernel name "EBRAINS-24.04 | Idle".

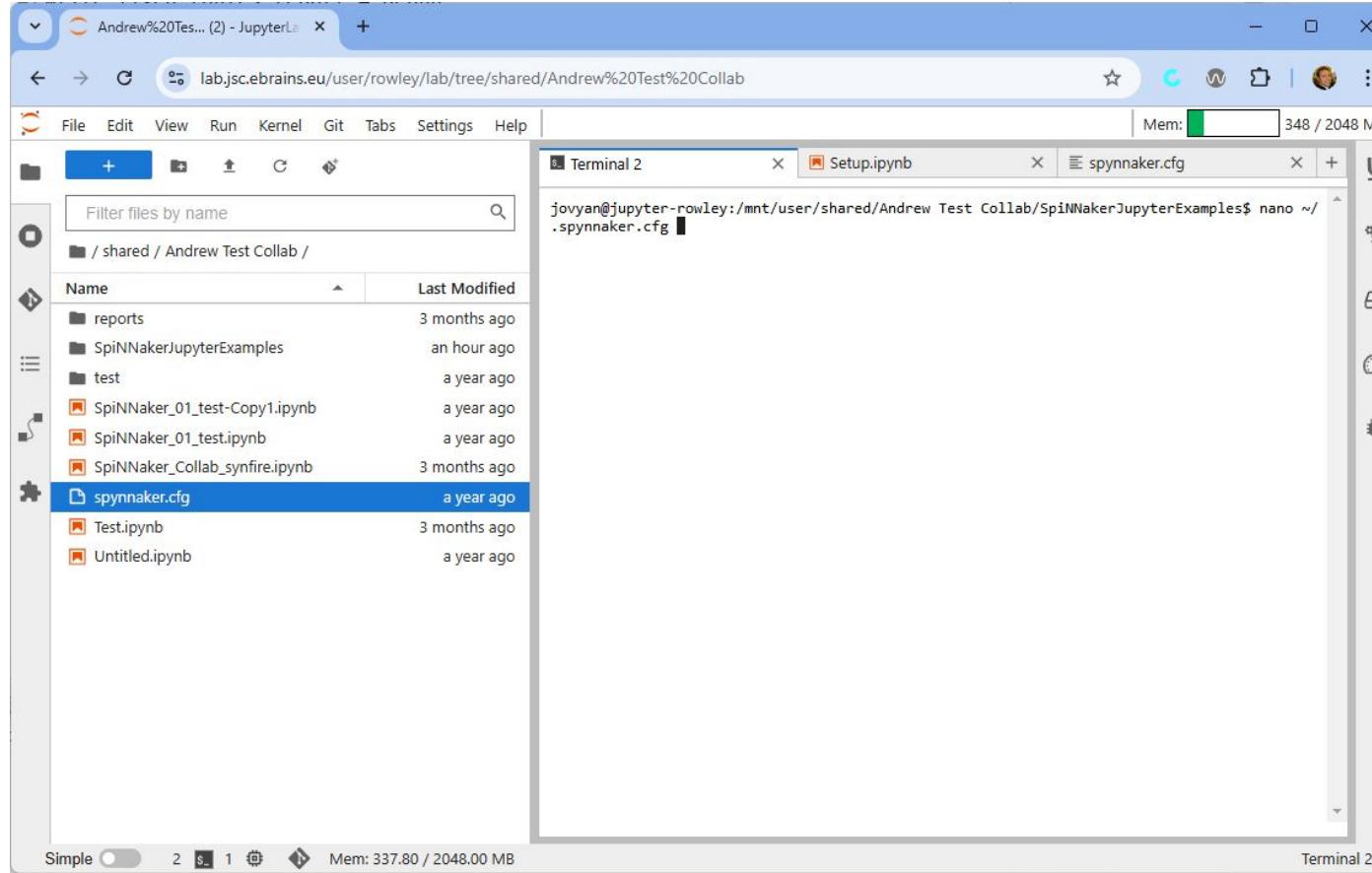
Terminal Access



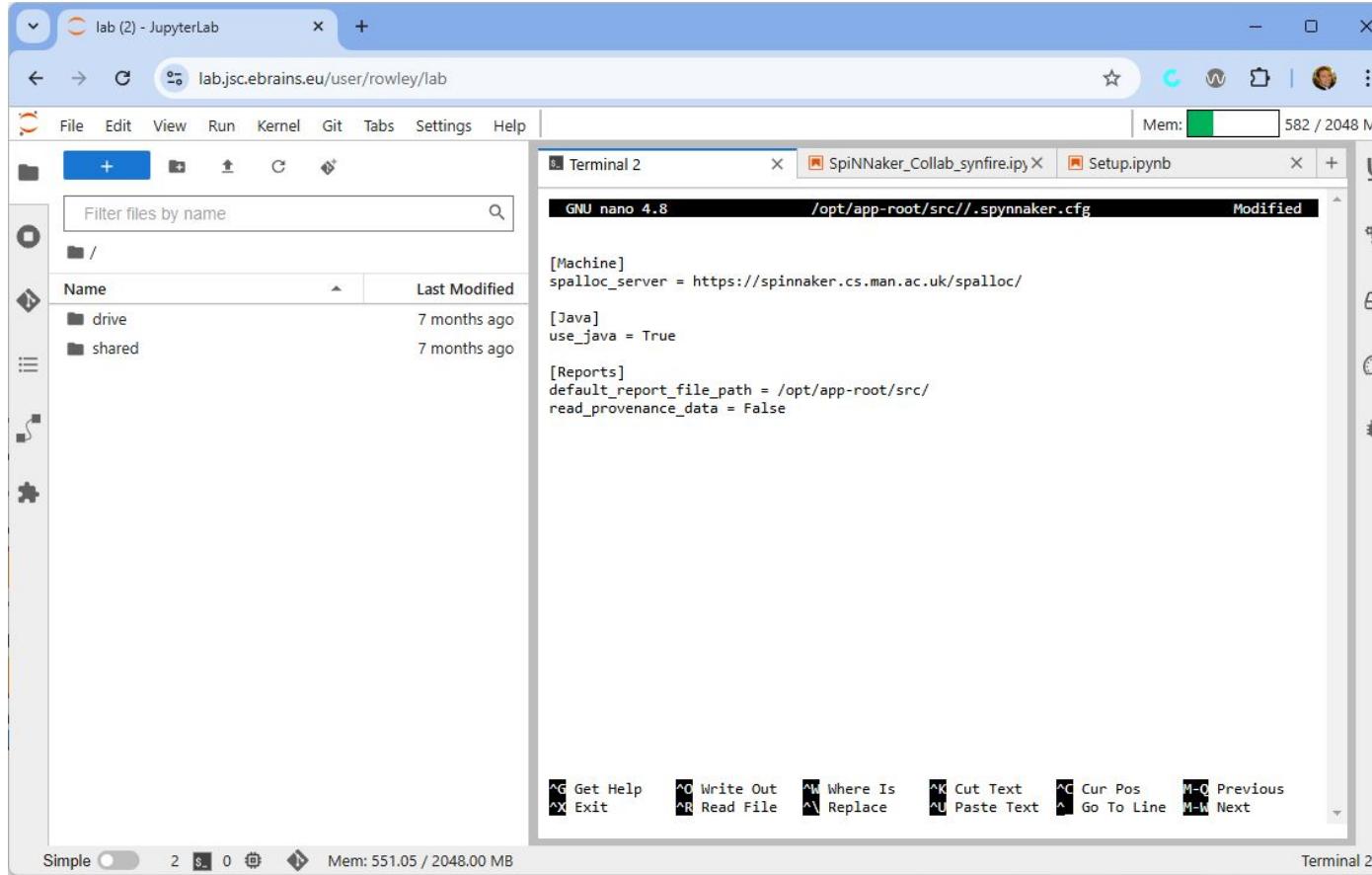
Terminal Access



Edit SpiNNaker Configuration

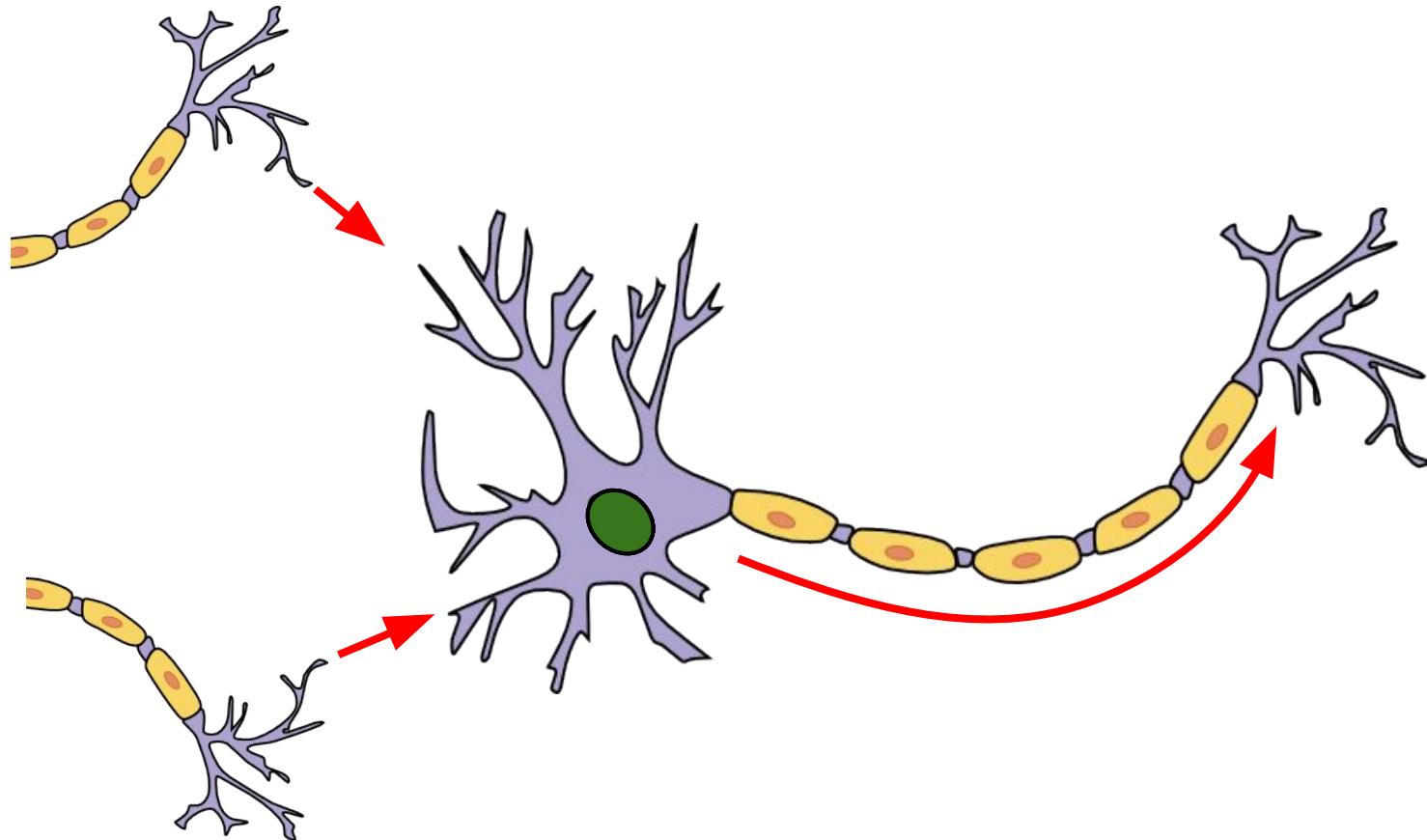


Set Reports Options

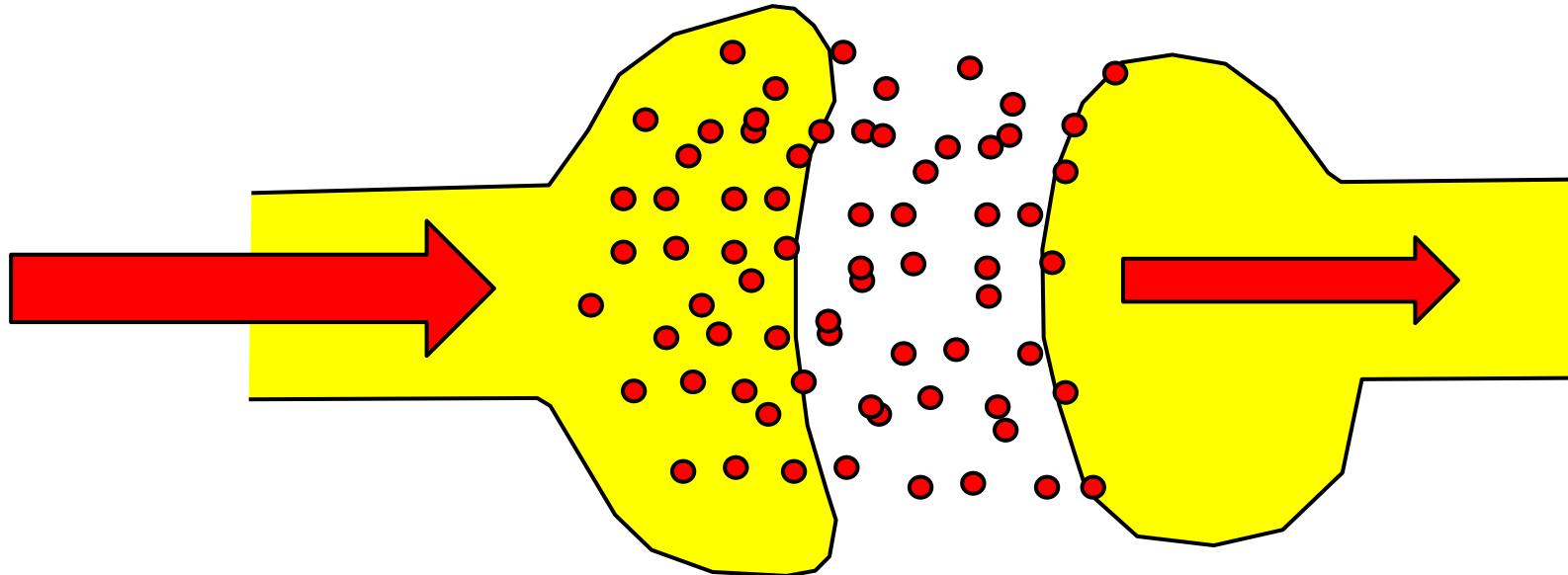


Spiking Neural Networks

Spiking Neural Networks



Spiking Neural Networks

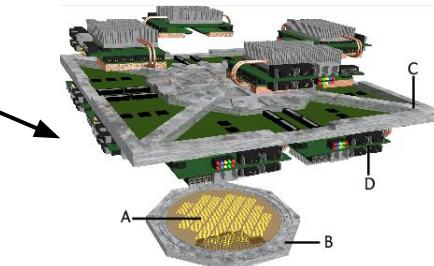
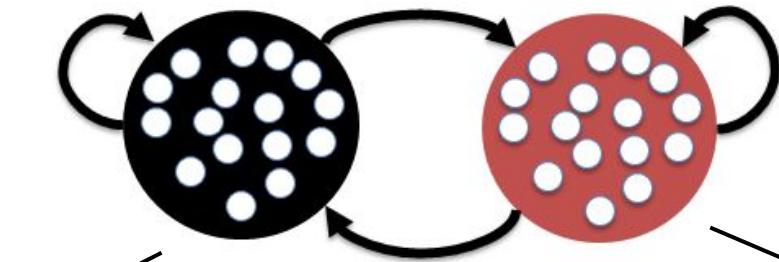


PyNN

What is PyNN?



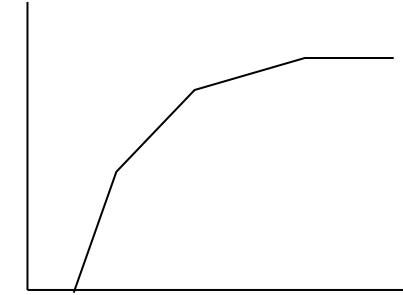
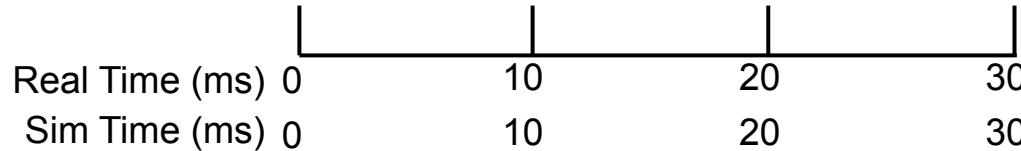
BRIAN



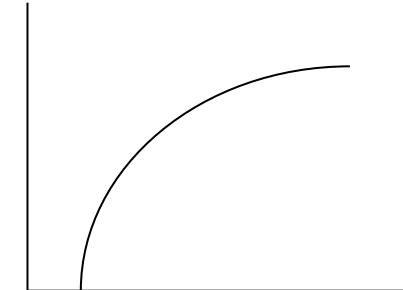
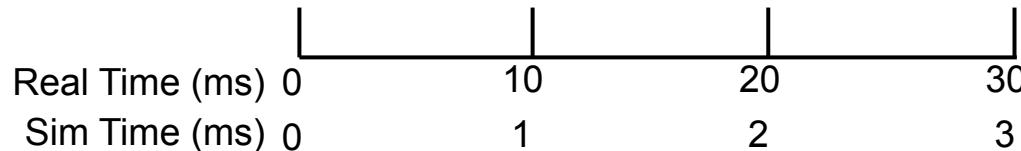
PyNN - Setup

```
import pyNN.spiNNaker as p
```

```
p.setup(timestep=1.0)
```

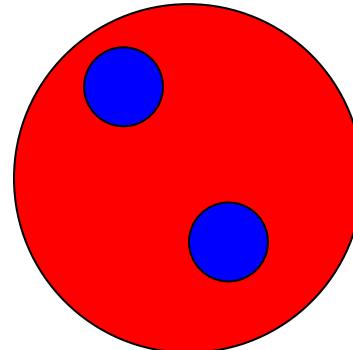
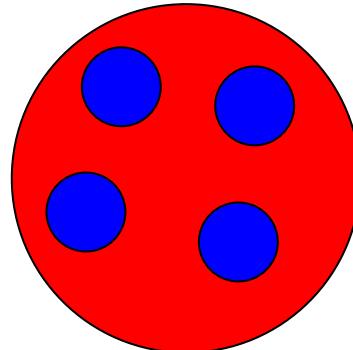


```
p.setup(timestep=0.1)
```



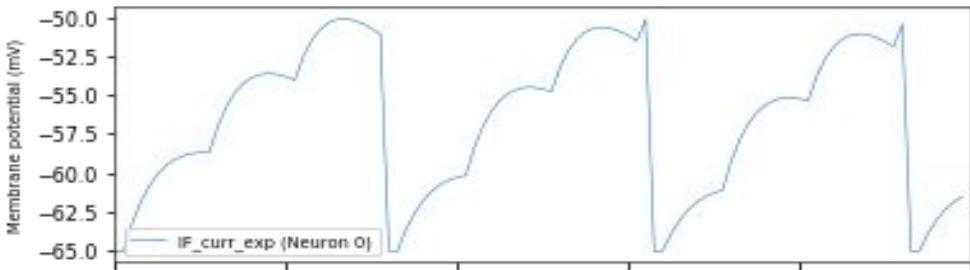
PyNN - Populations

```
pop_1 = p.Population(  
    4, p.IF_curr_exp(), label="Fred")  
pop_2 = p.Population(  
    2, p.IF_curr_exp(), label="Bob")
```

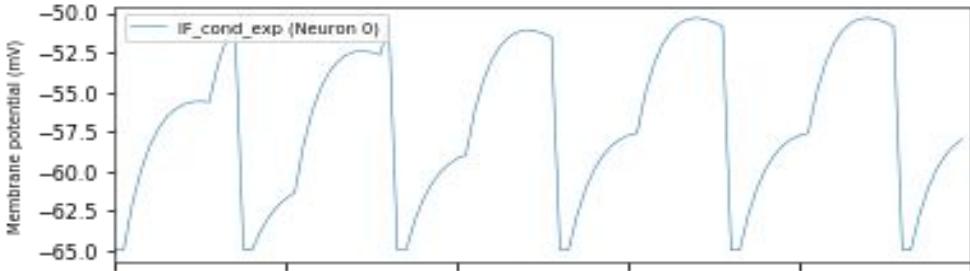


PyNN Populations - Models

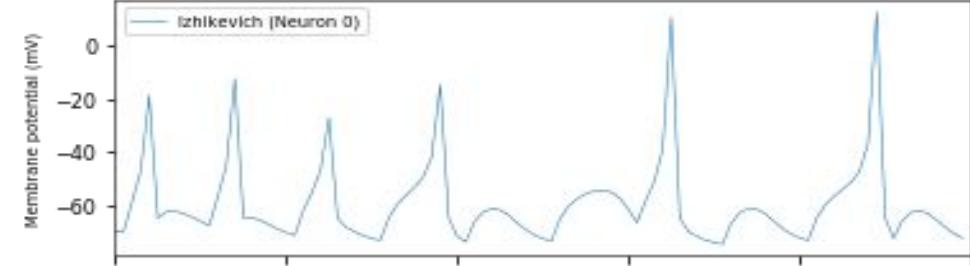
`p.IF_curr_exp(...)`



`p.IF_cond_exp(...)`

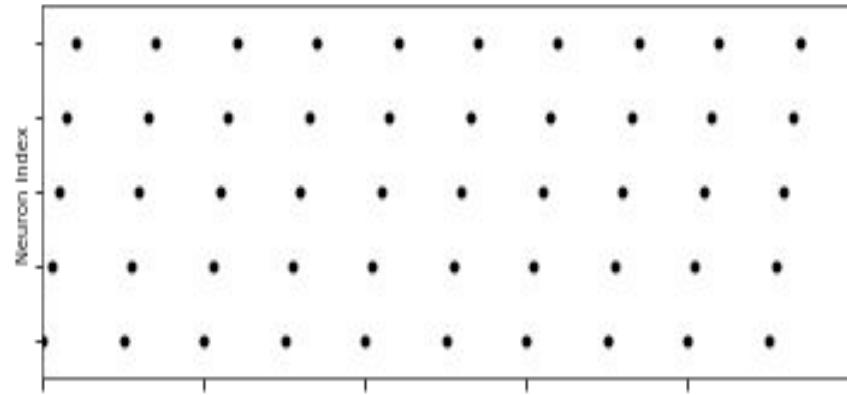


`p.Izhikevich(...)`

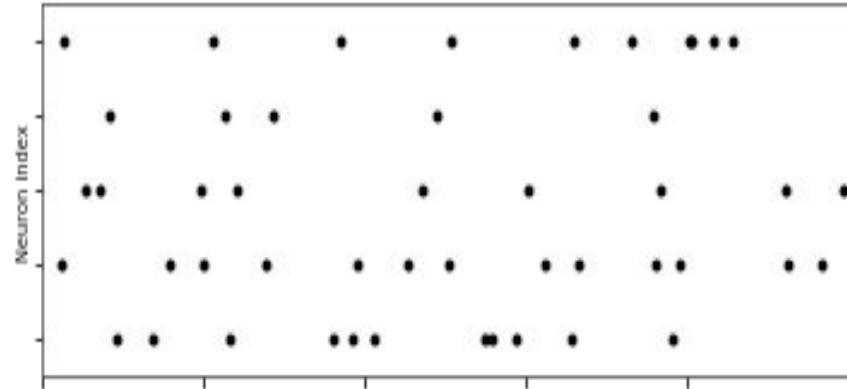


PyNN Populations - Models

```
p.SpikeSourceArray(  
    spike_times=[...])
```

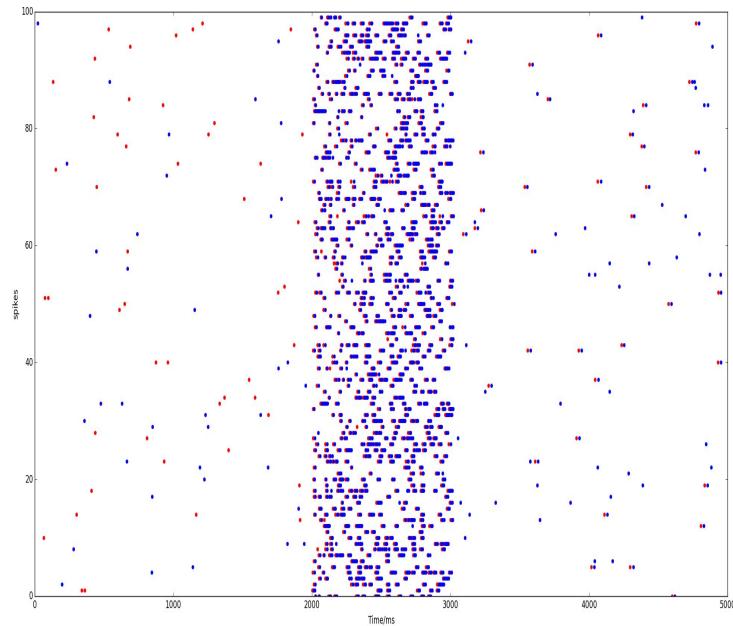
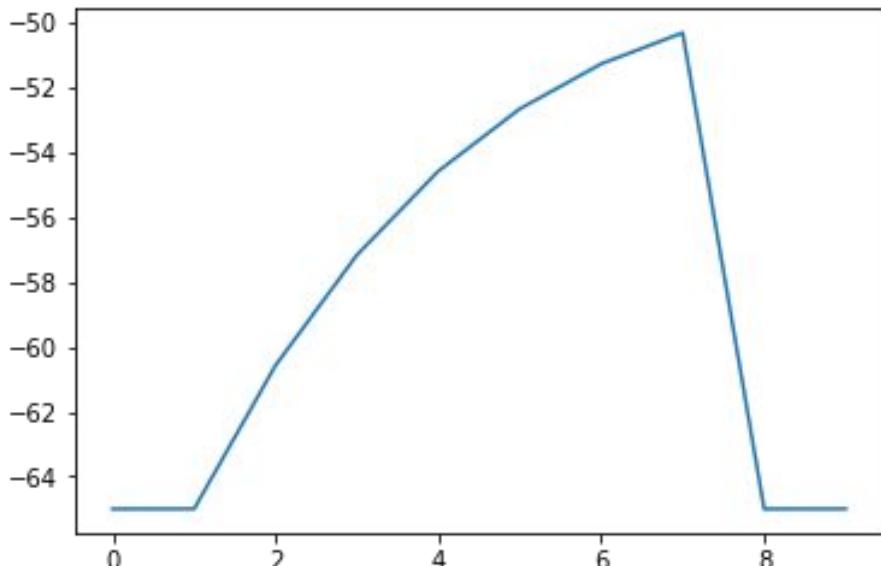


```
p.SpikeSourcePoisson(  
    rate=...)
```



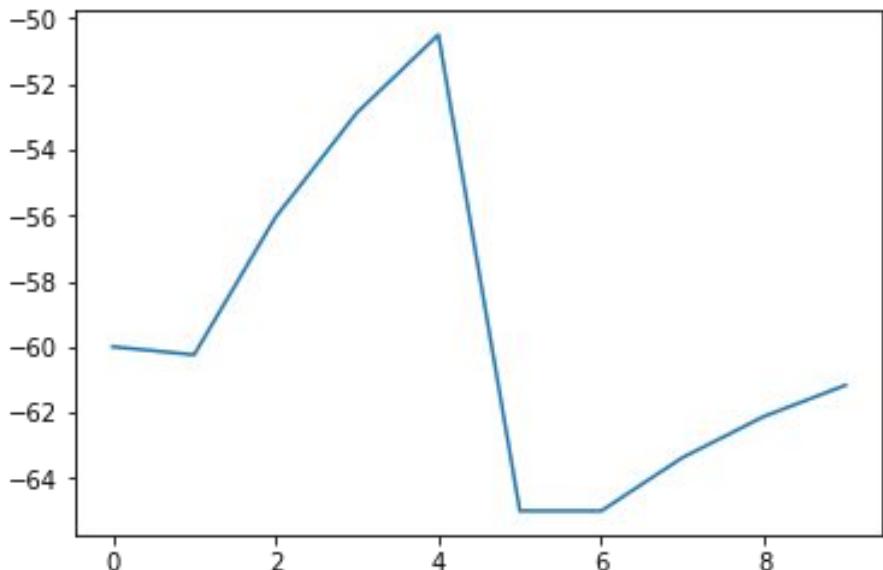
PyNN Populations - Recording

`pop_1.record(["v", "spikes"])`

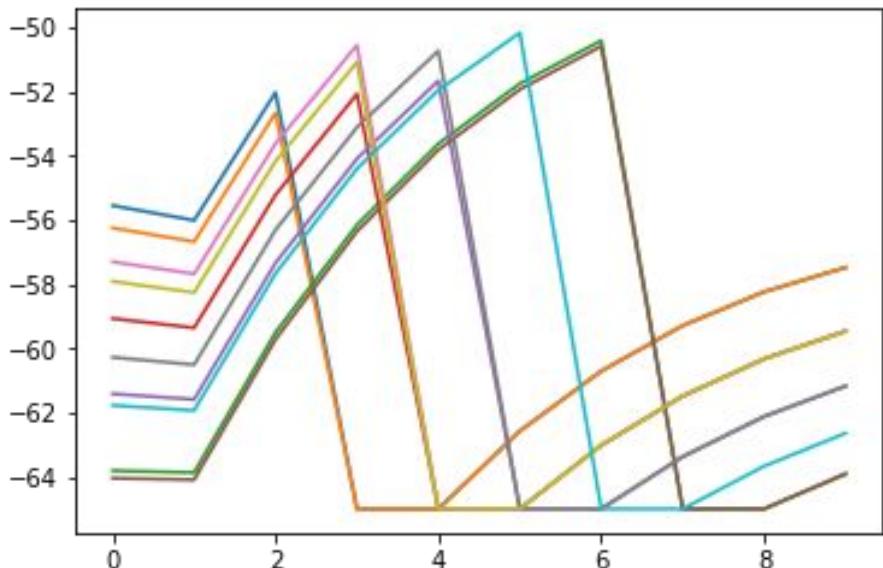


PyNN Populations - Initialize

`pop_1.initialize(v=-60)`

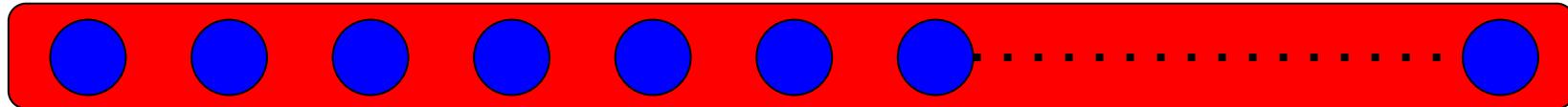


```
pop_1.initialize(v=p.RandomDistribution(  
    "uniform", low=-65.0, high=-55.0))
```



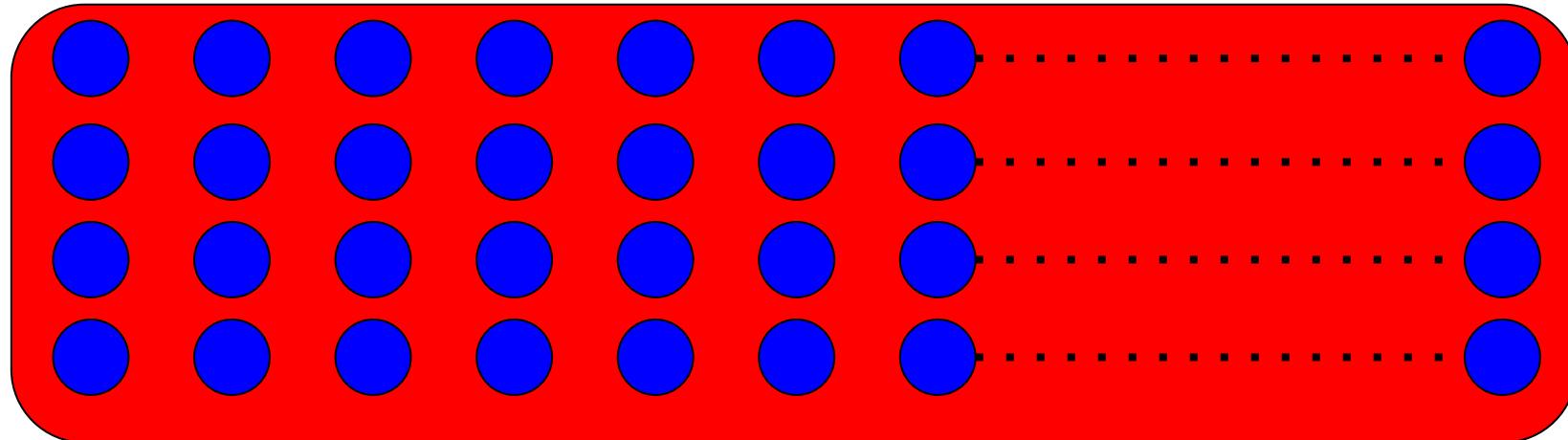
PyNN Populations - Structure

```
pop_1 = p.Population(  
    100, p.IF_curr_exp())
```



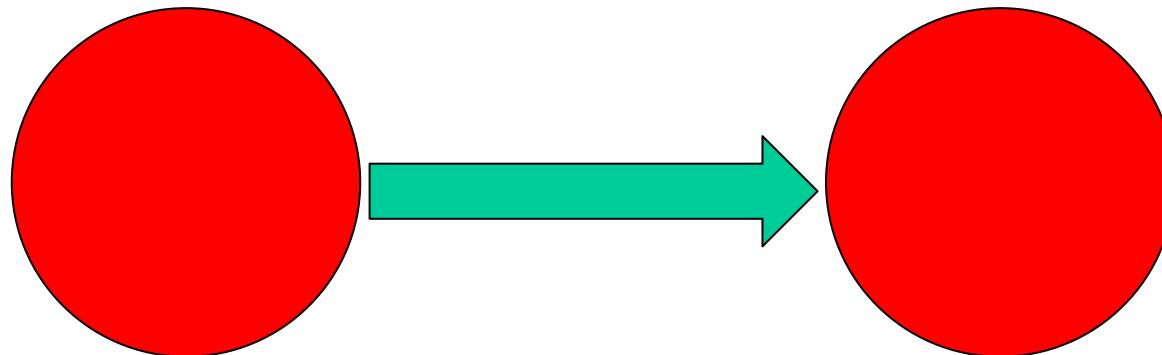
PyNN Populations - Structure

```
pop_1 = p.Population(  
    100, p.IF_curr_exp(),  
    structure=Grid2D(4 / 25))
```



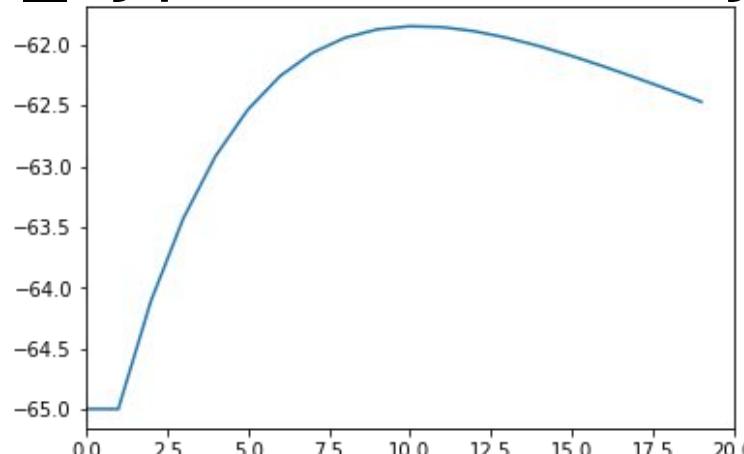
PyNN - Projections

```
proj = p.Projection(  
    pop_1, pop_2,  
    p.OneToOneConnector(),  
    p.StaticSynapse(  
        weight=1.0, delay=2.0))
```



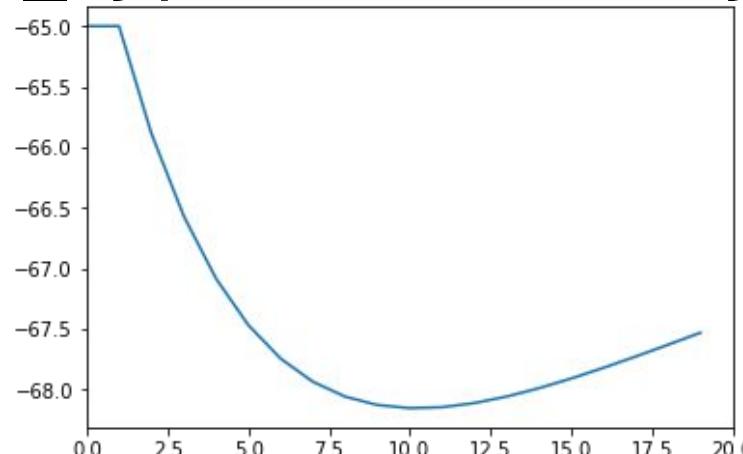
PyNN - Projections

```
proj = p.Projection(  
    pop_1, pop_2,  
    p.OneToOneConnector(),  
    p.StaticSynapse(weight=1.0),  
    receptor_type="excitatory")
```



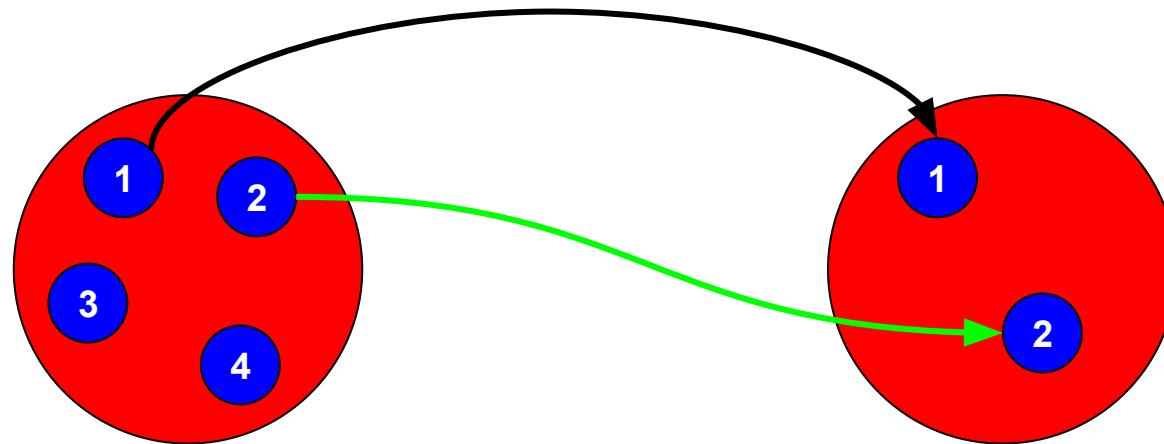
PyNN - Projections

```
proj = p.Projection(  
    pop_1, pop_2,  
    p.OneToOneConnector(),  
    p.StaticSynapse(weight=1.0),  
    receptor_type="inhibitory")
```



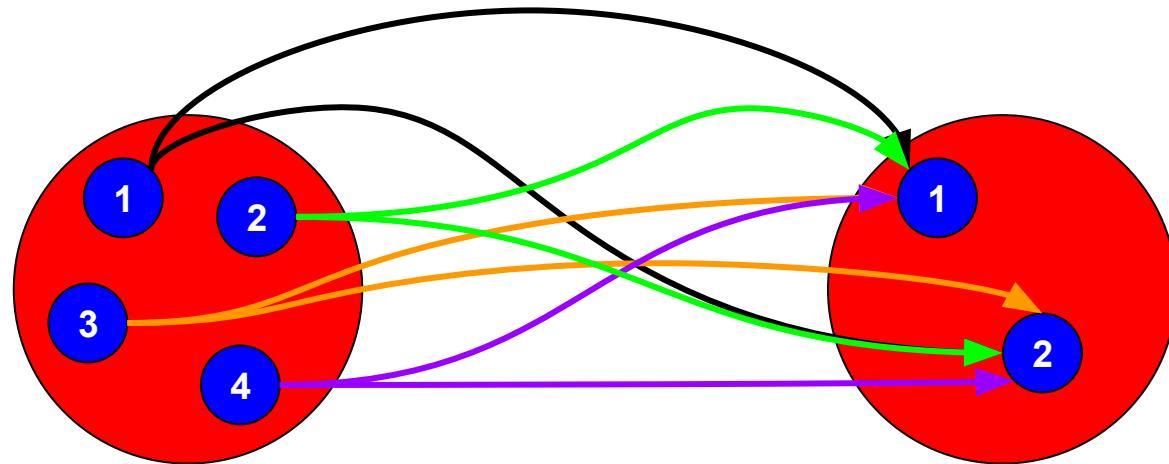
PyNN Projections - Connectors

p.OneToOneConnector()



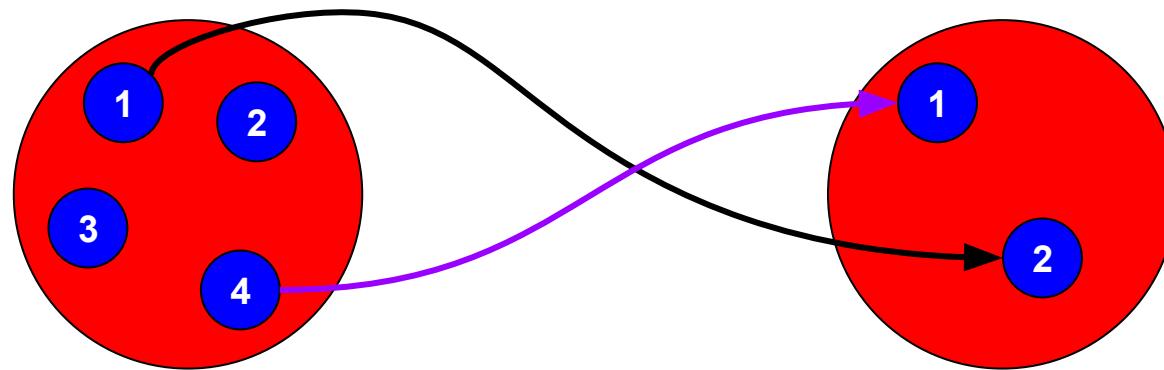
PyNN Projections - Connectors

p.AllToAllConnector()



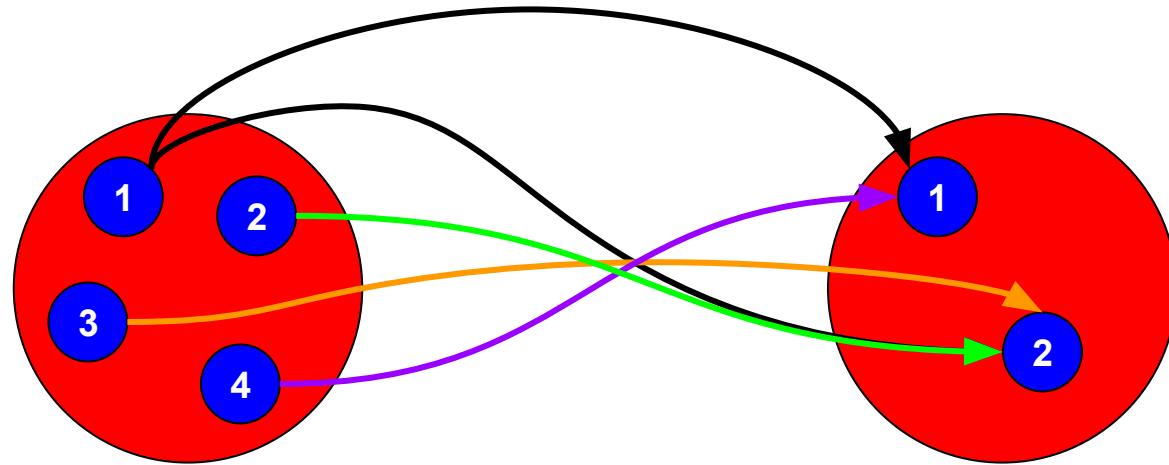
PyNN Projections - Connectors

`p.FixedProbabilityConnector(p=0.1)`



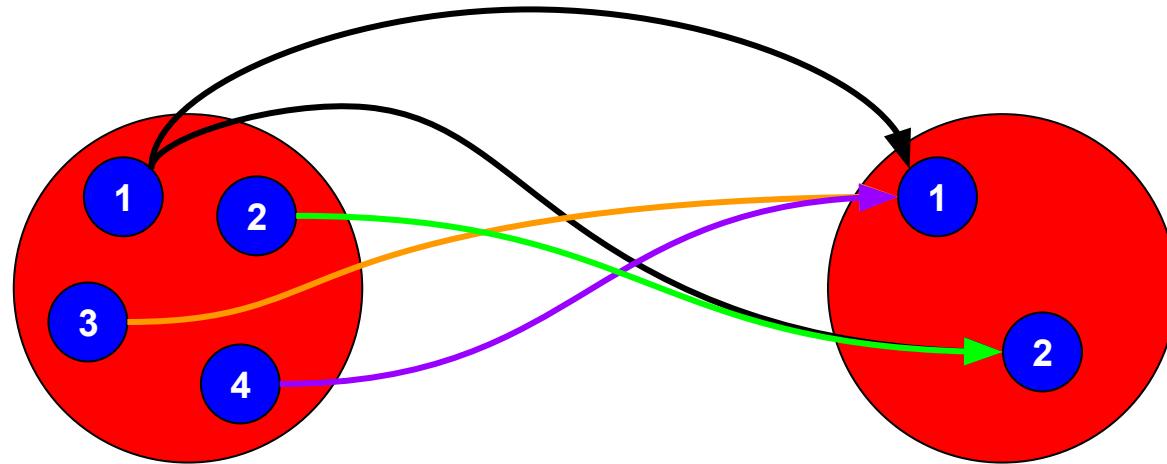
PyNN Projections - Connectors

`p.FixedProbabilityConnector(p=0.5)`



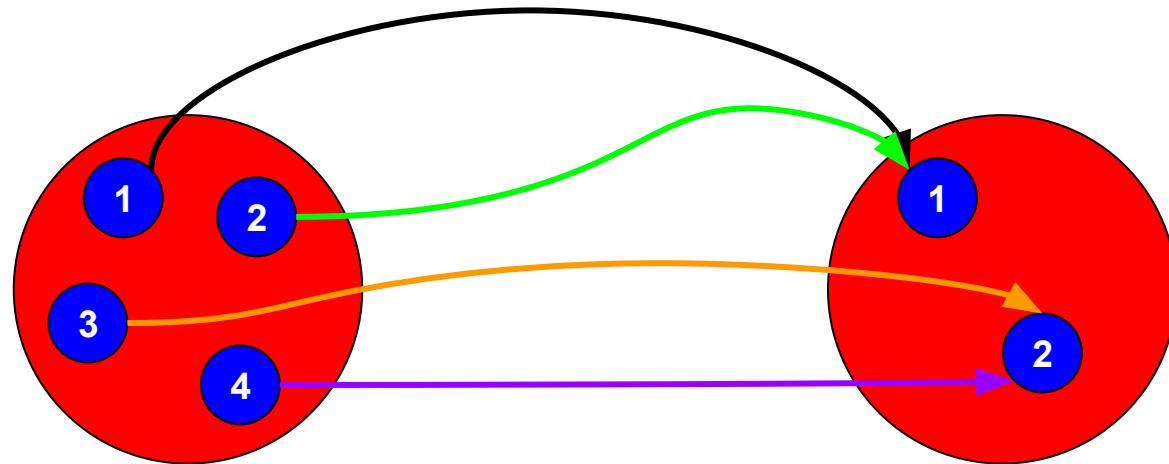
PyNN Projections - Connectors

p.FixedTotalNumberConnector(5)



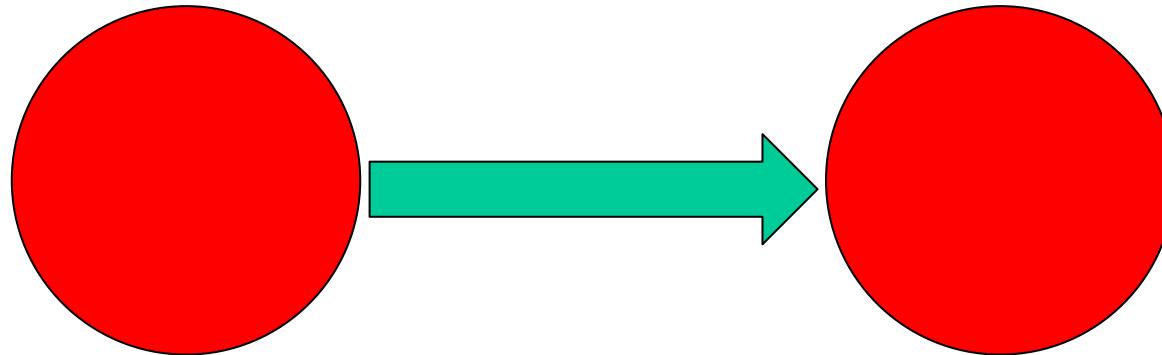
PyNN Projections - Connectors

```
p.FromListConnector(  
    [(1, 1), (2, 1), (3, 2), (4, 2)])
```



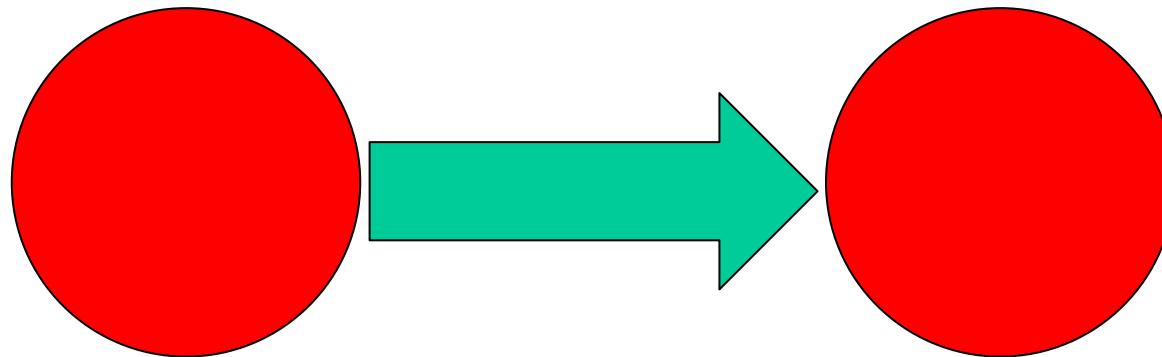
PyNN - Static Synapse Types

```
p.StaticSynapse(weight=1.0, delay=2.0)
```



PyNN - Static Synapse Types

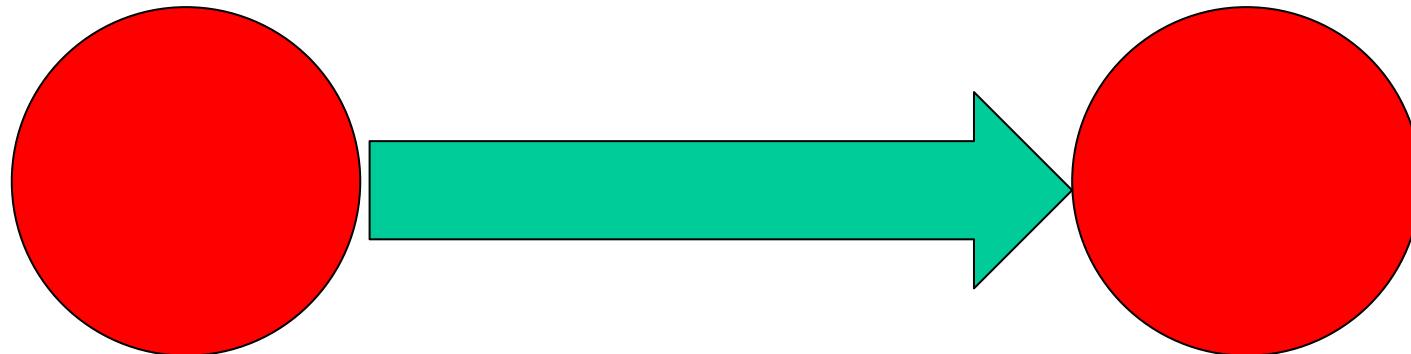
```
p.StaticSynapse(weight=5.0, delay=2.0)
```



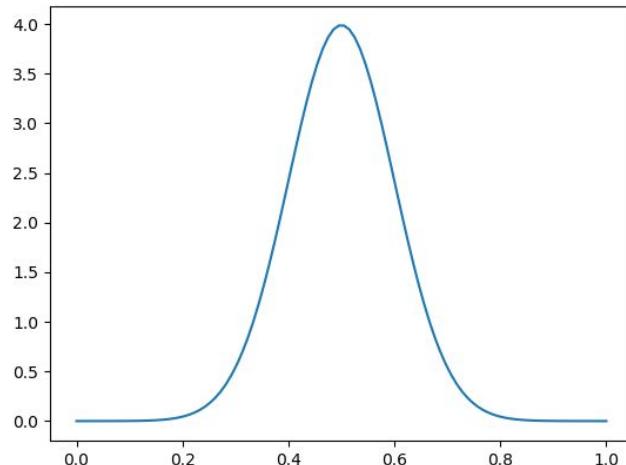
PyNN - Static Synapse Types

```
p.StaticSynapse(weight=5.0, delay=3.0)
```

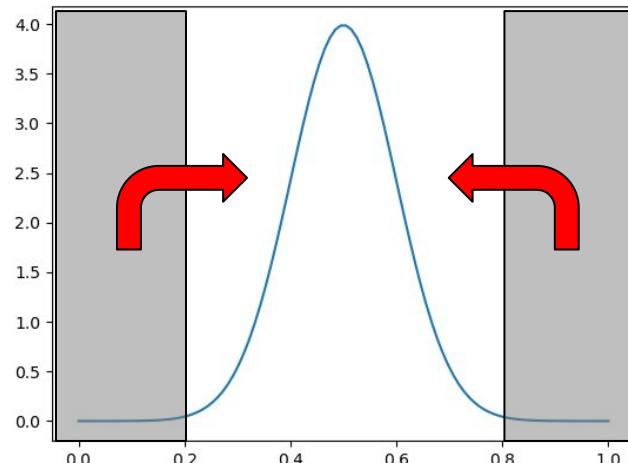
(timestep <= delay <= 144 * timestep)



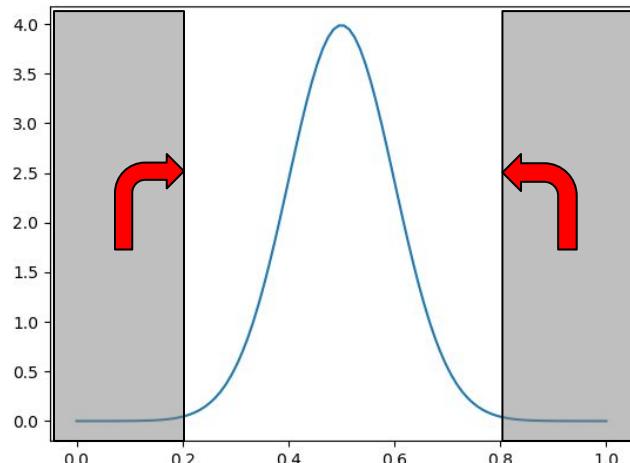
```
weight_dist = p.RandomDistribution(  
    "normal", mu=0.5, sigma=0.1)  
p.StaticSynapse(  
    weight=weight_dist, delay=3.0)
```



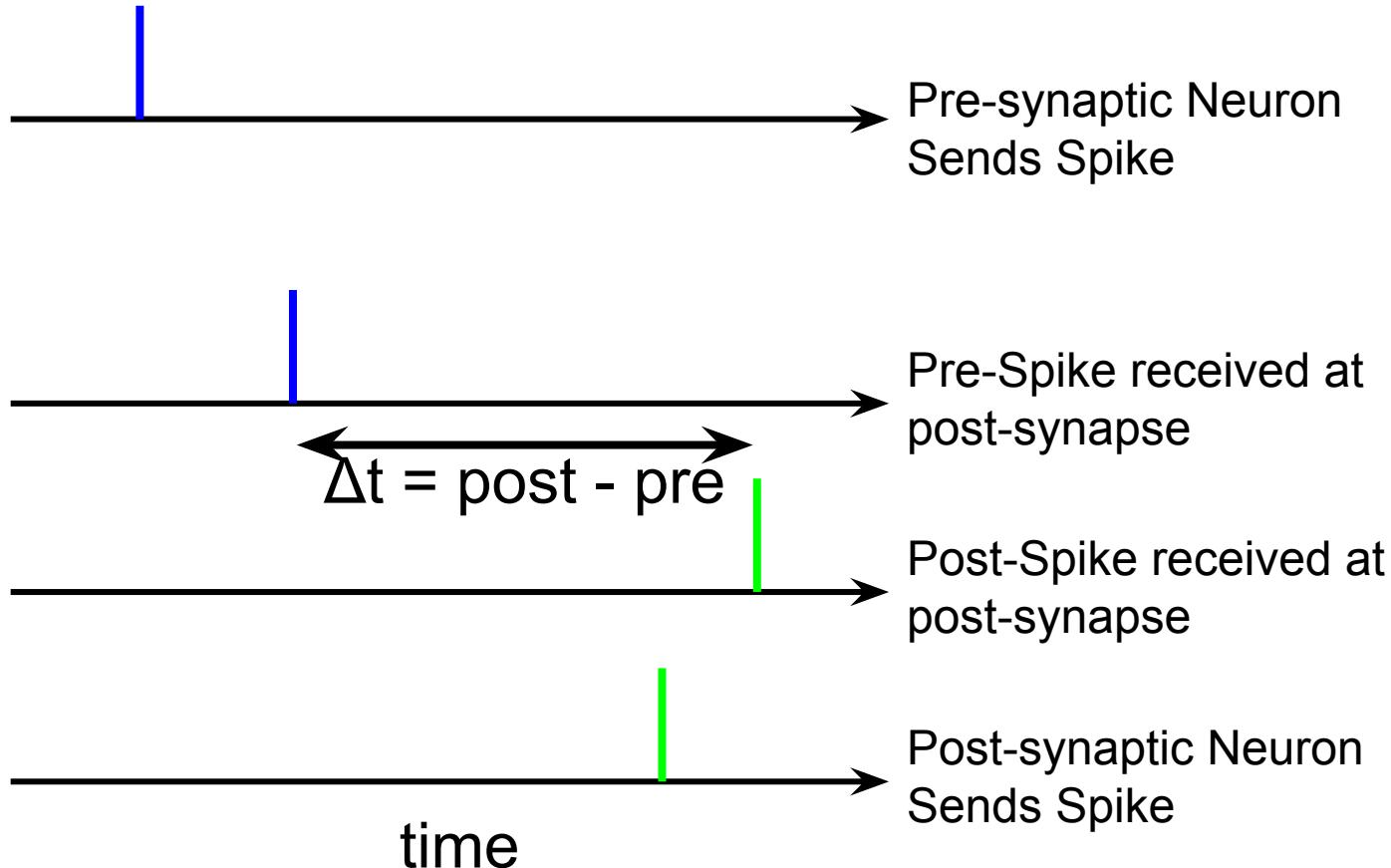
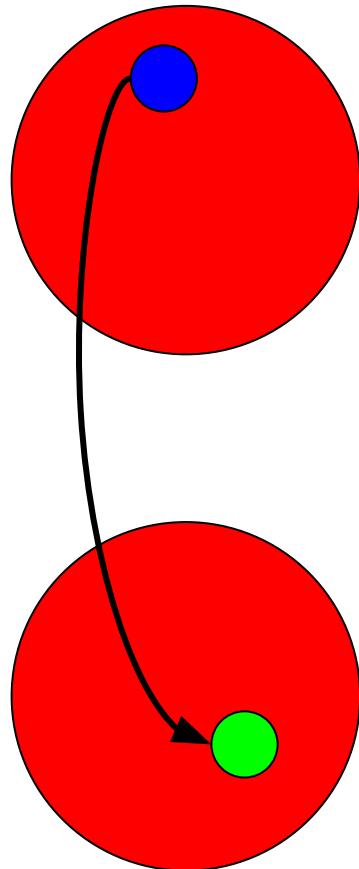
```
weight_dist = p.RandomDistribution(  
    "normal_clipped",  
    mu=0.5, sigma=0.1, low=0.2 high=0.8)
```



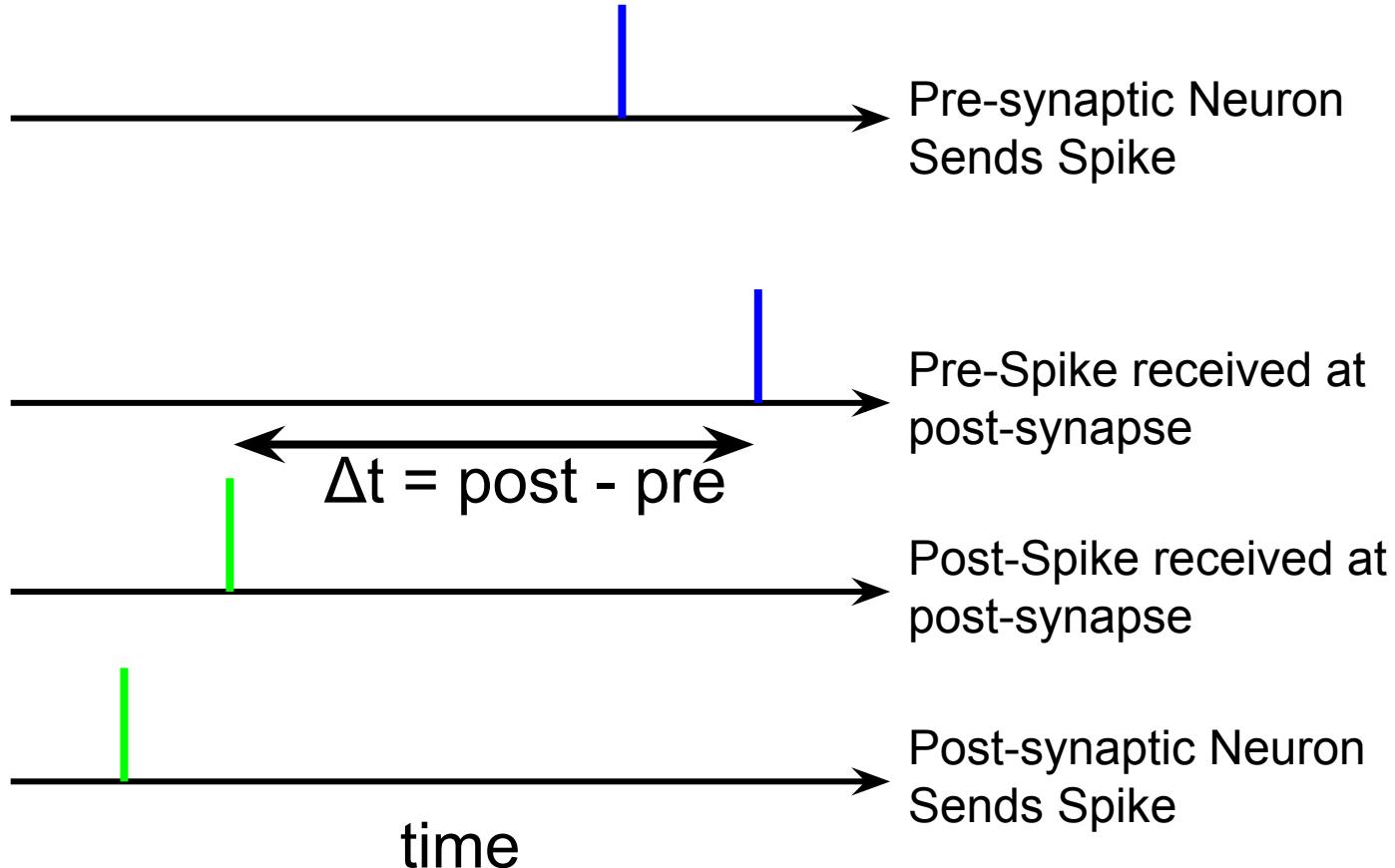
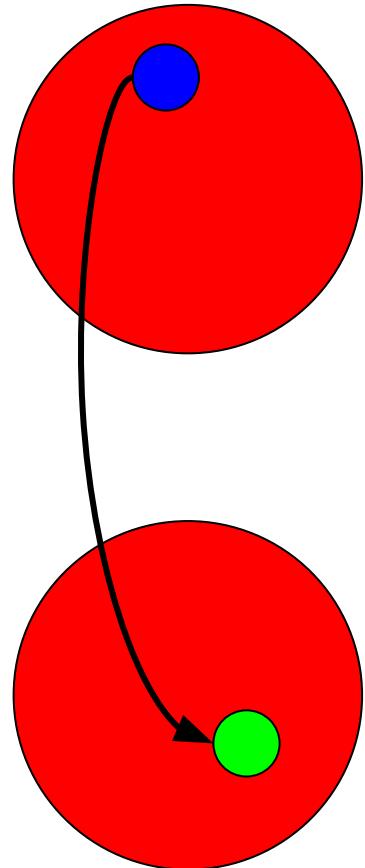
```
weight_dist = p.RandomDistribution(  
    "normal_clipped_to_boundary",  
    mu=0.5, sigma=0.1, low=0.2 high=0.8)
```



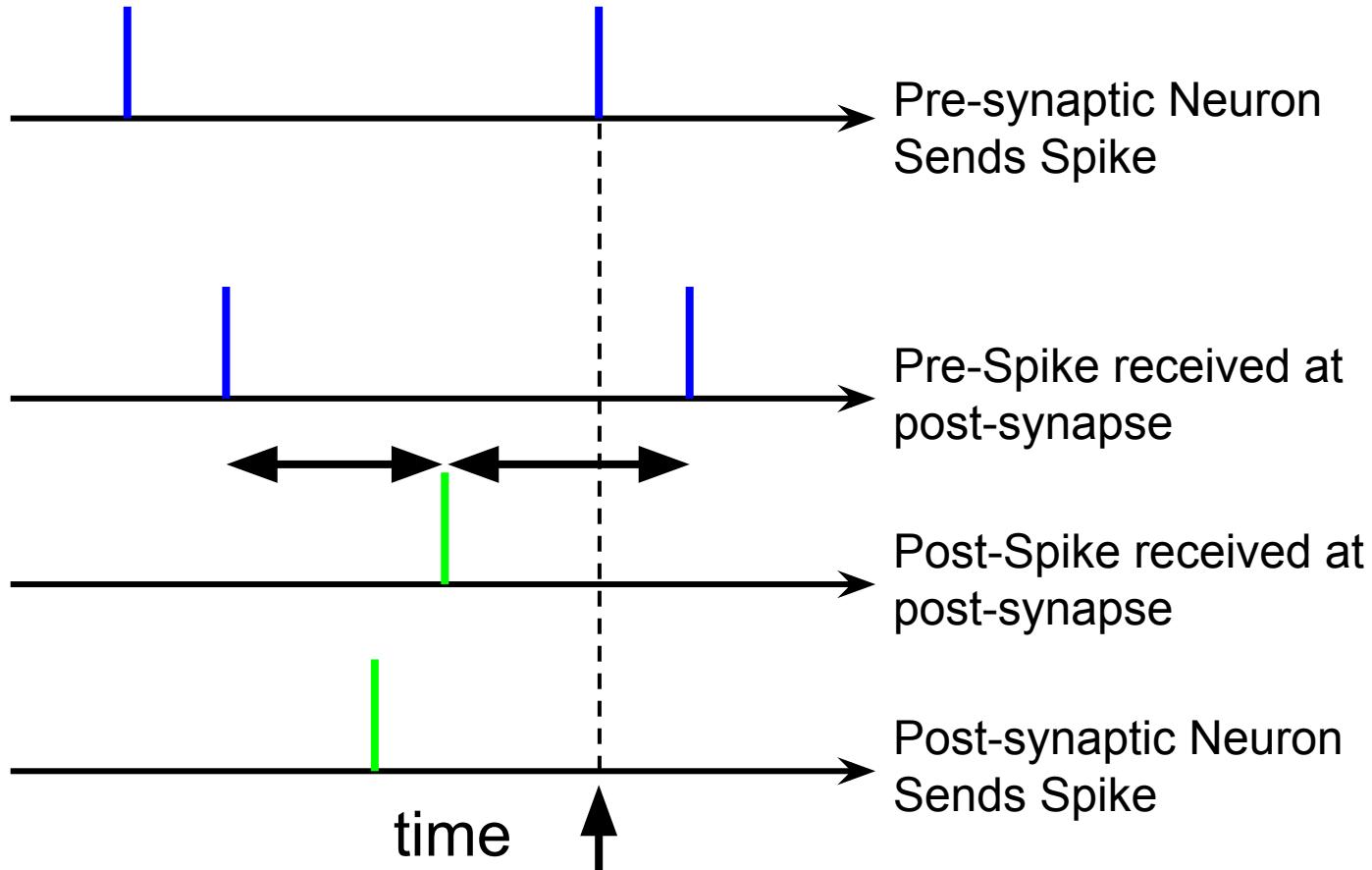
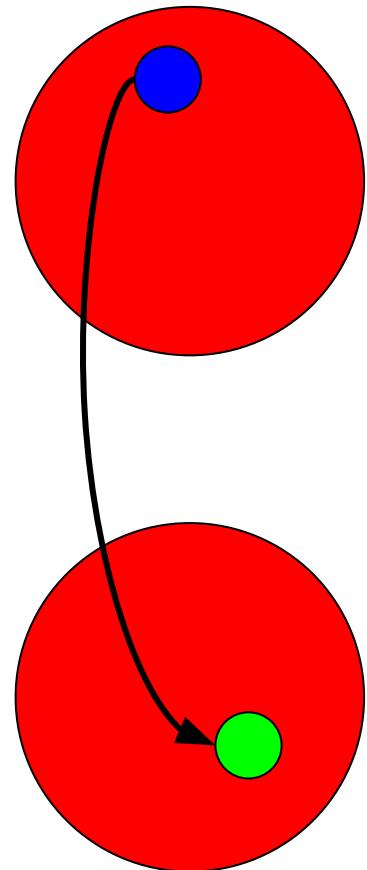
Spike Timing Dependent Plasticity



Spike Timing Dependent Plasticity

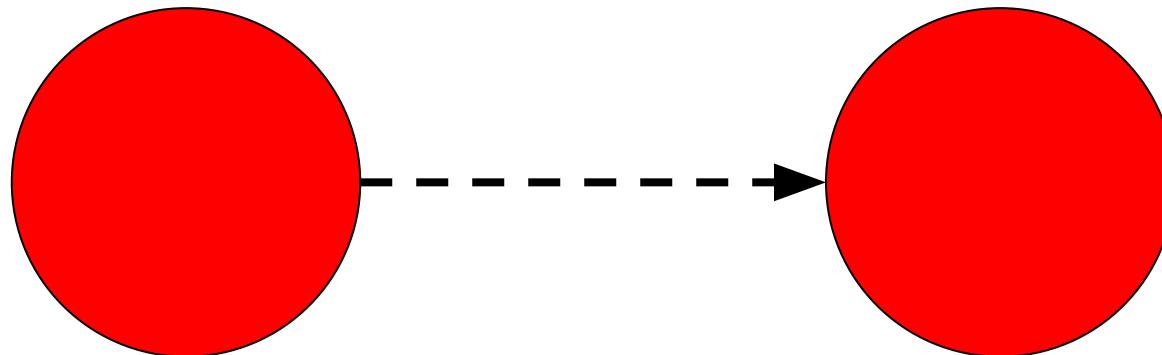


STDP - Deferred Execution



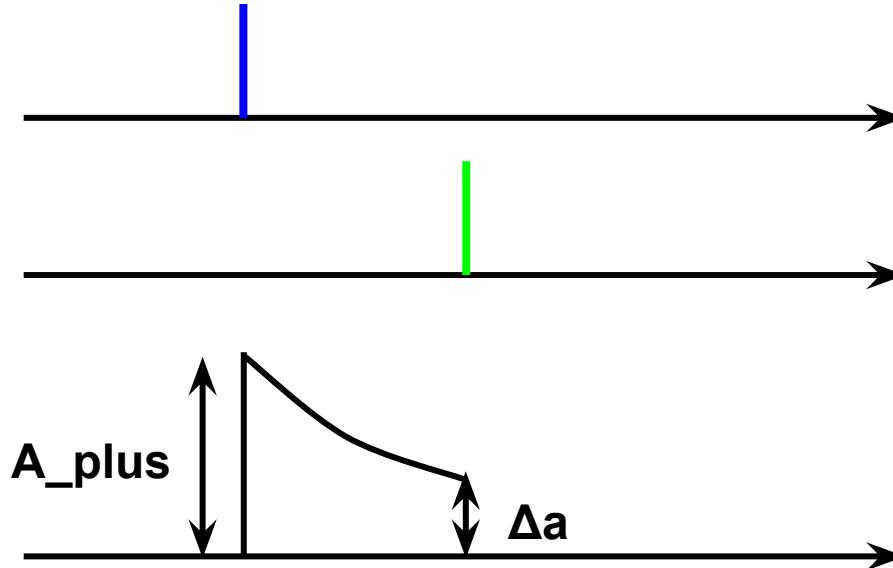
PyNN - STDP Synapse Types

```
p.STDPMechanism(  
    timing_dependence=?,  
    weight_dependence=?,  
    weight=0.0, delay=2.0)
```



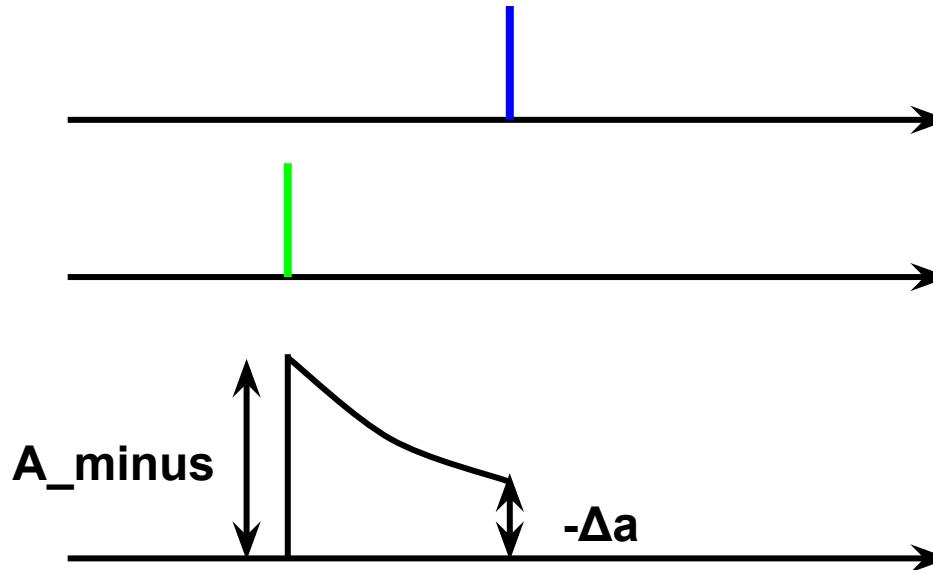
PyNN - Timing Dependence

```
sim.SpikePairRule(tau_plus=20.0, tau_minus=20.0,  
                   A_plus=0.5, A_minus=0.5)
```



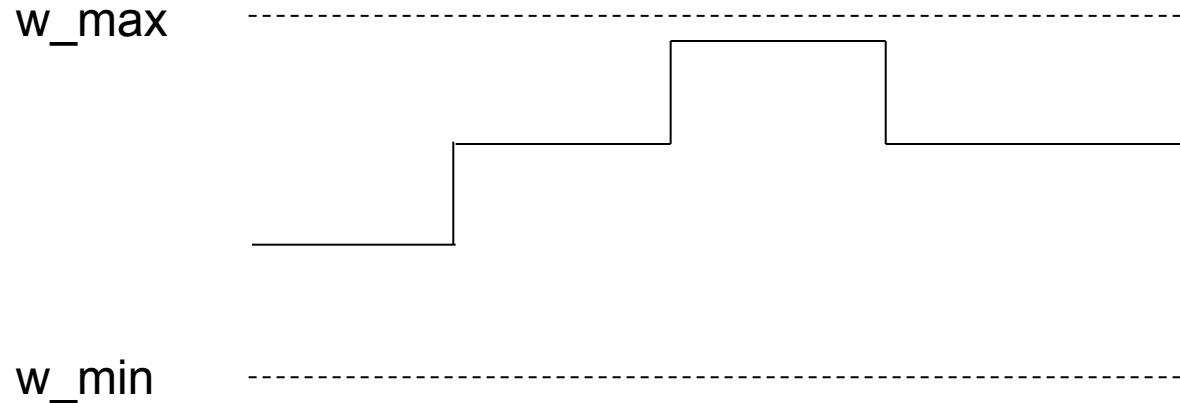
PyNN - Timing Dependence

```
sim.SpikePairRule(tau_plus=20.0, tau_minus=20.0,  
                  A_plus=0.5, A_minus=0.5)
```



PyNN - Weight Dependence

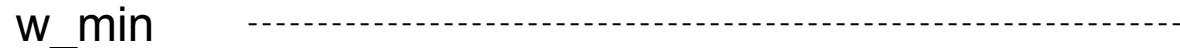
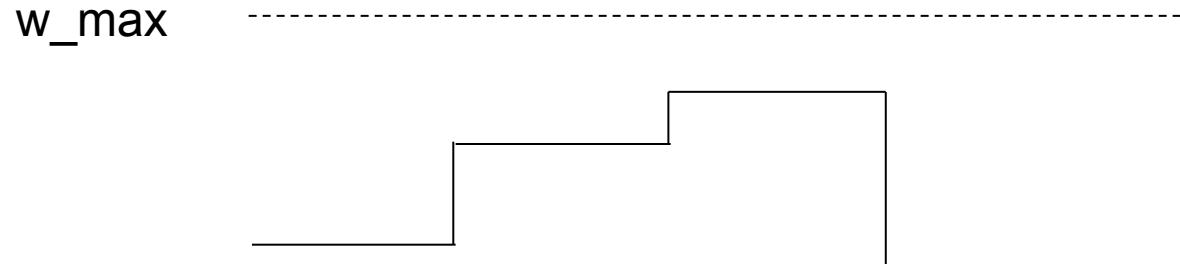
```
sim.AdditiveWeightDependence(w_max=5.0, w_min=0.0)
```



$$\Delta w = \Delta a (w_{\text{max}} - w_{\text{min}})$$

PyNN - Weight Dependence

sim.MultiplicativeWeightDependence(w_max=5.0,w_min=0.0)

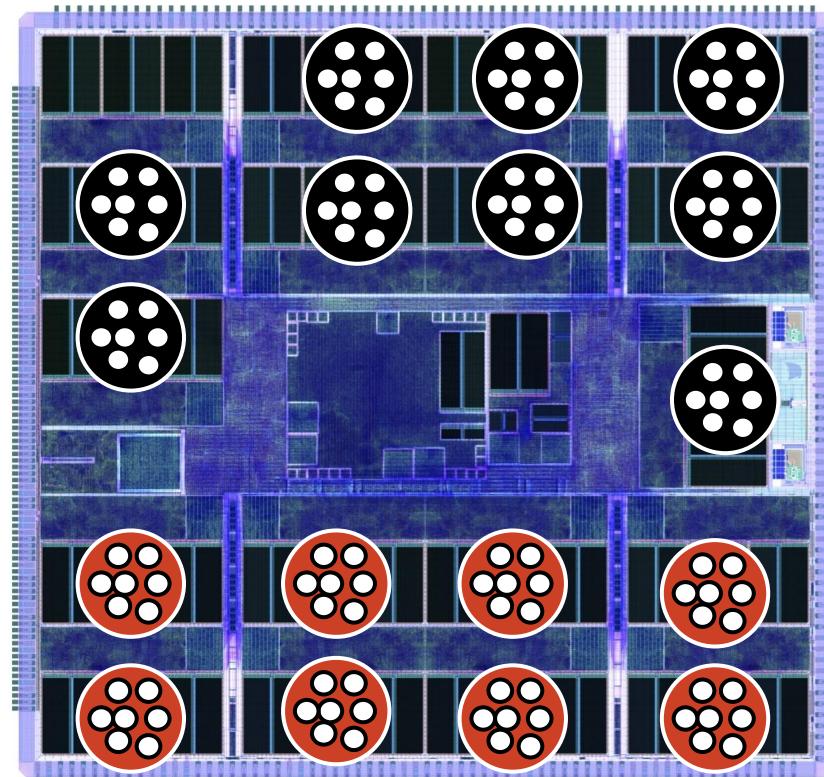
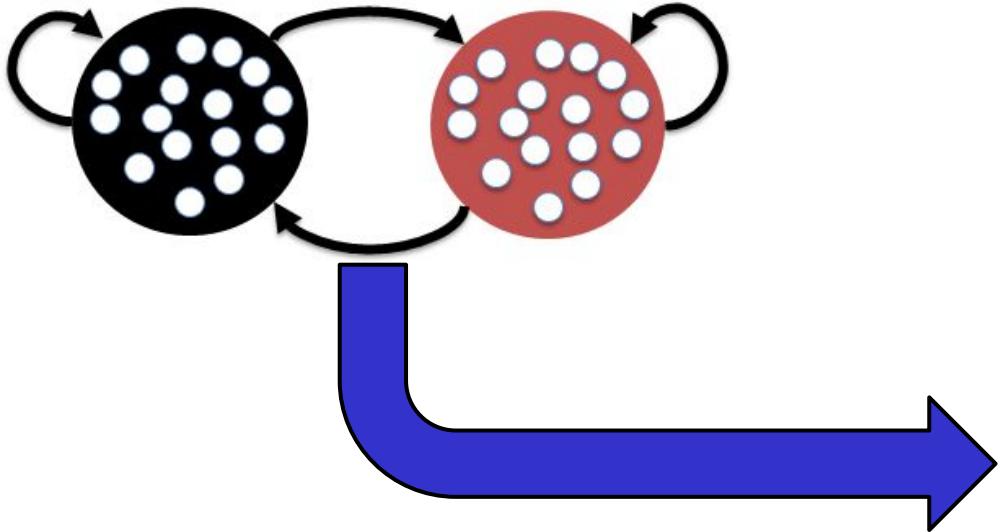


$$\Delta w = \Delta a (w - w_{\min}) \text{ if } \Delta a < 0 \text{ (Depression)}$$

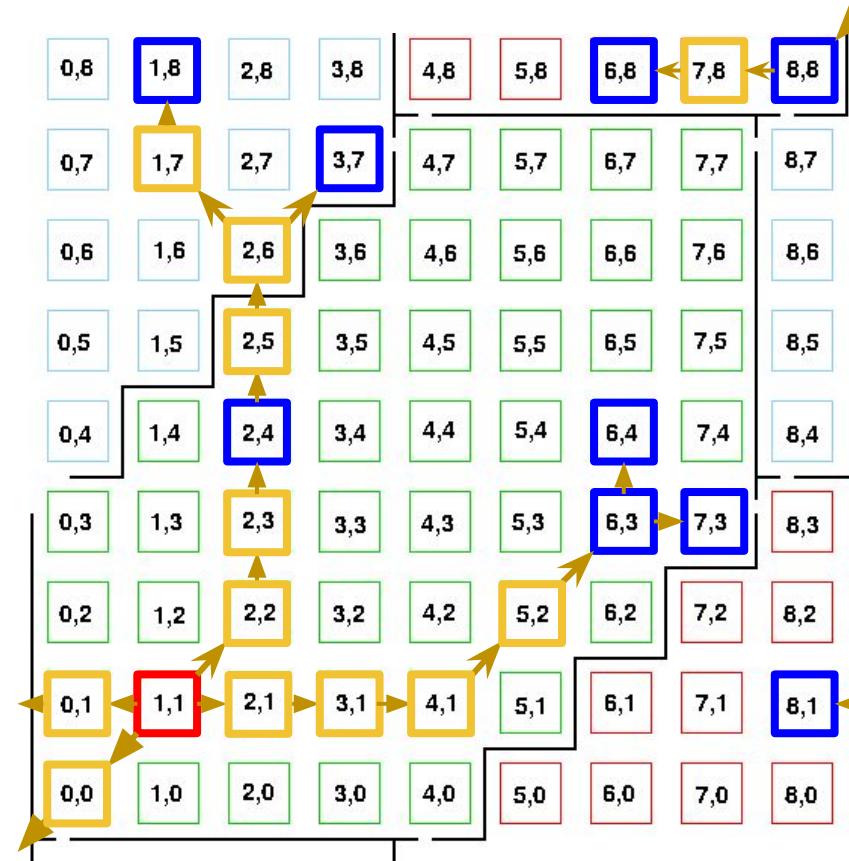
$$\Delta w = \Delta a (w_{\max} - w) \text{ if } \Delta a > 0 \text{ (Potentiation)}$$

Running on SpiNNaker

p.run(100)

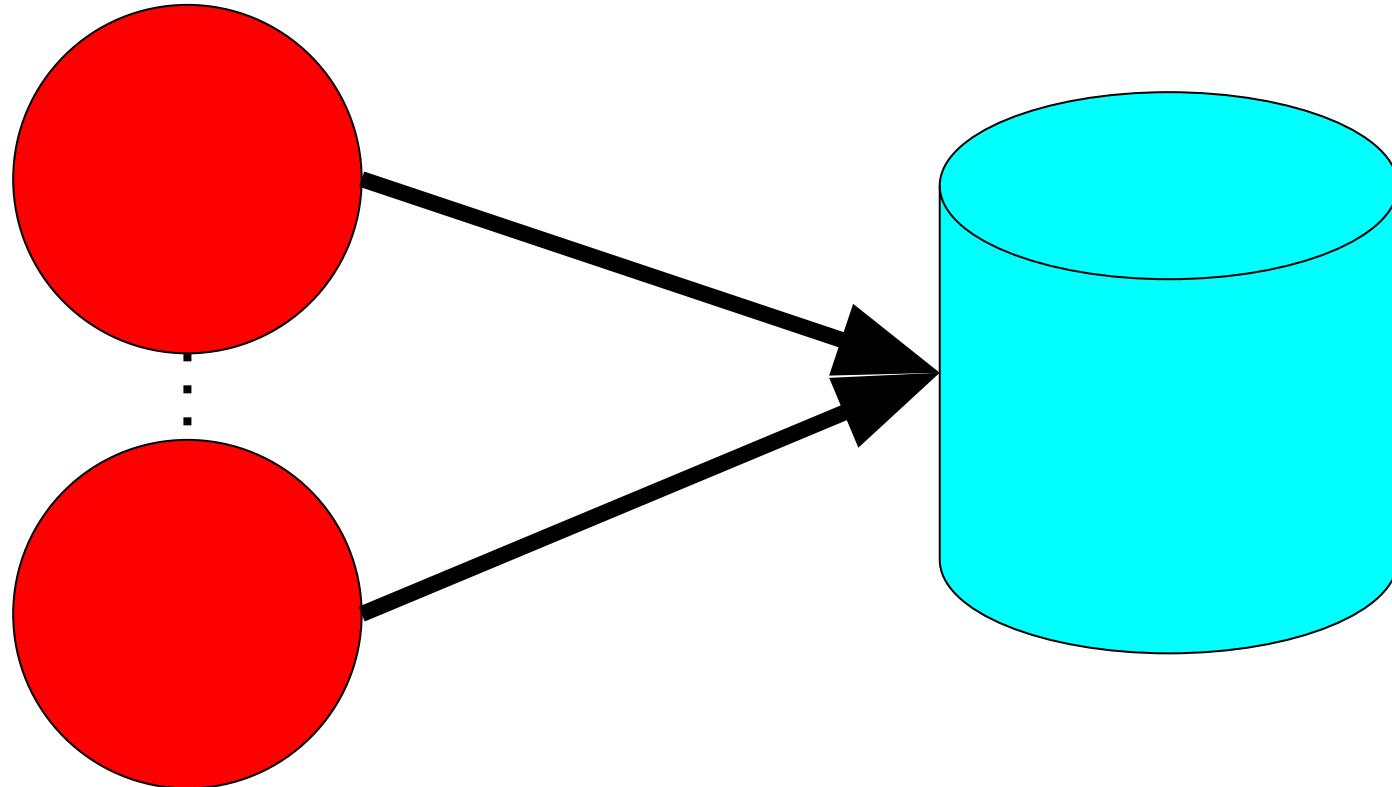


```
p.run(100)
```



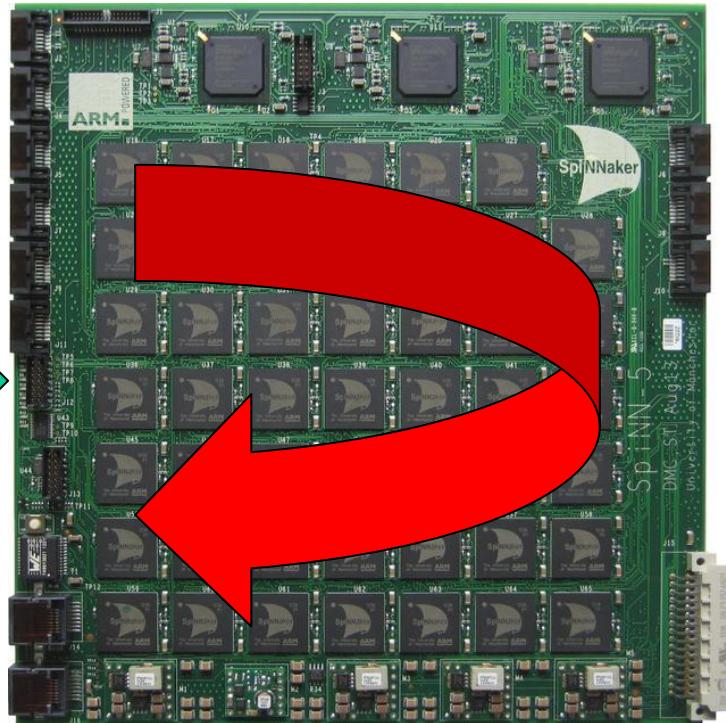
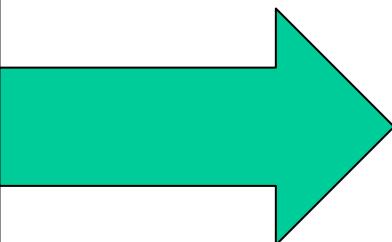
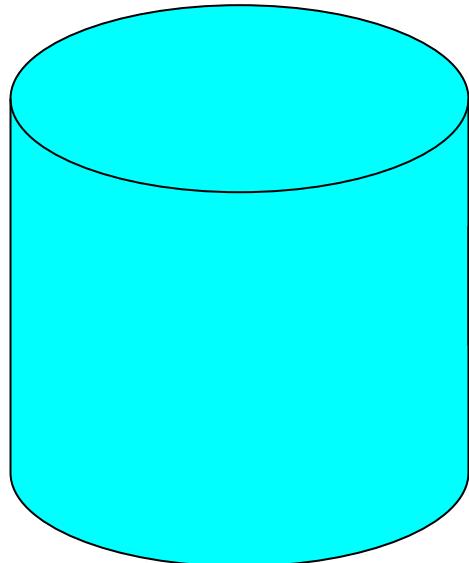
PyNN - Run

`p.run(100)`



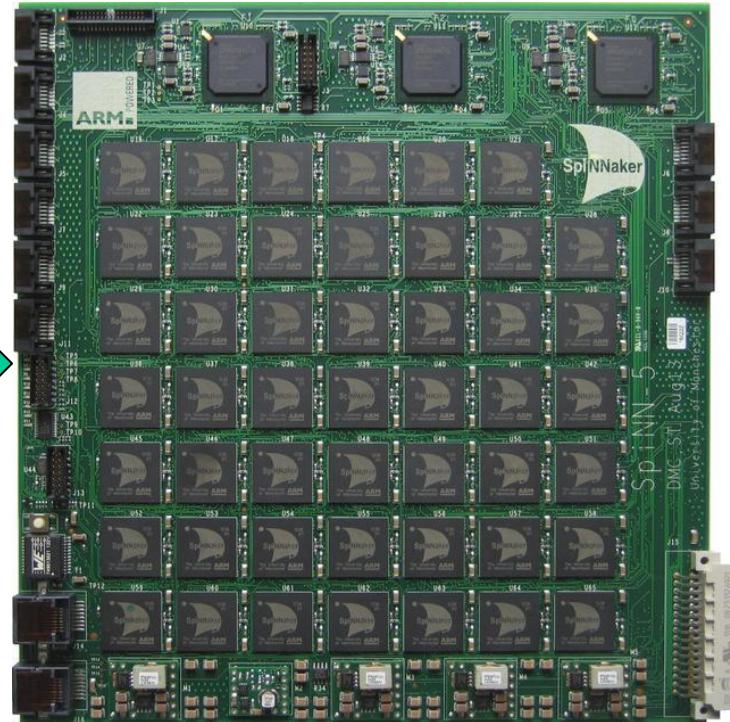
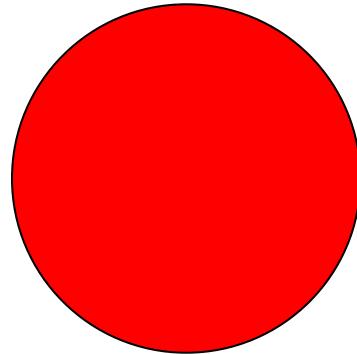
PyNN - Run

p.run(100)



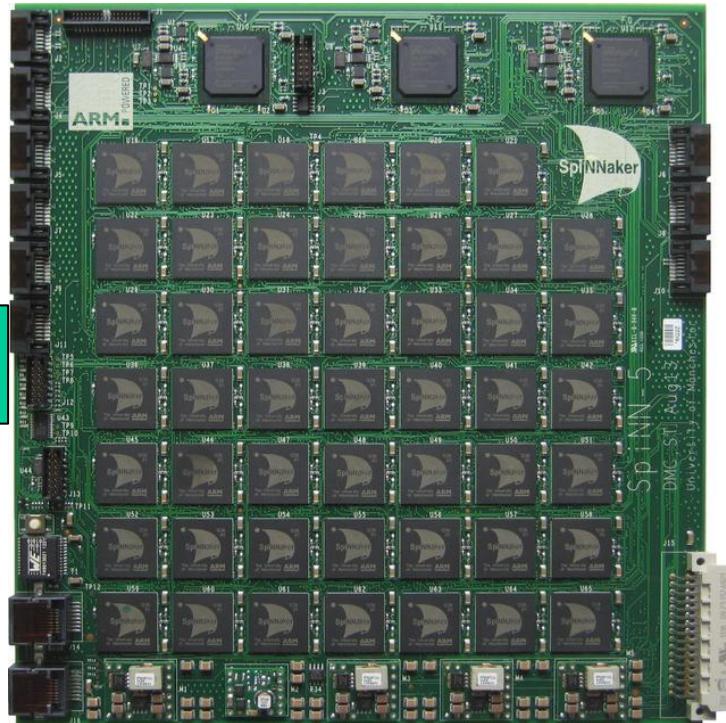
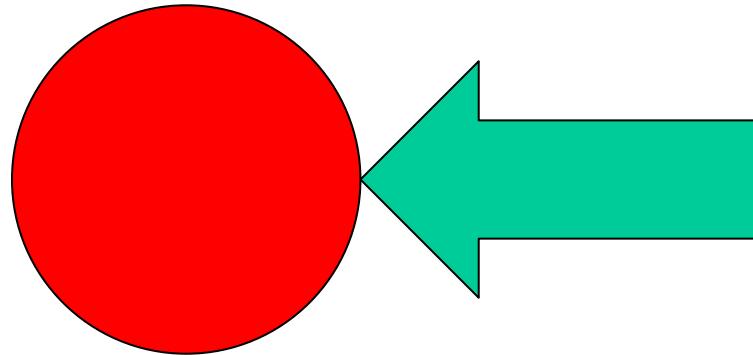
PyNN - Change and Run Again

```
pop_1.set(i_offset=5.0)  
p.run(50)
```



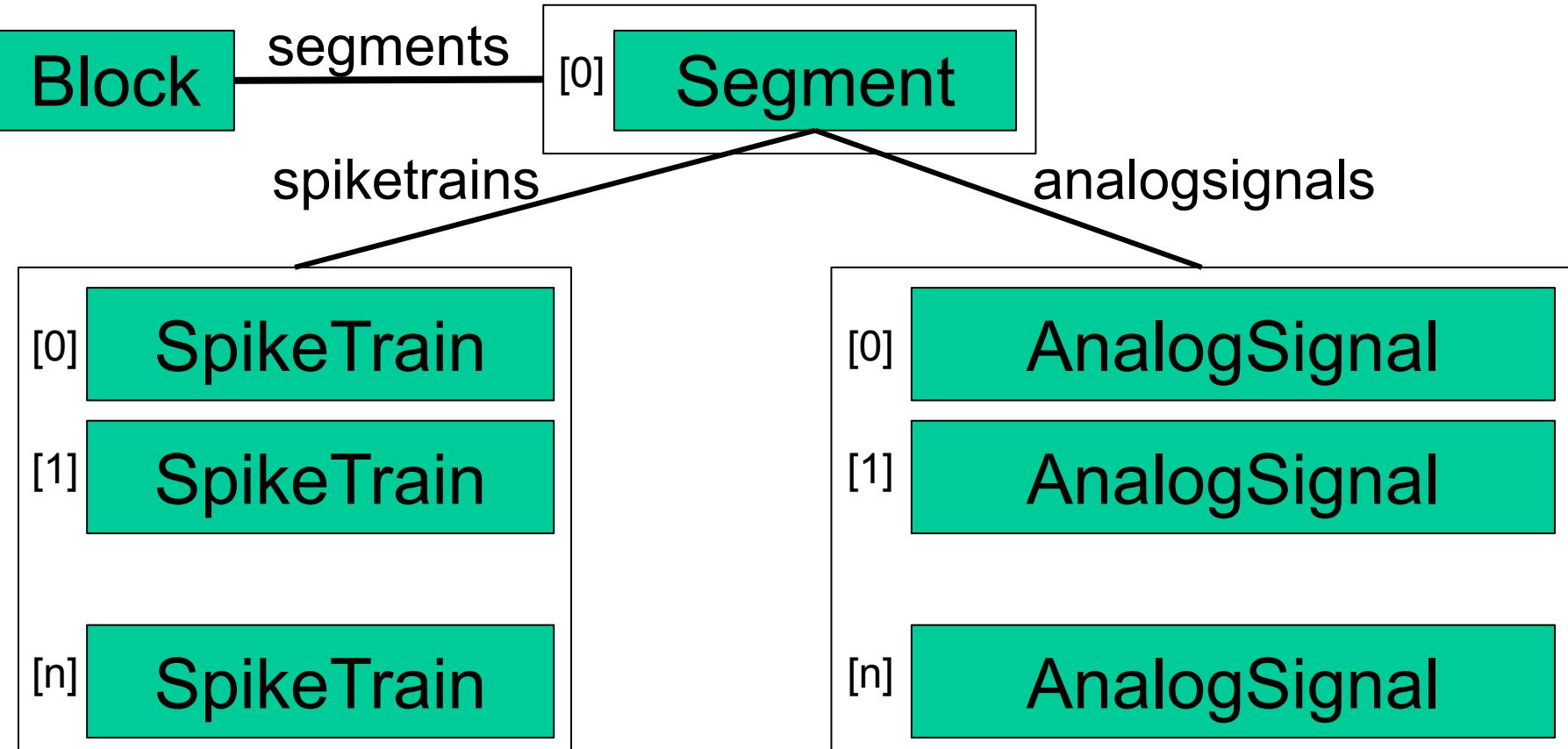
PyNN - Get Data

```
data = pop_1.get_data([“v”, “spikes”])
```

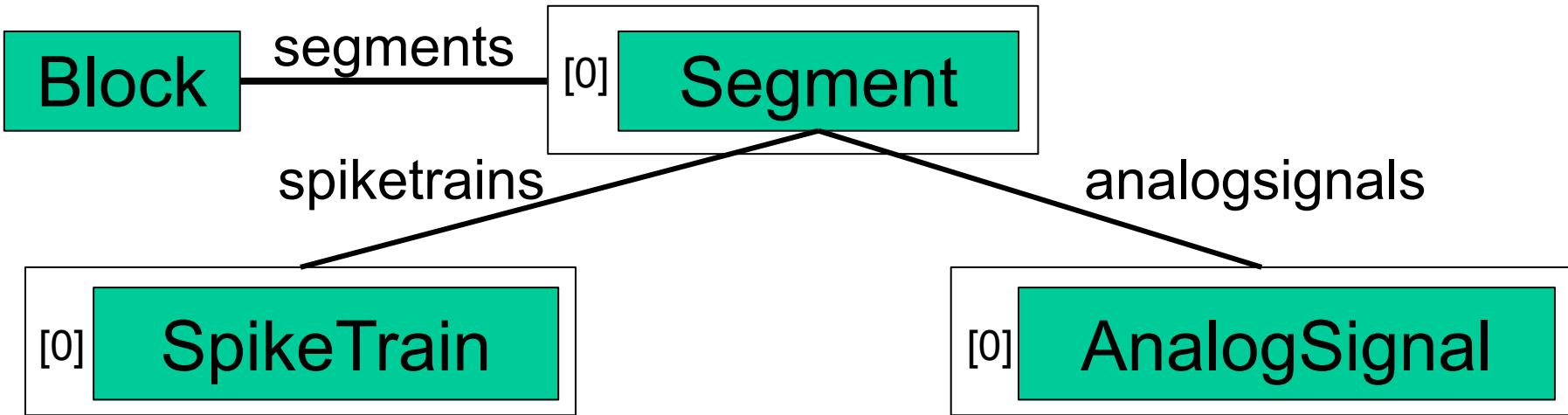


Reading Results

PyNN - Neo Data



PyNN - Neo Data

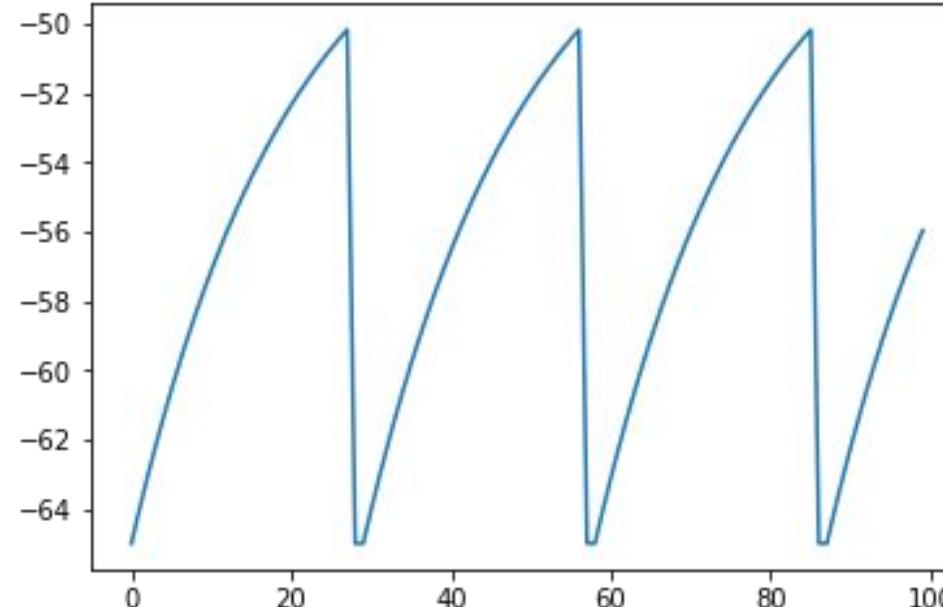


```
data = pop_1.get_data(["v", "spikes"])
v = data.segments[0].analogsignals
V = data.segments[0].filter(name="v")[0]
spikes = data.segments[0].spiketrains
```

PyNN - Plotting

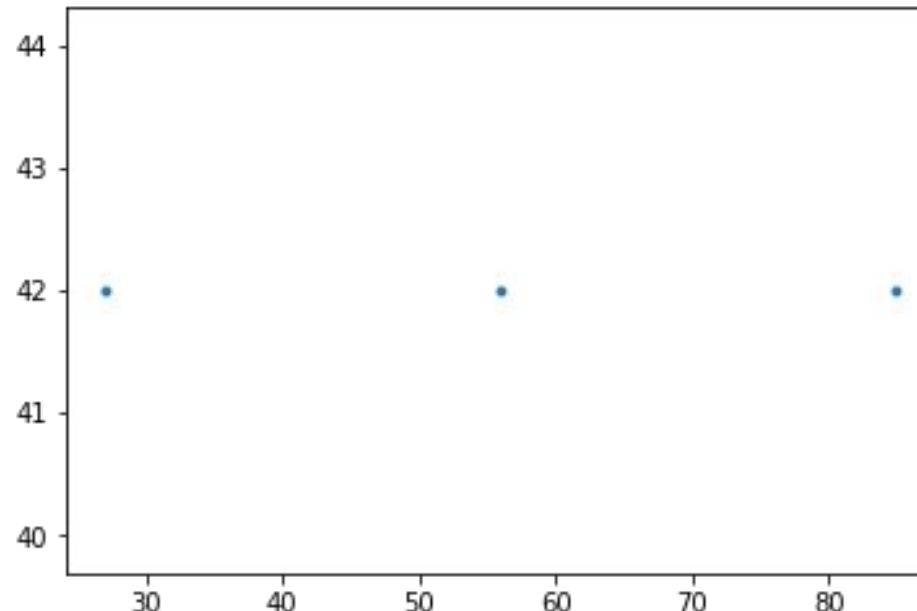
```
import matplotlib.pyplot as plt
```

```
plt.figure()  
plt.plot(v[0].times, v[0])  
plt.show()
```



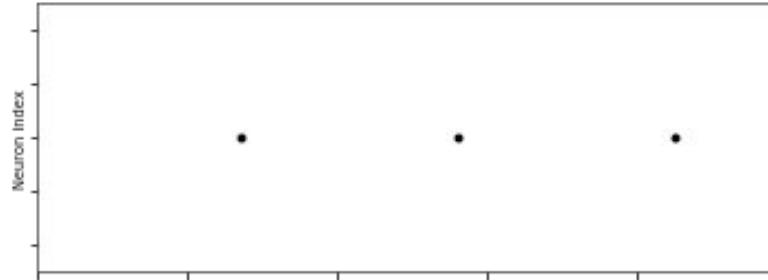
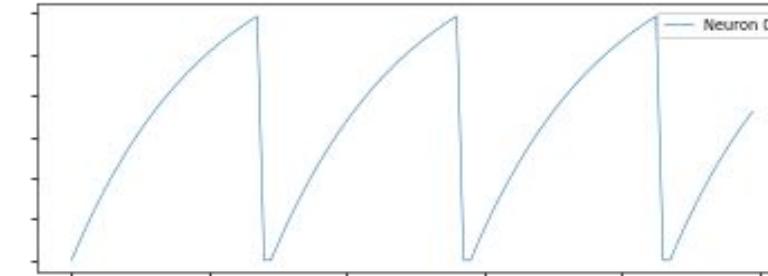
PyNN - Plotting

```
plt.figure()  
y = [1 for i in range(len(spikes[0]))]  
plt.plot(spikes[0], y, ".")  
plt.show()
```



PyNN - Plotting Neo Directly

```
from pyNN.utility.plotting import Figure, Panel
Figure(
    Panel(*data.segments[0].analogsignals),
    Panel(data.segments[0].spiketrains)
)
```



PyNN - Get Weights and Delays

```
synapses = proj.get(  
    ["weight", "delay"], "list")  
  
array([(0, 5, 0.756, 1.), (0, 6, 0.316, 1.), (0, 7, 0.885, 2.),  
       (0, 8, 0.421, 1.), (1, 4, 0.618, 1.), (1, 7, 0.438, 1.),  
       (1, 9, 1.607, 1.), (2, 0, 0.129, 1.), (2, 2, 1.055, 1.),  
       (2, 3, 1.319, 1.), (2, 9, 0.422, 1.), (3, 1, 0.328, 1.),  
       (3, 3, 0.456, 1.), (3, 6, 0.566, 1.), (4, 0, 1.046, 1.),  
       (4, 1, 1.199, 1.), (4, 2, 0.831, 1.), (5, 0, 1.643, 1.),  
       (5, 2, 1.165, 1.), (5, 3, 0.902, 1.), (5, 5, 1.627, 1.),  
       (6, 0, 2.143, 1.), (6, 5, 0.635, 1.), (6, 7, 0.704, 1.),  
       (7, 0, 1.914, 1.), (7, 4, 0.289, 1.), (7, 5, 2.058, 1.),  
       (7, 6, 0.428, 2.), (7, 7, 0.639, 1.), (7, 9, 0.616, 2.),  
       (8, 0, 1.039, 1.), (8, 1, 0.576, 1.), (8, 4, 1.563, 2.),  
       (8, 8, 0.995, 1.), (9, 0, 1.686, 1.), (9, 9, 0.631, 2.)])
```

PyNN - Get Weights and Delays

```
synapses = proj.get(  
    "weight", "array")
```

```
array([[  nan,  nan,  nan,  nan,  nan,  0.756,  0.316,  0.885,  0.421,  nan],  
       [  nan,  nan,  nan,  nan,  0.618,  nan,  nan,  0.438,  nan,  1.607],  
       [0.129,  nan,  1.055,  1.319,  nan,  nan,  nan,  nan,  0.422],  
       [  nan,  0.328,  nan,  0.456,  nan,  nan,  0.566,  nan,  nan,  nan],  
       [1.046,  1.199,  0.831,  nan,  nan,  nan,  nan,  nan,  nan,  nan],  
       [1.643,  nan,  1.165,  0.902,  nan,  1.627,  nan,  nan,  nan,  nan],  
       [2.143,  nan,  nan,  nan,  nan,  0.635,  nan,  0.704,  nan,  nan],  
       [1.914,  nan,  nan,  nan,  0.289,  2.058,  0.428,  0.639,  nan,  0.616],  
       [1.039,  0.576,  nan,  nan,  1.563,  nan,  nan,  nan,  0.995,  nan],  
       [1.686,  nan,  nan,  nan,  nan,  nan,  nan,  nan,  nan,  0.631]])
```

<http://neuralensemble.org/docs/PyNN/>

PyNN 0.9.4 documentation »

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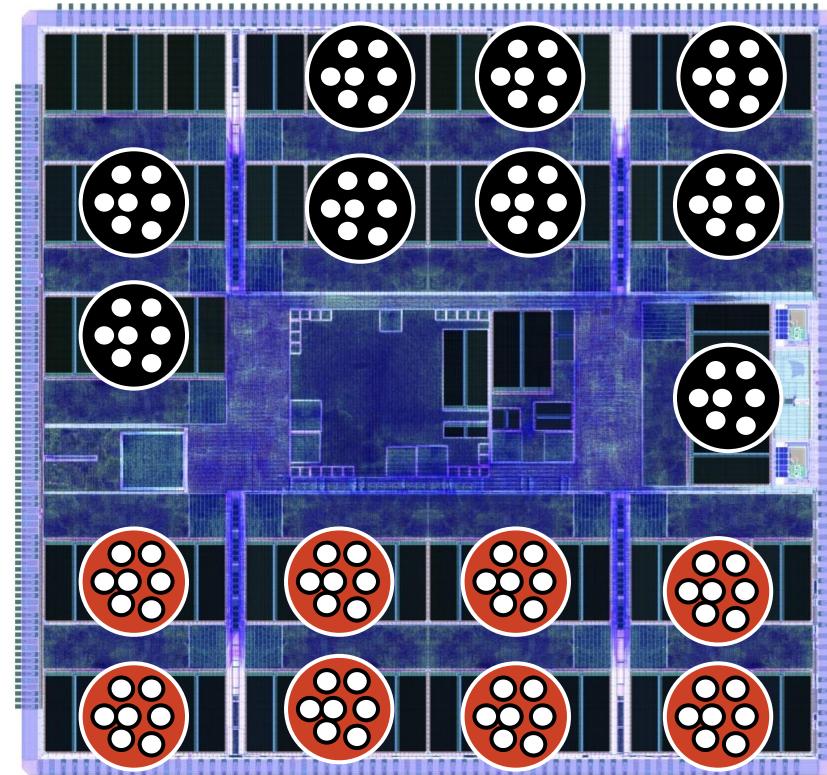
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Additional Non-PyNN Features

Neurons Per Core

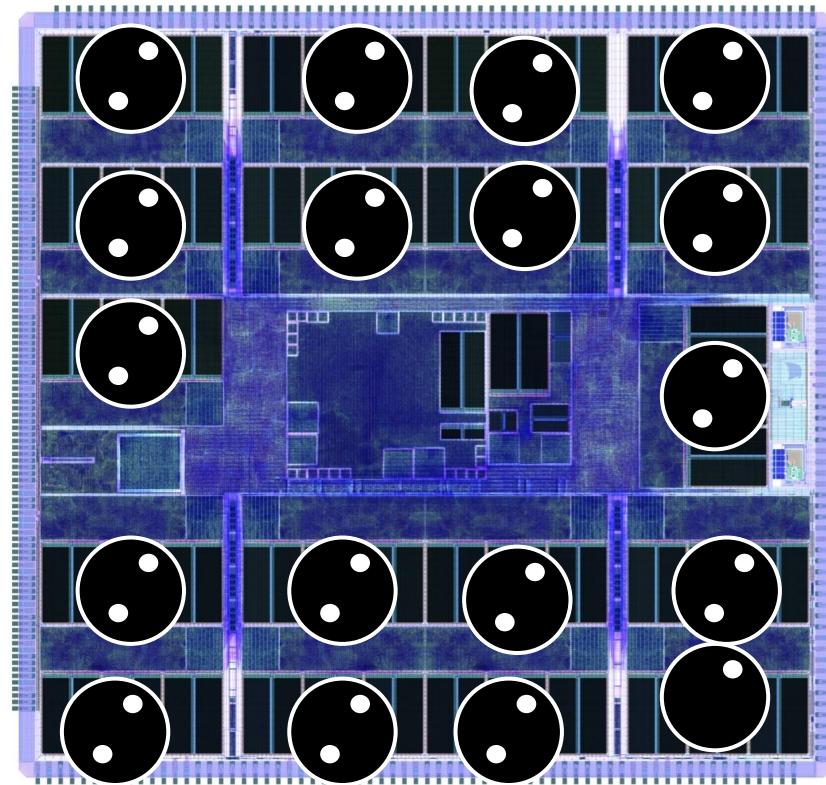
```
p.set_number_of_neurons_per_core(  
    p.IF_curr_exp, 7)
```

Default: 256



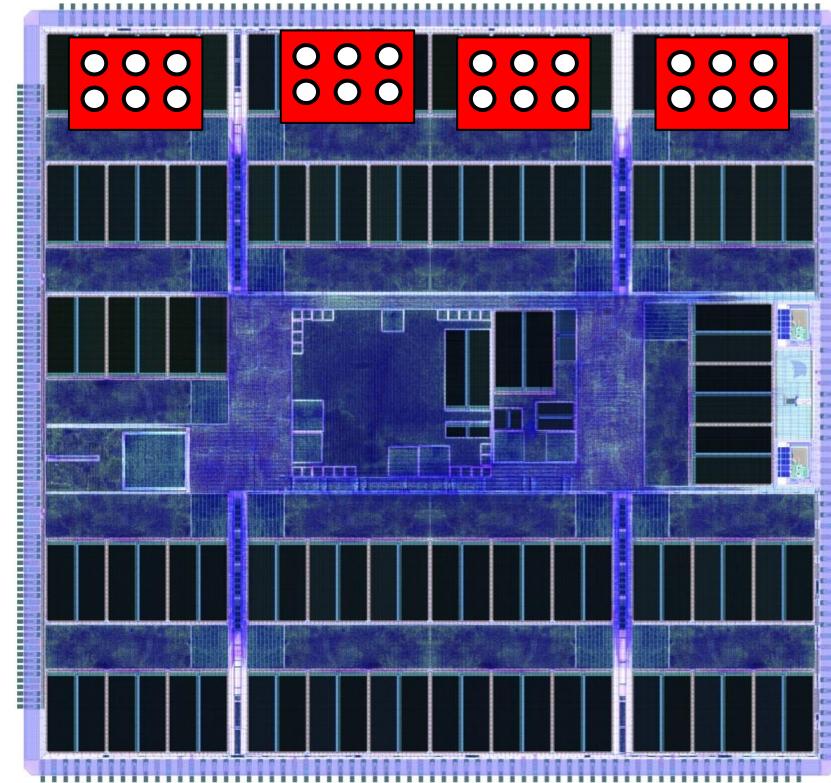
Neurons Per Core

```
p.set_number_of_neurons_per_core(  
    p.IF_curr_exp, 2)
```



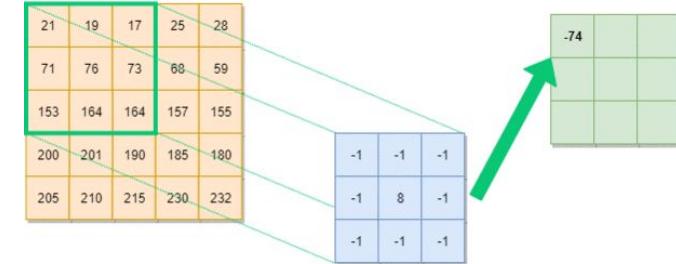
Neurons Per Core

```
p.set_number_of_neurons_per_core(  
    p.IF_curr_exp,  
    (3, 2))
```



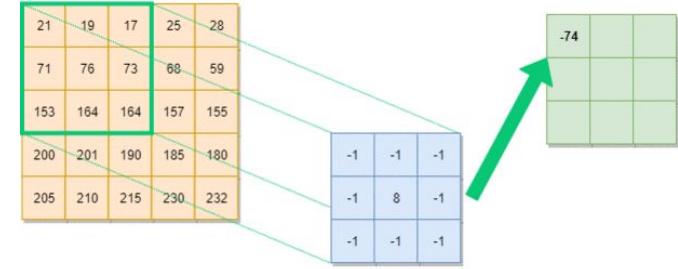
Convolution Connections

```
con = p.ConvolutionConnector(kernel=[...])  
  
in_sz = (640, 480)  
inp = p.Population(  
    in_sz[0] * in_sz[1], ...  
    structure=Grid2D(in_sz[0] / in_sz[1]))  
  
out_sz = conn.get_post_shape(in_sz)  
outp = p.Population(  
    out_sz[0] * out_sz[1], ...  
    structure=Grid2D(out_sz[0] / out_sz[1]))
```



Convolution Connections

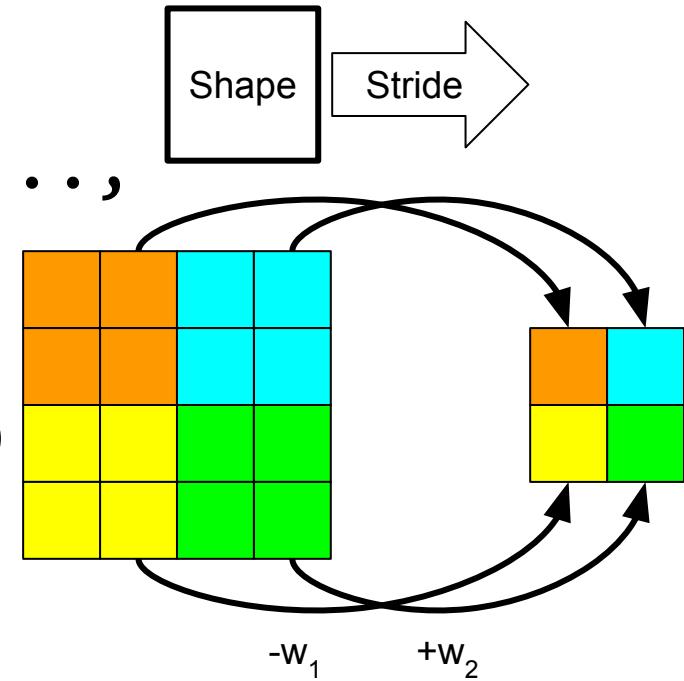
```
con = p.ConvolutionConnector(kernel=[...])
```



```
p.Projection(inp, outp, con, p.Convolution())
```

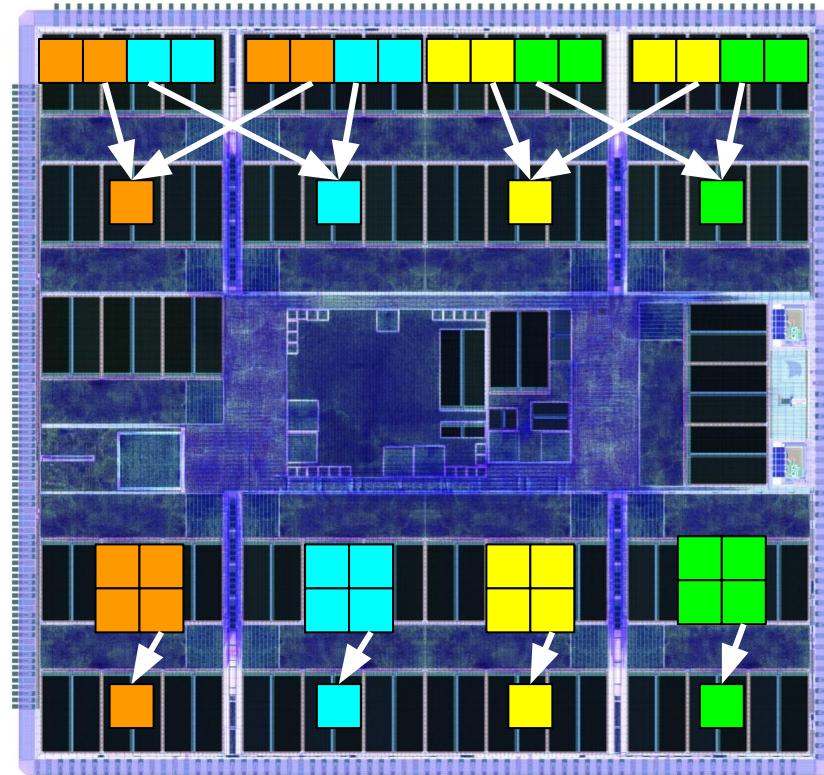
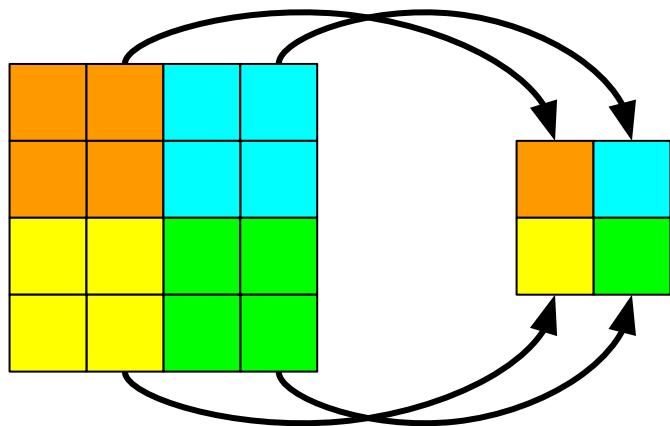
Pool Dense Connections

```
con = p.PoolDenseConnector(  
    kernel=[...], pool_shape=...,  
    pool_stride=...,  
    positive_synapse_type=...,  
    negative_synapse_type=...)
```



```
p.Projection(inp, outp, con, p.PoolDense())
```

Use of Population Structure

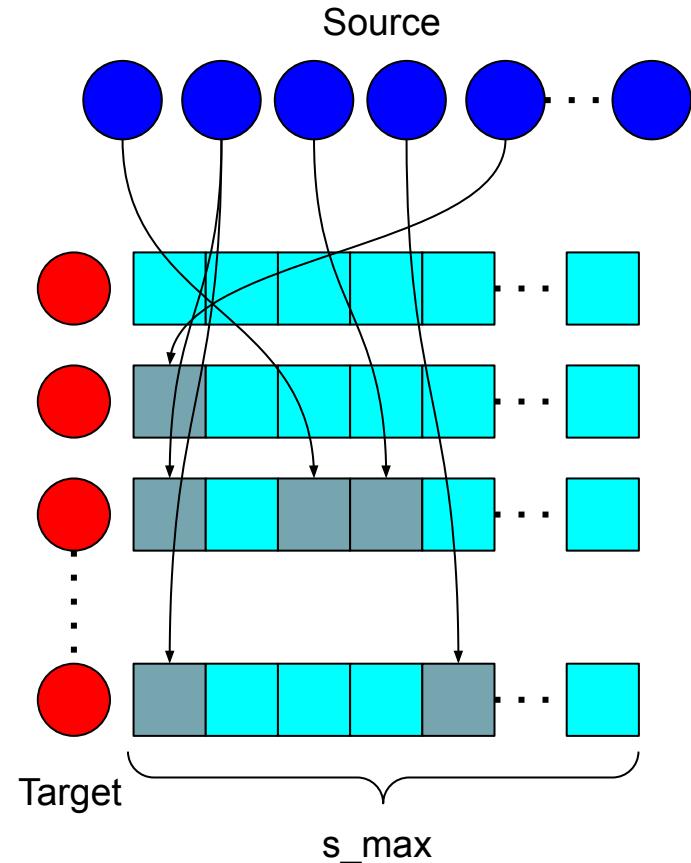


Structural Plasticity

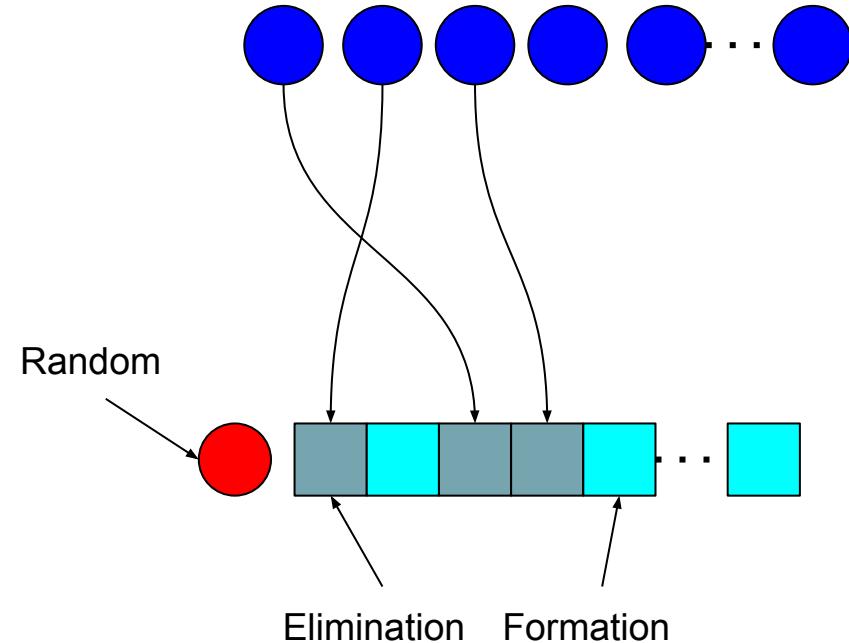
```
p.StructuralMechanism(  
    f_rew=..., s_max=...,  
    weight=..., delay=...,  
    ...)
```



f_rew



Structural Plasticity



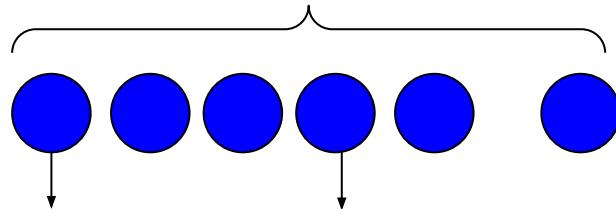
Structural Plasticity

p.StructuralMechanism(

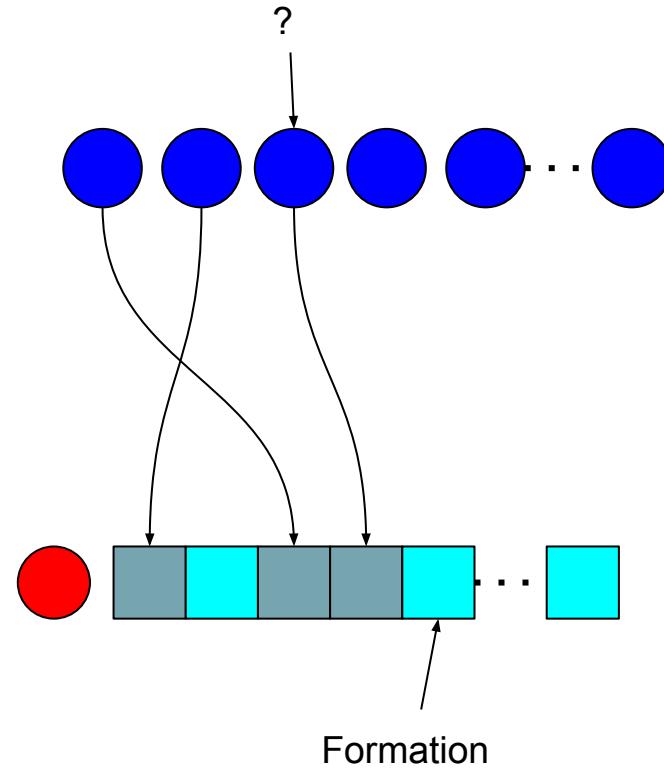
...

partner_selection=,
with_replacement=, ...)

p.RandomSelection()



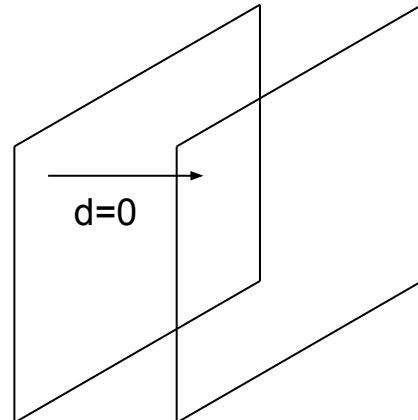
p.LastNeuronSelection()



```
p.StructuralMechanism(
```

```
...
```

```
formation=p.DistanceDependentFormation(  
    grid=[...], p_form_forward=...,  
    sigma_form_forward=...),  
    ...)
```



p.StructuralMechanism(

...

```
elimination=p.RandomByWeightElimination(  
    threshold=...,  
    prob_elim_depressed=...,  
    prob_elim_potentiated=...),  
    ...)
```



Live Input and Output

Input from Environment: Spikes

send_spikes

Spikelnjector
label="injector"

send_spikes("injector", [0])

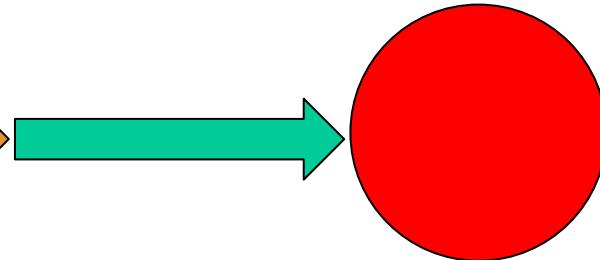
```
SpynnakerLiveSpikesConnection(  
    send_labels=[“injector”])
```

Multicast Key(s)
(Spike)



Input from Environment: Rates

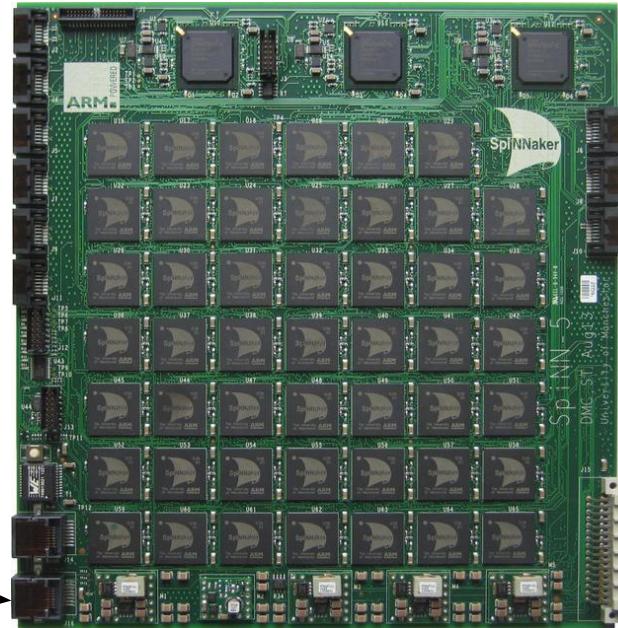
add_poisson_live_rate_control
set_rates



set_rates("input", [(0, 10)])

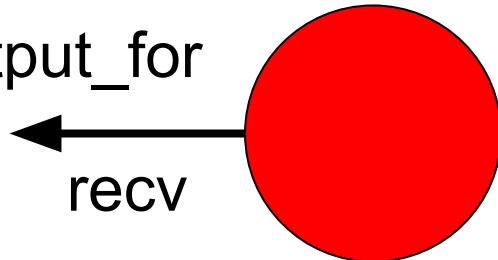
```
SpynnakerPoissonControlConnection(  
    poisson_labels=[“input”])
```

Multicast Key(s)
and Payload(s)



Output to Environment: Spikes

activate_live_output_for

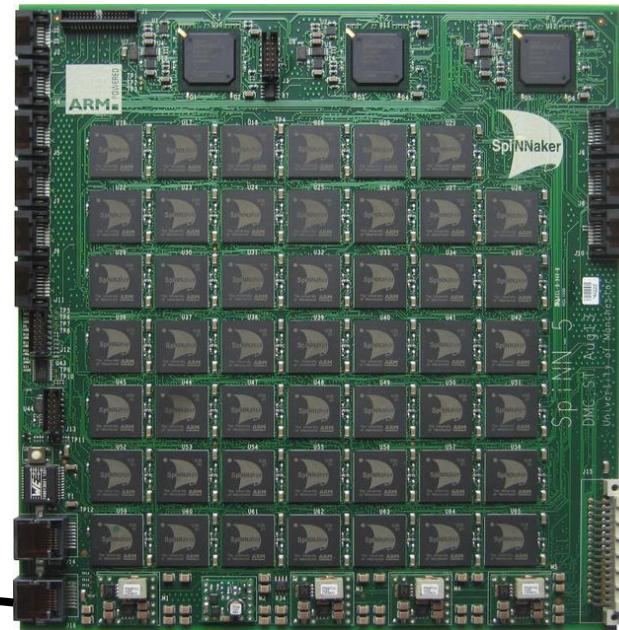


recv

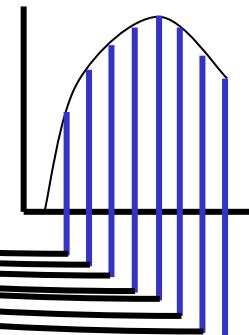
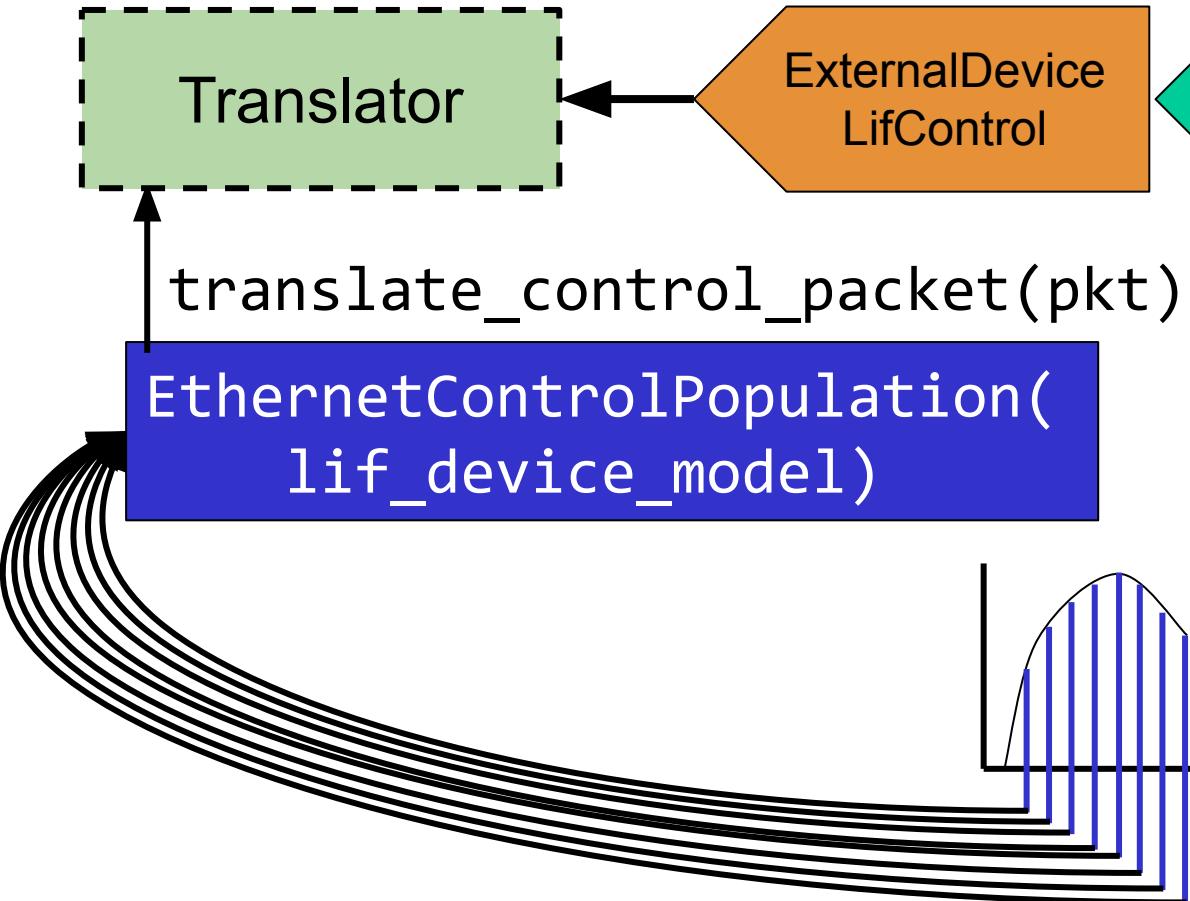
recv("pop", time, neuron_ids)

```
SpynnakerLiveSpikesConnection(  
    receive_labels=[“pop”])
```

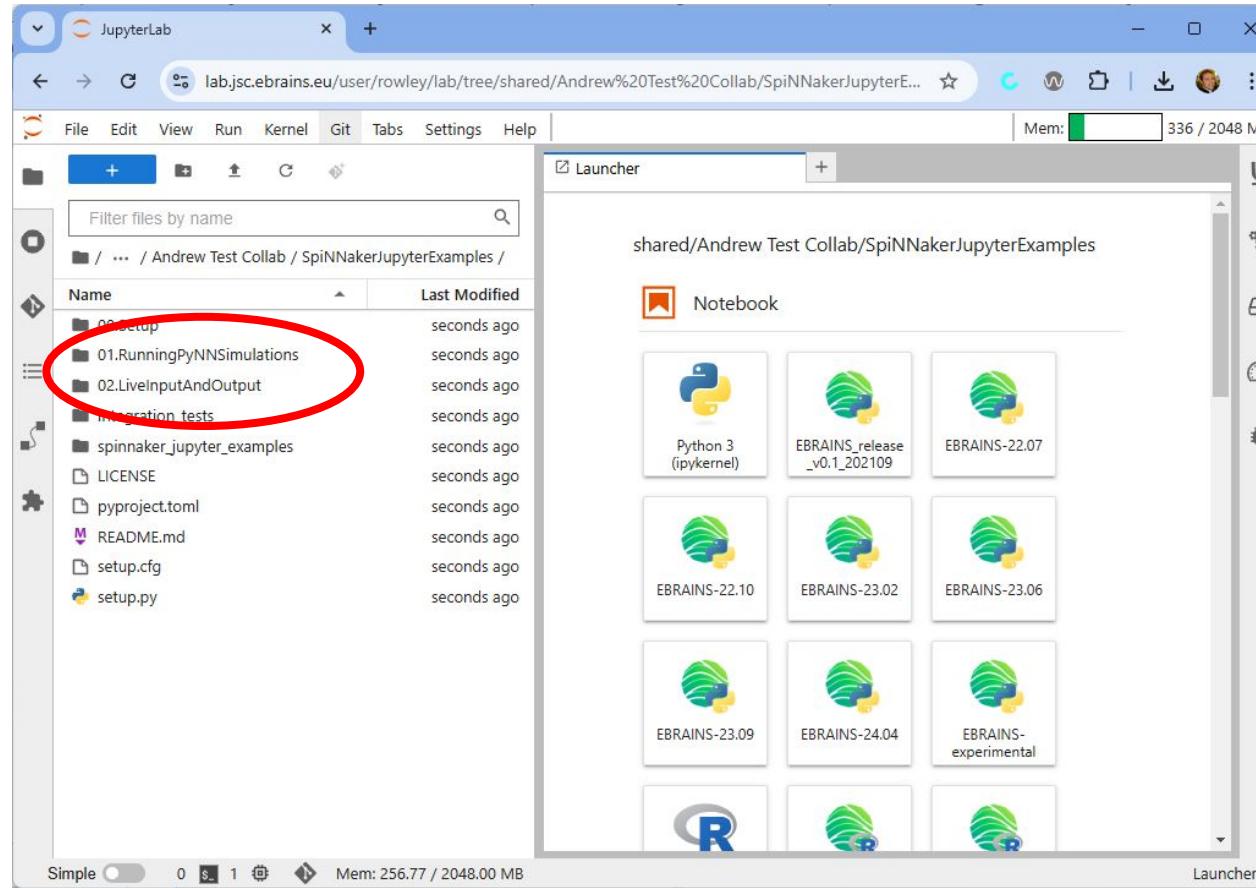
Multicast Key(s)
(Spike)



Output to Environment: Voltage



SpiNNaker Tutorials



SpiNNaker Tutorials on Jupyter

<https://lab.ebrains.eu/>

[https://github.com/SpiNNakerManchester/
SpiNNakerJupyterExamples](https://github.com/SpiNNakerManchester/SpiNNakerJupyterExamples)

```
import matplotlib.pyplot as plt  
...  
plt.savefig("fig.png")
```

01.RunningPyNNSimulations

02.LiveInputAndOutput

<https://shorturl.at/oJWFf>

PyNN Documentation:

<http://neuralensemble.org/docs/PyNN/>