Cleo

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CONTENTS

Hello there! Cleo has the goal of bridging theory and experiment for mesoscale neuroscience, facilitating electrode recording, optogenetic stimulation, and closed-loop experiments (e.g., real-time input and output processing) with the Brian 2 spiking neural network simulator. We hope users will find these components useful for prototyping experiments, innovating methods, and testing observations about a hypotheses *in silico*, incorporating into spiking neural network models laboratory techniques ranging from passive observation to complex model-based feedback control. Cleo also serves as an extensible, modular base for developing additional recording and stimulation modules for Brian simulations.

This package was developed by Kyle Johnsen and Nathan Cruzado under the direction of Chris Rozell at Georgia Institute of Technology. See the preprint here.

Cleo allows for flexible I/O processing in real time, enabling the simulation of closed-loop experiments such as event-triggered or feedback control. The user can also add latency to the stimulation to study the effects of computation delays.

CHAPTER

ONE

ELECTRODE RECORDING

Cleo provides functions for configuring electrode arrays and placing them in arbitrary locations in the simulation. The user can then specify parameters for probabilistic spike detection or a spike-based LFP approximation developed by Teleńczuk et al., 2020.

CHAPTER

TWO

1P/2P OPTOGENETIC STIMULATION

By modeling light propagation and opsins, Cleo enables users to flexibly add photostimulation to their model. Both a four-state Markov state model of opsin kinetics is available, as well as a minimal proportional current option for compatibility with simple neuron models. Cleo also accounts for opsin action spectra to model the effects of multi-light/wavelength/opsin crosstalk and heterogeneous expression. Parameters are for multiple opsins, and blue optic fiber (1P) and infrared spot (for 2P) illumination.

CHAPTER

THREE

2P IMAGING

Users can also inject a microscope into their model, selecting neurons on the specified plane of imaging or elsewhere, with signal and noise strength determined by indicator expression levels and position with respect to the focal plane. The calcium indicator model of Song et al., 2021 is implemented, with parameters included for GCaMP6 variants.

CHAPTER

FOUR

GETTING STARTED

Just use pip to install—the name on PyPI is `cleosim`:

```
pip install cleosim
```

Then head to the overview section of the documentation for a more detailed discussion of motivation, structure, and basic usage.

CHAPTER

FIVE

RELATED RESOURCES

Those using Cleo to simulate closed-loop control experiments may be interested in software developed for the execution of real-time, *in-vivo* experiments. Developed by members of Chris Rozell's and Garrett Stanley's labs at Georgia Tech, the CLOCTools repository can serve these users in two ways:

1. By providing utilities and interfaces with experimental platforms for moving from simulation to reality.
2. By providing performant control and estimation algorithms for feedback control. Although Cleo enables closed-loop manipulation of network simulations, it does not include any advanced control algorithms itself. The `ldsCtrlEst` library implements adaptive linear dynamical system-based control while the `hmm` library can generate and decode systems with discrete latent states and observations.

5.1 Publications

Cleo: A testbed for bridging model and experiment by simulating closed-loop stimulation, electrode recording, and optophysiology K.A. Johnsen, N.A. Cruzado, Z.C. Menard, A.A. Willats, A.S. Charles, and C.J. Rozell. *bioRxiv*, 2023.

CLOC Tools: A Library of Tools for Closed-Loop Neuroscience A.A. Willats, M.F. Bolus, K.A. Johnsen, G.B. Stanley, and C.J. Rozell. *In prep*, 2023.

State-Aware Control of Switching Neural Dynamics A.A. Willats, M.F. Bolus, C.J. Whitmire, G.B. Stanley, and C.J. Rozell. *In prep*, 2023.

Closed-Loop Identifiability in Neural Circuits A. Willats, M. O'Shaughnessy, and C. Rozell. *In prep*, 2023.

State-space optimal feedback control of optogenetically driven neural activity M.F. Bolus, A.A. Willats, C.J. Rozell and G.B. Stanley. *Journal of Neural Engineering*, 18(3), pp. 036006, March 2021.

Design strategies for dynamic closed-loop optogenetic neurocontrol in vivo M.F. Bolus, A.A. Willats, C.J. Whitmire, C.J. Rozell and G.B. Stanley. *Journal of Neural Engineering*, 15(2), pp. 026011, January 2018.

CHAPTER

SIX

DOCUMENTATION CONTENTS

6.1 Overview

6.1.1 Introduction

Who is this package for?

Cleo (Closed-Loop, Electrophysiology, and Optophysiology experiment simulation testbed) is a Python package developed to bridge theory and experiment for mesoscale neuroscience. We envision two primary uses cases:

1. For prototyping closed-loop control of neural activity *in silico*. Animal experiments are costly to set up and debug, especially with the added complexity of real-time intervention—our aim is to enable researchers, given a decent spiking model of the system of interest, to assess whether the type of control they desire is feasible and/or what configuration(s) would be most conducive to their goals.
2. The complexity of experimental interfaces means it's not always clear what a model would look like in a real experiment. Cleo can help anyone interested in observing or manipulating a model while taking into account the constraints present in real experiments. Because Cleo is built around the Brian simulator, we especially hope this is helpful for existing Brian users who for whatever reason would like a convenient way to inject recorders (e.g., electrodes or 2P imaging) or stimulators (e.g., optogenetics) into the core network simulation.

What is closed-loop control?

In short, determining the inputs to deliver to a system from its outputs. In neuroscience terms, making the stimulation parameters a function of the data recorded in real time.

Structure and design

Cleo wraps a spiking network simulator and allows for the injection of stimulators and/or recorders. The models used to emulate these devices are often non-trivial to implement or use in a flexible manner, so Cleo aims to make device injection and configuration as painless as possible, requiring minimal modification to the original network.

Cleo also orchestrates communication between the simulator and a user-configured `IOProcessor` object, modeling how experiment hardware takes samples, processes signals, and controls stimulation devices in real time.

For an explanation of why we choose to prioritize spiking network models and how we chose Brian as the underlying simulator, see *Design rationale*.

Why closed-loop control in neuroscience?

Fast, real-time, closed-loop control of neural activity enables intervention in processes that are too fast or unpredictable to control manually or with pre-defined stimulation, such as sensory information processing, motor planning, and oscillatory activity. Closed-loop control in a *reactive* sense enables the experimenter to respond to discrete events of interest, such as the arrival of a traveling wave or sharp wave ripple, whereas *feedback* control deals with driving the system towards a desired point or along a desired state trajectory. The latter has the effect of rejecting noise and disturbances, reducing variability across time and across trials, allowing the researcher to perform inference with less data and on a finer scale. Additionally, closed-loop control can compensate for model mismatch, allowing it to reach more complex targets where open-loop control based on imperfect models is bound to fail.

6.1.2 Installation

Make sure you have Python 3.7, then use pip: `pip install cleosim`.

> **Caution:** The name on PyPI is `cleosim` since `cleo` was already taken, but in code it is still used as `import cleo`. The other Cleo appears to actually be a fairly well developed package, so I'm sorry if you need to use it along with this Cleo in the same environment. In that case, there are workarounds.

Or, if you're a developer, install poetry and run `poetry install` from the repository root.

6.1.3 Usage

Brian network model

The starting point for using Cleo is a Brian spiking neural network model of the system of interest. For those new to Brian, the docs are a great resource. If you have a model built with another simulator or modeling language, you may be able to import it to Brian via NeuroML.

Perhaps the biggest change you may have to make to an existing model to make it compatible with Cleo's optogenetics and electrode recording is to give the neurons of interest coordinates in space. See the tutorials or the cleo.coords module for more info.

You'll need your model in a Brian `Network` object before you move on. E.g.,:

```
import brian2 as b2
ng = b2.NeuronGroup( # a simple population of 100 LIF neurons
    500,
    """dv/dt = (-v - 70*mV + (500*Mohm)*Iopto + 2*xi*sqrt(tau_m)*mvolt) / tau_m : volt
    Iopto : amp""",
    threshold='v>-50*mV',
    reset='v=-70*mV',
    namespace={'tau_m': 20*b2.ms},
)
ng.v = -70*b2.mV
net = b2.Network(ng)
```

Your neurons need x, y, and z coordinates for Cleo's spatially defined recording and stimulation models to work:

```
import cleo
cleo.coords.assign_coords_rand_rect_prism(
    ng, xlim=(-0.2, 0.2), ylim=(-0.2, 0.2), zlim=(0.2, 1), unit=b2.mm
)
```

CLSimulator

Once you have a network model, you can construct a *CLSimulator* object:

```
sim = cleo.CLSimulator(net)
```

The simulator object wraps the Brian network and coordinates device injection, processing input and output, and running the simulation.

Recording

Recording devices take measurements of the Brian network. To use a *Recorder*, you must inject it into the simulator via *cleo.CLSimulator.inject()*. The recorder will only record from the neuron groups specified on injection, allowing for such scenarios as singling out a cell type to record from. Some extremely simple implementations (which do little more than wrap Brian monitors) are available in the *cleo.recorders* module. See the *Electrode recording* and *All-optical control* tutorials for more detail on how to record from a simulation more realistically, but here's a quick example of how to record multi-unit spiking activity with an electrode:

```
# configure and inject a 32-channel shank
coords = cleo.ephys.linear_shank_coords(
    array_length=1*b2.mm, channel_count=32, start_location=(0, 0, 0.2)*b2.mm
)
mua = cleo.ephys.MultiUnitSpiking(
    r_perfect_detection=20 * b2.um,
    r_half_detection=40 * b2.um,
)
probe = cleo.ephys.Probe(coords, signals=[mua])
sim.inject(probe, ng)
```

```
---------------------------------------------------------------------------
DimensionMismatchError                    Traceback (most recent call last)
Cell In[4], line 10
      5 mua = cleo.ephys.MultiUnitSpiking(
      6     r_perfect_detection=20 * b2.um,
      7     r_half_detection=40 * b2.um,
      8 )
      9 probe = cleo.ephys.Probe(coords, signals=[mua])
---> 10 sim.inject(probe, ng)

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/cleo/base.py:383, in CLSimulator.inject(self, device, *neuron_groups,␣
↪**kwparams)
    381         device.sim = self
    382         device.init_for_simulator(self)
--> 383     device.connect_to_neuron_group(ng, **kwparams)
    384 for brian_object in device.brian_objects:
    385     if brian_object not in self.network.objects:

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/cleo/ephys/probes.py:158, in Probe.connect_to_neuron_group(self, neuron_group,
↪ **kwparams)
    146 """Configure probe to record from given neuron group
    147
```

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```
    148 Will call :meth:`Signal.connect_to_neuron_group` for each signal
   (...)
    155     Passed in to signals' connect functions, needed for some signals
    156 """
    157 for signal in self.signals:
--> 158     signal.connect_to_neuron_group(neuron_group, **kwparams)
    159     self.brian_objects.update(signal.brian_objects)

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/cleo/ephys/spiking.py:208, in MultiUnitSpiking.connect_to_neuron_group(self,␣
↪neuron_group, **kwparams)
    200 def connect_to_neuron_group(self, neuron_group: NeuronGroup, **kwparams) -> None:
    201     """Configure signal to record from specified neuron group
    202
    203     Parameters
   (...)
    206         group to record from
    207     """
--> 208     neuron_channel_dtct_probs = super(
    209         MultiUnitSpiking, self
    210     ).connect_to_neuron_group(neuron_group, **kwparams)
    211     if self._dtct_prob_array is None:
    212         self._dtct_prob_array = neuron_channel_dtct_probs

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/cleo/ephys/spiking.py:99, in Spiking.connect_to_neuron_group(self, neuron_
↪group, **kwparams)
     97 distances = np.sqrt(dist2) * meter  # since units stripped
     98 # probs is n_neurons by n_channels
---> 99 probs = self._detection_prob_for_distance(distances)
    100 # cut off to get indices of neurons to monitor
    101 # [0] since nonzero returns tuple of array per axis
    102 i_ng_to_keep = np.nonzero(np.all(probs > self.cutoff_probability, axis=1))[0]

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/cleo/ephys/spiking.py:148, in Spiking._detection_prob_for_distance(self, r)
    146 h = b - a
    147 with np.errstate(divide="ignore"):
--> 148     decaying_p = h / (r - c)
    149 decaying_p[decaying_p == np.inf] = 1  # to fix NaNs caused by /0
    150 p = 1 * (r <= a) + decaying_p * (r > a)

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/brian2/units/fundamentalunits.py:1193, in Quantity.__array_ufunc__(self, uf,␣
↪method, *inputs, **kwargs)
   1190 elif uf.__name__ in UFUNCS_MATCHING_DIMENSIONS + UFUNCS_COMPARISONS:
   1191     # Ok if dimension of arguments match (for reductions, they always do)
   1192     if method == "__call__":
-> 1193         fail_for_dimension_mismatch(
   1194             inputs[0],
   1195             inputs[1],
   1196             error_message=(
```

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```
   1197                 "Cannot calculate {val1} %s {val2}, the units do not match"
   1198             )
   1199             % uf.__name__,
   1200             val1=inputs[0],
   1201             val2=inputs[1],
   1202         )
   1203     if uf.__name__ in UFUNCS_COMPARISONS:
   1204         return uf_method(*[np.asarray(i) for i in inputs], **kwargs)

File ~/checkouts/readthedocs.org/user_builds/cleosim/envs/v0.14.1/lib/python3.12/site-
↪packages/brian2/units/fundamentalunits.py:266, in fail_for_dimension_mismatch(obj1,␣
↪obj2, error_message, **error_quantities)
    264         raise DimensionMismatchError(error_message, dim1)
    265     else:
--> 266         raise DimensionMismatchError(error_message, dim1, dim2)
    267 else:
    268     return dim1, dim2

DimensionMismatchError: Cannot calculate [[810.66587861 779.27314261 ... 255.16673068␣
↪278.62607216]
 [119.0777885   87.9475586  ... 852.14088745 884.38357572]
 ...
 [679.139645   646.89460055 ... 289.47648175 321.67306985]
 [ 65.16398162  64.029518   ... 951.3970552  983.58769558]] mm^2 subtract 0. m, the␣
↪units do not match (units are m^2 and m).
```

Stimulation

Stimulator devices manipulate the Brian network, and are likewise *inject()*ed into the simulator, into specified neuron groups. Optogenetics (1P and 2P) is the main stimulation modality currently implemented by Cleo. This requires injection of both a light source and an opsin—see the *Optogenetic stimulation* and *All-optical control* tutorials for more detail.

```
fiber = cleo.light.Light(
    coords=(0, 0, 0.5)*b2.mm,
    light_model=cleo.light.fiber473nm(),
    wavelength=473*b2.nmeter
)
chr2 = cleo.opto.chr2_4s()
sim.inject(fiber, ng).inject(chr2, ng)
```

Note: Markov opsin kinetics models require target neurons to have membrane potentials in realistic ranges and an `Iopto` term defined in amperes. If you need to interface with a model without these features, you may want to use the simplified *ProportionalCurrentOpsin*. You can find more details, including a comparison between the two model types, in the *optogenetics tutorial*.

Note: Recorders and stimulators need unique names which serve as keys to access/set values in the *IOProcessor*'s input/output dictionaries. The name defaults to the class name, but you can specify it on construction.

I/O Processor

Just as in a real experiment where the experiment hardware must be connected to signal processing equipment and/or computers for recording and control, the *CLSimulator* must be connected to an *IOProcessor*. If you are only recording, you may want to use the *RecordOnlyProcessor*. Otherwise you will want to implement the *LatencyIOProcessor*, which not only takes samples at the specified rate, but processes the data and delivers input to the network after a user-defined delay, emulating the latency inherent in real experiments. This is done by creating a subclass and defining the *process()* function:

```
class MyProcessor(cleo.ioproc.LatencyIOProcessor):
    def process(self, state_dict, sample_time_ms):
        # state_dict contains a {'recorder_name': value} dict of network.
        i_spikes, t_ms_spikes, y_spikes = state_dict['Probe']['MultiUnitSpiking']
        # on-off control
        irr0_mW_per_mm2 = 5 if len(i_spikes) < 10 else 0
        # output is a {'stimulator_name': value} dict and output time
        return {'Light': irr0_mW_per_mm2}, sample_time_ms + 3  # (3 ms delay)

sim.set_io_processor(MyProcessor(sample_period_ms=1))
```

The *On-off control*, *PI control*, and *LQR optimal control using ldsctrlest* tutorials give examples of closed-loop control ranging from simple to complex.

Visualization

cleo.viz.plot() allows you to easily visualize your experimental configuration:

```
cleo.viz.plot(ng, colors=['#c500cc'], sim=sim, zlim=(200, 1000))
```

Cleo also features some *video visualization capabilities*.

Running experiments

Use *cleo.CLSimulator.run()* function with the desired duration. This wrap's Brian's `brian2.core.network.Network.run()` function:

```
sim.run(50 * b2.ms)  # kwargs are passed to Brian's run function
```

Use *reset()* to restore the default state (right after initialization/injection) for the network and all devices. This could be useful for running a simulation multiple times under different conditions.

To facilitate access to data after the simulation, devices offer a *cleo.InterfaceDevice.save_history* option on construction, by default `True`. If true, that object will store relevant variables as attributes. For example:

```
import matplotlib.pyplot as plt
fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
ax1.scatter(mua.t_ms, mua.i, marker='.', c='white', s=2)
ax1.set(ylabel='channel index', title='spikes')
ax2.step(fiber.t_ms, fiber.values, c='#72b5f2')
ax2.set(xlabel='time (ms)', ylabel='irradiance (mW/mm$^2$)', title='photostimulation')
```

6.1.4 Design rationale

Why not prototype with more abstract models?

Cleo aims to be practical, and as such provides models at the level of abstraction corresponding to the variables the experimenter has available to manipulate. This means models of spatially defined, spiking neural networks.

Of course, neuroscience is studied at many spatial and temporal scales. While other projects may be better suited for larger segments of the brain and/or longer timescales (such as HNN or BMTK's PopNet or FilterNet), this project caters to finer-grained models because they can directly simulate the effects of alternate experimental configurations. For example, how would the model change when swapping one opsin for another, using multiple opsins simultaneously, or with heterogeneous expression? How does recording or stimulating one cell type vs. another affect the experiment? Would using a more sophisticated control algorithm be worth the extra compute time, and thus later stimulus delivery, compared to a simpler controller?

Questions like these could be answered using an abstract dynamical system model of a neural circuit, but they would require the extra step of mapping the afore-mentioned details to a suitable abstraction—e.g., estimating a transfer function to model optogenetic stimulation for a given opsin and light configuration. Thus, we haven't emphasized these sorts of models so far in our development of Cleo, though they should be possible to implement in Brian if you are interested. For example, one could develop a Poisson linear dynamical system (PLDS), record spiking output, and configure stimulation to act directly on the system's latent state.

And just as experiment prototyping could be done on a more abstract level, it could also be done on an even more realistic level, which we did not deem necessary. That brings us to the next point…

Why Brian?

Brian is a relatively new spiking neural network simulator written in Python. Here are some of its advantages:

- Flexibility: allowing (and requiring!) the user to define models mathematically rather than selecting from a pre-defined library of cell types and features. This enables us to define arbitrary models for recorders and stimulators and easily interface with the simulation
- Ease of use: it's all just Python
- Speed (at least when compiled to C++ or GPU—see Brian2GENN, Brian2CUDA)

NEST is a popular alternative to Brian also strong in point neuron simulations. However, it appears to be less flexible, and thus harder to extend. NEURON is another popular alternative to Brian. Its main advantage is its first-class support of detailed, morphological, multi-compartment neurons. In fact, strong alternatives to Brian for this project were BioNet (docs, paper) and NetPyNE (docs, paper), which already offer a high-level interface to NEURON with extracellular potential recording. Optogenetics could be incorporated with pre-existing .hoc code, though the light model would need to be implemented. From brief examination of the source code of BioNet, it appears that closed-loop stimulation would not be too difficult to add. It is unclear for NetPyNE.

In the end, we chose Brian since our priority was to model circuit/population-level dynamics over molecular/intra-neuron dynamics. Also, Brian does have support for multi-compartment neurons, albeit less fully featured, if that is needed.

PyNN would have been an ideal interface to build around, as it supports multiple simulator backends. The difficulty is, implementing objects not natively supported by SNN simulators (e.g., opsins, calcium indicators, and light source) has required bespoke, idiosyncratic code applicable only to one simulator. To do so in a native, efficient way, as we have attempted to do with Brian, would require significant work. A collaborative effort extending a multi-simulator framework such as PyNN for this purpose may be of value if there is enough community interest in expanding the open-source SNN experiment simulation toolbox.

6.1.5 Future development

Here are some features which are missing but could be useful to add:

- Electrode microstimulation
- A more accurate LFP signal (only usable for morphological neurons) based on the volume conductor forward model as in LFPy or Vertex
- The Mazzoni-Lindén LFP approximation for LIF point-neuron networks
- Voltage indicators
- An expanded calcium indicator library—currently the parameter set for the full NAOMi model is only available for GCaMP6f. The phenomenological S2F model should be easy to implement and fit to data, has parameters for several of the latest and greatest GECIs (jGCaMP7 and jGCaMP8 varieties), and should be cheaper to simulate as well.

6.2 Tutorials

6.2.1 Electrode recording

How to insert electrodes to measure different spiking and extracellular signals from a Brian network simulation.

Preamble:

```
import brian2.only as b2
from brian2 import np
import matplotlib.pyplot as plt
import cleo

# the default cython compilation target isn't worth it for
# this trivial example
b2.prefs.codegen.target = "numpy"
b2.seed(1919)
np.random.seed(1919)

cleo.utilities.style_plots_for_docs()

# colors
c = {
    "light": "#df87e1",
    "main": "#C500CC",
    "dark": "#8000B4",
    "exc": "#d6755e",
    "inh": "#056eee",
    "accent": "#36827F",
}
```

Network setup

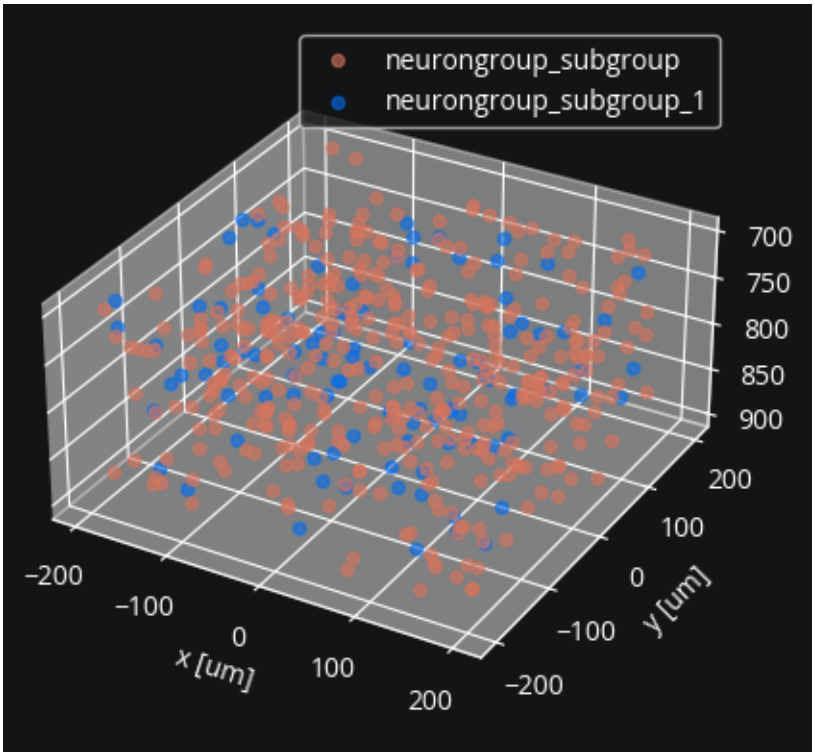
First we create a simple E-I network with external Poisson input and assign coordinates. We only need spiking neurons to record *TKLFPSignal*, but we need synapses onto pyramidal cells for *RWSLFPSignalFromSpikes*.

```
N = 500
n_e = int(N * 0.8)
n_i = int(N * 0.2)
n_ext = N

neurons = b2.NeuronGroup(
    N,
    "dv/dt = -v / (10*ms) : 1",
    threshold="v > 1",
    reset="v = 0",
    refractory=2 * b2.ms,
)
ext_input = b2.PoissonGroup(n_ext, 23 * b2.Hz, name="ext_input")
cleo.coords.assign_coords_rand_rect_prism(
    neurons, xlim=(-0.2, 0.2), ylim=(-0.2, 0.2), zlim=(0.7, 0.9)
)
# need to create subgroups after assigning coordinates
exc = neurons[:n_e]
inh = neurons[n_e:]

w0 = 0.06
syn_exc = b2.Synapses(
    exc,
    neurons,
    f"w = {w0} : 1",
    on_pre="v_post += w",
    name="syn_exc",
    delay=1.5 * b2.ms,
)
syn_exc.connect(p=0.1)
syn_inh = b2.Synapses(
    inh,
    neurons,
    f"w = -4*{w0} : 1",
    on_pre="v_post += w",
    name="syn_inh",
    delay=1.5 * b2.ms,
)
syn_inh.connect(p=0.1)
syn_ext = b2.Synapses(
    ext_input, neurons, "w = .05 : 1", on_pre="v_post += w", name="syn_ext"
)
syn_ext.connect(p=0.1)

net = b2.Network([neurons, exc, inh, syn_exc, syn_inh, ext_input, syn_ext])
sim = cleo.CLSimulator(net)
cleo.viz.plot(exc, inh, colors=[c["exc"], c["inh"]], scatterargs={"alpha": 0.6});
```



Specifying electrode coordinates

Now we insert an electrode shank probe in the center of the population by injecting a *Probe* device. Note that *Probe* takes arbitrary coordinates as arguments, so you can place contacts wherever you wish. However, the *cleo.ephys* module provides convenience functions to easily generate coordinates common in NeuroNexus probes. Here are some examples:

```
from cleo import ephys
from mpl_toolkits.mplot3d import Axes3D

array_length = 0.4 * b2.mm  # length of the array itself, not the shank
tetr_coords = ephys.tetrode_shank_coords(array_length, tetrode_count=3)
poly2_coords = ephys.poly2_shank_coords(
    array_length, channel_count=32, intercol_space=50 * b2.um
)
poly3_coords = ephys.poly3_shank_coords(
    array_length, channel_count=32, intercol_space=30 * b2.um
)
# by default start_location (location of first contact) is at (0, 0, 0)
single_shank = ephys.linear_shank_coords(
    array_length, channel_count=8, start_location=(-0.2, 0, 0) * b2.mm
)
# tile vector determines length and direction of tiling (repeating)
multishank = ephys.tile_coords(
    single_shank, num_tiles=3, tile_vector=(0.4, 0, 0) * b2.mm
)

fig = plt.figure(figsize=(8, 8))
```

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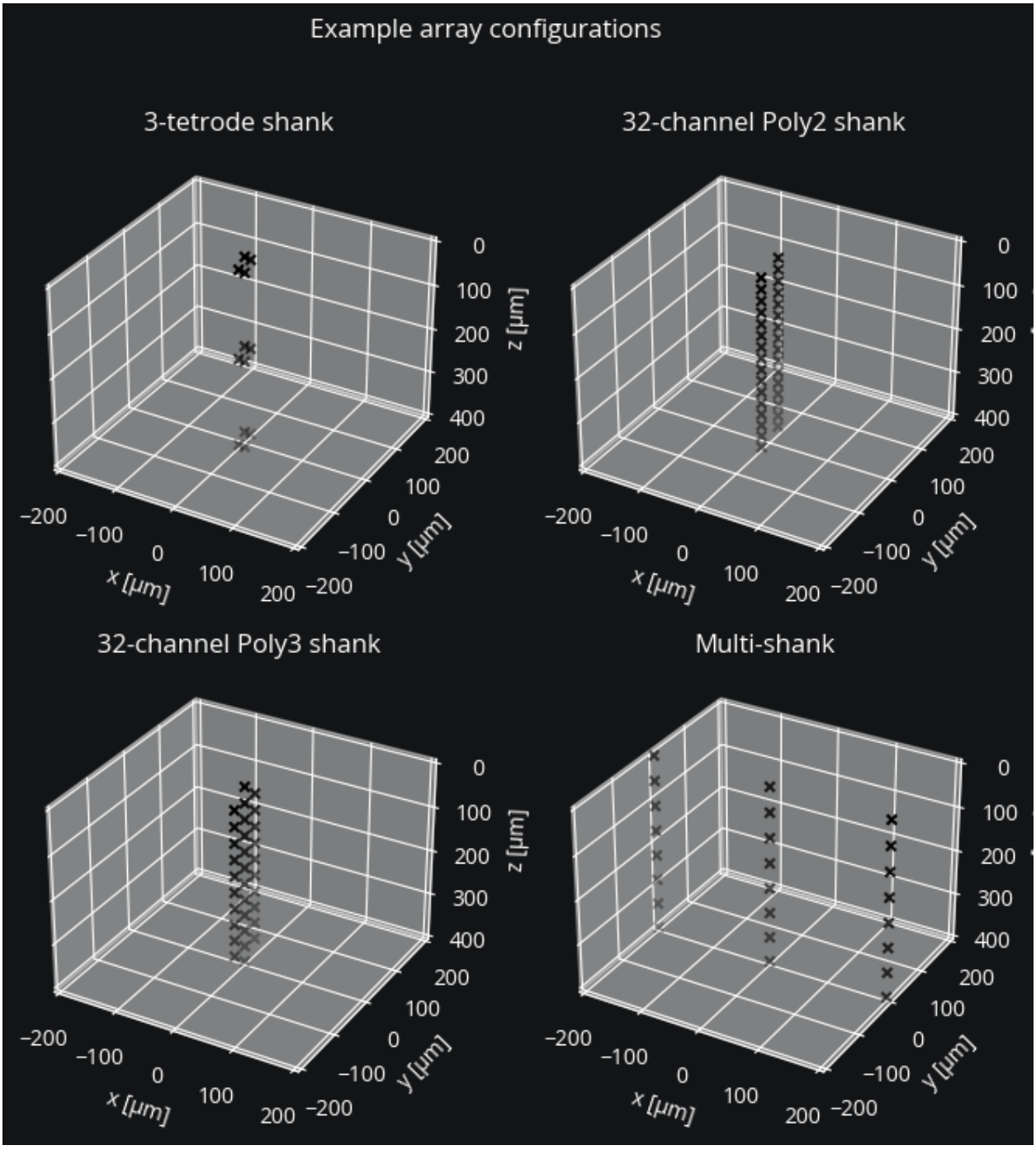
```
fig.suptitle("Example array configurations")
for i, (coords, title) in enumerate(
    [
        (tetr_coords, "3-tetrode shank"),
        (poly2_coords, "32-channel Poly2 shank"),
        (poly3_coords, "32-channel Poly3 shank"),
        (multishank, "Multi-shank"),
    ],
    start=1,
):
    ax = fig.add_subplot(2, 2, i, projection="3d")
    x, y, z = coords.T / b2.um
    ax.scatter(x, y, z, marker="x", c="black")
    ax.set(
        title=title,
        xlabel="x [m]",
        ylabel="y [m]",
        zlabel="z [m]",
        xlim=(-200, 200),
        ylim=(-200, 200),
        zlim=(400, 0),
    )
```

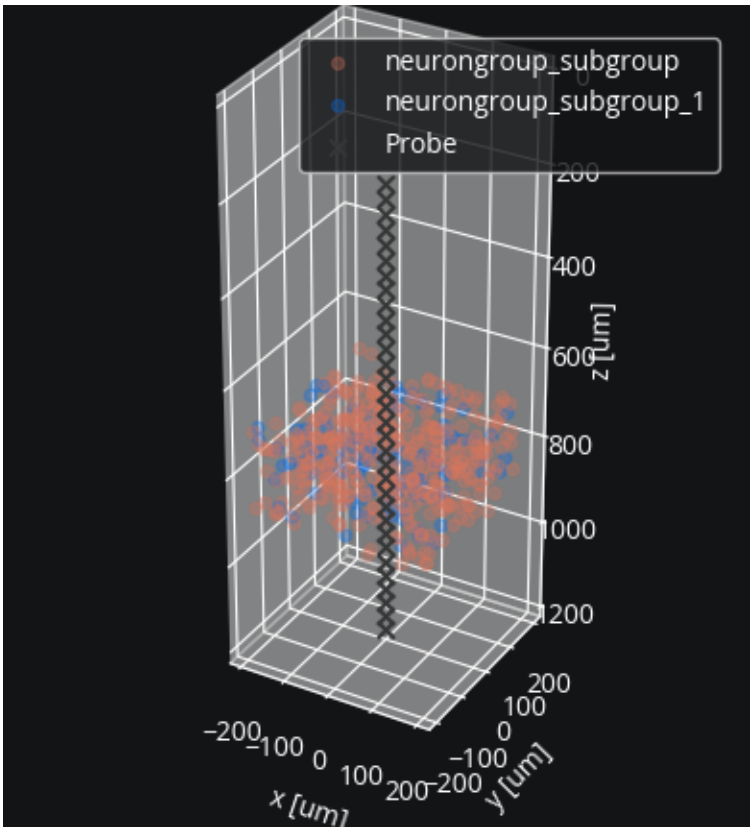


As seen above, the *tile_coords()* function can be used to repeat a single shank to produce coordinates for a multi-shank probe. Likewise it can be used to repeat multi-shank coordinates to achieve a 3D recording array (what NeuroNexus calls a MatrixArray).

For our example we will use a simple linear array. We configure the probe so it has 32 contacts ranging from 0.2 to 1.2 mm in depth. We could specify the orientation, but by default shank coordinates extend downwards (in the positive z direction).

We can add the electrode to the plotting function to visualize it along with the neurons:

```
coords = ephys.linear_shank_coords(1 * b2.mm, 32, start_location=(0, 0, 0.2) * b2.mm)
probe = ephys.Probe(coords, save_history=True)
cleo.viz.plot(
    exc,
    inh,
    colors=[c["exc"], c["inh"]],
    zlim=(0, 1200),
    devices=[probe],
    scatterargs={"alpha": 0.3},
);
```



Specifying signals to record

This looks right, but we need to specify what signals we want to pick up with our electrode. Let's try the two basic spiking signals and an LFP approximation for point neurons.

The two spiking signals (sorted and multi-unit) take the same parameters, mainly *r_perfect_detection*, within which all spikes will be detected, and *r_half_detection*, at which distance a spike has only a 50% chance of being detected. My choice to set these parameters at 50 and 100 m is arbitary, though from at least some published data that seems reasonable.

We use default parameters for the Teleńczuk kernel LFP approximation method (TKLFP), but will need to specify cell type (excitatory or inhibitory) and sampling period (if unavailable from a connected IO processor) upon injection.

The reference weighted sum of synaptic currents LFP proxy (RWSLFP) requires synaptic currents, which we synthesize by convolving spikes with a biexponential kernel. We need to pass in `ampa_syns` and `gaba_syns` on injection to compute the effect of incoming spikes on the population we're recording from. We only need to do this for pyramidal

cells, since RWSLFP ignores currents onto interneurons.

```
mua = ephys.MultiUnitSpiking(
    r_perfect_detection=0.05 * b2.mm,
    r_half_detection=0.1 * b2.mm,
)
ss = ephys.SortedSpiking(0.05 * b2.mm, 0.1 * b2.mm)
tklfp = ephys.TKLFPSignal()
rwslfp = ephys.RWSLFPSignalFromSpikes()

probe.add_signals(mua, ss, tklfp, rwslfp)

sim.set_io_processor(cleo.ioproc.RecordOnlyProcessor(sample_period_ms=1))
sim.inject(
    probe,
    exc,
    tklfp_type="exc",
    ampa_syns=[syn_exc[f"j < {n_e}"], syn_ext[f"j < {n_e}"]],
    gaba_syns=[syn_inh[f"j < {n_e}"]],
)
sim.inject(probe, inh, tklfp_type="inh")
```

```
CLSimulator(io_processor=RecordOnlyProcessor(sample_period_ms=1, sampling='fixed',␣
↪processing='parallel'), devices={Probe(name='Probe', save_history=True,␣
↪signals=[MultiUnitSpiking(name='MultiUnitSpiking', brian_objects={<SpikeMonitor,␣
↪recording from 'spikemonitor_6'>, <SpikeMonitor, recording from 'spikemonitor'>},␣
↪probe=..., r_perfect_detection=50. * umetre, r_half_detection=100. * umetre, cutoff_
↪probability=0.01), SortedSpiking(name='SortedSpiking', brian_objects={<SpikeMonitor,␣
↪recording from 'spikemonitor_1'>, <SpikeMonitor, recording from 'spikemonitor_7'>},␣
↪probe=..., r_perfect_detection=50. * umetre, r_half_detection=100. * umetre, cutoff_
↪probability=0.01), TKLFPSignal(name='TKLFPSignal', brian_objects={<SpikeMonitor,␣
↪recording from 'spikemonitor_2'>, <SpikeMonitor, recording from 'spikemonitor_8'>},␣
↪probe=..., uLFP_threshold_uV=0.001, _lfp_unit=uvolt), RWSLFPSignalFromSpikes(name=
↪'RWSLFPSignalFromSpikes', brian_objects={<SpikeMonitor, recording from 'spikemonitor_5
↪'>, <SpikeMonitor, recording from 'spikemonitor_4'>, <SpikeMonitor, recording from
↪'spikemonitor_3'>}, probe=..., amp_func=<function mazzoni15_nrn at 0x7faa69039080>,␣
↪pop_aggregate=False, _lfp_unit=1, tau1_ampa=2. * msecond, tau2_ampa=0.4 * msecond,␣
↪tau1_gaba=5. * msecond, tau2_gaba=250. * usecond, syn_delay=1. * msecond, I_
↪threshold=0.001, weight='w')], probe=NOTHING)})
```

Simulation and results

Now we'll run the simulation:

```
sim.run(250 * b2.ms)
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'exact' (took 0.18s). [brian2.stateupdaters.base.method_choice]
```

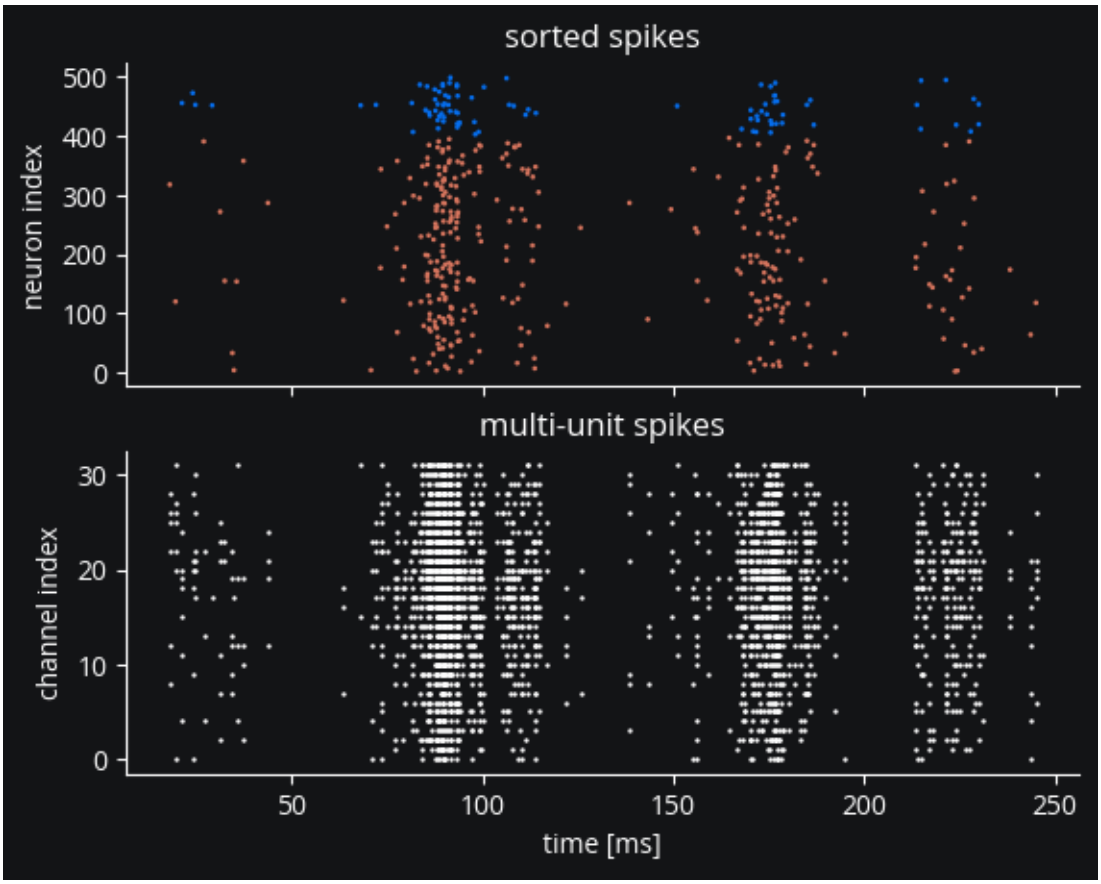
And plot the output of the four signals we've recorded:

```
from matplotlib.colors import ListedColormap, LinearSegmentedColormap

fig, axs = plt.subplots(2, 1, sharex=True)

# assuming all neurons are detectable for c=ss.i >= n_e to work
# in practice this will often not be the case and we'd have to map
# from probe index to neuron group index using ss.i_probe_by_i_ng.inverse
exc_inh_cmap = ListedColormap([c["exc"], c["inh"]])
axs[0].scatter(ss.t_ms, ss.i, marker=".", c=ss.i >= n_e, cmap=exc_inh_cmap, s=3)
axs[0].set(title="sorted spikes", ylabel="neuron index")

axs[1].scatter(mua.t_ms, mua.i, marker=".", s=2, c="white")
axs[1].set(title="multi-unit spikes", ylabel="channel index", xlabel="time [ms]");
```



TKLFP supposedly outputs a value with an absolute scale in terms of V, though it is quite high compared to ±0.1 V scale of RWSLFP as given in Mazzoni, Lindén et al., 2015. RWSLFP outputs unnormalized LFP instead of this ±0.1 V range to sidestep the complications of normalizing in a causal, stepwise manner.

```
fig, axs = plt.subplots(1, 2, figsize=(6, 7), sharey=True, layout="constrained")
channel_offsets = -12 * np.arange(probe.n)
lfp_to_plot = tklfp.lfp / b2.uvolt + channel_offsets
axs[0].plot(lfp_to_plot, color="w", lw=1)
axs[0].set(
    yticks=channel_offsets,
    yticklabels=range(1, 33),
```

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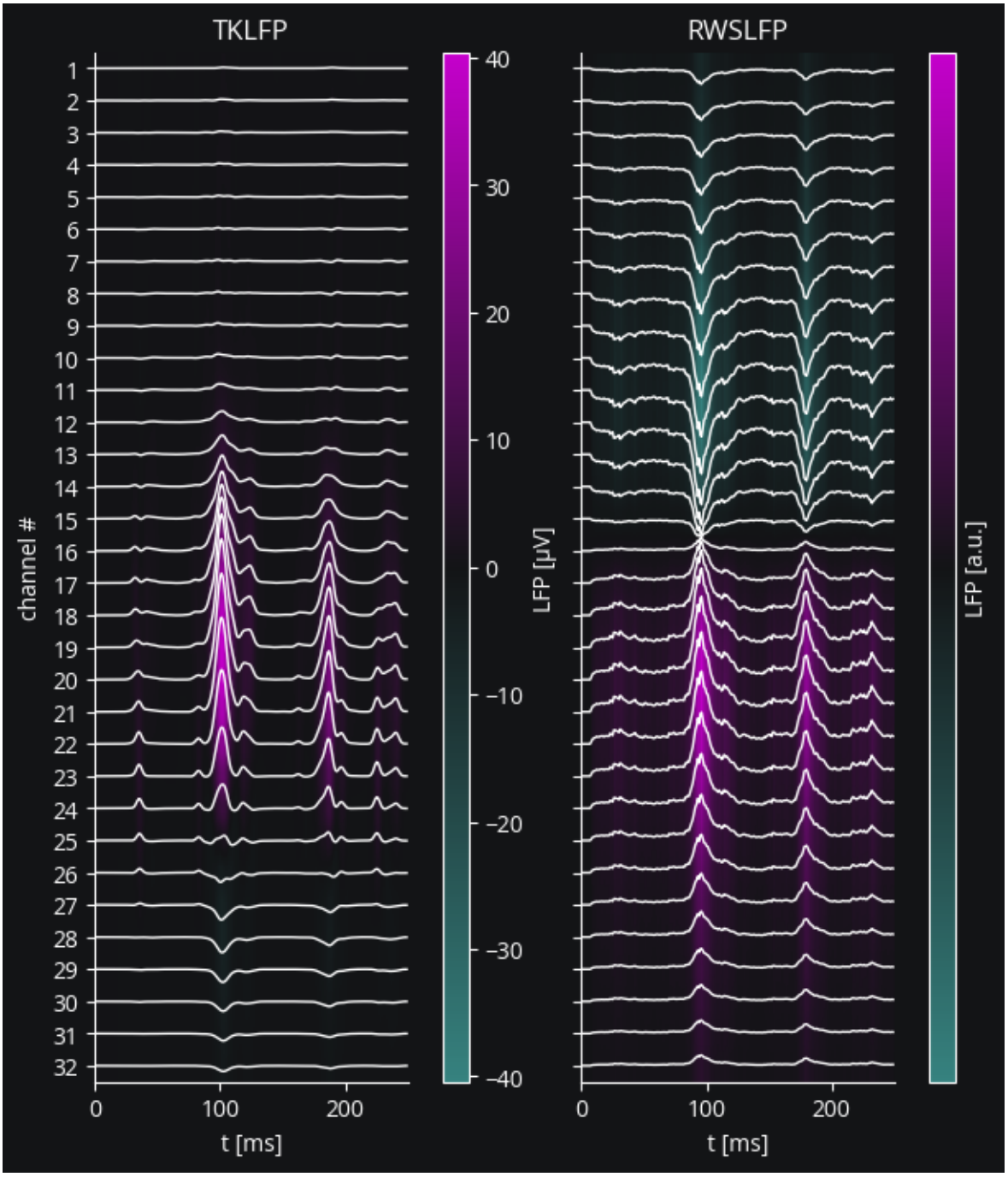
```
    xlabel="t [ms]",
    ylabel="channel #",
    title="TKLFP",
)

axs[1].plot(rwslfp.lfp + channel_offsets, color="w", lw=1)
axs[1].set(title="RWSLFP", xlabel="t [ms]")

extent = (0, 250, channel_offsets.min() - 6, channel_offsets.max() + 6)
cmap = LinearSegmentedColormap.from_list("lfp", [c["accent"], "#131416", c["main"]])
im1 = axs[0].imshow(
    tklfp.lfp.T / b2.uvolt,
    aspect="auto",
    cmap=cmap,
    extent=extent,
    vmin=-np.max(np.abs(tklfp.lfp / b2.uvolt)),
    vmax=np.max(np.abs(tklfp.lfp / b2.uvolt)),
)
fig.colorbar(im1, aspect=40, label="LFP [V]")
im2 = axs[1].imshow(
    rwslfp.lfp.T,
    aspect="auto",
    cmap=cmap,
    extent=extent,
    vmin=-np.max(np.abs(rwslfp.lfp)),
    vmax=np.max(np.abs(rwslfp.lfp)),
)
fig.colorbar(im2, aspect=40, label="LFP [a.u.]", ticks=[]);
```



See *Advanced LFP* for more options and comparison of different LFP signals.

6.2.2 Optogenetic stimulation

How to inject an optogenetic intervention (opsin and optic fiber) into a simulation.

Preamble:

```
%load_ext autoreload
%autoreload 2
from brian2 import *
import matplotlib.pyplot as plt

import cleo
from cleo import *

cleo.utilities.style_plots_for_docs()

# numpy faster than cython for lightweight example
prefs.codegen.target = 'numpy'
# for reproducibility
np.random.seed(1866)
```

```
The autoreload extension is already loaded. To reload it, use:
  %reload_ext autoreload
```

Create a Markov opsin-compatible network

Cleo enables two basic approaches to modeling opsin currents. One is a fairly accurate Markov state model and the other is a simple proportional current model. We will look at the Markov model here.

The established Markov opsin models (as presented in Evans et al., 2016), are conductance-based and so depend on somewhat realistic membrane voltages. Hence, we'll use the exponential integrate-and-fire (EIF) model. Note that we follow the conventions used in neuron modeling, where current is positive, rather than the conventions in opsin modeling, where the photocurrent is negative.

We'll use a small neuron group, biased by Poisson input spikes.

```
n = 10
ng = NeuronGroup(
    n,
    """
    dv/dt = (-(v - E_L) + Delta_T*exp((v-theta)/Delta_T) + Rm*I) / tau_m : volt
    I : amp
    """,
    threshold="v>30*mV",
    reset="v=-55*mV",
    namespace={
        "tau_m": 20 * ms,
        "Rm": 500 * Mohm,
        "theta": -50 * mV,
        "Delta_T": 2 * mV,
        "E_L": -70*mV,
    },
)
ng.v = -70 * mV
```

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```
input_group = PoissonInput(ng, "v", n, 100 * Hz, 1 * mV)

mon = SpikeMonitor(ng)

net = Network(ng, input_group, mon)
ng.equations
```

$$\frac{\mathrm{d}v}{\mathrm{d}t} = \frac{\Delta_T e^{\frac{-\theta+v}{\Delta_T}} + E_L + IRm - v}{\tau_m} \qquad \text{(unit of } v\text{: V)}$$

$$I \qquad \text{(unit: A)}$$

Assign coordinates and configure optogenetic model

The `OptogeneticIntervention` class implements the chosen opsin kinetics model with specified parameters. A standard four-state Markov model as well as channelrhodopsin-2 (ChR2) parameters are included with cleo and are accessible in the `cleo.opto` module. For extending to other models (such as three-state or six-state), see the source code—the state equations, opsin-specific parameters, and light wavelength-specific parameters (if not using 473-nm blue) would be needed.

For reference, cleo draws heavily on Foutz et al., 2012 for the light propagation model and on Evans et al., 2016 for the opsin kinetics model.

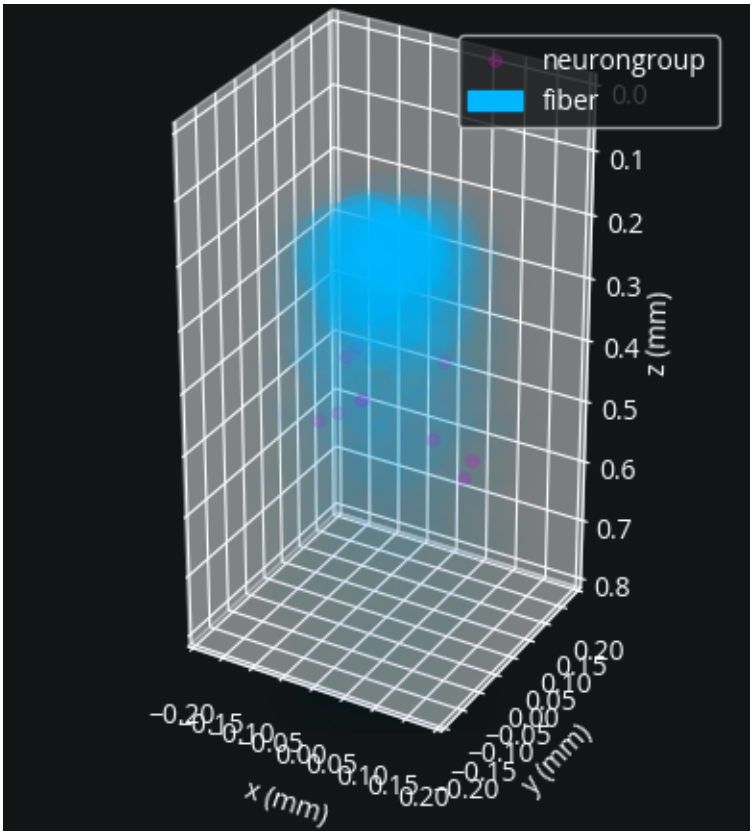
```
from cleo.coords import assign_coords_rand_rect_prism
from cleo.opto import *
from cleo.light import *

assign_coords_rand_rect_prism(ng, xlim=(-0.1, 0.1), ylim=(-0.1, 0.1), zlim=(0.4, 0.6))

opsin = chr2_4s()
fiber = Light(
    coords=(0, 0, 0.2) * mm,
    light_model=fiber473nm(),
    name="fiber",
)

cleo.viz.plot(
    ng,
    colors=["xkcd:fuchsia"],
    xlim=(-0.2, 0.2),
    ylim=(-0.2, 0.2),
    zlim=(0, 0.8),
    devices=[fiber],
)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (mm)', ylabel='y (mm)', zlabel='z (mm)'>)
```



Open-loop optogenetic stimulation

We need to inject our optogenetic intervention into the simulator. `cleo` handles all the object creation and equations needed to interact with the existing Brian model without the need to alter it, with the possible exception of adding a variable to represent the opsin current. This needs to be specified upon injection with `Iopto_var_name=...` if not the default `Iopto`. The membrane potential variable name also needs to be specified (with `v_var_name=...`) if not the default `v`.

```
sim = CLSimulator(net)
sim.inject(opsin, ng, Iopto_var_name='I')
sim.inject(fiber, ng)
```

```
CLSimulator(io_processor=None, devices={FourStateOpsin(brian_objects=
↪{NeuronGroup(clock=Clock(dt=100. * usecond, name='defaultclock'), when=start, order=0,␣
↪name='light_agg_ChR2_neurongroup'), Synapses(clock=Clock(dt=100. * usecond, name=
↪'defaultclock'), when=start, order=0, name='syn_ChR2_neurongroup')}, sim=..., name=
↪'ChR2', save_history=True, spectrum=[(400, 0.34), (422, 0.65), (460, 0.96), (470, 1),␣
↪(473, 1), (500, 0.57), (520, 0.22), (540, 0.06), (560, 0.01)], required_vars=[('Iopto',
↪ amp), ('v', volt)], g0=114. * nsiemens, gamma=0.00742, phim=2.33e+23 * (second ** -1)␣
↪/ (meter ** 2), k1=4.15 * khertz, k2=0.868 * khertz, p=0.833, Gf0=37.3 * hertz, kf=58.
↪1 * hertz, Gb0=16.1 * hertz, kb=63. * hertz, q=1.94, Gd1=105. * hertz, Gd2=13.8 *␣
↪hertz, Gr0=0.33 * hertz, E=0. * volt, v0=43. * mvolt, v1=17.1 * mvolt, model="\n      ␣
↪ dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\n        dO1/dt = Ga1*C1 + Gb*O2␣
↪- (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt = Ga2*C2 + Gf*O1 - (Gd2+Gb)*O2 : 1␣
↪(clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n        Theta = int(phi_pre >␣
```

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```
↪0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_pre**p + phim**p) : 1\n       ␣
↪Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n        Hq = Theta * phi_pre**q/(phi_
↪pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\n        Gb = kb*Hq + Gb0 :␣
↪hertz\n\n        fphi = O1 + gamma*O2 : 1\n        # v1/v0 when v-E == 0 via l'Hopital
↪'s rule\n        fv = f_unless_x0(\n            (1 - exp(-(V_VAR_NAME_post-E)/v0)) /␣
↪((V_VAR_NAME_post-E)/v1),\n            V_VAR_NAME_post - E,\n            v1/v0\n      ␣
↪ ) : 1\n\n        IOPTO_VAR_NAME_post = -g0*fphi*fv*(V_VAR_NAME_post-E)*rho_rel :␣
↪ampere (summed)\n        rho_rel : 1", extra_namespace={'f_unless_x0': <brian2.core.
↪functions.Function object at 0x7fa988672c80>}), Light(brian_objects=set(), sim=...,␣
↪name='fiber', save_history=True, value=array([0.]), light_model=OpticFiber(R0=100. *␣
↪umetre, NAfib=0.37, K=125. * metre ** -1, S=7370. * metre ** -1, ntis=1.36),␣
↪coords=array([[  0.,   0., 200.]]) * umetre, wavelength=0.473 * umetre,␣
↪direction=array([0., 0., 1.]), max_Irr0_mW_per_mm2=None, max_Irr0_mW_per_mm2_viz=None,␣
↪default_value=array([0.]))})
```

IO processor setup

Here we design an IO processor that ignores measurements and simply sets the light intensity according to the `stimulus(t)` function:

```
from cleo.ioproc import LatencyIOProcessor

def stimulus(time_ms):
    f = 30
    return 1 * (1 + np.sin(2*np.pi*f * time_ms/1000))

class OpenLoopOpto(LatencyIOProcessor):
    def __init__(self):
        super().__init__(sample_period_ms=1)

    # since this is open-loop, we don't use state_dict
    def process(self, state_dict, time_ms):
        opto_intensity = stimulus(time_ms)
        # return output dict and time
        return ({"fiber": opto_intensity}, time_ms)

sim.set_io_processor(OpenLoopOpto())
```

```
CLSimulator(io_processor=<__main__.OpenLoopOpto object at 0x7fa986024280>, devices=
↪{FourStateOpsin(brian_objects={NeuronGroup(clock=Clock(dt=100. * usecond, name=
↪'defaultclock'), when=start, order=0, name='light_agg_ChR2_neurongroup'),␣
↪Synapses(clock=Clock(dt=100. * usecond, name='defaultclock'), when=start, order=0,␣
↪name='syn_ChR2_neurongroup')}, sim=..., name='ChR2', save_history=True, spectrum=[(400,
↪ 0.34), (422, 0.65), (460, 0.96), (470, 1), (473, 1), (500, 0.57), (520, 0.22), (540,␣
↪0.06), (560, 0.01)], required_vars=[('Iopto', amp), ('v', volt)], g0=114. * nsiemens,␣
↪gamma=0.00742, phim=2.33e+23 * (second ** -1) / (meter ** 2), k1=4.15 * khertz, k2=0.
↪868 * khertz, p=0.833, Gf0=37.3 * hertz, kf=58.1 * hertz, Gb0=16.1 * hertz, kb=63. *␣
↪hertz, q=1.94, Gd1=105. * hertz, Gd2=13.8 * hertz, Gr0=0.33 * hertz, E=0. * volt,␣
↪v0=43. * mvolt, v1=17.1 * mvolt, model="\n        dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 :␣
↪1 (clock-driven)\n        dO1/dt = Ga1*C1 + Gb*O2 - (Gd1+Gf)*O1 : 1 (clock-driven)\n  ␣
```

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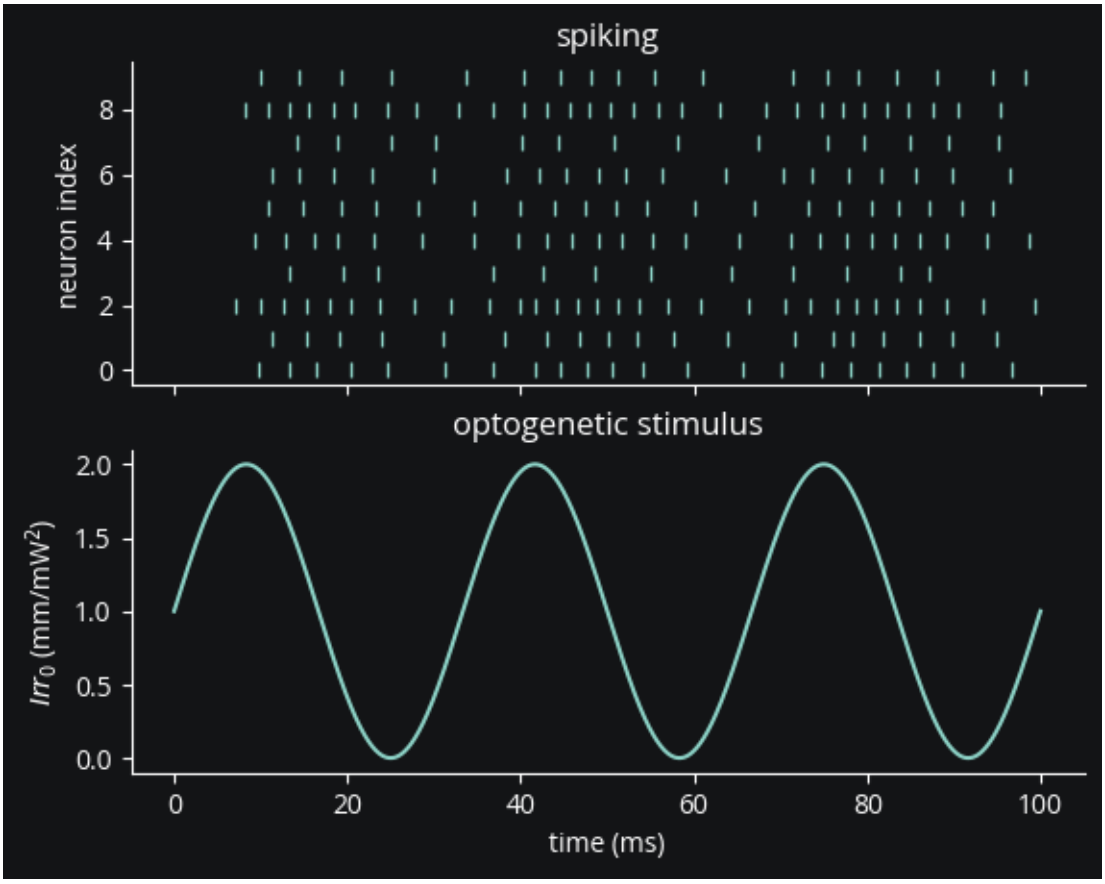
```
↪     dO2/dt = Ga2*C2 + Gf*O1 - (Gd2+Gb)*O2 : 1 (clock-driven)\n        C2 = 1 - C1 -␣
↪O1 - O2 : 1\n\n        Theta = int(phi_pre > 0*phi_pre) : 1\n        Hp = Theta * phi_
↪pre**p/(phi_pre**p + phim**p) : 1\n        Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp :␣
↪hertz\n        Hq = Theta * phi_pre**q/(phi_pre**q + phim**q) : 1\n        Gf = kf*Hq␣
↪+ Gf0 : hertz\n        Gb = kb*Hq + Gb0 : hertz\n\n        fphi = O1 + gamma*O2 : 1\n ␣
↪      # v1/v0 when v-E == 0 via l'Hopital's rule\n        fv = f_unless_x0(\n         ␣
↪  (1 - exp(-(V_VAR_NAME_post-E)/v0)) / ((V_VAR_NAME_post-E)/v1),\n            V_VAR_
↪NAME_post - E,\n            v1/v0\n        ) : 1\n\n        IOPTO_VAR_NAME_post = -
↪g0*fphi*fv*(V_VAR_NAME_post-E)*rho_rel : ampere (summed)\n        rho_rel : 1", extra_
↪namespace={'f_unless_x0': <brian2.core.functions.Function object at 0x7fa988672c80>}),␣
↪Light(brian_objects=set(), sim=..., name='fiber', save_history=True, value=array([0.]),
↪ light_model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=125. * metre ** -1, S=7370. *␣
↪metre ** -1, ntis=1.36), coords=array([[  0.,   0., 200.]]) * umetre, wavelength=0.473␣
↪* umetre, direction=array([0., 0., 1.]), max_Irr0_mW_per_mm2=None, max_Irr0_mW_per_mm2_
↪viz=None, default_value=array([0.]))})
```

Run simulation and plot results

```
sim.run(100*ms)

fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
ax1.plot(mon.t / ms, mon.i[:], '|')
ax1.set(ylabel='neuron index', title='spiking')
t_sim=np.linspace(0, 100, 1000)
ax2.plot(t_sim, stimulus(t_sim))
ax2.set(ylabel=r'$Irr_0$ (mm/mW$^2$)', title='optogenetic stimulus', xlabel='time (ms)');
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'euler' (took 0.01s, trying other methods took 0.04s). [brian2.stateupdaters.
↪base.method_choice]
INFO       No numerical integration method specified for group 'syn_ChR2_neurongroup',␣
↪using method 'euler' (took 0.02s, trying other methods took 0.05s). [brian2.
↪stateupdaters.base.method_choice]
```




```
opsin.synapses[ng.name].equations
```

$$C2 = -C_1 - O_1 - O_2 + 1 \quad \text{(unit of } C_2\text{: rad)}$$
$$Theta = \text{int}\left(\phi_{pre} > 0\right) \quad \text{(unit of } \Theta\text{: rad)}$$
$$fphi = O_1 + O_2\gamma \quad \text{(unit of } fphi\text{: rad)}$$
$$fv = f_{unlessx0}\left(\frac{v_1 \cdot \left(1 - e^{\frac{E - v_{post}}{v_0}}\right)}{-E + v_{post}}, -E + v_{post}, \frac{v_1}{v_0}\right) \quad \text{(unit of } fv\text{: rad)}$$
$$Hp = \frac{\Theta \phi_{pre}^{p}}{\phi_{pre}^{p} + phim^{p}} \quad \text{(unit of } Hp\text{: rad)}$$
$$Hq = \frac{\Theta \phi_{pre}^{q}}{\phi_{pre}^{q} + phim^{q}} \quad \text{(unit of } Hq\text{: rad)}$$
$$Ga1 = Hpk_1 \quad \text{(unit of } Ga_1\text{: Hz)}$$
$$Ga2 = Hpk_2 \quad \text{(unit of } Ga_2\text{: Hz)}$$
$$Gf = Gf_0 + Hqkf \quad \text{(unit of } Gf\text{: Hz)}$$
$$Gb = Gb_0 + Hqkb \quad \text{(unit of } Gb\text{: Hz)}$$
$$\frac{\mathrm{d}C_1}{\mathrm{d}t} = -C_1 Ga_1 + C_2 Gr_0 + Gd_1 O_1 \quad \text{(unit of } C_1\text{: rad, flags: clock-driven)}$$
$$\frac{\mathrm{d}O_1}{\mathrm{d}t} = C_1 Ga_1 + GbO_2 - O_1\left(Gd_1 + Gf\right) \quad \text{(unit of } O_1\text{: rad, flags: clock-driven)}$$
$$\frac{\mathrm{d}O_2}{\mathrm{d}t} = C_2 Ga_2 + GfO_1 - O_2\left(Gb + Gd_2\right) \quad \text{(unit of } O_2\text{: rad, flags: clock-driven)}$$
$$\rho_{rel} \quad \text{(unit: rad)}$$

Conclusion

We can see clearly that firing rate correlates with light intensity as expected.

As a recap, in this tutorial we've seen how to:

- configure an `OptogeneticIntervention`,
- inject it into the simulation,
- and control its light intensity in an open-loop fashion.

Appendix: alternative opsin and neuron models

Because it would be a pain and an obstacle to reproducibility to have to replace all pre-existing simple neuron models with more sophisticated ones with proper voltage ranges and units, we provide an approximation that is much more flexible, requiring only a current term, of any unit, in the target neurons.

The Markov models of opsin dynamics we've used so far produce a rise, peak, and fall to a steady-state plateau current when subjected to sustained light. Since they are conductance-based, the current also varies with membrane voltage, including during spikes. The `ProportionalCurrentModel`, on the other hand, simply delivers current proportional to light intensity. This should be adequate for a wide range of use cases where the exact opsin current dynamics on short timescales don't matter so much and a sort of average current-light relationship will suffice.

Speaking of realistic membrane voltages, does the Markov model's voltage-dependent current render it unsuitable for the most basic leaky integrate-and-fire (LIF) neuron model? LIF neurons reset on reaching their rheobase threshold,

staying perpetually in a subthreshold region producing exaggerated opsin currents. How much does this affect the output? We will explore this question by comparing a variety of opsin/neuron model combinations.

First, we introduce exponential integrate-and-fire neurons, which maintain simplicity while modeling an upward membrane potential swing during a spike. For more info, see the related section in the Neuronal Dynamics online textbook and their example parameters table.

```
neuron_params = {
    "tau_m": 20 * ms,
    "Rm": 500 * Mohm,
    "theta": -50 * mV,
    "Delta_T": 2 * mV,
    "E_L": -70*mV,
}

def prep_ng(ng, neuron_type, markov_opsin):
    ng.v = neuron_params['E_L']
    assign_coords_rand_rect_prism(ng, xlim=(0, 0), ylim=(0, 0), zlim=(0, 0))
    state_mon = StateMonitor(ng,("Iopto", "v"), record=True)
    spike_mon = SpikeMonitor(ng)
    return neuron_type, ng, state_mon, spike_mon, markov_opsin

experiments = []

eif = NeuronGroup(
    1,
    """
    dv/dt = (-(v - E_L) + Delta_T*exp((v-theta)/Delta_T) + Rm*Iopto) / tau_m : volt
    Iopto : amp
    """,
    threshold="v > -10*mV",
    reset="v = E_L - 0*mV",
    namespace=neuron_params,
)

experiments.append(prep_ng(eif, 'EIF', True))
```

Configure LIF models

Here we define LIF neurons with biological parameters for the sake of comparison, but the `ProportionalCurrentModel` is compatible with models of any voltage range and units, so long as it has an `Iopto` term.

```
def prep_lif(markov_opsin):
    ng = NeuronGroup(
        1,
        """dv/dt = (-(v - E_L) + Rm*Iopto) / tau_m : volt
        Iopto : amp""",
        threshold="v > theta + 4*mV",
        reset="v = E_L - 0*mV",
        namespace=neuron_params,
    )
    return prep_ng(ng, "LIF", markov_opsin)
```

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```
experiments.append(prep_lif(True))
experiments.append(prep_lif(False))
```

Comparing to more realistic models

To see how well simplified neuron and opsin models do, we'll also compare to the more complex AdEx neuron (with "tonic" firing pattern parameters) and a Hodgkin-Huxley model (code from Neuronal Dynamics).

```
adex = NeuronGroup(
    1,
    """dv/dt = (-(v - E_L) + 2*mV*exp((v-theta)/Delta_T) + Rm*(Iopto-w)) / tau_m : volt
    dw/dt = (0*nsiemens*(v-E_L) - w) / (100*ms) : amp
    Iopto : amp""",
    threshold="v>=-10*mV",
    reset="v=-55*mV; w+=5*pamp",
    namespace=neuron_params,
)
experiments.append(prep_ng(adex, "AdEx", True))

# Parameters
# Cm = 1*ufarad*cm**-2 * area
Cm = neuron_params["tau_m"] / neuron_params["Rm"]
# area = 5000*umetre**2
area = Cm / (1*ufarad*cm**-2)
gl = 0.3*msiemens*cm**-2 * area
El = -65*mV
EK = -90*mV
ENa = 50*mV
g_na = 40*msiemens*cm**-2 * area
g_kd = 35*msiemens*cm**-2 * area
VT = -63*mV

# The model
eqs = Equations('''
dv/dt = (gl*(El-v) - g_na*(m*m*m)*h*(v-ENa) - g_kd*(n*n*n*n)*(v-EK) + Iopto)/Cm : volt
dm/dt = 0.32*(mV**-1)*4*mV/exprel((13.*mV-v+VT)/(4*mV))/ms*(1-m)-0.28*(mV**-1)*5*mV/
↪exprel((v-VT-40.*mV)/(5*mV))/ms*m : 1
dn/dt = 0.032*(mV**-1)*5*mV/exprel((15.*mV-v+VT)/(5*mV))/ms*(1.-n)-.5*exp((10.*mV-v+VT)/
↪(40.*mV))/ms*n : 1
dh/dt = 0.128*exp((17.*mV-v+VT)/(18.*mV))/ms*(1.-h)-4./(1+exp((40.*mV-v+VT)/(5.*mV)))/
↪ms*h : 1
Iopto : amp
''')
# Threshold and refractoriness are only used for spike counting
hh = NeuronGroup(1, eqs,
                 threshold='v > -40*mV',
                 reset='',
                 method='exponential_euler')

experiments.append(prep_ng(hh, "HH", True))
```

Opsin configuration

Note that the only parameter we need to set for the simple opsin model is the gain on light intensity, `I_per_Irr`. This term defines what the neuron receives for every 1 mW/mm2 of light intensity. Here that term is defined in amperes, but it could have been unitless for a simpler model.

The gain is tuned somewhat by hand (in relation to the membrane resistance and the 20 mV gap between rest and threshold potential) to achieve similar outputs to the Markov model.

```
light = Light(light_model=fiber473nm())
simple_opsin = ProportionalCurrentOpsin(
    name="simple_opsin",
    # handpicked gain to make firing rate roughly comparable to EIF
    I_per_Irr=140/neuron_params['Rm']*20*mV,
)
markov_opsin = chr2_4s()
markov_opsin.name = "markov_opsin"
```

Simulation

And we set up the simulator:

```
net = Network()
sim = CLSimulator(net)
for ng_type, ng, state_mon, spike_mon, use_markov_opsin in experiments:
    net.add(ng, state_mon, spike_mon)
    sim.inject(light, ng)
    if use_markov_opsin:
        sim.inject(markov_opsin, ng)
    else:
        sim.inject(simple_opsin, ng)
```

We'll now run the simulation with light pulses of increasing amplitudes to observe the effect on the current.

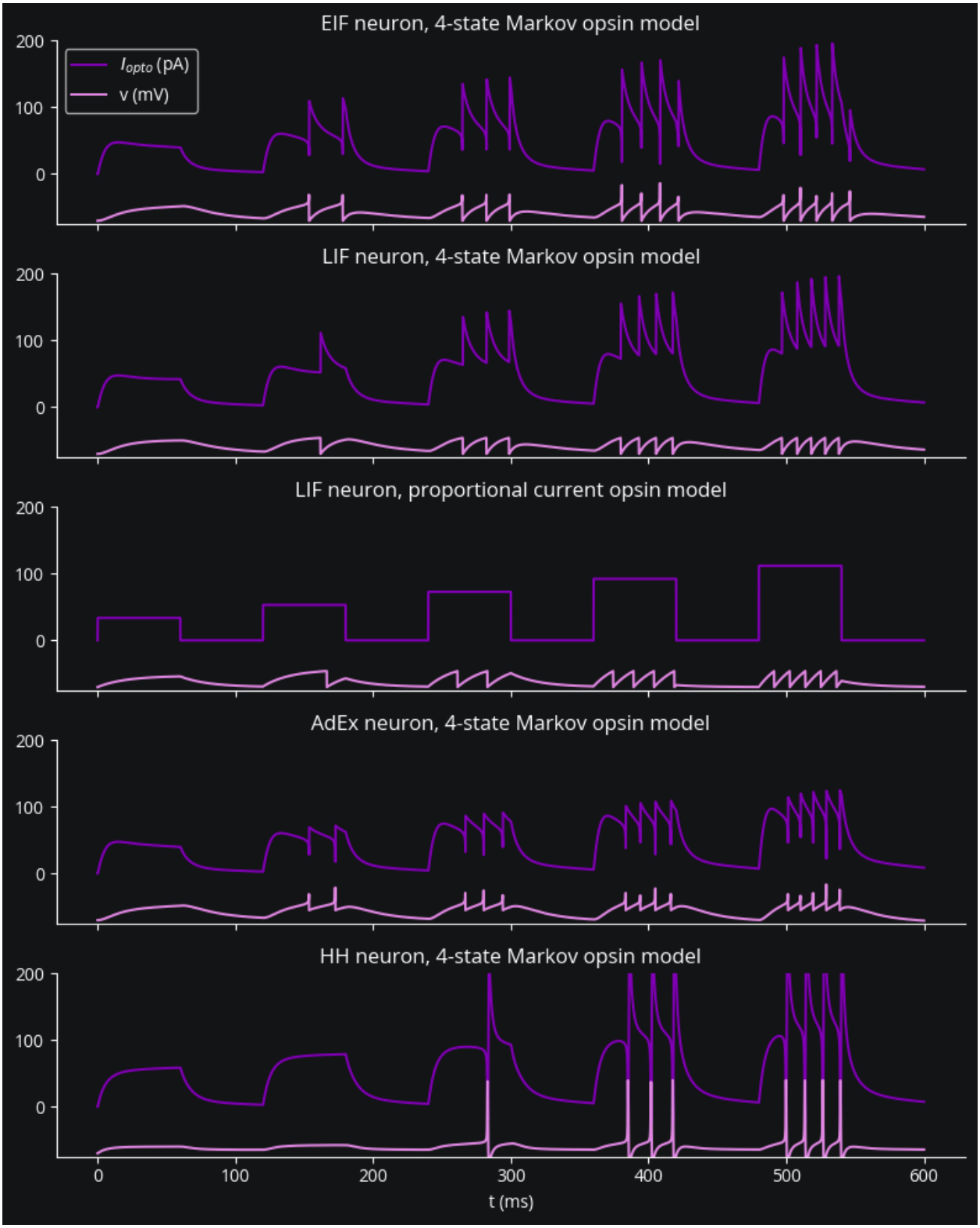
```
# hand-picked range of amplitudes to show 0 to moderate firing rates
for Irr0_mW_per_mm2 in np.linspace(0.015, 0.05, 5):
    light.update(Irr0_mW_per_mm2)
    sim.run(60 * ms)
    light.update(0)
    sim.run(60 * ms)
```

```
INFO       No numerical integration method specified for group 'neurongroup_1', using␣
↪method 'euler' (took 0.01s, trying other methods took 0.02s). [brian2.stateupdaters.
↪base.method_choice]
INFO       No numerical integration method specified for group 'neurongroup_2', using␣
↪method 'exact' (took 0.04s). [brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'neurongroup_3', using␣
↪method 'exact' (took 0.02s). [brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'neurongroup_4', using␣
↪method 'euler' (took 0.01s, trying other methods took 0.05s). [brian2.stateupdaters.
↪base.method_choice]
```

```
WARNING    'n' is an internal variable of group 'neurongroup_5', but also exists in the␣
↪run namespace with the value 10. The internal variable will be used. [brian2.groups.
↪group.Group.resolve.resolution_conflict]
INFO       No numerical integration method specified for group 'syn_markov_opsin_
↪neurongroup_1', using method 'euler' (took 0.01s, trying other methods took 0.01s).␣
↪[brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_markov_opsin_
↪neurongroup_2', using method 'euler' (took 0.01s, trying other methods took 0.01s).␣
↪[brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_markov_opsin_
↪neurongroup_4', using method 'euler' (took 0.01s, trying other methods took 0.01s).␣
↪[brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_markov_opsin_
↪neurongroup_5', using method 'euler' (took 0.01s, trying other methods took 0.01s).␣
↪[brian2.stateupdaters.base.method_choice]
```

Results

```
c1 = '#8000b4'
c2 = '#df87e1'

fig, axs = plt.subplots(
    len(experiments), 1, figsize=(8, 2*len(experiments)), sharex=True
)

for ax, (ng_type, _, state_mon, spike_mon, markov_opsin) in zip(axs, experiments):
    ax.plot(state_mon.t / ms, state_mon.Iopto[0] / pamp, c=c1, label="$I_{opto}$ (pA)")
    ax.plot(state_mon.t / ms, state_mon.v[0] / mV, c=c2, label="v (mV)")
    opsin_name = "4-state Markov" if markov_opsin else "proportional current"
    ax.set(title=f"{ng_type} neuron, {opsin_name} opsin model")

axs[-1].set_xlabel('t (ms)')
axs[0].legend();

max_ylim = max([ax.get_ylim()[1] for ax in axs])
for ax in axs:
    ax.set_ylim([-75, 200])

fig.tight_layout()
```



Qualitatively we can see that the proportional current model doesn't capture the rise, peak, plateau, and fall dynamics that a Markov model can produce, but is a reasonable approximation if all you need is a roughly linear light intensity-firing rate relationship. We also see that a variety of neuron/opsin model combinations all produce similar firing responses to light.

6.2.3 Multi-channel, bidirectional optogenetics

Cleo supports the simultaneous use of multiple `Light` devices, multiple channels per device, and multiple opsins per neuron group. Here' we'll see how to use all these features.

```
# boilerplate
%load_ext autoreload
%autoreload 2
from brian2 import *
import matplotlib.pyplot as plt

import cleo
from cleo import *

cleo.utilities.style_plots_for_docs()

# numpy faster than cython for lightweight example
prefs.codegen.target = 'numpy'
# for reproducibility
np.random.seed(1866)

# colors
c = {
    'main': '#C500CC',
    '473nm': '#72b5f2',
    '590nm': (1, .875, 0),
}
```

```
The autoreload extension is already loaded. To reload it, use:
  %reload_ext autoreload
```

Network setup

We'll use excitatory and inhibitory populations of exponential integrate-and-fire neurons.

```
n = 500
ng = NeuronGroup(
    n,
    """
    dv/dt = (
        -(v - E_L)
        + Delta_T*exp((v-theta)/Delta_T)
        + Rm*(I_exc + I_inh + I_bg)
    ) / tau_m + sigma*sqrt(2/tau_m)*xi: volt
    I_exc : amp
    I_inh : amp
    """,
    threshold="v > -10*mV",
    reset="v=E_L",
    namespace={
        "tau_m": 20 * ms,
        "Rm": 500 * Mohm,
```

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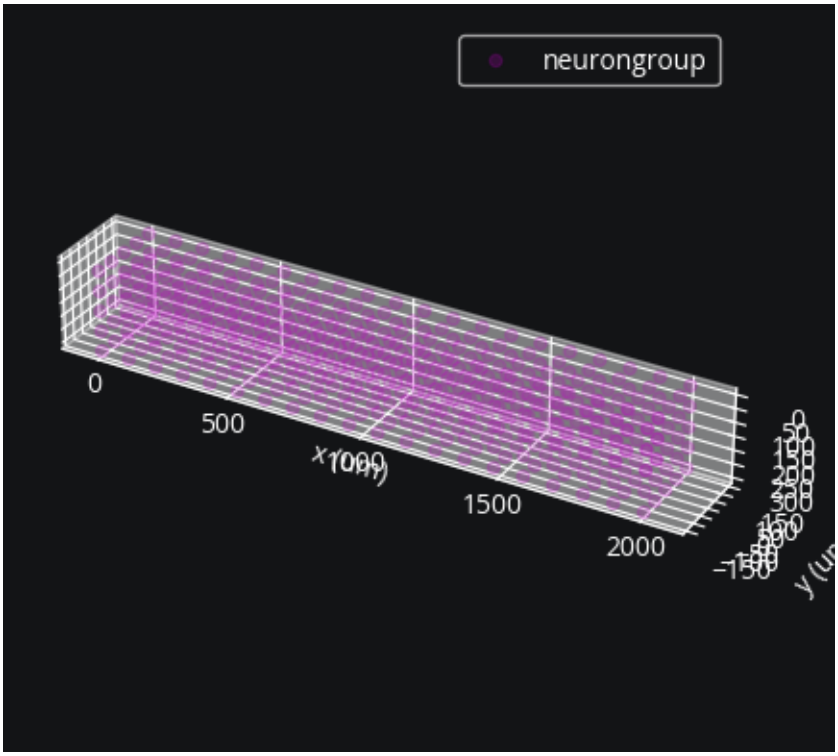
```
        "theta": -50 * mV,
        "Delta_T": 2 * mV,
        "E_L": -70*mV,
        "sigma": 5 * mV,
        "I_bg": 60 * pamp,
    },
)
ng.v = np.random.uniform(-70, -50, n) * mV

W = 1 * mV
p_S = 0.3
n_neighbors = 40
S_ee = Synapses(ng, model='w: 1', on_pre="v_post+=W*w/sqrt(N)")
S_ee.connect(condition='abs(i-j)<=n_neighbors and i!=j')
S_ee.w = np.exp(np.random.randn(int(S_ee.N - 0))) * np.random.choice([-1, 1], int(S_ee.N␣
↪- 0))

spike_mon = SpikeMonitor(ng)
# for visualizing currents
Imon = StateMonitor(ng, ('I_exc', 'I_inh'), record=range(50))
net = Network(ng, S_ee, spike_mon, Imon)
sim = cleo.CLSimulator(net)
```

```
from cleo.coords import assign_coords_grid_rect_prism
xmax_mm = 2
assign_coords_grid_rect_prism(ng, xlim=(0, xmax_mm), ylim=(-.15, .15), zlim=(0, .3),␣
↪shape=(20, 5, 5))
cleo.viz.plot(ng, colors=[c['main']])
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (um)', ylabel='y (um)', zlabel='z (um)'>)
```



Injecting a multi-channel `Light`

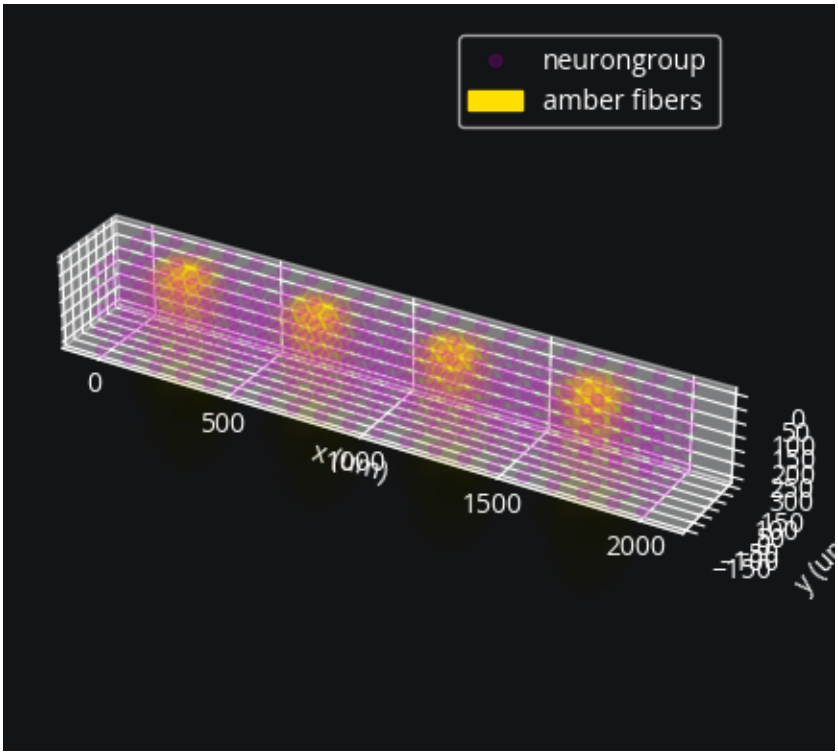
A `Light` device can have multiple channels; all the user needs is to specify the coordinates (and optionally direction) of each light source (channel). A `LightModel` (e.g., that of an optical fiber) defines how light propagates from each source.

Here we inject 590 nm light for activating Vf-Chrimson. Lacking a more rigorous quantification, we assume absorption and scattering coefficients of 590 nm light in the brain are roughly 0.8 times that of 470 nm light (see Jacques 2013 for some justification).

```
from cleo.light import Light, OpticFiber
from cleo.opto import vfchrimson_4s

n_fibers = 4
coords = np.zeros((n_fibers, 3))
end_space = 1 / (2 * n_fibers)
coords[:, 0] = np.linspace(end_space, 1 - end_space, n_fibers) * xmax_mm
coords[:, 1] = -0.025
amber_fibers = Light(
    name="amber fibers",
    coords=coords * mm,
    light_model=OpticFiber(K=0.125 * 0.8 / mm, S=7.37 * 0.8 / mm),
    wavelength=590 * nmeter,
)
sim.inject(amber_fibers, ng)
vfc = vfchrimson_4s()
sim.inject(vfc, ng, Iopto_var_name="I_exc")
cleo.viz.plot(ng, colors=[c["main"]], sim=sim)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (um)', ylabel='y (um)', zlabel='z (um)'>)
```



Bidirectional control via a second opsin

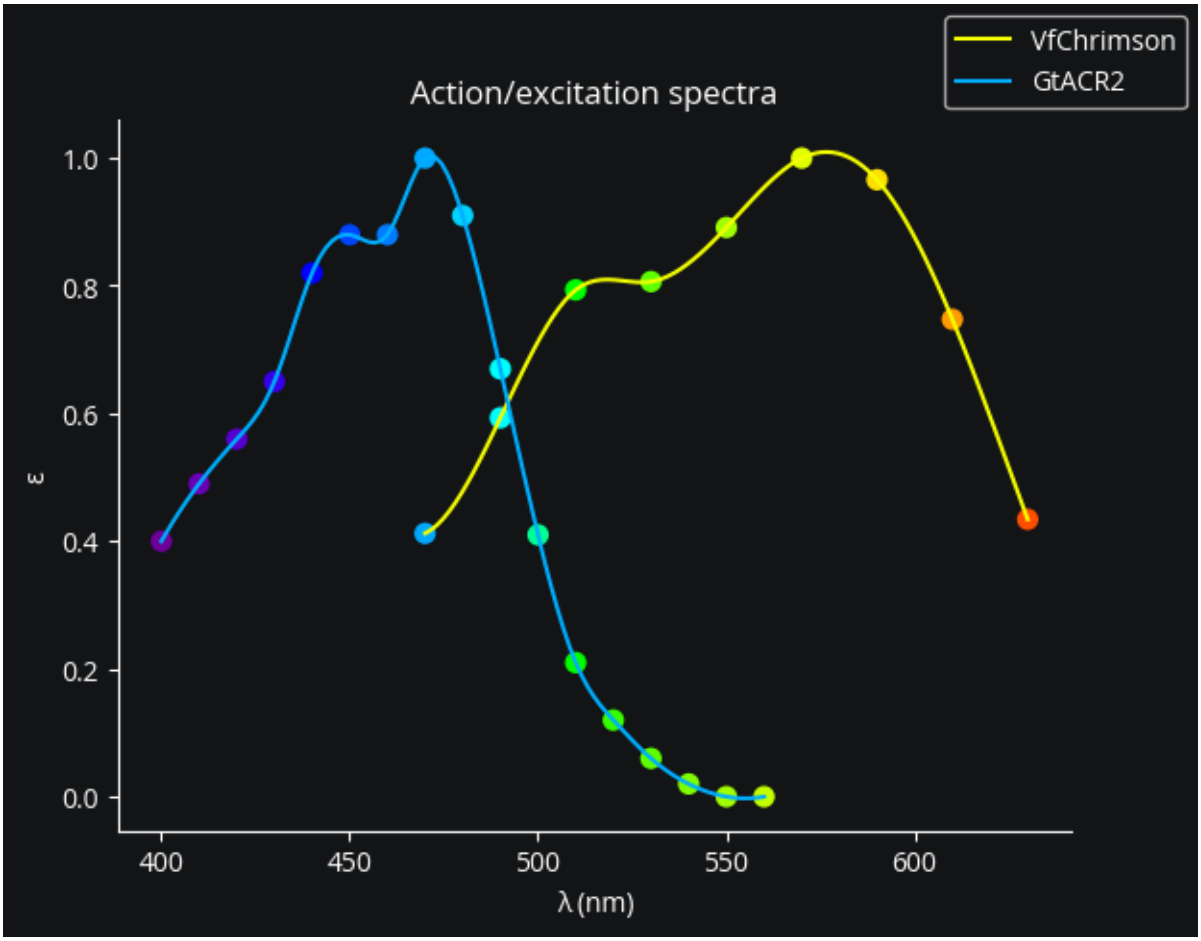
Here we will demonstrate increasing and decreasing activity in the same experiment by injecting an inhibitory opsin with a minimally overlapping activation spectrum. Alternatively, we could achieve bidirectional control with excitatory opsins on excitatory and inhibitory neurons.

We will use the anion channel GtACR2 which is maximally activated by 470 nm light.

Let's first visualize how the action spectra for the two opsins overlap:

```
gtacr2 = cleo.opto.gtacr2_4s()
cleo.light.plot_spectra(vfc, gtacr2)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes: title={'center': 'Action/excitation spectra'}, xlabel=' (nm)', ylabel=''>)
```

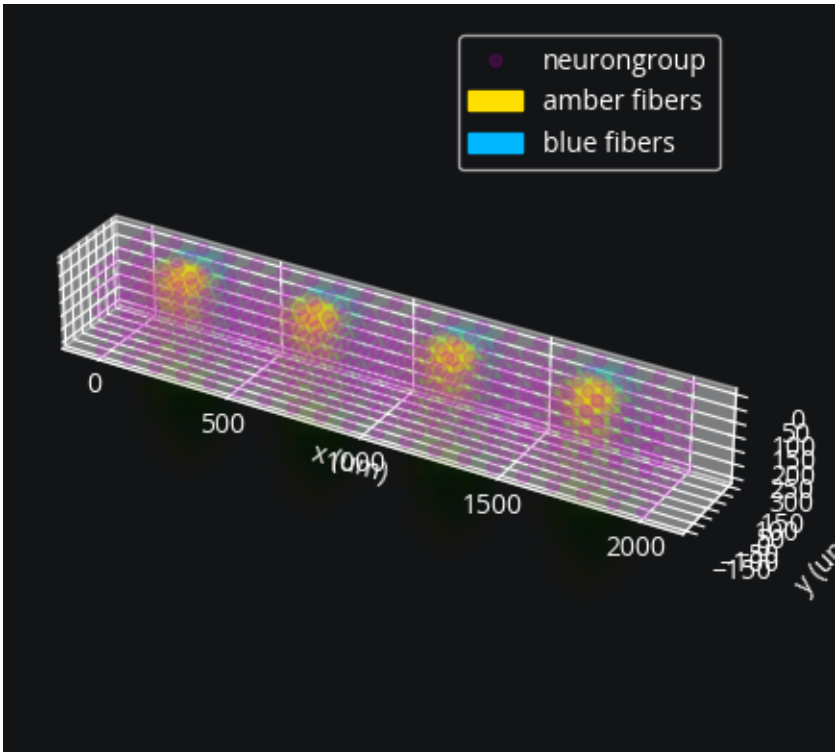


We see that GtACR2 will be totally unaffected by amber (590 nm) light, while Vf-Chrimson will be slightly activated by blue (470 nm) light.

```
coords[:, 1] = 0.025
blue_fibers = Light(
    name="blue fibers",
    coords=coords * mm,
    light_model=cleo.light.fiber473nm(),
)
sim.inject(blue_fibers, ng)
sim.inject(gtacr2, ng, Iopto_var_name="I_inh")
cleo.viz.plot(ng, colors=[c["main"]], sim=sim)
```

```
WARNING    /home/kyle/Dropbox (GaTech)/projects/cleo/cleo/light/light_dependence.py:107:␣
↪UserWarning:  = 590.0 nm is outside the range of the action spectrum data for GtACR2.␣
↪Assuming  = 0.
  warnings.warn(
 [py.warnings]
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (um)', ylabel='y (um)', zlabel='z (um)'>)
```



Open-loop stimulation

We will now design a stimulus pattern to demonstrate bidirectional control segregated by channel.

```
from cleo.ioproc import LatencyIOProcessor

class OpenLoopOpto(LatencyIOProcessor):
    def __init__(self):
        super().__init__(sample_period_ms=1)

    # since this is open-loop, we don't use state_dict
    def process(self, state_dict, time_ms):
        amplitude_mW_mm2 = 1
        time_offsets = np.array([0, -20, -40, -60])
        t = time_ms + time_offsets
        amber = ((t >= 20) & (t < 40)) * amplitude_mW_mm2
        blue = ((t >= 60) & (t < 63)) * amplitude_mW_mm2

        # return output dict and time
        return ({"amber fibers": amber, "blue fibers": blue}, time_ms)

sim.set_io_processor(OpenLoopOpto())
```

```
CLSimulator(io_processor=<__main__.OpenLoopOpto object at 0x7fe758a361d0>, devices=
↪{BansalFourStateOpsin(sim=..., name='GtACR2', save_history=True, on_pre='',␣
↪spectrum=[(400, 0.4), (410, 0.49), (420, 0.56), (430, 0.65), (440, 0.82), (450, 0.88),␣
↪(460, 0.88), (470, 1.0), (480, 0.91), (490, 0.67), (500, 0.41), (510, 0.21), (520, 0.
↪12), (530, 0.06), (540, 0.02), (550, 0.0), (560, 0.0)], required_vars=[('Iopto', amp),␣
```

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```
↪('v', volt)], Gd1=17. * hertz, Gd2=10. * hertz, Gr0=0.58 * hertz, g0=44. * nsiemens,␣
↪phim=2.e+23 * (second ** -1) / (meter ** 2), k1=40. * khertz, k2=20. * khertz, Gf0=1.␣
↪* hertz, Gb0=3. * hertz, kf=1. * hertz, kb=5. * hertz, gamma=0.05, p=1, q=0.1, E=-69.5␣
↪* mvolt, model='\n        dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\n      ␣
↪ dO1/dt = Ga1*C1 + Gb*O2 - (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt = Ga2*C2 +␣
↪Gf*O1 - (Gd2+Gb)*O2 : 1 (clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n       ␣
↪Theta = int(phi_pre > 0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_pre**p +␣
↪phim**p) : 1\n        Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n        Hq =␣
↪Theta * phi_pre**q/(phi_pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\n     ␣
↪  Gb = kb*Hq + Gb0 : hertz\n\n        fphi = O1 + gamma*O2 : 1\n\n        IOPTO_VAR_
↪NAME_post = -g0*fphi*(V_VAR_NAME_post-E)*rho_rel : ampere (summed)\n        rho_rel : 1
↪'), Light(sim=..., name='amber fibers', save_history=True, value=array([0., 0., 0., 0.
↪]), light_model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=100. * metre ** -1, S=5896.␣
↪* metre ** -1, ntis=1.36), wavelength=0.59 * umetre, direction=array([0., 0., 1.]),␣
↪max_Irr0_mW_per_mm2=None, max_Irr0_mW_per_mm2_viz=None), BansalFourStateOpsin(sim=...,␣
↪name='VfChrimson', save_history=True, on_pre='', spectrum=[(470.0, 0.4123404255319149),
↪ (490.0, 0.593265306122449), (510.0, 0.7935294117647058), (530.0, 0.8066037735849055),␣
↪(550.0, 0.8912727272727272), (570.0, 1.0), (590.0, 0.9661016949152542), (610.0, 0.
↪7475409836065574), (630.0, 0.4342857142857143)], required_vars=[('Iopto', amp), ('v',␣
↪volt)], Gd1=0.37 * khertz, Gd2=175. * hertz, Gr0=0.667 * mhertz, g0=17.5 * nsiemens,␣
↪phim=1.5e+22 * (second ** -1) / (meter ** 2), k1=3. * khertz, k2=200. * hertz, Gf0=20.␣
↪* hertz, Gb0=3.2 * hertz, kf=10. * hertz, kb=10. * hertz, gamma=0.05, p=1, q=1, E=0. *␣
↪volt, model='\n        dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\n       ␣
↪dO1/dt = Ga1*C1 + Gb*O2 - (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt = Ga2*C2 +␣
↪Gf*O1 - (Gd2+Gb)*O2 : 1 (clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n       ␣
↪Theta = int(phi_pre > 0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_pre**p +␣
↪phim**p) : 1\n        Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n        Hq =␣
↪Theta * phi_pre**q/(phi_pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\n     ␣
↪  Gb = kb*Hq + Gb0 : hertz\n\n        fphi = O1 + gamma*O2 : 1\n\n        IOPTO_VAR_
↪NAME_post = -g0*fphi*(V_VAR_NAME_post-E)*rho_rel : ampere (summed)\n        rho_rel : 1
↪'), Light(sim=..., name='blue fibers', save_history=True, value=array([0., 0., 0., 0.
↪]), light_model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=125. * metre ** -1, S=7370.␣
↪* metre ** -1, ntis=1.36), wavelength=0.473 * umetre, direction=array([0., 0., 1.]),␣
↪max_Irr0_mW_per_mm2=None, max_Irr0_mW_per_mm2_viz=None)})
```

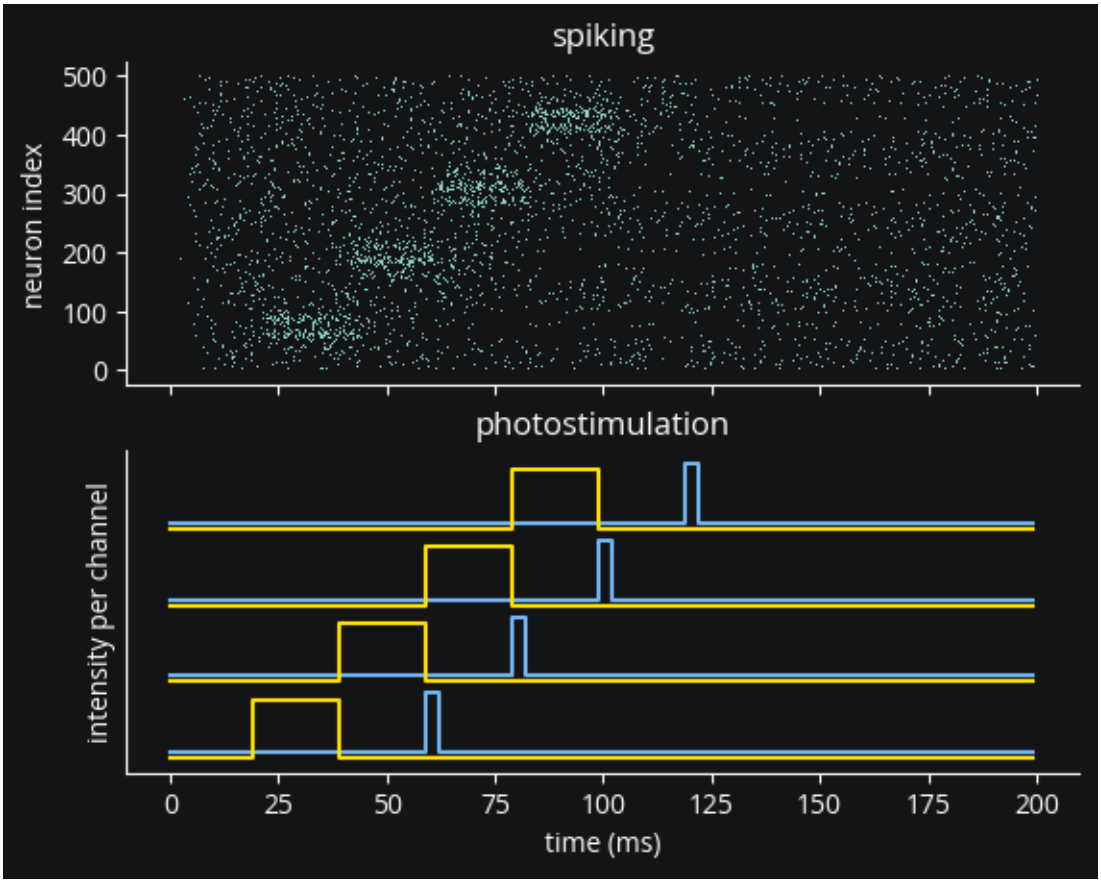
Run simulation and plot results

```
sim.reset()
sim.run(200*ms)
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'euler' (took 0.15s, trying other methods took 0.00s). [brian2.stateupdaters.
↪base.method_choice]
INFO       No numerical integration method specified for group 'syn_GtACR2_neurongroup',␣
↪using method 'euler' (took 0.02s, trying other methods took 0.06s). [brian2.
↪stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_VfChrimson_
↪neurongroup', using method 'euler' (took 0.01s, trying other methods took 0.01s).␣
↪[brian2.stateupdaters.base.method_choice]
```

```
fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)

ax1.plot(spike_mon.t / ms, spike_mon.i[:], ",")
ax1.set(ylabel="neuron index", title="spiking")

ax2.step(
    blue_fibers.t_ms, blue_fibers.values + np.arange(n_fibers) * 1.3 + 0.1, c=c["473nm"]
)
ax2.step(amber_fibers.t_ms, amber_fibers.values + np.arange(n_fibers) * 1.3, c=c["590nm
↪"])
ax2.set(
    yticks=[],
    ylabel="intensity per channel",
    title="photostimulation",
    xlabel="time (ms)",
)
```

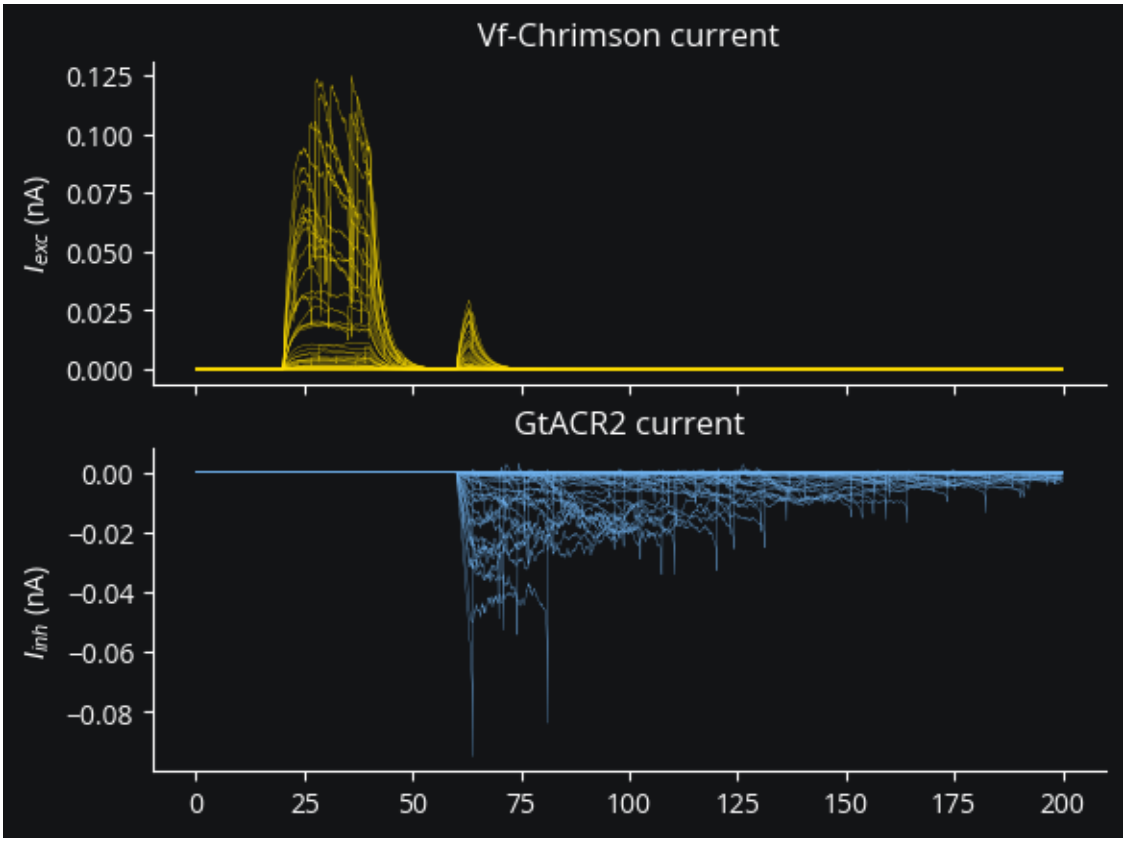
```
[[],
 Text(0, 0.5, 'intensity per channel'),
 Text(0.5, 1.0, 'photostimulation'),
 Text(0.5, 0, 'time (ms)')]
```



As you can see, Vf-Chrimson has fast dynamics, enabling high-frequency control. GtACR2, on the other hand, continues acting long after the light is removed due to its slow deactivation kinetics. We can confirm this by plotting the current from each of the opsins in the first segment of neurons:

```
fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
ax1.plot(Imon.t / ms, Imon.I_exc.T / namp, lw=0.2, c=c["590nm"])
ax1.set(title="Vf-Chrimson current", ylabel="$I_{exc}$ (nA)")
ax2.plot(Imon.t / ms, Imon.I_inh.T / namp, lw=0.2, c=c["473nm"])
ax2.set(title="GtACR2 current", ylabel="$I_{inh}$ (nA)")
```

```
[Text(0.5, 1.0, 'GtACR2 current'), Text(0, 0.5, '$I_{inh}$ (nA)')]
```



We can also confirm that blue light has a non-negligible effect on Vf-Chrimson.

Conclusion

As a recap, in this tutorial we've seen how to:

- configure a multi-channel `Light` device,
- use more than one of them simultaneously, and
- inject multiple opsins of overlapping action spectra into the same network.

6.2.4 On-off control

Here we will see how to set up a minimum, working closed loop with a very simple threshold-triggered control scheme.

Preamble:

```
from brian2 import *
from cleo import *

import matplotlib.pyplot as plt

utilities.style_plots_for_docs()

# the default cython compilation target isn't worth it for
# this trivial example
prefs.codegen.target = "numpy"
```

Set up network

We will use a simple leaky integrate-and-fire network with Poisson spike train input. We use Brian's standard `SpikeMonitor` to view resulting spikes here for simplicity, but see the electrodes tutorial for a more realistic electrode recording scheme.

```
n = 10
population = NeuronGroup(n, '''
             dv/dt = (-v - 70*mV + Rm*I) / tau : volt
             tau: second
             Rm: ohm
             I: amp''',
        threshold='v>-50*mV',
        reset='v=-70*mV'
)
population.tau = 10*ms
population.Rm = 100*Mohm
population.I = 0*mA
population.v = -70*mV

input_group = PoissonGroup(n, np.linspace(0, 100, n)*Hz + 10*Hz)

S = Synapses(input_group, population, on_pre='v+=5*mV')
S.connect(condition='abs(i-j)<=3')

pop_mon = SpikeMonitor(population)

net = Network([population, input_group,S, pop_mon])

print("Recorded population's equations:")
population.user_equations
```

```
Recorded population's equations:
```

$$\frac{\mathrm{d}v}{\mathrm{d}t} = \frac{IRm - 70mV - v}{\tau} \quad \text{(unit of } v\text{: V)}$$

τ (unit: s)

Rm (unit: ohm)

I (unit: A)

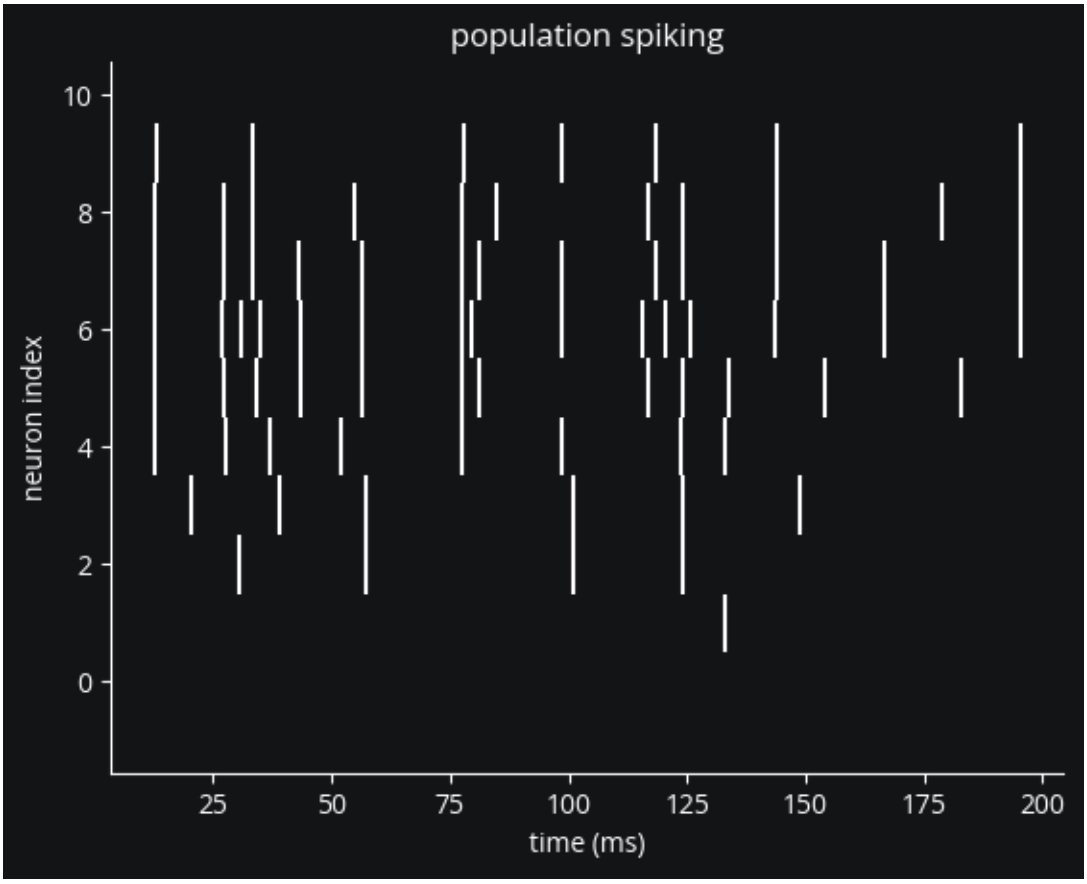
Run simulation

```
net.run(200*ms)
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'exact' (took 0.15s). [brian2.stateupdaters.base.method_choice]
```

```
sptrains = pop_mon.spike_trains()
fig, ax = plt.subplots()
ax.eventplot([t / ms for t in sptrains.values()], lineoffsets=list(sptrains.keys()))
ax.set(title='population spiking', ylabel='neuron index', xlabel='time (ms)')
```

```
[Text(0.5, 1.0, 'population spiking'),
 Text(0, 0.5, 'neuron index'),
 Text(0.5, 0, 'time (ms)')]
```



Because lower neuron indices receive very little input, we see no spikes for neuron 0. Let's change that with closed-loop control.

IO processor setup

We use the `IOProcessor` class to define interactions with the network. To achieve our goal of making neuron 0 fire, we'll use a contrived, simplistic setup where

1. the recorder reports the voltage of a given neuron (of index 5 in our case),
2. the controller outputs a pulse whenever that voltage is below a certain threshold, and
3. the stimulator applies that pulse to the specified neuron.

So if everything is wired correctly, we'll see bursts of activity in just the first neuron.

```
from cleo.recorders import RateRecorder, VoltageRecorder
from cleo.stimulators import StateVariableSetter

i_rec = int(n / 2)
i_ctrl = 0
sim = CLSimulator(net)
v_rec = VoltageRecorder(name="rec")
sim.inject(v_rec, population[i_rec])
sim.inject(
    StateVariableSetter(name="stim", variable_to_ctrl="I", unit=nA), population[i_ctrl]
)
```

```
CLSimulator(io_processor=None, devices={VoltageRecorder(brian_objects={<StateMonitor,␣
↪recording ['v'] from 'neurongroup_subgroup'>}, sim=..., name='rec', voltage_var_name='v
↪', mon=<StateMonitor, recording ['v'] from 'neurongroup_subgroup'>),␣
↪StateVariableSetter(brian_objects=set(), sim=..., name='stim', value=0, default_
↪value=0, save_history=True, variable_to_ctrl='I', unit=namp, neuron_groups=[<Subgroup
↪'neurongroup_subgroup_1' of 'neurongroup' from 0 to 1>])})
```

We need to implement the `LatencyIOProcessor` object. For a more sophisticated case we'd use `ProcessingBlock` objects to decompose the computation in the `process` function.

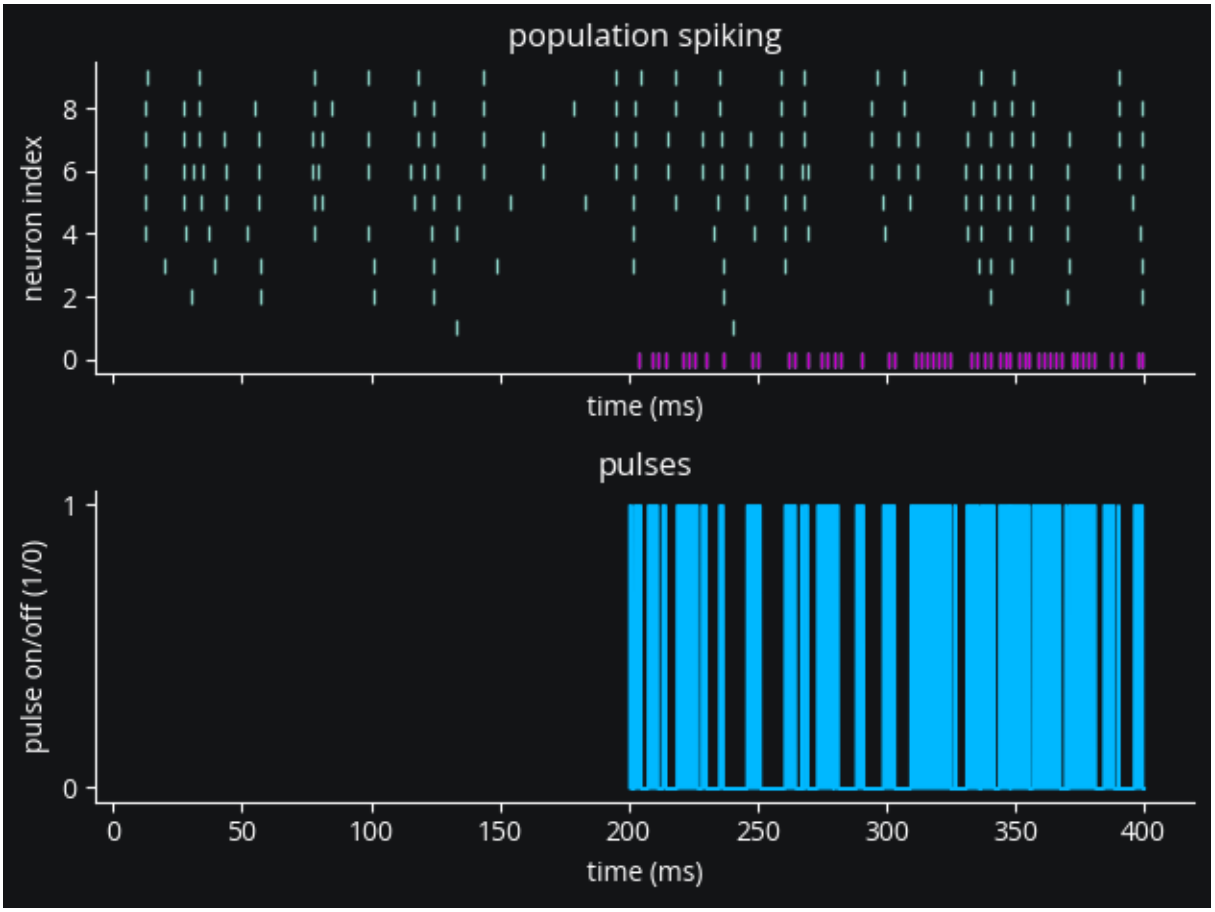
```
from cleo.ioproc import LatencyIOProcessor

trigger_threshold = -60*mV
class ReactivePulseIOProcessor(LatencyIOProcessor):
    def __init__(self, pulse_current=1):
        super().__init__(sample_period_ms=1)
        self.pulse_current = pulse_current
        self.out = {}

    def process(self, state_dict, time_ms):
        v = state_dict['rec']
        if v is not None and v < trigger_threshold:
            self.out['stim'] = self.pulse_current
        else:
            self.out['stim'] = 0

        return (self.out, time_ms)

sim.set_io_processor(ReactivePulseIOProcessor(pulse_current=1))
```

```
CLSimulator(io_processor=<__main__.ReactivePulseIOProcessor object at 0x7f57975a1600>,␣
↪devices={VoltageRecorder(brian_objects={<StateMonitor, recording ['v'] from
↪'neurongroup_subgroup'>}, sim=..., name='rec', voltage_var_name='v', mon=<StateMonitor,
↪ recording ['v'] from 'neurongroup_subgroup'>), StateVariableSetter(brian_
↪objects=set(), sim=..., name='stim', value=0, default_value=0, save_history=True,␣
↪variable_to_ctrl='I', unit=namp, neuron_groups=[<Subgroup 'neurongroup_subgroup_1' of
↪'neurongroup' from 0 to 1>])})
```

And run the simulation:

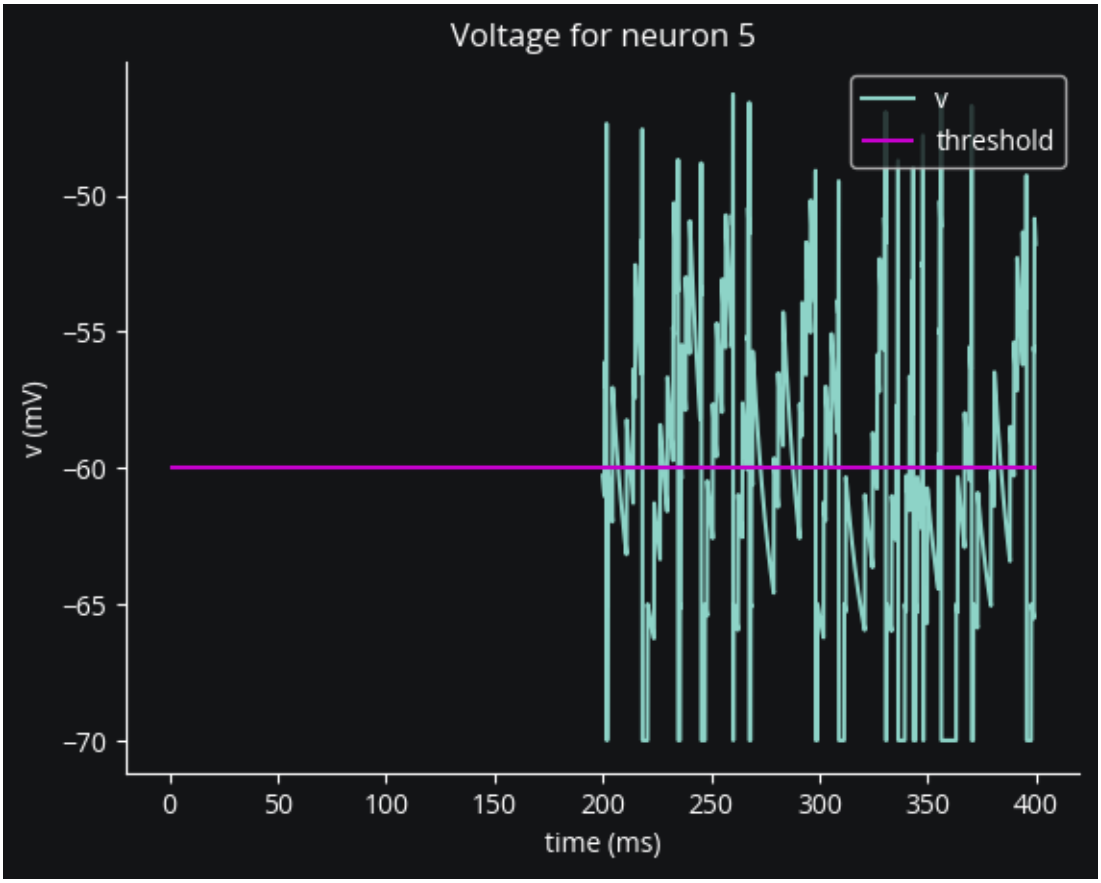
```
sim.run(200*ms)
```

```
fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
ax1.plot(pop_mon.t / ms, pop_mon.i[:], "|")
ax1.plot(
    pop_mon.t[pop_mon.i == i_ctrl] / ms,
    pop_mon.i[pop_mon.i == i_ctrl],
    "|",
    c="#C500CC",
)
ax1.set(title="population spiking", ylabel="neuron index", xlabel="time (ms)")
ax2.fill_between(
    v_rec.mon.t / ms, (v_rec.mon.v.T < trigger_threshold)[:, 0], color=(0.0, 0.72, 1.0)
)
ax2.set(title="pulses", xlabel="time (ms)", ylabel="pulse on/off (1/0)", yticks=[0, 1])
plt.tight_layout()
```



Yes, we see the IO processor triggering pulses as expected. And here's a plot of neuron 5's voltage to confirm that those pulses are indeed where we expect them to be, whenever the voltage is below -60 mV.

```
fig, ax = plt.subplots()
ax.set(title=f"Voltage for neuron {i_rec}", ylabel="v (mV)", xlabel='time (ms)')
ax.plot(v_rec.mon.t/ms, v_rec.mon.v.T / mV);
ax.hlines(-60, 0, 400, color='#c500cc');
ax.legend(['v', 'threshold'], loc='upper right');
```



Conclusion

In this tutorial we've seen the basics of configuring an `IOProcessor` to implement a closed-loop intervention on a Brian network simulation.

6.2.5 PI control

In this tutorial we'll introduce

1. PI control, a commonly used model-free control method,
2. the concept of decomposing the `IOProcessor`'s computation into `ProcessingBlock`s, and
3. modeling computation delays on those blocks to reflect hardware and algorithmic speed limitations present in a real experiment.

Preamble:

```
from brian2 import *
import matplotlib.pyplot as plt
from cleo import *

utilities.style_plots_for_docs()

np.random.seed(7000)
```

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```
# the default cython compilation target isn't worth it for
# this trivial example
prefs.codegen.target = "numpy"
```

Create the Brian network

We'll create a population of 10 LIF neurons mainly driven by feedforward input but with some recurrent connections as well.

```
n = 10
population = NeuronGroup(n, '''
            dv/dt = (-v - 70*mV + Rm*I) / tau : volt
            tau: second
            Rm: ohm
            I: amp''',
        threshold='v>-50*mV',
        reset='v=-70*mV'
)
population.tau = 10*ms
population.Rm = 100*Mohm
population.I = 0*mA
population.v = -70*mV

input_group = PoissonGroup(n, np.linspace(20, 200, n)*Hz)

S = Synapses(input_group, population, on_pre='v+=5*mV')
S.connect(condition=f'abs(i-j)<={3}')
S2 = Synapses(population, population, on_pre='v+=2*mV')
S2.connect(p=0.2)

pop_mon = SpikeMonitor(population)

net = Network(population, input_group, S, S2, pop_mon)
population.equations
```

$$\frac{\mathrm{d}v}{\mathrm{d}t} = \frac{IRm - 70mV - v}{\tau} \quad \text{(unit of } v\text{: V)}$$

I (unit: A)

Rm (unit: ohm)

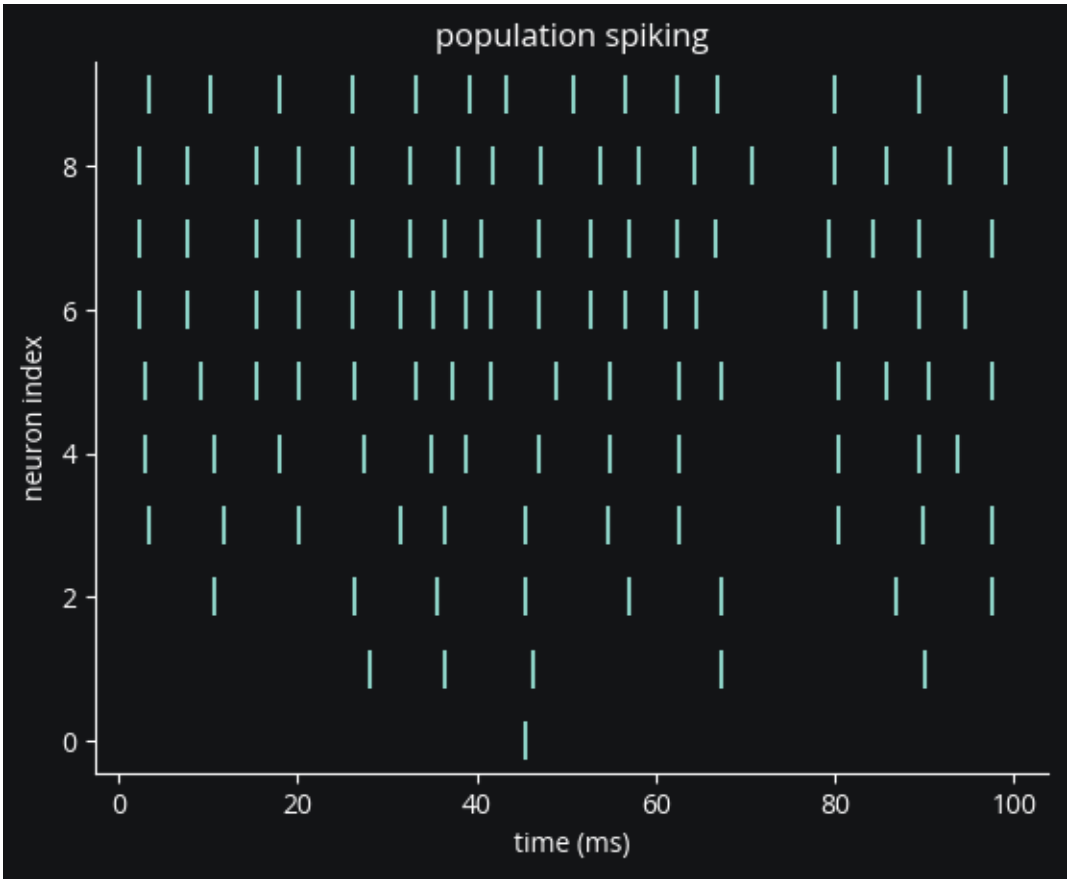
τ (unit: s)

Run simulation without control:

```
net.run(100*ms)
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'exact' (took 0.06s). [brian2.stateupdaters.base.method_choice]
```

```
fig, ax = plt.subplots()
ax.scatter(pop_mon.t / ms, pop_mon.i, marker='|', s=200);
ax.set(title='population spiking', ylabel='neuron index', xlabel='time (ms)');
```



Constructing a closed-loop simulation

We will use the popular model-free PI control to control a single neuron's firing rate. PI stands for proportional-integral, referring to a feedback gain *proportional* to the instantaneous error as well as the *integrated* error over time.

First we construct a `CLSimulator` from the network:

```
from cleo import CLSimulator
sim = CLSimulator(net)
```

Then, to control neuron i, we need to:

1. capture spiking using a `GroundTruthSpikeRecorder`

```
from cleo.recorders import GroundTruthSpikeRecorder
i = 0  # neuron to control
rec = GroundTruthSpikeRecorder(name='spike_rec')
sim.inject(rec, population[i])
```

```
CLSimulator(io_processor=None, devices={GroundTruthSpikeRecorder(brian_objects={
↪<SpikeMonitor, recording from 'spikemonitor_1'>}, sim=..., name='spike_rec', _mon=
↪<SpikeMonitor, recording from 'spikemonitor_1'>, _num_spikes_seen=0, neuron_group=
↪<Subgroup 'neurongroup_subgroup' of 'neurongroup' from 0 to 1>)})
```

2. define the firing rate trajectory we want our target neuron to follow

```
# the target firing rate trajectory, as a function of time
def target_Hz(t_ms):
    if t_ms < 250:  # constant target at first
        return 400
    else:  # sinusoidal afterwards
        a = 200
        t_s = t_ms / 1000
        return a + a * np.sin(2 * np.pi * 20 * t_s)
```

2. estimating its firing rate from incoming spikes using a `FiringRateEstimator`
3. compute the stimulus intensity with a `PIController`
4. output that value for a `StateVariableSetter` stimulator to use

Here we initialize blocks when the `IOProcessor` is created and define how to process network output and set the control signal in the `process` function.

```
from cleo.ioproc import (
    LatencyIOProcessor,
    FiringRateEstimator,
    ConstantDelay,
    PIController,
)

class PIRateIOProcessor(LatencyIOProcessor):
    delta = 1  # ms

    def __init__(self):
        super().__init__(sample_period_ms=self.delta, processing="parallel")
        self.rate_estimator = FiringRateEstimator(
            tau_ms=15,
            sample_period_ms=self.delta,
            delay=ConstantDelay(4.1),  # latency in ms
            save_history=True,  # lets us plot later
        )

        # using hand-tuned gains that seem reasonable
        self.pi_controller = PIController(
            target_Hz,
            Kp=0.005,
            Ki=0.04,
```

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```
            sample_period_ms=self.delta,
            delay=ConstantDelay(2.87),  # latency in ms
            save_history=True,  # lets us plot later
        )

    def process(self, state_dict, sample_time_ms):
        spikes = state_dict["spike_rec"]
        # feed output and out_time through each block
        out, time_ms = self.rate_estimator.process(
            spikes, sample_time_ms, sample_time_ms=sample_time_ms
        )
        out, time_ms = self.pi_controller.process(
            out, time_ms, sample_time_ms=sample_time_ms
        )
        # this dictionary output format allows for the flexibility
        # of controlling multiple stimulators
        if out < 0:  # limit to positive current
            out = 0
        out_dict = {"I_stim": out}
        # time_ms at the end reflects the delays added by each block
        return out_dict, time_ms

io_processor = PIRateIOProcessor()
sim.set_io_processor(io_processor)
```

```
CLSimulator(io_processor=<__main__.PIRateIOProcessor object at 0x7f6be05fdb70>, devices=
↪{GroundTruthSpikeRecorder(brian_objects={<SpikeMonitor, recording from 'spikemonitor_1
↪'>}, sim=..., name='spike_rec', _mon=<SpikeMonitor, recording from 'spikemonitor_1'>, _
↪num_spikes_seen=0, neuron_group=<Subgroup 'neurongroup_subgroup' of 'neurongroup' from␣
↪0 to 1>)})
```

Note that we can set delays for individual `ProcessingBlock`s in the IO processor to better approximate the experiment. We use simple constant delays here, but a `GaussianDelay` class is also available and others could be easily implemented.

Now we inject the stimulator:

```
from cleo.stimulators import StateVariableSetter
sim.inject(
        StateVariableSetter(
            name='I_stim', variable_to_ctrl='I', unit=nA),
        population[i]
)
```

```
CLSimulator(io_processor=<__main__.PIRateIOProcessor object at 0x7f6be05fdb70>, devices=
↪{StateVariableSetter(brian_objects=set(), sim=..., name='I_stim', value=0, default_
↪value=0, save_history=True, variable_to_ctrl='I', unit=namp, neuron_groups=[<Subgroup
↪'neurongroup_subgroup_1' of 'neurongroup' from 0 to 1>]),␣
↪GroundTruthSpikeRecorder(brian_objects={<SpikeMonitor, recording from 'spikemonitor_1'>
↪}, sim=..., name='spike_rec', _mon=<SpikeMonitor, recording from 'spikemonitor_1'>, _
↪num_spikes_seen=0, neuron_group=<Subgroup 'neurongroup_subgroup' of 'neurongroup' from␣
↪0 to 1>)})
```

Run the simulation

```
sim.run(300*ms)
```

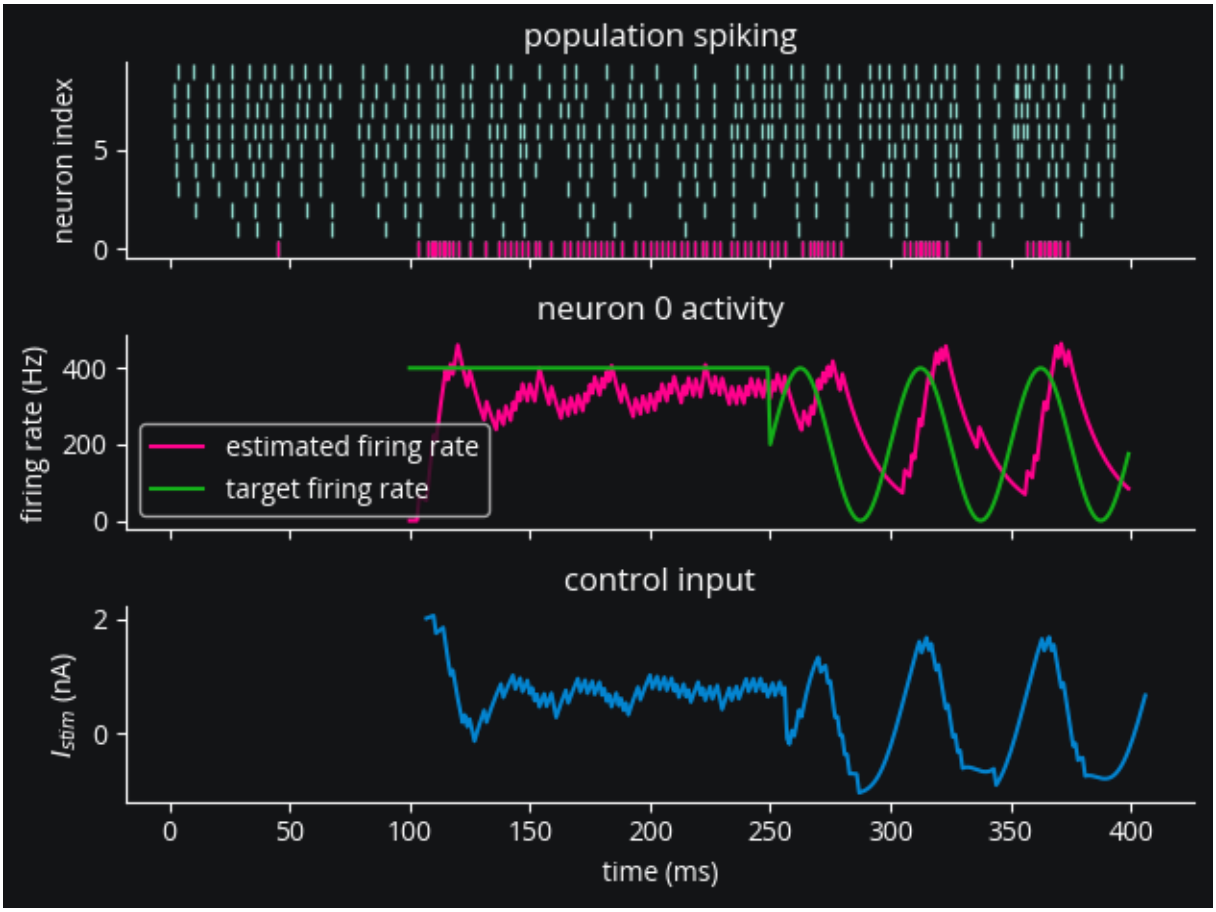
```
fig, (ax1, ax2, ax3) = plt.subplots(3, 1, sharex=True);
ax1.plot(pop_mon.t / ms, pop_mon.i[:], '|');
ax1.plot(pop_mon.t[pop_mon.i == i]/ms, pop_mon.i[pop_mon.i==i], '|', c='xkcd:hot pink')
ax1.set(title='population spiking', ylabel='neuron index')

ax2.plot(io_processor.rate_estimator.t_in_ms, io_processor.rate_estimator.values, c=
↪'xkcd:hot pink');
ax2.plot(io_processor.rate_estimator.t_in_ms, [target_Hz(t) for t in io_processor.rate_
↪estimator.t_in_ms],\
         c='xkcd:green');
ax2.set(ylabel='firing rate (Hz)', title=f'neuron {i} activity');
ax2.legend(['estimated firing rate', 'target firing rate']);

ax3.plot(io_processor.pi_controller.t_out_ms, io_processor.pi_controller.values, c=
↪'xkcd:cerulean')
ax3.set(title='control input', ylabel='$I_{stim}$ (nA)', xlabel='time (ms)')

fig.tight_layout()
fig.show()
```

```
WARNING    /tmp/ipykernel_28526/1609733203.py:16: UserWarning: Matplotlib is currently␣
↪using module://matplotlib_inline.backend_inline, which is a non-GUI backend, so cannot␣
↪show the figure.
  fig.show()
 [py.warnings]
```



Note the lag in keeping up with the target firing rate, which can be directly attributed to the ~7 ms delay we coded in to the IO processor.

Conclusion

In this tutorial, we've learned how to

- use PI control to interact with a Brian simulation,
- decompose processing steps into blocks, and
- assign delays to processing blocks to model real-life latency.

6.2.6 LQR optimal control using `ldsctrlest`

This tutorial will be more comprehensive than the others, bringing together all of `cleo`'s main capabilities—electrode recording, optogenetics, and latency modeling—as well as introducing more sophisticated model-based feedback control. To achieve the latter, we will use the `ldsctrlest` Python bindings to the `ldsCtrlEst` C++ library.

Preamble:

```
from brian2 import *
import matplotlib.pyplot as plt
import cleo
```

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```
cleo.utilities.style_plots_for_docs()

# numpy faster than cython for lightweight example
prefs.codegen.target = 'numpy'
np.random.seed(1856)
```

Network setup

As in the optogenetics tutorial, we'll use a trivial network of a small neuron group biased by Poisson input spikes. We'll use the exponential integrate-and-fire neuron model, which maintains simplicity while modeling an upward membrane potential swing when spiking.

```
n = 2
ng = NeuronGroup(
    n,
    """
    dv/dt = (-(v - E_L) + Delta_T*exp((v-theta)/Delta_T) + Rm*I) / tau_m : volt
    I : amp
    """,
    threshold="v>30*mV",
    reset="v=-55*mV",
    namespace={
        "tau_m": 20 * ms,
        "Rm": 500 * Mohm,
        "theta": -50 * mV,
        "Delta_T": 2 * mV,
        "E_L": -70 * mV,
    },
)
ng.v = -70 * mV

input_group = PoissonInput(ng, "v", 10, 100 * Hz, 2.5 * mV)

net = Network(ng, input_group)
```

Coordinates, stimulation, and recording

Here we assign coordinates to the neurons and configure the optogenetic intervention and recording setup:

```
from cleo.coords import assign_coords_rand_rect_prism
from cleo.opto import *
from cleo.light import Light, fiber473nm
from cleo.ephys import Probe, SortedSpiking

hor_lim = 0.05
assign_coords_rand_rect_prism(
    ng, xlim=(-hor_lim, hor_lim), ylim=(-hor_lim, hor_lim), zlim=(0.4, 0.6)
)

fiber = Light(
```

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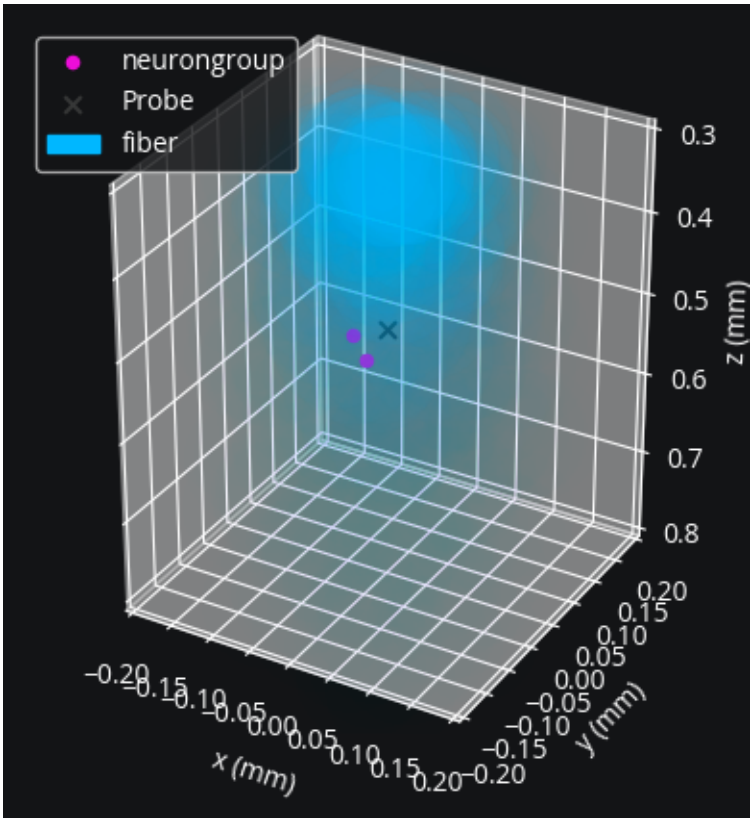
```
    name="fiber",
    light_model=fiber473nm(),
    coords=(0, 0, 0.3) * mm,
)

opsin = chr2_4s()

spikes = SortedSpiking(
    name="spikes",
    r_perfect_detection=40 * umeter,
    r_half_detection=80 * umeter,
)
probe = Probe(
    coords=[0, 0, 0.5] * mm,
    signals=[spikes],
    save_history=True,
)

cleo.viz.plot(
    ng,
    colors=["xkcd:fuchsia"],
    xlim=(-0.2, 0.2),
    ylim=(-0.2, 0.2),
    zlim=(0.3, 0.8),
    devices=[probe, fiber],
    scatterargs={"alpha": 1},
    axis_scale_unit=mm,
)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (mm)', ylabel='y (mm)', zlabel='z (mm)'>)
```



Looks right. Let's set up the simulation and inject the devices:

```
sim = cleo.CLSimulator(net)
sim.inject(fiber, ng)
sim.inject(opsin, ng, Iopto_var_name='I')
sim.inject(probe, ng)
```

```
CLSimulator(io_processor=None, devices={Probe(sim=..., name='Probe', save_history=True,␣
↪signals=[SortedSpiking(name='spikes', brian_objects={<SpikeMonitor, recording from
↪'spikemonitor'>}, probe=..., r_perfect_detection=40. * umetre, r_half_detection=80. *␣
↪umetre, cutoff_probability=0.01)], probe=NOTHING), FourStateOpsin(sim=..., name='ChR2',
↪ save_history=True, on_pre='', spectrum=[(400, 0.34), (422, 0.65), (460, 0.96), (470,␣
↪1), (473, 1), (500, 0.57), (520, 0.22), (540, 0.06), (560, 0.01)], required_vars=[(
↪'Iopto', amp), ('v', volt)], g0=114. * nsiemens, gamma=0.00742, phim=2.33e+23 *␣
↪(second ** -1) / (meter ** 2), k1=4.15 * khertz, k2=0.868 * khertz, p=0.833, Gf0=37.3␣
↪* hertz, kf=58.1 * hertz, Gb0=16.1 * hertz, kb=63. * hertz, q=1.94, Gd1=105. * hertz,␣
↪Gd2=13.8 * hertz, Gr0=0.33 * hertz, E=0. * volt, v0=43. * mvolt, v1=17.1 * mvolt,␣
↪model="\n        dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\n        dO1/dt␣
↪= Ga1*C1 + Gb*O2 - (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt = Ga2*C2 + Gf*O1 -␣
↪(Gd2+Gb)*O2 : 1 (clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n        Theta =␣
↪int(phi_pre > 0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_pre**p + phim**p) :␣
↪1\n        Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n        Hq = Theta * phi_
↪pre**q/(phi_pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\n        Gb =␣
↪kb*Hq + Gb0 : hertz\n\n        fphi = O1 + gamma*O2 : 1\n        # v1/v0 when v-E == 0␣
↪via l'Hopital's rule\n        fv = f_unless_x0(\n            (1 - exp(-(V_VAR_NAME_
↪post-E)/v0)) / ((V_VAR_NAME_post-E)/v1),\n            V_VAR_NAME_post - E,\n          ␣
↪ v1/v0\n        ) : 1\n\n        IOPTO_VAR_NAME_post = -g0*fphi*fv*(V_VAR_NAME_post-
```

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```
↪E)*rho_rel : ampere (summed)\n        rho_rel : 1", extra_namespace={'f_unless_x0':
↪<brian2.core.functions.Function object at 0x7f5971fba6e0>}), Light(sim=..., name='fiber
↪', save_history=True, value=array([0.]), light_model=OpticFiber(R0=100. * umetre,␣
↪NAfib=0.37, K=125. * metre ** -1, S=7370. * metre ** -1, ntis=1.36), wavelength=0.473␣
↪* umetre, direction=array([0., 0., 1.]), max_Irr0_mW_per_mm2=None, max_Irr0_mW_per_mm2_
↪viz=None)})
```

Prepare controller

Our goal will be to control two neuron's firing rates simultaneously. To do this, we will use the LQR technique explained in Bolus et al., 2021 ("State-space optimal feedback control of optogenetically driven neural activity)".

Fit model

Our controller needs a model of the system's dynamics, which we can obtain by fitting to training data. We will generate training data using Gaussian random walk inputs. `ldsCtrlEst` is designed for data coming from an experiment, organized into trials, so we will run the simulation repeatedly, resetting after each run. Here u represents the input and z the spike output.

We will intentionally use very little training data so the importance of adaptive control will become apparent later on.

```
n_trials = 5
n_samp = 100
u = []
z = []
n_u = 1  # 1-dimensional input (just one optogenetic actuator)
n_z = 2  # we'll be controlling two neurons
for trial in range(n_trials):
    # one-sided normally distributed training data, stdev of 10 mW/mm2
    u_trial = 10*np.abs(np.random.randn(n_u, n_samp))
    u.append(u_trial)
    z.append(np.zeros((n_z, n_samp)))
```

The IO processor is simple enough here that we won't bother separating steps using :class:`~cleo.ioproc.ProcessingBlock` objects, which is recommended for more complex scenarios where modularity is more important.

```
from cleo.ioproc import LatencyIOProcessor

class TrainingStimIOP(LatencyIOProcessor):
    i_samp = 0
    i_trial = 0

    # here we just feed in the training inputs and record the outputs
    def process(self, state_dict, sample_time_ms):
        i, t, z_t = state_dict['Probe']['spikes']
        z[self.i_trial][:, self.i_samp] = z_t[:n_z]  # just first two neurons
        out = {'fiber': u[self.i_trial][:, self.i_samp]}
        self.i_samp += 1
        return out, sample_time_ms

training_stim_iop = TrainingStimIOP(sample_period_ms=1)
```

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```
sim.set_io_processor(training_stim_iop)

for i_trial in range(n_trials):
    training_stim_iop.i_trial = i_trial
    training_stim_iop.i_samp = 0
    sim.run(n_samp*ms)
    sim.reset()
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'euler' (took 0.02s, trying other methods took 0.07s). [brian2.stateupdaters.
↪base.method_choice]
```

```
INFO       No numerical integration method specified for group 'syn_ChR2_neurongroup',␣
↪using method 'euler' (took 0.02s, trying other methods took 0.09s). [brian2.
↪stateupdaters.base.method_choice]
```

Now we have `u` and `z` in the form we need for `ldsctrlest`'s fitting functions: `n_trial`-length lists of `n` by `n_samp` arrays. We will now fit Gaussian linear dynamical systems using the SSID algorithm. See the documentation for more detailed explanations.

```
import ldsctrlest as lds
import ldsctrlest.gaussian as glds
n_x_fit = 2  # latent dimensionality of system
n_h = 50  # size of block Hankel data matrix
dt = 0.001  # timestep (in seconds)
u_train = lds.UniformMatrixList(u, free_dim=2)
z_train = lds.UniformMatrixList(z, free_dim=2)
ssid = glds.FitSSID(n_x_fit, n_h, dt, u_train, z_train)
fit, sing_vals = ssid.Run(lds.SSIDWt.kMOESP)
```

Design controller

LQR optimal control

We now use the fit parameters to create the controller system and set additional parameters. The feedback gain, $ K_c $, is especially important, determining how the controller responds to the current "error"—the difference between where the system is (estimated to be) now and where we want it to be. The field of optimal control deals with how to design the controller so as to minimize a cost function reflecting what we care about.

With a linear system (obtained from the fitting procedure above) and quadratic per-timestep cost function L penalizing distance from the reference x^* and the input u

$$ L = \frac{1}{2} (x - x^)^T Q (x - x^) + \frac{1}{2} u^T R u $$

we can use the closed-form optimal solution called the Linear Quadratic Regulator (LQR).

$$ K = (R + B^T P B)^{-1}(B^T P A) \quad\quad u = -Kx$$

The P matrix is obtained by numerically solving the discrete algebraic Riccati equation:

$$ P=A^{T} P A-\left(A^{T} P B\right)\left(R+B^{T} P B\right)^{-1}\left(B^{T} P A\right)+Q $$

```
fit_sys = glds.System(fit)
# upper and lower bounds on control signal (optic fiber light intensity)
u_lb = 0  # mW/mm2
u_ub = 30  # mW/mm2
controller = glds.Controller(fit_sys, u_lb, u_ub)
# careful not to use this anymore since controller made a copy
del fit_sys

from scipy.linalg import solve_discrete_are
# cost matrices
# Q reflects how much we care about state error
# we use C'C since we really care about output error, not latent state
Q_cost = controller.sys.C.T @ controller.sys.C
R_cost = 1e-4 * np.eye(n_u)  # reflects how much we care about minimizing the stimulus
A, B = controller.sys.A, controller.sys.B
P = solve_discrete_are(A, B, Q_cost, R_cost)
controller.Kc = np.linalg.inv(R_cost + B.T @ P @ B) @ (B.T @ P @ A)
controller.Print()
```

```
 ********** SYSTEM **********
x:
        0
        0

P:
   1.0000e-06            0
            0   1.0000e-06

A:
   0.5877   0.7122
  -0.7679   0.4800

B:
  -0.0152
  -0.0124

g:
   1.0000

m:
        0
        0

Q:
   0.0783   0.0510
   0.0510   0.1465

Q_m:
   1.0000e-06            0
            0   1.0000e-06

d:
```

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```
        0
        0

C:
  -0.1074   0.0030
  -0.0810   0.1761

y:
        0
        0

R:
   0.0943   0.0164
   0.0164   0.1574

g_design :    1.0000

u_lb : 0
u_ub : 30
```

We now configure the `IOProcessor` to use our controller:

```
class CtrlLoop(LatencyIOProcessor):
    def __init__(self, samp_period_ms, controller, y_ref: callable):
        super().__init__(samp_period_ms)
        self.controller = controller
        self.sys = controller.sys
        self.y_ref = y_ref
        self.do_control = False  # allows us to turn on and off control

        # for post hoc visualization/analysis:
        self.u = np.empty((n_u, 0))
        self.x_hat = np.empty((n_x_fit, 0))
        self.y_hat = np.empty((n_z, 0))
        self.z = np.empty((n_z, 0))

    def process(self, state_dict, sample_time_ms):
        i, t, z_t = state_dict["Probe"]["spikes"]
        z_t = z_t[:n_z].reshape((-1, 1))  # just first n_z neurons
        self.controller.y_ref = self.y_ref(sample_time_ms)

        u_t = self.controller.ControlOutputReference(z_t, do_control=self.do_control)
        out = {fiber.name: u_t.squeeze()}

        # record variables from this timestep
        self.u = np.hstack([self.u, u_t])
        self.y_hat = np.hstack([self.y_hat, self.sys.y])
        self.x_hat = np.hstack([self.x_hat, self.sys.x])
        self.z = np.hstack((self.z, z_t))

        return out, sample_time_ms + 3  # 3 ms delay
```

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```
y_ref = 200 * dt  # target rate in Hz
ctrl_loop = CtrlLoop(
    samp_period_ms=1, controller=controller, y_ref=lambda t: np.ones((n_z, 1)) * y_ref
)
```

Run the experiment

We'll now run the simulation with and without control to compare.

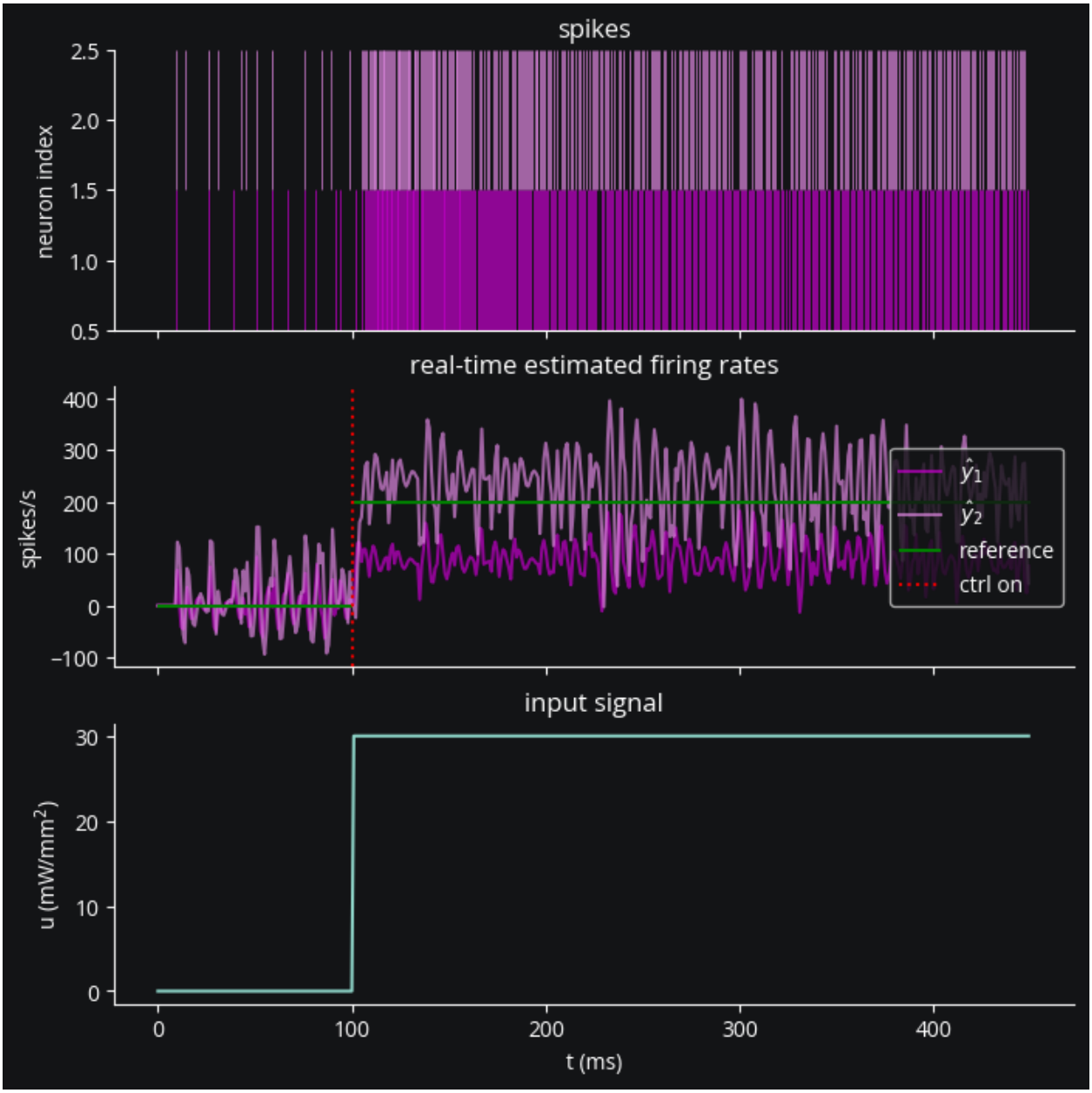
```
sim.set_io_processor(ctrl_loop)
T0 = 100
sim.run(T0*ms)

ctrl_loop.do_control = True
T1 = 350
sim.run(T1*ms)
```

```
WARNING    'dt' is an internal variable of group 'syn_ChR2_neurongroup', but also exists␣
↪in the run namespace with the value 0.001. The internal variable will be used. [brian2.
↪groups.group.Group.resolve.resolution_conflict]
```

Now we plot the results to see how well the controller was able to match the desired firing rate:

```
fig, (ax1, ax2, ax3) = plt.subplots(3, 1, sharex=True, figsize=(8,8))
c1 = "#C500CC"
c2 = "#df87e1"
spikes1 = spikes.t_ms[spikes.i == 0]
spikes2 = spikes.t_ms[spikes.i == 1]
ax1.eventplot([spikes1, spikes2], lineoffsets=[1, 2], colors=[c1, c2], lw=0.5)
ax1.set(ylabel='neuron index', ylim=(0.5, 2.5), title='spikes')
ax2.set(ylabel='spikes/s', title='real-time estimated firing rates')
ax2.plot(ctrl_loop.y_hat[0]/dt, c=c1, alpha=0.7, label='$\hat{y}_1$')
ax2.plot(ctrl_loop.y_hat[1]/dt, c=c2, alpha=0.7, label='$\hat{y}_2$')
ax2.hlines(y_ref/dt, 100, T0+T1, color='green', label='reference')
ax2.hlines(0, 0, 100, color='green')
ax2.axvline(T0, c='xkcd:red', linestyle=':', label='ctrl on')
ax2.legend(loc="right")
ax3.plot(range(T0+T1), ctrl_loop.u.T)
ax3.set(xlabel='t (ms)', ylabel='u (mW/mm$^2$)', title='input signal');
```



Looks all right, but in addition to the system's estimated firing rate let's count the spikes over the control period to see how well we hit the target on average:

```
print("Results (spikes/second):")
print('baseline =', np.sum(ctrl_loop.z[:, :T0], axis=1)/(T0/1000))
print('target =', [y_ref*1000, y_ref*1000])
print('lqr achieved =', (np.sum(ctrl_loop.z[:, T0:T0+T1], axis=1)/(T1/1000)).round(1))
```

```
Results (spikes/second):
baseline = [100. 120.]
target = [200.0, 200.0]
lqr achieved = [928.6 748.6]
```

We can see that the system consistently underestimates the true firing rate. And as we could expect, we weren't able

to maintain the target firing rate with both neurons simultaneously since one was exposed to more light than the other. However, the controller was able to achieve something. See the appendix for how we can avoid overshooting with both neurons, which should be avoidable.

Conclusion

As a recap, in this tutorial we've seen how to:

- inject optogenetic stimulation into an existing Brian network
- inject an electrode into an existing Brian network to record spikes
- generate training data and fit a Gaussian linear dynamical system to the spiking output using `ldsctrlest`
- configure an `ldsctrlest` LQR controller based on that linear system and design optimal gains
- use that controller in running a complete simulated feedback control experiment

Appendix

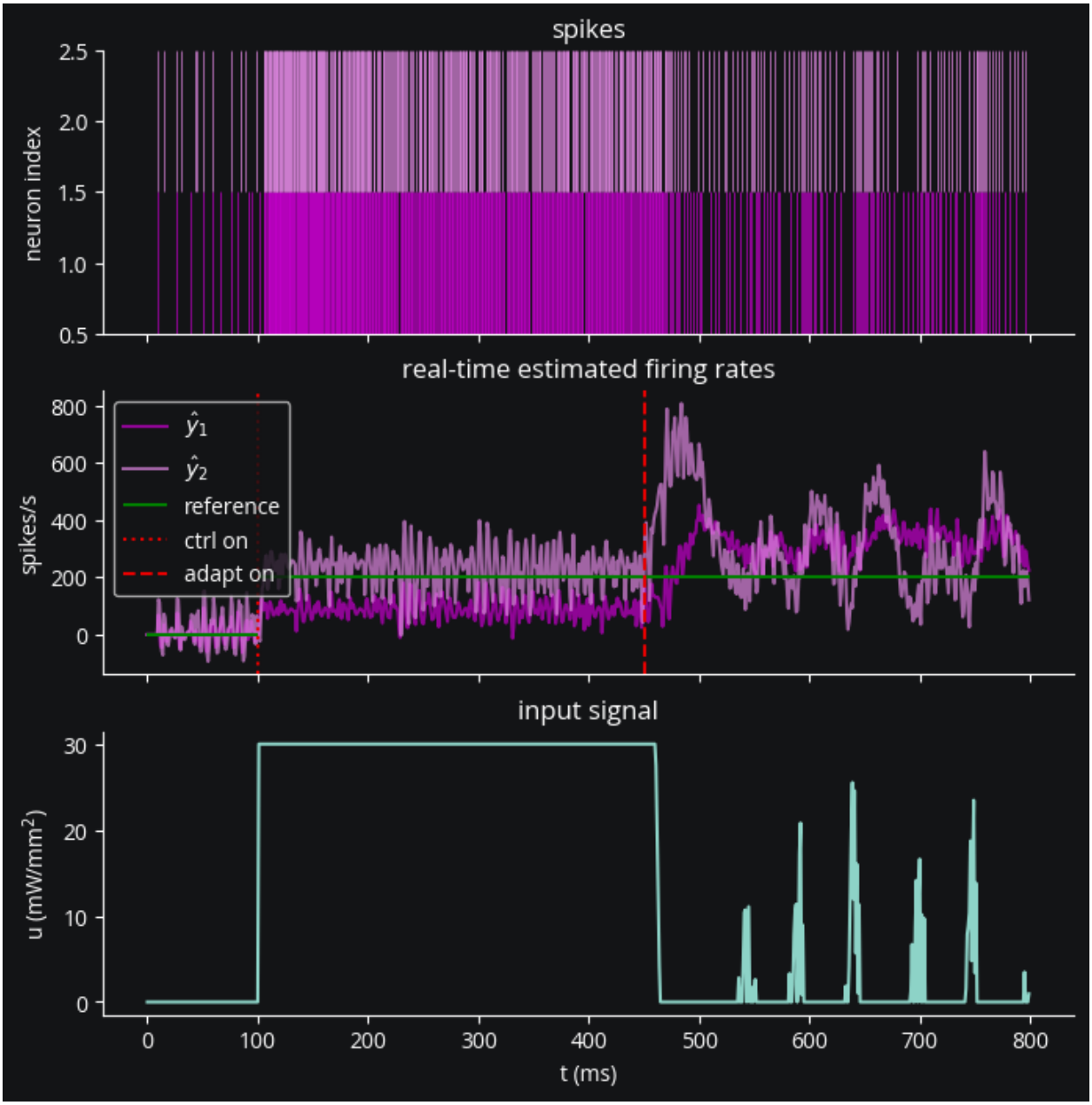
Adaptive control

ldsCtrlEst also provides an *adaptive* variation on LQR, capable of inferring state beyond our static, linear model and thus able to account for unmodeled disturbances and noise. Let's see how it compares:

```
controller.sys.do_adapt_m = True  # enable adaptive disturbance estimation
# set covariance for the disturbance state
# larger values mean the system more readily ascribes changes to unmodeled disturbance
controller.sys.Q_m = 1e-2 * np.eye(n_x_fit)
controller.control_type = lds.kControlTypeAdaptM  # enable adaptive control
```

```
ctrl_loop.sys.do_adapt_m = True
T2 = 350
sim.run(T2*ms)
T = T0 + T1 + T2
```

```
fig, (ax1, ax2, ax3) = plt.subplots(3, 1, sharex=True, figsize=(8,8))
spikes1 = spikes.t_ms[spikes.i == 0]
spikes2 = spikes.t_ms[spikes.i == 1]
ax1.eventplot([spikes1, spikes2], lineoffsets=[1, 2], colors=[c1, c2], lw=0.5)
ax1.set(ylabel='neuron index', ylim=(.5, 2.5), title='spikes')
ax2.set(ylabel='spikes/s', title='real-time estimated firing rates')
ax2.plot(ctrl_loop.y_hat[0]/dt, c=c1, alpha=0.7, label='$\hat{y}_1$')
ax2.plot(ctrl_loop.y_hat[1]/dt, c=c2, alpha=0.7, label='$\hat{y}_2$')
ax2.hlines(y_ref/dt, 100, T, color='green', label='reference')
ax2.hlines(0, 0, 100, color='green')
ax2.axvline(T0, c='xkcd:red', linestyle=':', label='ctrl on')
ax2.axvline(T0+T1, c='xkcd:red', linestyle='--', label='adapt on')
ax2.legend(loc="upper left")
ax3.plot(range(T), ctrl_loop.u.T)
ax3.set(xlabel='t (ms)', ylabel='u (mW/mm$^2$)', title='input signal');
```



We can see the effect most easily in the input signal, which has much more variation now. Let's confirm that the firing rates were better balanced around the target:

```
print("Results (spikes/second):")
print('baseline =', np.sum(ctrl_loop.z[:, :T0], axis=1)/(T0/1000))
print('target =', [y_ref*1000, y_ref*1000])
print('static achieved =', (np.sum(ctrl_loop.z[:, T0:T0+T1], axis=1)/(T1/1000)).round(1))
print('adaptive achieved =', (np.sum(ctrl_loop.z[:, T0+T1:T], axis=1)/(T2/1000)).
↪round(1))
```

```
Results (spikes/second):
baseline = [100. 120.]
target = [200.0, 200.0]
```

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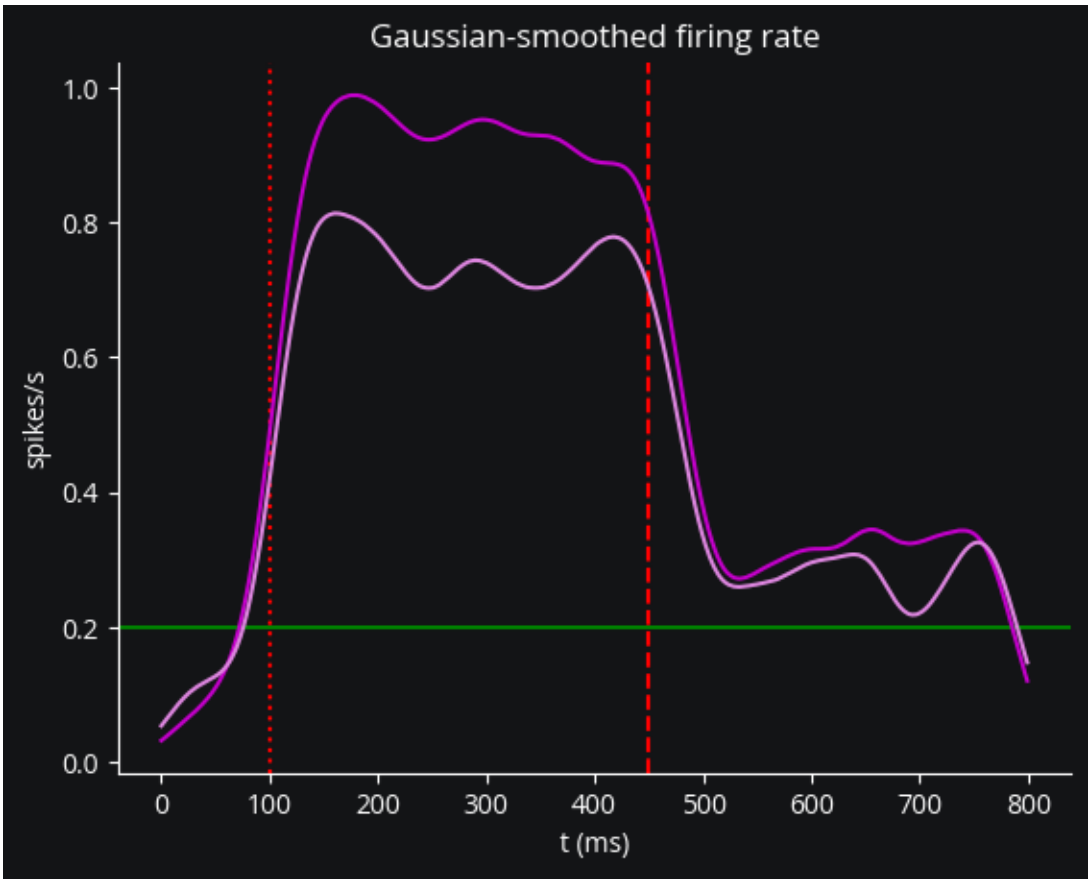
```
static achieved = [928.6 748.6]
adaptive achieved = [354.3 317.1]
```

That looks better. Adaptive control achieves a balance between the two neurons, as we would expect.

Post-hoc firing rate estimate

To see if the system's online estimation of firing rates is reasonable, we compute a Gaussian-smoothed version with a 25-ms standard deviation:

```
from scipy.stats import norm
kernel = norm.pdf(np.linspace(-75, 75, 151), scale=25)  # 25-ms  Gaussian window
smoothed1 = np.convolve(ctrl_loop.z[0, :], kernel, mode='same')
smoothed2 = np.convolve(ctrl_loop.z[1, :], kernel, mode='same')
plt.axhline(y_ref, c='g')
plt.axvline(T0, c='r', ls=':')
plt.axvline(T0+T1, c='r', ls='--')
plt.xlabel("t (ms)")
plt.ylabel("spikes/s")
plt.title("Gaussian-smoothed firing rate")
plt.plot(smoothed1, c=c1)
plt.plot(smoothed2, c=c2);
```



6.2.7 All-optical control

In this tutorial we'll see how to

- configure and inject a microscope for two-photon imaging and stimulation
- inject a calcium indicator for neurons visible to the microscope
- set up two-photon optogenetics by
  - injecting an opsin with an extended action spectrum and
  - injecting a 2P light source targeting neurons imaged by the microscope

Preamble

```
import brian2 as b2
from brian2 import np
import cleo
from cleo import opto, imaging, light
import matplotlib.pyplot as plt

# for reproducibility
rng = np.random.default_rng(92)
np.random.seed(92)

cleo.utilities.style_plots_for_docs()
```

Brian network setup

All we need are LIF neurons that will spike in response to photostimulation for us to see the resulting fluorescence traces.

```
ng = b2.NeuronGroup(
    200,
    """dv/dt = (-(v - E_L) + Rm*Iopto) / tau_m : volt
    Iopto : amp""",
    threshold="v > -50*mV",
    reset="v=E_L",
    namespace={
        "tau_m": 20 * b2.ms,
        "Rm": 500 * b2.Mohm,
        "E_L": -70 * b2.mV,
    },
)
ng.v = -70 * b2.mV
cleo.coords.assign_coords_rand_rect_prism(ng, [-0.2, 0.2], [-0.2, 0.2], [0, 0.4])
sim = cleo.CLSimulator(b2.Network(ng))
```

Microscope configuration

By default a scope selects neurons based on focus depth and assigns them a signal-to-noise ratio (SNR) based on soma size. (Larger cells' SNR decays more slowly with distance from the focal plane.) `focus_depth` and `soma_radius` are taken from scope parameters but can be overridden on injection.

We'll use GCaMP6f as our indicator and leave the default parameters, though those can be changed in the function call *gcamp6f()*.

```
scope = imaging.Scope(
    focus_depth=100 * b2.um,
    img_width=500 * b2.um,
    sensor=imaging.gcamp6f(),
)
```

Heterogeneous expression is simulated by providing a `rho_rel_generator` function that takes the number of neurons as an argument and returns a vector of relative expression levels. This is done on scope injection (as opposed to sensor injection afterward) because the scope needs this information to select ROIs with sufficiently high SNR.

```
expr_level_gen = lambda n: rng.lognormal(0, 0.2, n)
sim.inject(scope, ng, rho_rel_generator=expr_level_gen)  # uses scope's parameters
# optional overrides (we'll use a small soma to intentionally get few targets)
sim.inject(scope, ng, focus_depth=200 * b2.um, soma_radius=5 * b2.um, rho_rel_
↪generator=expr_level_gen)
```

```
CLSimulator(io_processor=None, devices={Scope(sim=..., name='Scope', save_history=True,␣
↪sensor=GECI(sim=None, name='gcamp6f', save_history=True, model='\n            dCa/dt =␣
↪-gamma * (Ca - Ca_rest) / (1 + kappa_S + kappa_B) : mmolar (clock-driven)\n           ␣
↪kappa_B = B_T * K_d / (Ca + K_d)**2 : 1\n\n            CaB_active = Ca_rest + b :␣
↪mmolar  # add tiny bit to avoid /0\n            db/dt = beta : mmolar (clock-driven)\n␣
↪           lam = 1/tau_off + 1/tau_on : 1/second\n            kap = 1/tau_off : 1/
↪second\n            dbeta/dt = (                    # should be M/s/s\n               ␣
↪A * (lam - kap) * (Ca - Ca_rest)  # M/s/s\n                - (kap + lam) * beta
↪# M/s/s\n                - kap * lam * b    # M/s/s\n            ) : mmolar/second␣
↪(clock-driven)\n            \nexc_factor = 1 : 1\n\n            dFF_baseline = 1 / (1␣
↪+ (K_d / Ca_rest) ** n_H) : 1\n            dFF = exc_factor * rho_rel * dFF_max  * (\n␣
↪               1 / (1 + (K_d / CaB_active) ** n_H)\n                - dFF_baseline\n  ␣
↪         ) : 1\n            rho_rel : 1\n        ', on_pre='Ca += dCa_T / (1 + kappa_S␣
↪+ kappa_B)', sigma_noise=0.03748181818181818, dFF_1AP=0.09775500000000001, location=
↪'cytoplasm', cal_model=DynamicCalcium(on_pre='Ca += dCa_T / (1 + kappa_S + kappa_B)',␣
↪model='\n            dCa/dt = -gamma * (Ca - Ca_rest) / (1 + kappa_S + kappa_B) :␣
↪mmolar (clock-driven)\n            kappa_B = B_T * K_d / (Ca + K_d)**2 : 1', Ca_
↪rest=50. * nmolar, gamma=292.3 * hertz, B_T=200. * umolar, kappa_S=110, dCa_T=7.6 *␣
↪umolar), bind_act_model=DoubExpCalBindingActivation(model='\n            CaB_active =␣
↪Ca_rest + b : mmolar  # add tiny bit to avoid /0\n            db/dt = beta : mmolar␣
↪(clock-driven)\n            lam = 1/tau_off + 1/tau_on : 1/second\n            kap = 1/
↪tau_off : 1/second\n            dbeta/dt = (                    # should be M/s/s\n   ␣
↪            A * (lam - kap) * (Ca - Ca_rest)  # M/s/s\n                - (kap + lam) *␣
↪beta        # M/s/s\n                - kap * lam * b    # M/s/s\n            ) :␣
↪mmolar/second (clock-driven)\n            ', A=7.61251 * khertz, tau_on=1.17164616 *␣
↪second, tau_off=10.14020867 * msecond, Ca_rest=50. * nmolar), exc_
↪model=NullExcitation(model='exc_factor = 1 : 1'), fluor_model='\n            dFF_
↪baseline = 1 / (1 + (K_d / Ca_rest) ** n_H) : 1\n            dFF = exc_factor * rho_
↪rel * dFF_max  * (\n                1 / (1 + (K_d / CaB_active) ** n_H)\n            ␣
```

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```
↪  - dFF_baseline\n            ) : 1\n            rho_rel : 1\n        ', K_d=290. *␣
↪nmolar, n_H=2.7, dFF_max=25.2), img_width=0.5 * mmetre, focus_depth=100. * umetre,␣
↪location=array([0., 0., 0.]) * metre, direction=array([0., 0., 1.]), soma_radius=10. *␣
↪umetre, snr_cutoff=1)})
```

Signal strength (F/F for 1 spike) per ROI is thus defined as *dFF_1AP* * rho_rel.

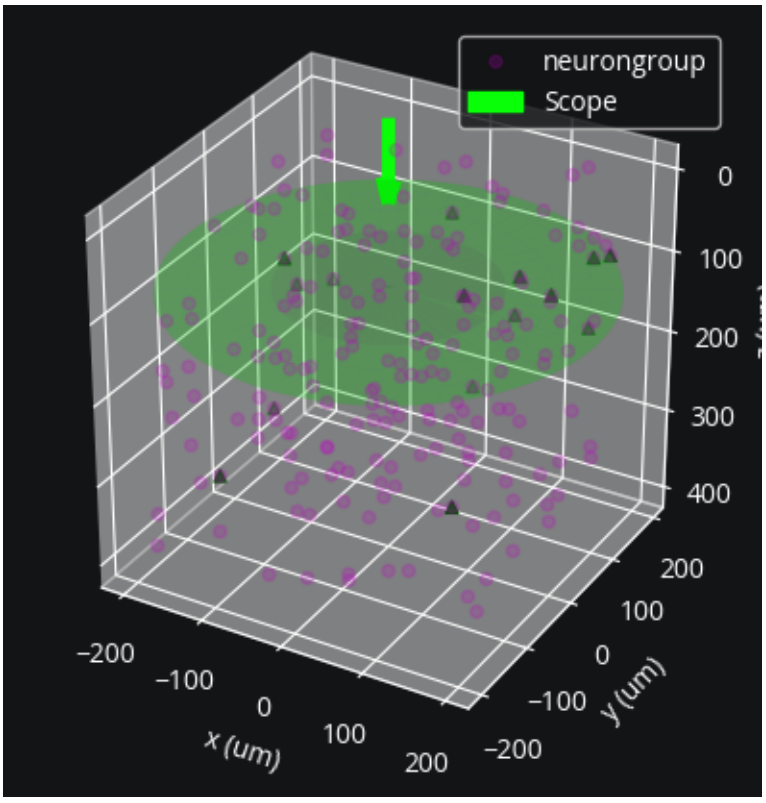
While Cleo adjusts noise levels according to distance from the focal plane automatically, other adjustments can be made manually by calling *target_neurons_in_plane()* to reflect factors such as cell heterogeneity or indicator expression or increased noise with depth.

Neurons with SNR (defined as *dFF_1AP* / *sigma_noise*) below the scope's *snr_cutoff* parameter are discarded.

```
i_targets, noise_focus_factor, focus_coords = scope.target_neurons_in_plane(ng, focus_
↪depth=300 * b2.um, soma_radius=5 * b2.um)
# scale noise std  randomly to simulate biological variability
std_noise = scope.sensor.sigma_noise * noise_focus_factor * rng.normal(1, .2, len(i_
↪targets))
sim.inject(scope, ng, focus_depth=None, i_targets=i_targets, sigma_noise=std_noise, rho_
↪rel_generator=expr_level_gen)

cleo.viz.plot(ng, colors=['#c500cc'], sim=sim)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (um)', ylabel='y (um)', zlabel='z (um)'>)
```



We can see targets off the visualized plane, resulting from our injections at 200 and 300 m depths, resembling a multi-plane imaging experiment.

When `focus_depth` is set to `None`, corresponding to sculpted holographic imaging, the scope will select all neurons in the volume, or the user can specify a list of neurons to select via `i_targets` on injection.

After all targets are specified, the sensor protein must also be injected. Doing it this way allows for efficiency: the sensor protein is only simulated for the imaged neurons. Expression levels are as sampled previously on scope injection.

```
scope.inject_sensor_for_targets()
```

2p stimulation configuration

Future work will address how to better quantify the relationship between 2P and the 1P action spectra, but for now we'll pretend that Vf-Chrimson activation at 1060 nm is 1/100th that of peak 1P activation for the same power density.

```
opsin = opto.vfchrimson_4s()
opsin.spectrum.append((1060, .01))
sim.inject(opsin, ng)
```

```
CLSimulator(io_processor=None, devices={GECI(sim=..., name='gcamp6f', save_history=True,␣
↪model='\n            dCa/dt = -gamma * (Ca - Ca_rest) / (1 + kappa_S + kappa_B) :␣
↪mmolar (clock-driven)\n            kappa_B = B_T * K_d / (Ca + K_d)**2 : 1\n\n        ␣
↪   CaB_active = Ca_rest + b : mmolar  # add tiny bit to avoid /0\n            db/dt =␣
↪beta : mmolar (clock-driven)\n            lam = 1/tau_off + 1/tau_on : 1/second\n     ␣
↪      kap = 1/tau_off : 1/second\n            dbeta/dt = (                    # should␣
↪be M/s/s\n                A * (lam - kap) * (Ca - Ca_rest)  # M/s/s\n                -␣
↪(kap + lam) * beta        # M/s/s\n                - kap * lam * b    # M/s/s\n       ␣
↪    ) : mmolar/second (clock-driven)\n            \nexc_factor = 1 : 1\n\n           ␣
↪dFF_baseline = 1 / (1 + (K_d / Ca_rest) ** n_H) : 1\n            dFF = exc_factor *␣
↪rho_rel * dFF_max  * (\n                1 / (1 + (K_d / CaB_active) ** n_H)\n         ␣
↪      - dFF_baseline\n            ) : 1\n            rho_rel : 1\n        ', on_pre=
↪'Ca += dCa_T / (1 + kappa_S + kappa_B)', sigma_noise=0.03748181818181818, dFF_1AP=0.
↪09775500000000001, location='cytoplasm', cal_model=DynamicCalcium(on_pre='Ca += dCa_T /
↪ (1 + kappa_S + kappa_B)', model='\n            dCa/dt = -gamma * (Ca - Ca_rest) / (1␣
↪+ kappa_S + kappa_B) : mmolar (clock-driven)\n            kappa_B = B_T * K_d / (Ca +␣
↪K_d)**2 : 1', Ca_rest=50. * nmolar, gamma=292.3 * hertz, B_T=200. * umolar, kappa_
↪S=110, dCa_T=7.6 * umolar), bind_act_model=DoubExpCalBindingActivation(model='\n      ␣
↪     CaB_active = Ca_rest + b : mmolar  # add tiny bit to avoid /0\n            db/dt␣
↪= beta : mmolar (clock-driven)\n            lam = 1/tau_off + 1/tau_on : 1/second\n   ␣
↪        kap = 1/tau_off : 1/second\n            dbeta/dt = (                    #␣
↪should be M/s/s\n                A * (lam - kap) * (Ca - Ca_rest)  # M/s/s\n         ␣
↪     - (kap + lam) * beta        # M/s/s\n                - kap * lam * b    # M/s/s\n␣
↪           ) : mmolar/second (clock-driven)\n            ', A=7.61251 * khertz, tau_
↪on=1.17164616 * second, tau_off=10.14020867 * msecond, Ca_rest=50. * nmolar), exc_
↪model=NullExcitation(model='exc_factor = 1 : 1'), fluor_model='\n            dFF_
↪baseline = 1 / (1 + (K_d / Ca_rest) ** n_H) : 1\n            dFF = exc_factor * rho_
↪rel * dFF_max  * (\n                1 / (1 + (K_d / CaB_active) ** n_H)\n            ␣
↪  - dFF_baseline\n            ) : 1\n            rho_rel : 1\n        ', K_d=290. *␣
↪nmolar, n_H=2.7, dFF_max=25.2), Scope(sim=..., name='Scope', save_history=True,␣
↪sensor=GECI(sim=..., name='gcamp6f', save_history=True, model='\n            dCa/dt = -
↪gamma * (Ca - Ca_rest) / (1 + kappa_S + kappa_B) : mmolar (clock-driven)\n            ␣
↪kappa_B = B_T * K_d / (Ca + K_d)**2 : 1\n\n            CaB_active = Ca_rest + b :␣
↪mmolar  # add tiny bit to avoid /0\n            db/dt = beta : mmolar (clock-driven)\n␣
↪           lam = 1/tau_off + 1/tau_on : 1/second\n            kap = 1/tau_off : 1/
↪second\n            dbeta/dt = (                    # should be M/s/s\n            ␣
```

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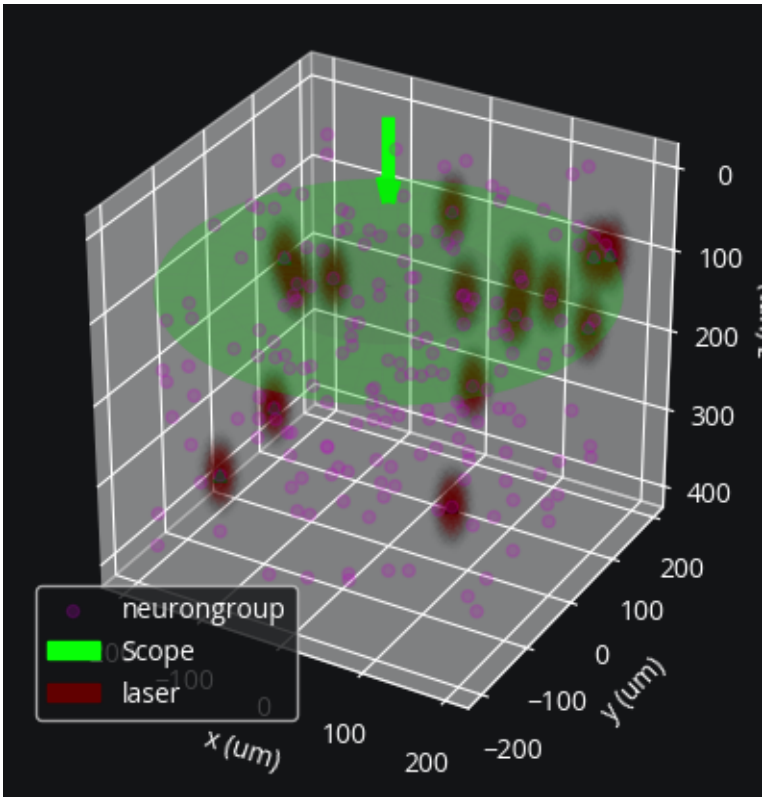
```
↪A * (lam - kap) * (Ca - Ca_rest)  # M/s/s\n                - (kap + lam) * beta
↪# M/s/s\n                - kap * lam * b    # M/s/s\n            ) : mmolar/second␣
↪(clock-driven)\n            \nexc_factor = 1 : 1\n\n            dFF_baseline = 1 / (1␣
↪+ (K_d / Ca_rest) ** n_H) : 1\n            dFF = exc_factor * rho_rel * dFF_max  * (\n␣
↪               1 / (1 + (K_d / CaB_active) ** n_H)\n                - dFF_baseline\n  ␣
↪         ) : 1\n            rho_rel : 1\n        ', on_pre='Ca += dCa_T / (1 + kappa_S␣
↪+ kappa_B)', sigma_noise=0.03748181818181818, dFF_1AP=0.09775500000000001, location=
↪'cytoplasm', cal_model=DynamicCalcium(on_pre='Ca += dCa_T / (1 + kappa_S + kappa_B)',␣
↪model='\n            dCa/dt = -gamma * (Ca - Ca_rest) / (1 + kappa_S + kappa_B) :␣
↪mmolar (clock-driven)\n            kappa_B = B_T * K_d / (Ca + K_d)**2 : 1', Ca_
↪rest=50. * nmolar, gamma=292.3 * hertz, B_T=200. * umolar, kappa_S=110, dCa_T=7.6 *␣
↪umolar), bind_act_model=DoubExpCalBindingActivation(model='\n            CaB_active =␣
↪Ca_rest + b : mmolar  # add tiny bit to avoid /0\n            db/dt = beta : mmolar␣
↪(clock-driven)\n            lam = 1/tau_off + 1/tau_on : 1/second\n            kap = 1/
↪tau_off : 1/second\n            dbeta/dt = (                    # should be M/s/s\n  ␣
↪            A * (lam - kap) * (Ca - Ca_rest)  # M/s/s\n                - (kap + lam) *␣
↪beta        # M/s/s\n                - kap * lam * b    # M/s/s\n            ) :␣
↪mmolar/second (clock-driven)\n            ', A=7.61251 * khertz, tau_on=1.17164616 *␣
↪second, tau_off=10.14020867 * msecond, Ca_rest=50. * nmolar), exc_
↪model=NullExcitation(model='exc_factor = 1 : 1'), fluor_model='\n            dFF_
↪baseline = 1 / (1 + (K_d / Ca_rest) ** n_H) : 1\n            dFF = exc_factor * rho_
↪rel * dFF_max  * (\n                1 / (1 + (K_d / CaB_active) ** n_H)\n            ␣
↪  - dFF_baseline\n            ) : 1\n            rho_rel : 1\n        ', K_d=290. *␣
↪nmolar, n_H=2.7, dFF_max=25.2), img_width=0.5 * mmetre, focus_depth=100. * umetre,␣
↪location=array([0., 0., 0.]) * metre, direction=array([0., 0., 1.]), soma_radius=10. *␣
↪umetre, snr_cutoff=1), BansalFourStateOpsin(sim=..., name='VfChrimson', save_
↪history=True, on_pre='', spectrum=[(470.0, 0.4123404255319149), (490.0, 0.
↪593265306122449), (510.0, 0.7935294117647058), (530.0, 0.8066037735849055), (550.0, 0.
↪8912727272727272), (570.0, 1.0), (590.0, 0.9661016949152542), (610.0, 0.
↪7475409836065574), (630.0, 0.4342857142857143), (1060, 0.01)], required_vars=[('Iopto',
↪ amp), ('v', volt)], Gd1=0.37 * khertz, Gd2=175. * hertz, Gr0=0.667 * mhertz, g0=17.5␣
↪* nsiemens, phim=1.5e+22 * (second ** -1) / (meter ** 2), k1=3. * khertz, k2=200. *␣
↪hertz, Gf0=20. * hertz, Gb0=3.2 * hertz, kf=10. * hertz, kb=10. * hertz, gamma=0.05,␣
↪p=1, q=1, E=0. * volt, model='\n        dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-
↪driven)\n        dO1/dt = Ga1*C1 + Gb*O2 - (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/
↪dt = Ga2*C2 + Gf*O1 - (Gd2+Gb)*O2 : 1 (clock-driven)\n        C2 = 1 - C1 - O1 - O2 :␣
↪1\n\n        Theta = int(phi_pre > 0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/
↪(phi_pre**p + phim**p) : 1\n        Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n␣
↪       Hq = Theta * phi_pre**q/(phi_pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 :␣
↪hertz\n        Gb = kb*Hq + Gb0 : hertz\n\n        fphi = O1 + gamma*O2 : 1\n\n       ␣
↪IOPTO_VAR_NAME_post = -g0*fphi*(V_VAR_NAME_post-E)*rho_rel : ampere (summed)\n       ␣
↪rho_rel : 1')})
```

Now, to target these neurons with 2P laser power, we use *tp_light_from_scope()* to create a `Light` object with a 2P laser *GaussianEllipsoid* light profile centered on each of the scope's targets:

```
laser = light.tp_light_from_scope(scope, wavelength=1060*b2.nmeter, name='laser')
sim.inject(laser, ng)
cleo.viz.plot(ng, colors=['#c500cc'], sim=sim)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (um)', ylabel='y (um)', zlabel='z (um)'>)
```



Simulating an all-optical experiment

We'll stimulate each neuron with a different number of laser pulses and see the resulting calcium traces.

```
from cleo.ioproc import LatencyIOProcessor

# for seeing ground-truth spikes
i_all_targets = scope.i_targets_for_neuron_group(ng)
smon = b2.SpikeMonitor(ng, record=i_all_targets)
sim.network.add(smon)

amplitude_mW = 2.5
pulse_width_ms = 2
interpulse_ms = 20

num_pulses = np.arange(1, scope.n + 1)
train_ends_ms = interpulse_ms * num_pulses


class IOProc(LatencyIOProcessor):
    def process(self, state_dict, time_ms):
        t_in_cycle = time_ms % interpulse_ms
        on = (0 <= t_in_cycle) & (t_in_cycle < pulse_width_ms) & (time_ms < (interpulse_
↪ms * num_pulses))

        return {"laser": on * amplitude_mW}, time_ms
```

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```
sim.set_io_processor(IOProc(1))

sim.reset()
tmax = 1000
sim.run(tmax * b2.ms)
```

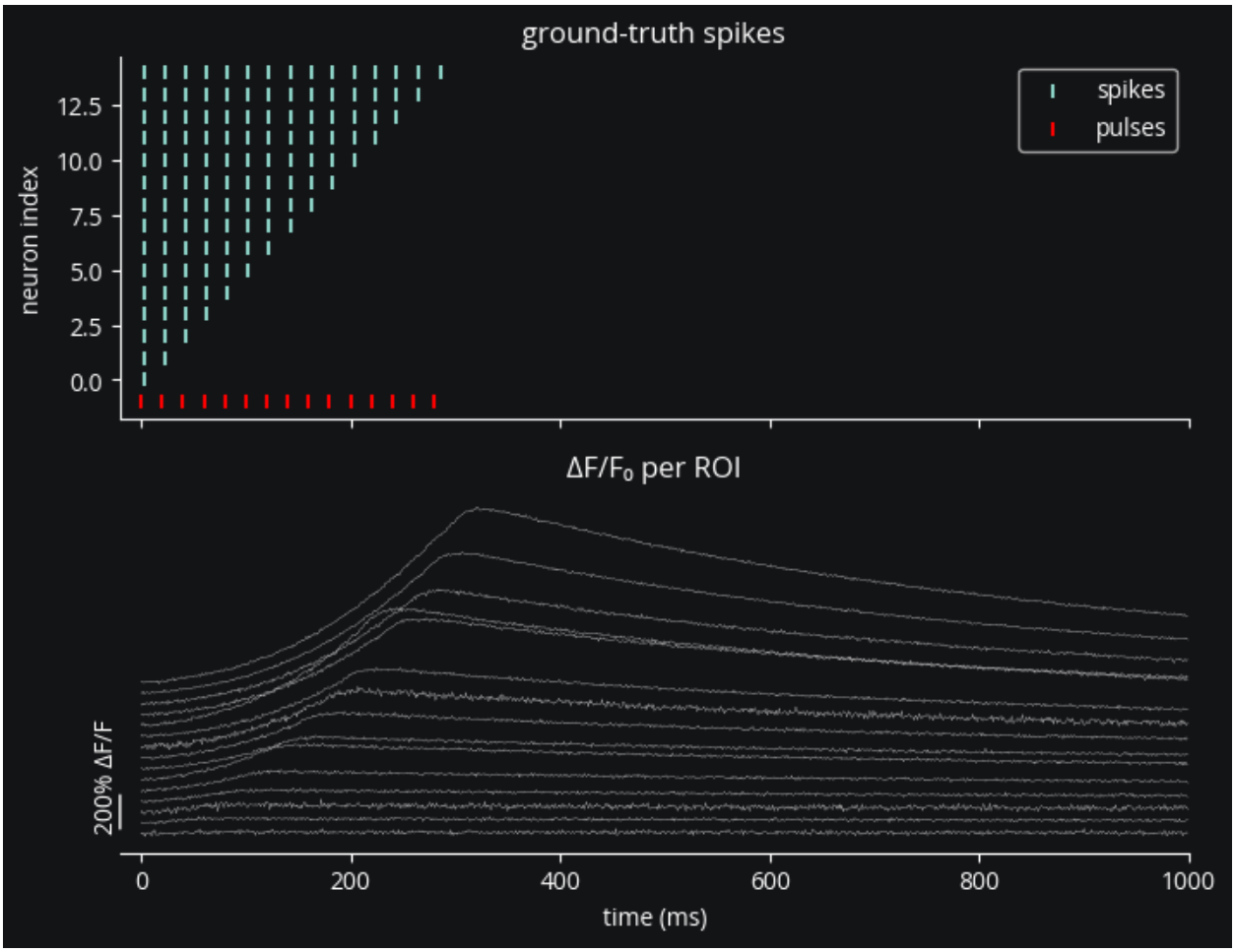
```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'exact' (took 0.18s). [brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_VfChrimson_
↪neurongroup', using method 'euler' (took 0.02s, trying other methods took 0.06s).␣
↪[brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_gcamp6f_neurongroup',
↪ using method 'euler' (took 0.02s, trying other methods took 0.05s). [brian2.
↪stateupdaters.base.method_choice]
```

Now we'll plot the result:

```
import matplotlib.pyplot as plt
sep = .5
n2plot = len(i_all_targets)
fig, (ax1, ax2) = plt.subplots(2, 1, figsize=(8, 6), sharex=True)

spt = np.empty((0,))
spi = np.empty((0,))
for i_target, i_ng in enumerate(i_all_targets):
    single_spt = smon.t[smon.i == i_ng]
    spt = np.concatenate((spt, single_spt))
    spi = np.concatenate((spi, np.full_like(single_spt, i_target)))
ax1.scatter(spt / b2.ms, spi, marker='|', label='spikes')
t_pulse_ms = np.arange(0, num_pulses.max() * interpulse_ms, interpulse_ms)
ax1.scatter(t_pulse_ms, np.full_like(t_pulse_ms, -1), marker='|', color='r', label=
↪'pulses')
ax1.set(ylabel='neuron index', title='ground-truth spikes', xlim=(0, tmax))
ax1.legend()

ax2.plot(scope.t_ms[:], np.array(scope.dFF)[:, :n2plot] + sep*np.arange(n2plot), lw=.2,␣
↪c='w')
y_scale = 2
y0 = 0
x0 = -20
ax2.set(xlabel='time (ms)', title='F/F₀ per ROI', xlim=(x0, tmax))
ax2.annotate('', xy=(x0, y0), xytext=(x0, y0 + y_scale), arrowprops=dict(arrowstyle='-'))
ax2.annotate(f'{y_scale * 100}% F/F', xy=(x0, y0), va='bottom', ha='right', rotation=90)
ax2.yaxis.set_visible(False)
ax2.spines['left'].set_visible(False)
```



Results are as expected:

- We see one spike for every pulse, though for longer trains we might start to see missed spikes due to the opsin activation plateauing.
- If neurons were closer together, we'd expect to see some off-target effects; if there are any here, they are apparently subthreshold.
- Signal strength is proportional to the number of spikes, as expected, but varies somewhat due to heterogeneous expression.
- We also see that noise levels vary from ROI to ROI due to varying distances from the focal plane.

6.2.8 Video visualization

In this tutorial we'll see how to inject a video visualizer into a simulation.

Preamble:

```
import brian2.only as b2
from brian2 import np
import matplotlib.pyplot as plt

import cleo
```

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```
cleo.utilities.style_plots_for_docs()

# numpy faster than cython for lightweight example
b2.prefs.codegen.target = 'numpy'
# for reproducibility
np.random.seed(1866)

c_exc = 'xkcd:tomato'
c_inh = 'xkcd:cerulean blue'
```

```
WARNING    /home/kyle/miniforge3/envs/cleo/lib/python3.12/site-packages/attr/_make.
↪py:918: RuntimeWarning: Running interpreter doesn't sufficiently support code object␣
↪introspection.  Some features like bare super() or accessing __class__ will not work␣
↪with slotted classes.
  set_closure_cell(cell, cls)
 [py.warnings]
```

Set up the simulation

Network

We'll use excitatory and inhibitory populations of exponential integrate-and-fire neurons.

```
n_e = 400
n_i = n_e // 4
def eif(n, name):
    ng = b2.NeuronGroup(
        n,
        """
        dv/dt = (-(v - E_L) + Delta_T*exp((v-theta)/Delta_T) + Rm*I) / tau_m : volt
        I : amp
        """,
        threshold="v>30*mV",
        reset="v=-55*mV",
        namespace={
            "tau_m": 20 * b2.ms,
            "Rm": 500 * b2.Mohm,
            "theta": -50 * b2.mV,
            "Delta_T": 2 * b2.mV,
            "E_L": -70*b2.mV,
        },
        name=name,
    )
    ng.v = -70 * b2.mV
    return ng

exc = eif(n_e, "exc")
inh = eif(n_i, "inh")
W = 250
```

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```
p_S = 0.3
S_ei = b2.Synapses(exc, inh, on_pre="v_post+=W*mV/n_e")
S_ei.connect(p=p_S)
S_ie = b2.Synapses(inh, exc, on_pre="v_post-=W*mV/n_i")
S_ie.connect(p=p_S)
S_ee = b2.Synapses(exc, exc, on_pre="v_post+=W*mV/n_e")
S_ee.connect(condition='abs(i-j)<=20')

mon_e = b2.SpikeMonitor(exc)
mon_i = b2.SpikeMonitor(inh)

net = b2.Network(exc, inh, S_ei, S_ie, S_ee, mon_e, mon_i)
```

Coordinates and optogenetics

Here we configure the coordinates and optogenetic stimulation. For more details, see the *"Optogenetic stimulation" tutorial*. Note that we save the arguments used in the plotting function for reuse later on when generating the video.

```
from cleo.coords import assign_coords_uniform_cylinder
from cleo.viz import plot

r = 1
assign_coords_uniform_cylinder(
    exc, xyz_start=(0, 0, 0.3), xyz_end=(0, 0, 0.4), radius=r
)
assign_coords_uniform_cylinder(
    inh, xyz_start=(0, 0, 0.3), xyz_end=(0, 0, 0.4), radius=r
)
```

```
from cleo.opto import chr2_4s
from cleo.light import fiber473nm, Light

opsin = chr2_4s()
fibers = Light(
    coords=[[0, 0, 0], [700, 0, 0]] * b2.um,
    light_model=fiber473nm(),
    max_Irr0_mW_per_mm2=30,
    save_history=True,
)

plotargs = {
    "colors": [c_exc, c_inh],
    "zlim": (0, 600),
    "scatterargs": {"s": 20},  # to adjust neuron marker size
    "axis_scale_unit": b2.um,
}

plot(
    exc,
    inh,
```

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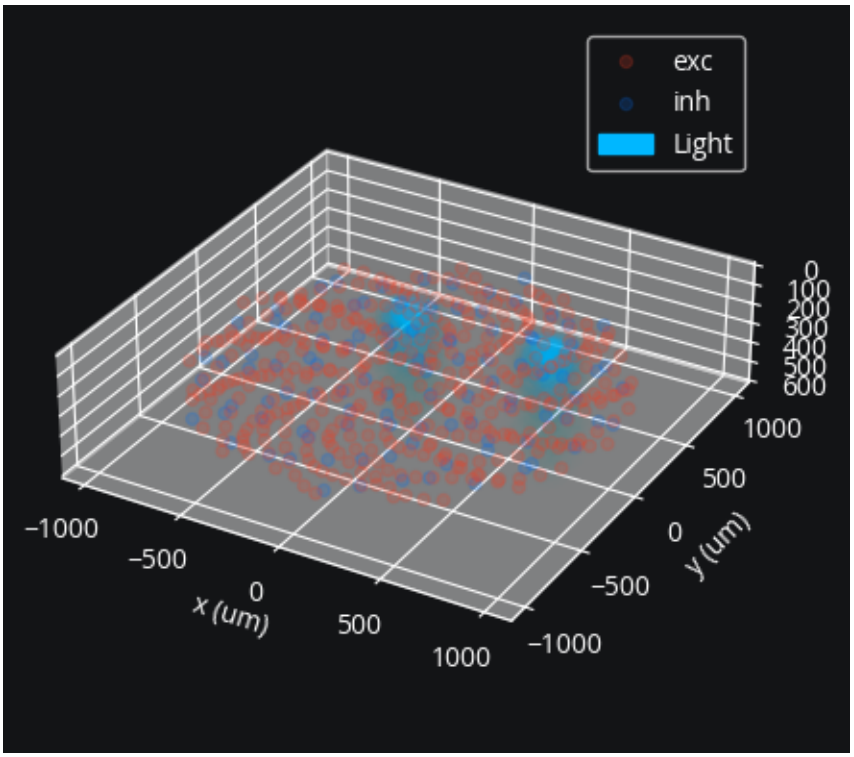
```
    **plotargs,
    devices=[fibers],
)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (um)', ylabel='y (um)', zlabel='z (um)'>)
```



Simulator, optogenetics injection

Here we create the simulator and inject the `OptogeneticIntervention`.

```
sim = cleo.CLSimulator(net)
sim.inject(opsin, exc, Iopto_var_name='I')
sim.inject(fibers, exc)
```

```
CLSimulator(io_processor=None, devices={Light(name='Light', save_history=True,␣
↪value=array([0., 0.]), light_model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=125. *␣
↪metre ** -1, S=7370. * metre ** -1, ntis=1.36), wavelength=0.473 * umetre,␣
↪direction=array([0., 0., 1.]), max_Irr0_mW_per_mm2=30, max_Irr0_mW_per_mm2_viz=None),␣
↪FourStateOpsin(name='ChR2', save_history=True, on_pre='', spectrum=[(400, 0.34), (422,␣
↪0.65), (460, 0.96), (470, 1), (473, 1), (500, 0.57), (520, 0.22), (540, 0.06), (560, 0.
↪01)], required_vars=[('Iopto', amp), ('v', volt)], g0=114. * nsiemens, gamma=0.00742,␣
↪phim=2.33e+23 * (second ** -1) / (meter ** 2), k1=4.15 * khertz, k2=0.868 * khertz,␣
↪p=0.833, Gf0=37.3 * hertz, kf=58.1 * hertz, Gb0=16.1 * hertz, kb=63. * hertz, q=1.94,␣
↪Gd1=105. * hertz, Gd2=13.8 * hertz, Gr0=0.33 * hertz, E=0. * volt, v0=43. * mvolt,␣
↪v1=17.1 * mvolt, model="\n        dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\
```

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```
↪n        dO1/dt = Ga1*C1 + Gb*O2 - (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt =␣
↪Ga2*C2 + Gf*O1 - (Gd2+Gb)*O2 : 1 (clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n␣
↪       Theta = int(phi_pre > 0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_
↪pre**p + phim**p) : 1\n        Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n     ␣
↪  Hq = Theta * phi_pre**q/(phi_pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\
↪n        Gb = kb*Hq + Gb0 : hertz\n\n        fphi = O1 + gamma*O2 : 1\n        # v1/v0␣
↪when v-E == 0 via l'Hopital's rule\n        fv = f_unless_x0(\n            (1 - exp(-
↪(V_VAR_NAME_post-E)/v0)) / ((V_VAR_NAME_post-E)/v1),\n            V_VAR_NAME_post - E,\
↪n            v1/v0\n        ) : 1\n\n        IOPTO_VAR_NAME_post = -g0*fphi*fv*(V_VAR_
↪NAME_post-E)*rho_rel : ampere (summed)\n        rho_rel : 1", extra_namespace={'f_
↪unless_x0': <brian2.core.functions.Function object at 0x7f4f3c391c40>})})
```

Processor

And we set up open-loop optogenetic stimulation:

```
fibers.update([5, 0])
class OpenLoopOpto(cleo.ioproc.LatencyIOProcessor):
    def process(self, state_dict, time_ms):
        # random walk stimulation
        fiber_intensities = fibers.value + np.random.randn(2)*.5
        fiber_intensities[fiber_intensities < 0] = 0
        if time_ms > 50:
            fiber_intensities = [0, 5]
        return ({"Light": fiber_intensities}, time_ms)

sim.set_io_processor(OpenLoopOpto(sample_period_ms=1))
```

```
CLSimulator(io_processor=OpenLoopOpto(sample_period_ms=1, sampling='fixed', processing=
↪'parallel'), devices={Light(name='Light', save_history=True, value=array([5, 0]),␣
↪light_model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=125. * metre ** -1, S=7370. *␣
↪metre ** -1, ntis=1.36), wavelength=0.473 * umetre, direction=array([0., 0., 1.]), max_
↪Irr0_mW_per_mm2=30, max_Irr0_mW_per_mm2_viz=None), FourStateOpsin(name='ChR2', save_
↪history=True, on_pre='', spectrum=[(400, 0.34), (422, 0.65), (460, 0.96), (470, 1),␣
↪(473, 1), (500, 0.57), (520, 0.22), (540, 0.06), (560, 0.01)], required_vars=[('Iopto',
↪ amp), ('v', volt)], g0=114. * nsiemens, gamma=0.00742, phim=2.33e+23 * (second ** -1)␣
↪/ (meter ** 2), k1=4.15 * khertz, k2=0.868 * khertz, p=0.833, Gf0=37.3 * hertz, kf=58.
↪1 * hertz, Gb0=16.1 * hertz, kb=63. * hertz, q=1.94, Gd1=105. * hertz, Gd2=13.8 *␣
↪hertz, Gr0=0.33 * hertz, E=0. * volt, v0=43. * mvolt, v1=17.1 * mvolt, model="\n      ␣
↪ dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\n        dO1/dt = Ga1*C1 + Gb*O2␣
↪- (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt = Ga2*C2 + Gf*O1 - (Gd2+Gb)*O2 : 1␣
↪(clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n        Theta = int(phi_pre >␣
↪0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_pre**p + phim**p) : 1\n       ␣
↪Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n        Hq = Theta * phi_pre**q/(phi_
↪pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\n        Gb = kb*Hq + Gb0 :␣
↪hertz\n\n        fphi = O1 + gamma*O2 : 1\n        # v1/v0 when v-E == 0 via l'Hopital
↪'s rule\n        fv = f_unless_x0(\n            (1 - exp(-(V_VAR_NAME_post-E)/v0)) /␣
↪((V_VAR_NAME_post-E)/v1),\n            V_VAR_NAME_post - E,\n            v1/v0\n      ␣
↪ ) : 1\n\n        IOPTO_VAR_NAME_post = -g0*fphi*fv*(V_VAR_NAME_post-E)*rho_rel :␣
↪ampere (summed)\n        rho_rel : 1", extra_namespace={'f_unless_x0': <brian2.core.
↪functions.Function object at 0x7f4f3c391c40>})})
```

Inject VideoVisualizer

A `VideoVisualizer` is an `InterfaceDevice` like recorders and stimulators and needs to be injected in order to properly interact with the Brian network. Keep in mind the following:

- It must be injected *after* all other devices for the `devices='all'` argument to work as expected.
- Similarly to recording and stimulation, you must specify the target neuron groups (to display, in this case) on injection
- The `dt` argument makes a huge difference on the amount of time it takes to generate the video. You may want to keep this high while experimenting and only lower it when you are ready to generate a high-quality video since the process is so slow.

```
vv = cleo.viz.VideoVisualizer(dt=1 * b2.ms, devices="all")
sim.inject(vv, exc, inh)
```

```
CLSimulator(io_processor=OpenLoopOpto(sample_period_ms=1, sampling='fixed', processing=
↪'parallel'), devices={VideoVisualizer(name='VideoVisualizer', save_history=True,␣
↪devices=[Light(name='Light', save_history=True, value=array([5, 0]), light_
↪model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=125. * metre ** -1, S=7370. * metre␣
↪** -1, ntis=1.36), wavelength=0.473 * umetre, direction=array([0., 0., 1.]), max_Irr0_
↪mW_per_mm2=30, max_Irr0_mW_per_mm2_viz=None)], dt=1. * msecond, fig=None, ax=None,␣
↪neuron_groups=[NeuronGroup(clock=Clock(dt=100. * usecond, name='defaultclock'),␣
↪when=start, order=0, name='exc'), NeuronGroup(clock=Clock(dt=100. * usecond, name=
↪'defaultclock'), when=start, order=0, name='inh')], _spike_mons=[<SpikeMonitor,␣
↪recording from 'spikemonitor_2'>, <SpikeMonitor, recording from 'spikemonitor_3'>], _
↪num_old_spikes=[0, 0], _value_per_device_per_frame=[], _i_spikes_per_ng_per_frame=[]),␣
↪Light(name='Light', save_history=True, value=array([5, 0]), light_
↪model=OpticFiber(R0=100. * umetre, NAfib=0.37, K=125. * metre ** -1, S=7370. * metre␣
↪** -1, ntis=1.36), wavelength=0.473 * umetre, direction=array([0., 0., 1.]), max_Irr0_
↪mW_per_mm2=30, max_Irr0_mW_per_mm2_viz=None), FourStateOpsin(name='ChR2', save_
↪history=True, on_pre='', spectrum=[(400, 0.34), (422, 0.65), (460, 0.96), (470, 1),␣
↪(473, 1), (500, 0.57), (520, 0.22), (540, 0.06), (560, 0.01)], required_vars=[('Iopto',
↪ amp), ('v', volt)], g0=114. * nsiemens, gamma=0.00742, phim=2.33e+23 * (second ** -1)␣
↪/ (meter ** 2), k1=4.15 * khertz, k2=0.868 * khertz, p=0.833, Gf0=37.3 * hertz, kf=58.
↪1 * hertz, Gb0=16.1 * hertz, kb=63. * hertz, q=1.94, Gd1=105. * hertz, Gd2=13.8 *␣
↪hertz, Gr0=0.33 * hertz, E=0. * volt, v0=43. * mvolt, v1=17.1 * mvolt, model="\n      ␣
↪ dC1/dt = Gd1*O1 + Gr0*C2 - Ga1*C1 : 1 (clock-driven)\n        dO1/dt = Ga1*C1 + Gb*O2␣
↪- (Gd1+Gf)*O1 : 1 (clock-driven)\n        dO2/dt = Ga2*C2 + Gf*O1 - (Gd2+Gb)*O2 : 1␣
↪(clock-driven)\n        C2 = 1 - C1 - O1 - O2 : 1\n\n        Theta = int(phi_pre >␣
↪0*phi_pre) : 1\n        Hp = Theta * phi_pre**p/(phi_pre**p + phim**p) : 1\n       ␣
↪Ga1 = k1*Hp : hertz\n        Ga2 = k2*Hp : hertz\n        Hq = Theta * phi_pre**q/(phi_
↪pre**q + phim**q) : 1\n        Gf = kf*Hq + Gf0 : hertz\n        Gb = kb*Hq + Gb0 :␣
↪hertz\n\n        fphi = O1 + gamma*O2 : 1\n        # v1/v0 when v-E == 0 via l'Hopital
↪'s rule\n        fv = f_unless_x0(\n            (1 - exp(-(V_VAR_NAME_post-E)/v0)) /␣
↪((V_VAR_NAME_post-E)/v1),\n            V_VAR_NAME_post - E,\n            v1/v0\n      ␣
↪ ) : 1\n\n        IOPTO_VAR_NAME_post = -g0*fphi*fv*(V_VAR_NAME_post-E)*rho_rel :␣
↪ampere (summed)\n        rho_rel : 1", extra_namespace={'f_unless_x0': <brian2.core.
↪functions.Function object at 0x7f4f3c391c40>})})
```

Run simulation and visualize

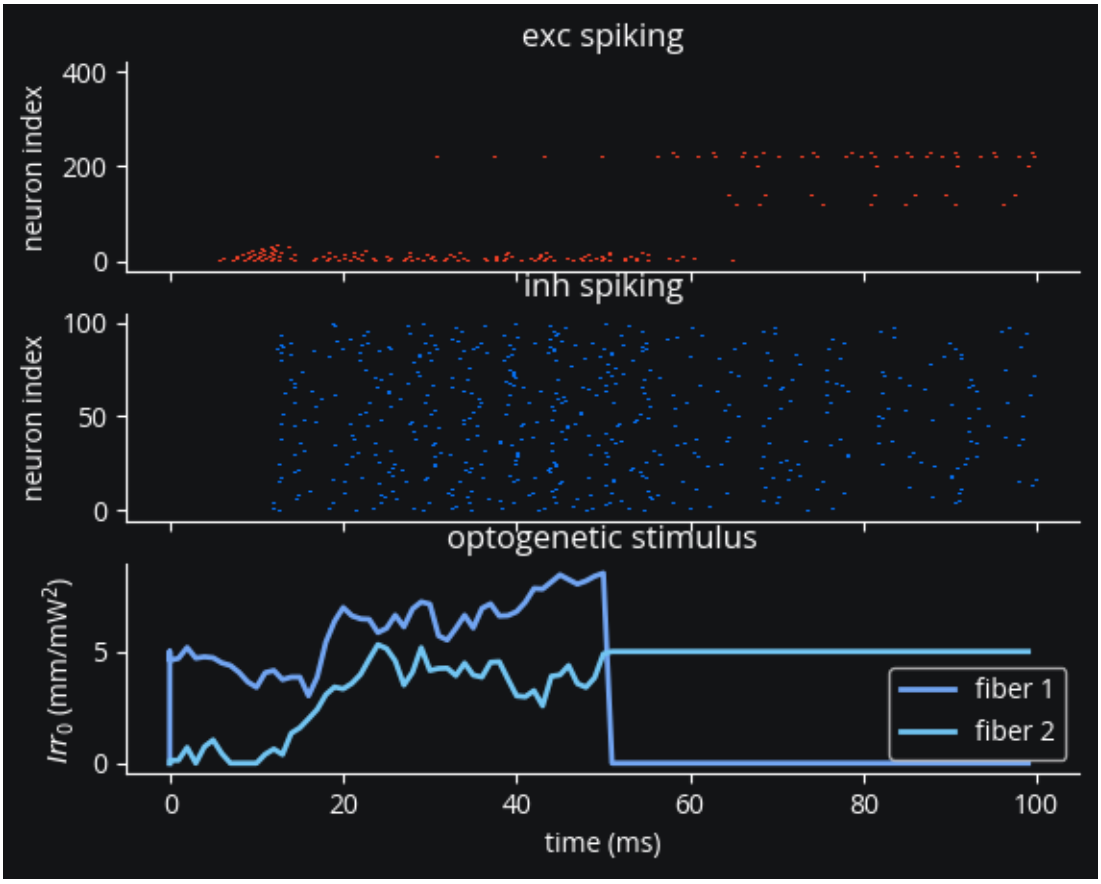
Here we display a quick plot before generating the video:

```
T = 100
sim.run(T * b2.ms)
```

```
WARNING    'T' is an internal variable of group 'light_prop_ChR2_exc', but also exists␣
↪in the run namespace with the value 100. The internal variable will be used. [brian2.
↪groups.group.Group.resolve.resolution_conflict]
INFO       No numerical integration method specified for group 'exc', using method 'euler
↪' (took 0.01s, trying other methods took 0.06s). [brian2.stateupdaters.base.method_
↪choice]
INFO       No numerical integration method specified for group 'inh', using method 'euler
↪' (took 0.01s, trying other methods took 0.01s). [brian2.stateupdaters.base.method_
↪choice]
```

```
INFO       No numerical integration method specified for group 'syn_ChR2_exc', using␣
↪method 'euler' (took 0.02s, trying other methods took 0.15s). [brian2.stateupdaters.
↪base.method_choice]
```

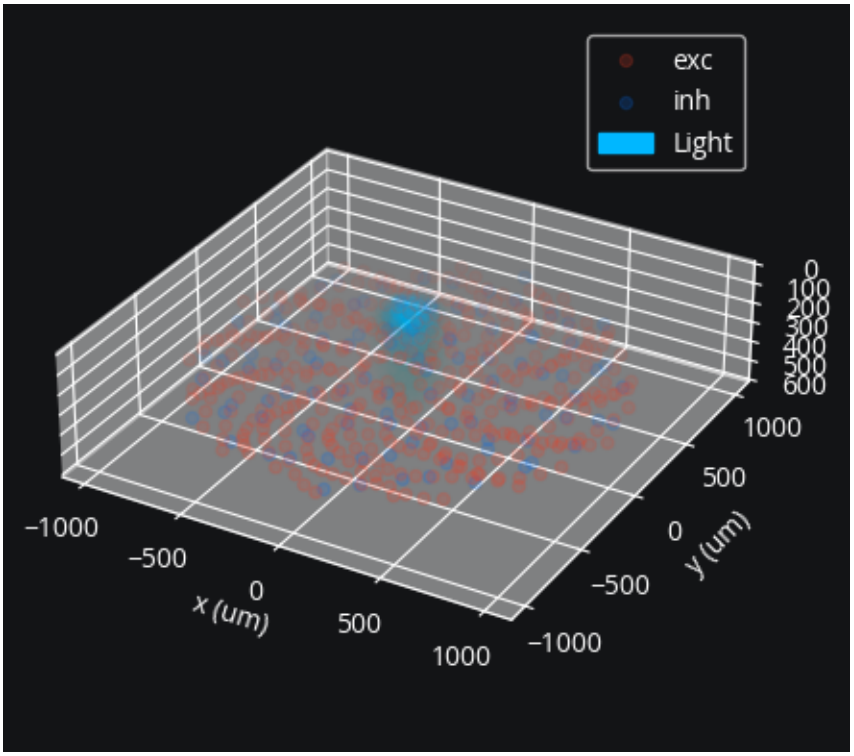
```
fig, (ax1, ax2, ax3) = plt.subplots(3, 1, sharex=True)
stim_vals = np.array(fibers.values)
sptexc = mon_e.spike_trains()
ax1.eventplot([t/b2.ms for t in sptexc.values()], lineoffsets=list(sptexc.keys()),␣
↪color=c_exc)
ax1.set(ylabel="neuron index", title="exc spiking")
sptinh = mon_i.spike_trains()
ax2.eventplot([t/b2.ms for t in sptinh.values()], lineoffsets=list(sptinh.keys()),␣
↪color=c_inh)
ax2.set(ylabel="neuron index", title="inh spiking")
ax3.plot(fibers.t_ms, stim_vals[:, 0], c="#72a5f2", lw=2, label='fiber 1')
ax3.plot(fibers.t_ms, stim_vals[:, 1], c="#72c5f2", lw=2, label='fiber 2')
ax3.legend()
ax3.set(ylabel=r"$Irr_0$ (mm/mW$^2$)", title="optogenetic stimulus", xlabel="time (ms)");
```



The `VideoVisualizer` stores the data it needs during the simulation, but hasn't yet produced any visual output. We first use the `generate_Animation()`, plugging in the arguments we used for the original plot.

Also, we set the `max_Irr0_mW_per_mm2_viz` attribute of the optogenetic intervention. This effectively scales how bright the light appears in the visualization. That is, a high maximum irradiance makes the stimulus values small in comparison and produces a faint light, while a low ceiling makes the values relatively large and produces a bright light in the resulting video.

```
fibers.max_Irr0_mW_per_mm2_viz = np.max(stim_vals)
ani = vv.generate_Animation(plotargs, slowdown_factor=10)
```



The `generate_Animation()` function returns a matplotlib `FuncAnimation` object, which you can then use however you want. You will probably want to save a video.

Note that at this point the video still hasn't been rendered; that happens when you try and save or visualize the animation. This step takes a while if your temporal resolution is high, so we suggest you do this only after your experiment is finalized and after you've experimented with low framerate videos to finalize video parameters.

Here we embed the video using HTML so you can see the output:

```
from matplotlib import rc
rc('animation', html='jshtml')

ani
```

```
<matplotlib.animation.FuncAnimation at 0x7f4f33cad250>
```

6.2.9 Neo export

Cleo allows you to export data from the whole *CLSimulator* or from individual *InterfaceDevice*s objects to Neo objects. This facilitates data analysis and visualization with packages that take Neo as an input format, as well as export to various open and proprietary ephys data file formats, which could be useful for integration with existing pipelines developed for experimental data.

Setup

```
import brian2 as b2
from brian2 import np
import cleo
from cleo import opto, ephys, light
import neo

# numpy faster than cython for lightweight example
b2.prefs.codegen.target = 'numpy'
# for reproducibility
np.random.seed(33)

cleo.utilities.style_plots_for_docs()
```

We'll set up a basic simulation to see how export works for different devices and the whole simulation.

```
ng = b2.NeuronGroup(
    100,
    """dv/dt = ((-70*mV - v) + (500*Mohm)*Iopto) / (20*ms) : volt
    Iopto : amp""",
    threshold="v > -50*mV",
    reset="v = -70*mV",
)
ng.v = -70 * b2.mV
syn = b2.Synapses(ng, on_pre="v += 3*mV")
cleo.coords.assign_coords_rand_rect_prism(ng, (-.2, .2), (-.2, .2), (0, .4))

light = light.Light(
    coords=[[-0.1, 0, 0], [0.1, 0, 0]] * b2.mm, light_model=light.fiber473nm()
)
probe = ephys.Probe(
    coords=[[0, 0, 50], [0, 0, 150], [0, 0, 250]] * b2.um,
    signals=[
        ephys.TKLFPSignal(),
        ephys.MultiUnitSpiking(
            r_perfect_detection=50 * b2.um, r_half_detection=100 * b2.um
        ),
        ephys.SortedSpiking(
            r_perfect_detection=50 * b2.um, r_half_detection=100 * b2.um
        ),
    ],
)
sim = cleo.CLSimulator(b2.Network(ng))
```

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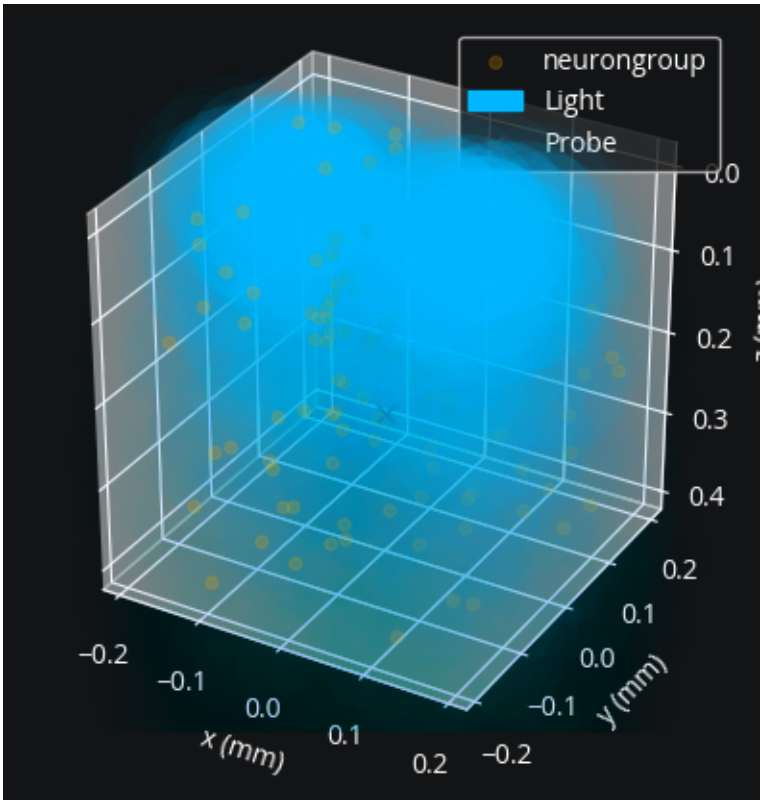
```
class IOProc(cleo.ioproc.LatencyIOProcessor):
    def process(self, state_dict, t_samp_ms):
        return {'Light': .5 * np.random.rand(light.n)}, t_samp_ms
sim.set_io_processor(IOProc(1))
sim.inject(light, ng).inject(probe, ng, tklfp_type="exc")
sim.inject(opto.chr2_4s(), ng)

cleo.viz.plot(ng, colors=['orange'], sim=sim)
```

```
(<Figure size 640x480 with 1 Axes>,
 <Axes3D: xlabel='x (mm)', ylabel='y (mm)', zlabel='z (mm)'>)
```




```
sim.run(50 * b2.ms)
```

```
INFO       No numerical integration method specified for group 'neurongroup', using␣
↪method 'exact' (took 0.23s). [brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'syn_ChR2_neurongroup',␣
↪using method 'euler' (took 0.02s, trying other methods took 0.06s). [brian2.
↪stateupdaters.base.method_choice]
```

Exporting individual devices

Depending on whether time values are regularly spaced, data is exported to either `AnalogSignal` or `IrregularlySampledSignal` objects, with appropriate annotations and per-channel annotations.

```
light.to_neo()
```

```
AnalogSignal with 2 channels of length 50; units mW/mm**2; datatype float64
name: 'Light'
description: 'Exported from Cleo Light device'
annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 181618)}
sampling rate: 1.0 1/ms
time: 0.0 ms to 50.0 ms
```

```
light.to_neo().array_annotations
```

```
{'x': array([-0.1,  0.1]) * mm,
 'y': array([0., 0.]) * mm,
 'z': array([0., 0.]) * mm,
 'direction_x': array([0., 0.]),
 'direction_y': array([0., 0.]),
 'direction_z': array([1., 1.]),
 'i_channel': array([0, 1])}
```

Different signals from the same device are grouped together:

```
probe_neo = probe.to_neo()
probe_neo
```

```
Group with 2 groups, 1 analogsignals
name: 'Probe'
description: 'Exported from Cleo Probe device'
```

```
probe_neo.children
```

```
(AnalogSignal with 3 channels of length 50; units uV; datatype float64
 name: 'Probe.TKLFPSignal'
 description: 'Exported from Cleo TKLFPSignal object'
 annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 239616)}
 sampling rate: 1.0 1/ms
 time: 0.0 ms to 50.0 ms,
 Group with 3 spiketrains
 name: 'Probe.MultiUnitSpiking'
 description: 'Exported from Cleo MultiUnitSpiking object'
 annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 241341)},
 Group with 55 spiketrains
 name: 'Probe.SortedSpiking'
 description: 'Exported from Cleo SortedSpiking object'
 annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 265177)})
```

Whole-simulation export

Exporting the whole *CLSimulator* object generates a Block object with a single Segment object containing all the data from the simulation.

```
sim.to_neo()
```

```
Block with 1 segments, 1 groups
description: 'Exported from Cleo simulation'
annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 320150)}
# segments (N=1)
0: Segment with 2 analogsignals, 58 spiketrains
   # analogsignals (N=2)
   0: AnalogSignal with 2 channels of length 50; units mW/mm**2; datatype float64
      name: 'Light'
      description: 'Exported from Cleo Light device'
      annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 320674)}
      sampling rate: 1.0 1/ms
      time: 0.0 ms to 50.0 ms
   1: AnalogSignal with 3 channels of length 50; units uV; datatype float64
      name: 'Probe.TKLFPSignal'
      description: 'Exported from Cleo TKLFPSignal object'
      annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 321221)}
      sampling rate: 1.0 1/ms
      time: 0.0 ms to 50.0 ms
```

Trial structure

Using the convention that a Segment represents a single "trial," there are a couple ways we can generate trial-structured Neo data:

1. Resetting the simulation and exporting the data from each trial individually, merging them into a single Block object.
2. Structuring multiple trials into a single call to *run()* and segmenting the data on export. This is not implemented, but could be in the future if there is sufficient demand.

Let's try the first of these options:

```
block1 = sim.to_neo()
block1.segments[0].name = 'trial 1'
sim.reset()
sim.run(50 * b2.ms)
block2 = sim.to_neo()
block2.segments[0].name = 'trial 2'

block = neo.Block()
block.segments.extend(block1.segments)
block.segments.extend(block2.segments)
block.groups.extend(block1.groups)
block.groups.extend(block2.groups)
block
```

```
Block with 2 segments, 2 groups
# segments (N=2)
0: Segment with 2 analogsignals, 58 spiketrains
   name: 'trial 1'
   # analogsignals (N=2)
   0: AnalogSignal with 2 channels of length 50; units mW/mm**2; datatype float64
      name: 'Light'
      description: 'Exported from Cleo Light device'
      annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 375717)}
      sampling rate: 1.0 1/ms
      time: 0.0 ms to 50.0 ms
   1: AnalogSignal with 3 channels of length 50; units uV; datatype float64
      name: 'Probe.TKLFPSignal'
      description: 'Exported from Cleo TKLFPSignal object'
      annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 33, 376227)}
      sampling rate: 1.0 1/ms
      time: 0.0 ms to 50.0 ms
1: Segment with 2 analogsignals, 63 spiketrains
   name: 'trial 2'
   # analogsignals (N=2)
   0: AnalogSignal with 2 channels of length 50; units mW/mm**2; datatype float64
      name: 'Light'
      description: 'Exported from Cleo Light device'
      annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 34, 138750)}
      sampling rate: 1.0 1/ms
      time: 0.0 ms to 50.0 ms
   1: AnalogSignal with 3 channels of length 50; units uV; datatype float64
      name: 'Probe.TKLFPSignal'
      description: 'Exported from Cleo TKLFPSignal object'
      annotations: {'export_datetime': datetime.datetime(2023, 9, 6, 9, 59, 34, 139149)}
      sampling rate: 1.0 1/ms
      time: 0.0 ms to 50.0 ms
```

The more attractive approach suggested by Neo's API of `block1.merge(block2)` does not work, but could potentially be fixed in the future.

Example analysis use case

Let's try elephant, following their statistics tutorial:

```
import matplotlib.pyplot as plt
from elephant.statistics import instantaneous_rate, time_histogram, mean_firing_rate
import quantities as pq

fig, ax = plt.subplots()
st1 = block.segments[0].spiketrains[0]
histogram_rate = time_histogram([st1], 5*pq.ms, output='rate')
inst_rate = instantaneous_rate(st1, sampling_period=1*pq.ms)

# plotting the original spiketrain
ax.plot(
    st1,
```

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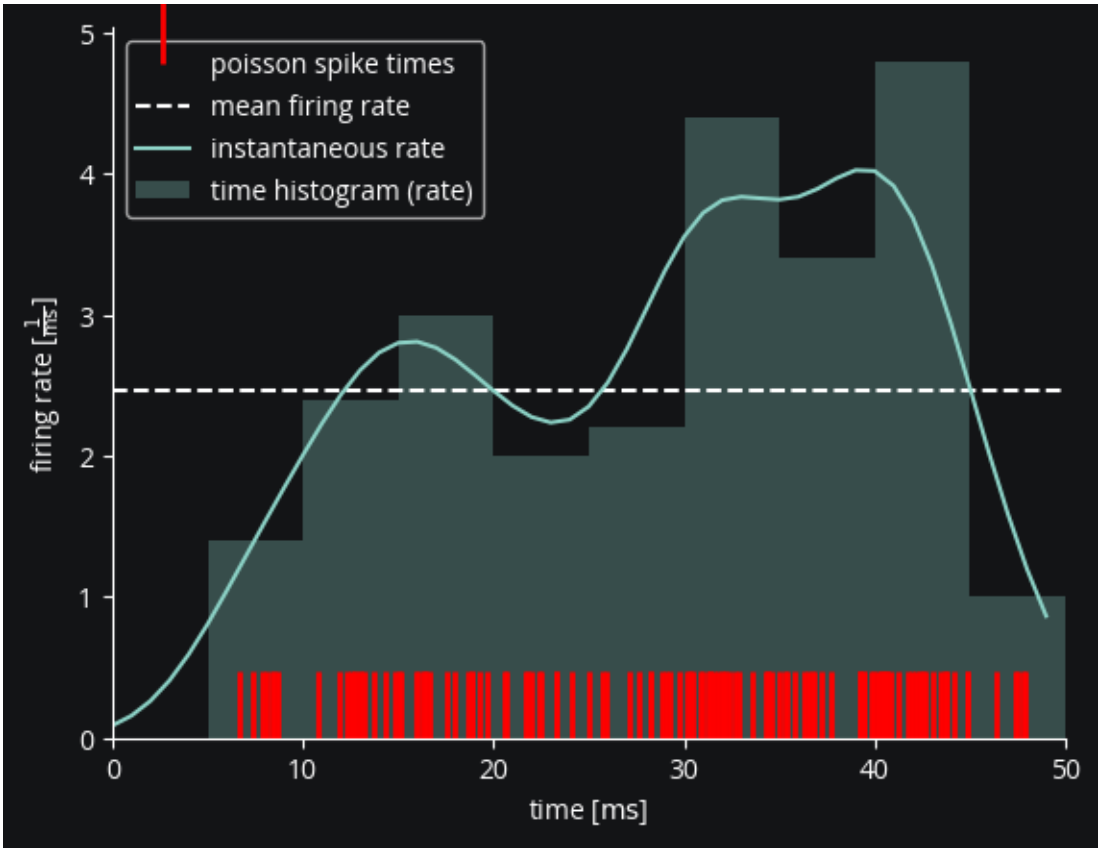
```
    [0] * len(st1),
    "r",
    marker=2,
    ms=25,
    markeredgewidth=2,
    lw=0,
    label="poisson spike times",
)

# mean firing rate
ax.hlines(
    mean_firing_rate(st1),
    xmin=st1.t_start,
    xmax=st1.t_stop,
    linestyle="--",
    label="mean firing rate",
)

# time histogram
ax.bar(
    histogram_rate.times,
    histogram_rate.magnitude.flatten(),
    width=histogram_rate.sampling_period,
    align="edge",
    alpha=0.3,
    label="time histogram (rate)",
)

# instantaneous rate
ax.plot(
    inst_rate.times.rescale(pq.ms),
    inst_rate.rescale(histogram_rate.dimensionality).magnitude.flatten(),
    label="instantaneous rate",
)

# axis labels and legend
ax.set(
    xlabel=f"time [{st1.times.dimensionality.latex}]",
    ylabel=f"firing rate [{histogram_rate.dimensionality.latex}]",
    xlim=(st1.t_start, st1.t_stop),
)
ax.legend()
```

```
<matplotlib.legend.Legend at 0x7f527c923e20>
```



6.2.10 Advanced LFP

Here we will demonstrate the diverse ways the different LFP proxies can be computed and compare them to each other.

```
# preamble:
import brian2.only as b2
from brian2 import np
import matplotlib.pyplot as plt
import cleo
from cleo import ephys
import cleo.utilities

# the default cython compilation target isn't worth it for
# this trivial example
b2.prefs.codegen.target = "numpy"
b2.seed(18010601)
np.random.seed(18010601)
rng = np.random.default_rng(18010601)

cleo.utilities.style_plots_for_docs()

# colors
c = {
    "light": "#df87e1",
    "main": "#C500CC",
```

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```
    "dark": "#8000B4",
    "exc": "#d6755e",
    "inh": "#056eee",
    "accent": "#36827F",
}
```

Network setup

First we need a point neuron simulation to approximate the LFP for. Here we adapt a balanced E/I network implementation from the Neuronal Dynamics textbook, using some parameters from Mazzoni, Lindén et al., 2015.

```
n_exc = 800
n_inh = None  # None = N_excit / 4
n_ext = 100
connection_probability = 0.2
w0 = 0.07 * b2.nA
g = 4
synaptic_delay = 1 * b2.ms
poisson_input_rate = 220 * b2.Hz
w_ext = 0.091 * b2.nA
v_rest = -70 * b2.mV
v_reset = -60 * b2.mV
firing_threshold = -50 * b2.mV
membrane_time_scale = 20 * b2.ms
Rm = 100 * b2.Mohm
abs_refractory_period = 2 * b2.ms

if n_inh is None:
    n_inh = int(n_exc / 4)
N_tot = n_exc + n_inh
if n_ext is None:
    n_ext = int(n_exc * connection_probability)
if w_ext is None:
    w_ext = w0

J_excit = w0
J_inhib = -g * w0

lif_dynamics = """
    dv/dt = (-(v-v_rest) + Rm*(I_exc + I_ext + I_gaba)) / membrane_time_scale : volt␣
↪(unless refractory)
    I_gaba : amp
    I_exc : amp
    I_ext : amp
"""

neurons = b2.NeuronGroup(
    N_tot,
    model=lif_dynamics,
    threshold="v>firing_threshold",
    reset="v=v_reset",
```

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```
    refractory=abs_refractory_period,
    method="linear",
)
neurons.v = (
    np.random.uniform(
        v_rest / b2.mV, high=firing_threshold / b2.mV, size=(n_exc + n_inh)
    )
    * b2.mV
)
cleo.coords.assign_coords_rand_cylinder(
    neurons, (0, 0, 700), (0, 0, 900), 250, unit=b2.um
)

exc = neurons[:n_exc]
inh = neurons[n_exc:]

syn_eqs = """
    dI_syn_syn/dt = (s - I_syn_syn)/tau_dsyn : amp (clock-driven)
    I_TYPE_post = I_syn_syn : amp (summed)
    ds/dt = -s/tau_rsyn : amp (clock-driven)
"""

exc_synapses = b2.Synapses(
    exc,
    target=neurons,
    model=syn_eqs.replace("TYPE", "exc"),
    on_pre="s += J_excit",
    delay=synaptic_delay,
    namespace={"tau_rsyn": 0.4 * b2.ms, "tau_dsyn": 2 * b2.ms},
)
exc_synapses.connect(p=connection_probability)

inh_synapses = b2.Synapses(
    inh,
    target=neurons,
    model=syn_eqs.replace("TYPE", "gaba"),
    on_pre="s += J_inhib",
    delay=synaptic_delay,
    namespace={"tau_rsyn": 0.25 * b2.ms, "tau_dsyn": 5 * b2.ms},
)
inh_synapses.connect(p=connection_probability)

ext_input = b2.PoissonGroup(n_ext, poisson_input_rate, name="ext_input")
ext_synapses = b2.Synapses(
    ext_input,
    target=neurons,
    model=syn_eqs.replace("TYPE", "ext"),
    on_pre="s += w_ext",
    delay=synaptic_delay,
    namespace={"tau_rsyn": 0.4 * b2.ms, "tau_dsyn": 2 * b2.ms},
)
ext_synapses.connect(p=connection_probability)
```

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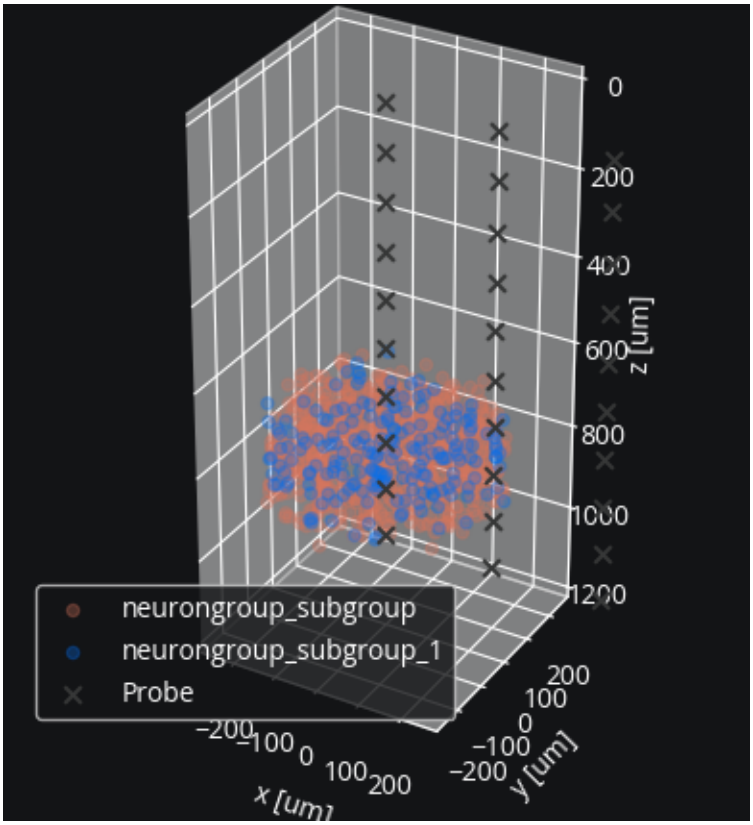
```
net = b2.Network(
    neurons,
    exc_synapses,
    inh_synapses,
    ext_input,
    ext_synapses,
)
sim = cleo.CLSimulator(net)
```

Electrode setup

```
elec_coords = cleo.ephys.linear_shank_coords(1 * b2.mm, channel_count=10)
elec_coords = cleo.ephys.tile_coords(
    elec_coords, num_tiles=3, tile_vector=(500, 0, 0) * b2.um
)
probe = cleo.ephys.Probe(elec_coords)
```

```
cleo.viz.plot(
    exc,
    inh,
    colors=[c["exc"], c["inh"]],
    zlim=(0, 1200),
    devices=[probe],
    scatterargs={"alpha": 0.3},
);
```




```
mua = ephys.MultiUnitSpiking(
    r_perfect_detection=0.05 * b2.mm,
    r_half_detection=0.1 * b2.mm,
)
ss = ephys.SortedSpiking(0.05 * b2.mm, 0.1 * b2.mm)
tklfp = ephys.TKLFPSignal()
```

RWSLFP recording options

There are a few important variations on how to record RWSLFP:

- Currents can be summed over the population, so that a postsynaptic current (PSC) in one location has the same effect on LFP as one on the other side of the population. The main advantage to this approach is it saves some memory storing currents. To use this, set *pop_aggregate* to `True`. You'll also want to set *amp_func* to `wslfp.mazzoni15_pop` to get the population amplitude profile from Mazzoni et al., 2015. The default is to not sum over the population, and use `wslfp.mazzoni15_nrn` to get per-neuron contributions to LFP instead.
- The LFP can be computed from PSCs if your model simulates them or from spikes (after synthesizing PSCs from them). Use *RWSLFPSignalFromSpikes* or *RWSLFPSignalFromPSCs* accordingly. In this example, we are simulating synaptic dynamics in the form of biexponential currents, which happens to be the form used to generate synthetic PSCs.

RWSLFPSignalFromSpikes needs to know about all spikes transmitted to the population being recorded from, so `ampa_syns` and `gaba_syns` must be passed on injection. To account for the relative impact of incoming spikes on synaptic currents, Cleo needs to be able to find the weight as well. It looks for a variable or parameter named `w` in the synapses by default, but you can pass in an alternate name or a value on injection instead.

RWSLFPSignalFromSpikes has sensible defaults, but can be overridden with the exact parameters used in our model.

These are used in the synthetic current generation process. These parameters then serve as the default for the signal, which can be overridden on a per-injection basis.

```
import wslfp

rwslfp_spk_nrn = ephys.RWSLFPSignalFromSpikes(
    tau1_ampa=exc_synapses.namespace["tau_dsyn"],
    tau2_ampa=exc_synapses.namespace["tau_rsyn"],
    tau1_gaba=inh_synapses.namespace["tau_dsyn"],
    tau2_gaba=inh_synapses.namespace["tau_rsyn"],
    syn_delay=synaptic_delay,
    name="per-neuron RWSLFP from spikes",
)

rwslfp_spk_pop = ephys.RWSLFPSignalFromSpikes(
    pop_aggregate=True,
    amp_func=wslfp.mazzoni15_pop,
    name="population-aggregated RWSLFP from spikes",
)
```

All that's needed for *RWSLFPSignalFromPSCs* is `Iampa_var_names` and `Igaba_var_names` on injection, which are lists of the variables representing AMPA and GABA currents.

```
rwslfp_psc_nrn = ephys.RWSLFPSignalFromPSCs(name="per-neuron RWSLFP from PSCs")
rwslfp_psc_pop = ephys.RWSLFPSignalFromPSCs(
    pop_aggregate=True,
    amp_func=wslfp.mazzoni15_pop,
    name="population-aggregated RWSLFP from PSCs",
)
```

All signals are grouped together on the probe, but we can avoid RWSLFP being recorded from interneurons by omitting `ampa_syns`, `gaba_syns`, `Iampa_var_names`, and `Igaba_var_names` from the injection.

```
probe.add_signals(
    mua,
    ss,
    tklfp,
    rwslfp_spk_nrn,
    rwslfp_spk_pop,
    rwslfp_psc_nrn,
    rwslfp_psc_pop,
)

sim.set_io_processor(cleo.ioproc.RecordOnlyProcessor(sample_period_ms=1))
sim.inject(
    probe,
    exc,
    # for TKLFPSignal:
    tklfp_type="exc",
    # for RWSLFPSignalFromSpikes:
    synaptic_delay=synaptic_delay,  # can override for all synapses
    ampa_syns=[  # or per synapse by with (syn, kwargs) tuples:
        # want only synapses onto pyramidal cells
        (exc_synapses[f"j < {n_exc}"], {"weight": J_excit}),
```

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```
        (ext_synapses[f"j < {n_exc}"], {"weight": w_ext}),
    ],
    gaba_syns=[(inh_synapses[f"j < {n_exc}"], {"weight": J_inhib})],
    # for RWSLFPSignalFromPSCs:
    Iampa_var_names=["I_exc", "I_ext"],
    Igaba_var_names=["I_gaba"],
)
# we don't include ampa_syns, gaba_syns, Iampa_var_name, or Igaba_var_name since RWSLFP
# is only recorded from pyramidal cells
sim.inject(probe, inh, tklfp_type="inh")
```

```
CLSimulator(io_processor=RecordOnlyProcessor(sample_period_ms=1, sampling='fixed',␣
↪processing='parallel'), devices={Probe(name='Probe', save_history=True,␣
↪signals=[MultiUnitSpiking(name='MultiUnitSpiking', brian_objects={<SpikeMonitor,␣
↪recording from 'spikemonitor'>, <SpikeMonitor, recording from 'spikemonitor_9'>},␣
↪probe=..., r_perfect_detection=50. * umetre, r_half_detection=100. * umetre, cutoff_
↪probability=0.01), SortedSpiking(name='SortedSpiking', brian_objects={<SpikeMonitor,␣
↪recording from 'spikemonitor_1'>, <SpikeMonitor, recording from 'spikemonitor_10'>},␣
↪probe=..., r_perfect_detection=50. * umetre, r_half_detection=100. * umetre, cutoff_
↪probability=0.01), TKLFPSignal(name='TKLFPSignal', brian_objects={<SpikeMonitor,␣
↪recording from 'spikemonitor_11'>, <SpikeMonitor, recording from 'spikemonitor_2'>},␣
↪probe=..., uLFP_threshold_uV=0.001, _lfp_unit=uvolt), RWSLFPSignalFromSpikes(name='per-
↪neuron RWSLFP from spikes', brian_objects={<SpikeMonitor, recording from 'spikemonitor_
↪4'>, <SpikeMonitor, recording from 'spikemonitor_5'>, <SpikeMonitor, recording from
↪'spikemonitor_3'>}, probe=..., amp_func=<function mazzoni15_nrn at 0x7f80f62c99e0>,␣
↪pop_aggregate=False, _lfp_unit=1, tau1_ampa=2. * msecond, tau2_ampa=0.4 * msecond,␣
↪tau1_gaba=5. * msecond, tau2_gaba=250. * usecond, syn_delay=1. * msecond, I_
↪threshold=0.001, weight='w'), RWSLFPSignalFromSpikes(name='population-aggregated␣
↪RWSLFP from spikes', brian_objects={<SpikeMonitor, recording from 'spikemonitor_7'>,
↪<SpikeMonitor, recording from 'spikemonitor_8'>, <SpikeMonitor, recording from
↪'spikemonitor_6'>}, probe=..., amp_func=<function mazzoni15_pop at 0x7f80f62c9940>,␣
↪pop_aggregate=True, _lfp_unit=1, tau1_ampa=2. * msecond, tau2_ampa=0.4 * msecond, tau1_
↪gaba=5. * msecond, tau2_gaba=250. * usecond, syn_delay=1. * msecond, I_threshold=0.001,
↪ weight='w'), RWSLFPSignalFromPSCs(name='per-neuron RWSLFP from PSCs', brian_
↪objects=set(), probe=..., amp_func=<function mazzoni15_nrn at 0x7f80f62c99e0>, pop_
↪aggregate=False, _lfp_unit=1), RWSLFPSignalFromPSCs(name='population-aggregated RWSLFP␣
↪from PSCs', brian_objects=set(), probe=..., amp_func=<function mazzoni15_pop at␣
↪0x7f80f62c9940>, pop_aggregate=True, _lfp_unit=1)], probe=NOTHING)})
```

Run simulation and plot results

```
sim.reset()
sim.run(500 * b2.ms)
```

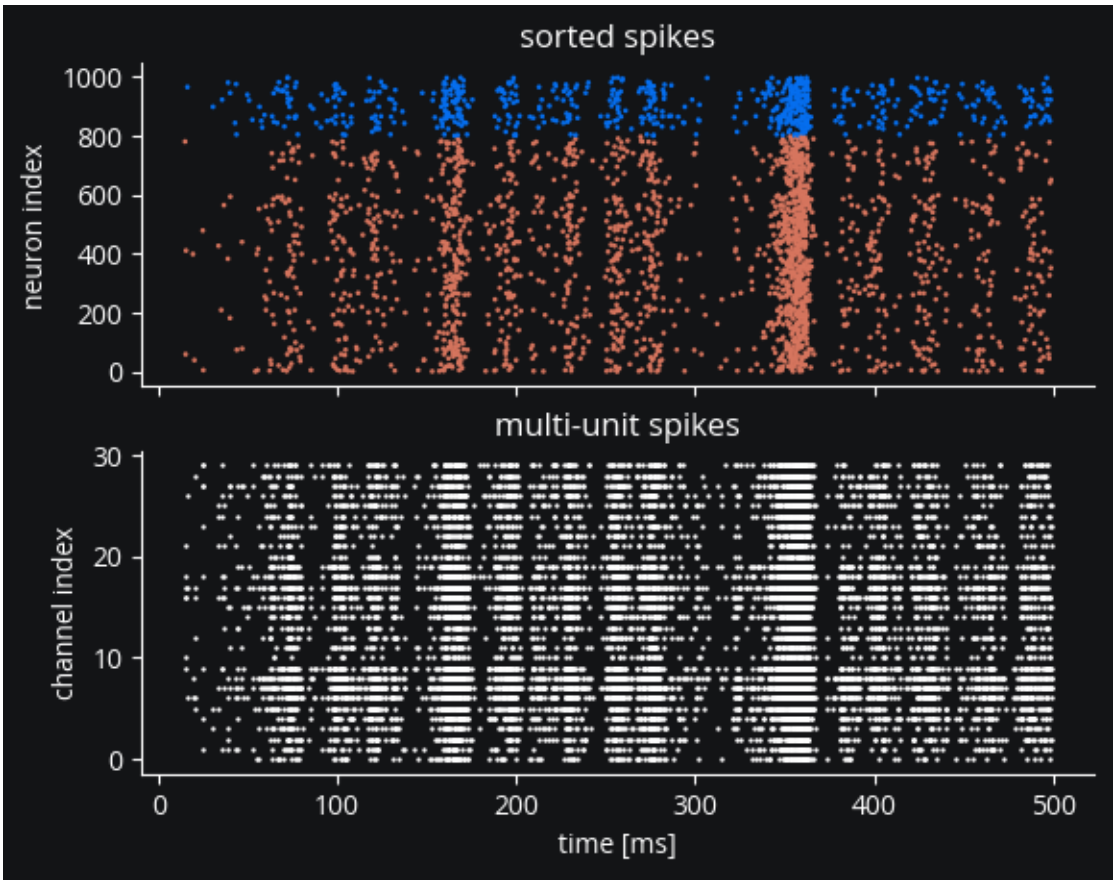
```
INFO       No numerical integration method specified for group 'synapses_1', using␣
↪method 'exact' (took 0.21s). [brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'synapses_2', using␣
↪method 'exact' (took 0.10s). [brian2.stateupdaters.base.method_choice]
INFO       No numerical integration method specified for group 'synapses', using method
↪'exact' (took 0.00s). [brian2.stateupdaters.base.method_choice]
```

```
from matplotlib.colors import ListedColormap

fig, axs = plt.subplots(2, 1, sharex=True)

# assuming all neurons are detectable for c=ss.i >= n_e to work
# in practice this will often not be the case and we'd have to map
# from probe index to neuron group index using ss.i_probe_by_i_ng.inverse
exc_inh_cmap = ListedColormap([c["exc"], c["inh"]])
axs[0].scatter(ss.t_ms, ss.i, marker=".", c=ss.i >= n_exc, cmap=exc_inh_cmap, s=3)
axs[0].set(title="sorted spikes", ylabel="neuron index")

axs[1].scatter(mua.t_ms, mua.i, marker=".", s=2, c="white")
axs[1].set(title="multi-unit spikes", ylabel="channel index", xlabel="time [ms]");
```




```
def plot_lfp(t_ms, lfp, title=None):
    n_shanks = 3
    n_contacts_per_shank = 10
    fig, axs = plt.subplots(1, n_shanks, sharey=True, figsize=(8, 4))
    for i, color, r_rec, ax in zip(
        range(n_shanks), [c["light"], c["main"], c["dark"]], [0, 250, 500], axs
    ):
        lfp_for_shank = lfp[
            :, i * n_contacts_per_shank : (i + 1) * n_contacts_per_shank
        ]
```

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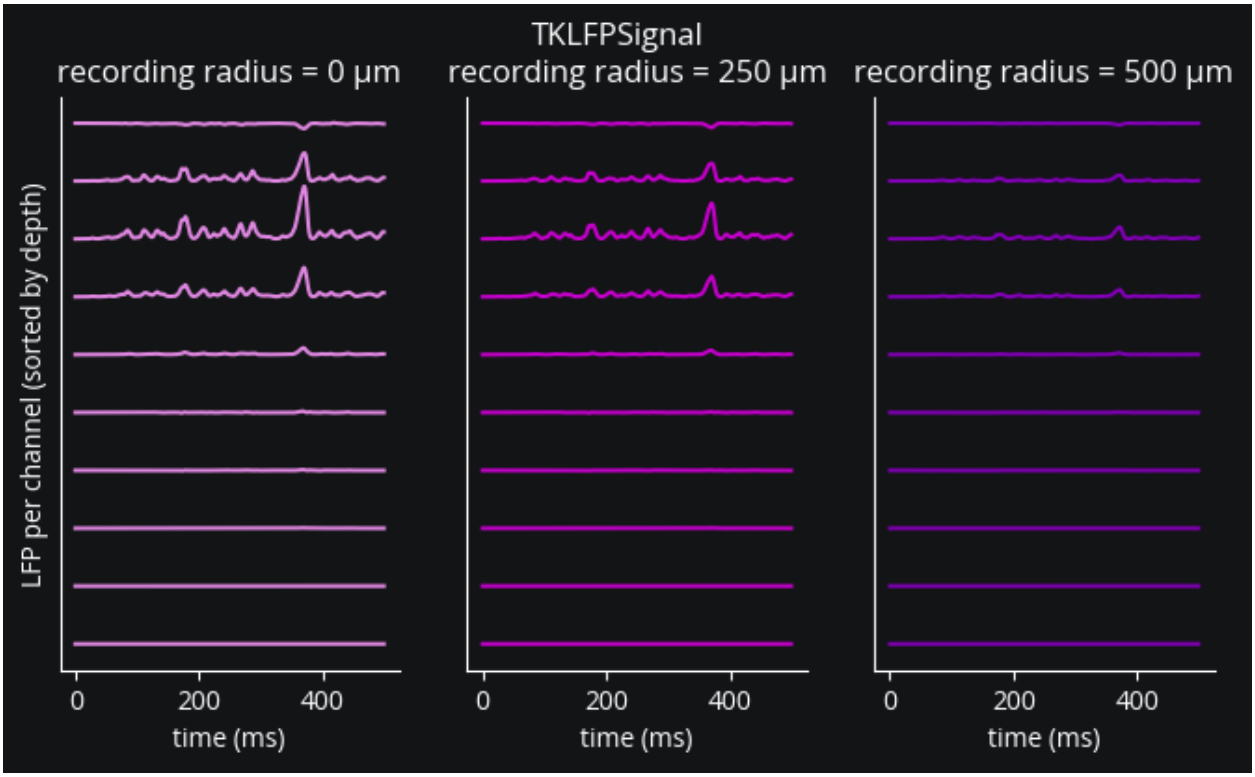
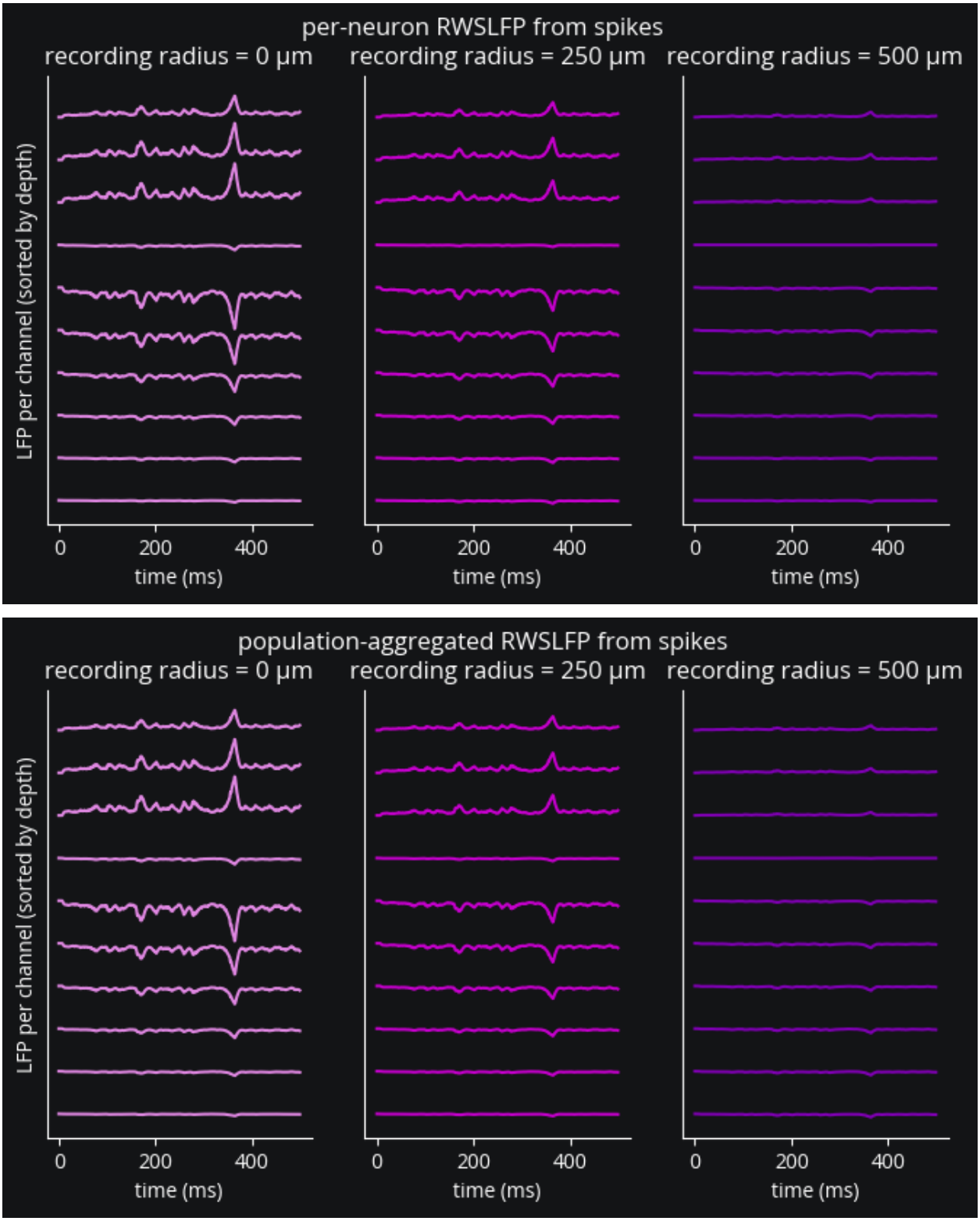
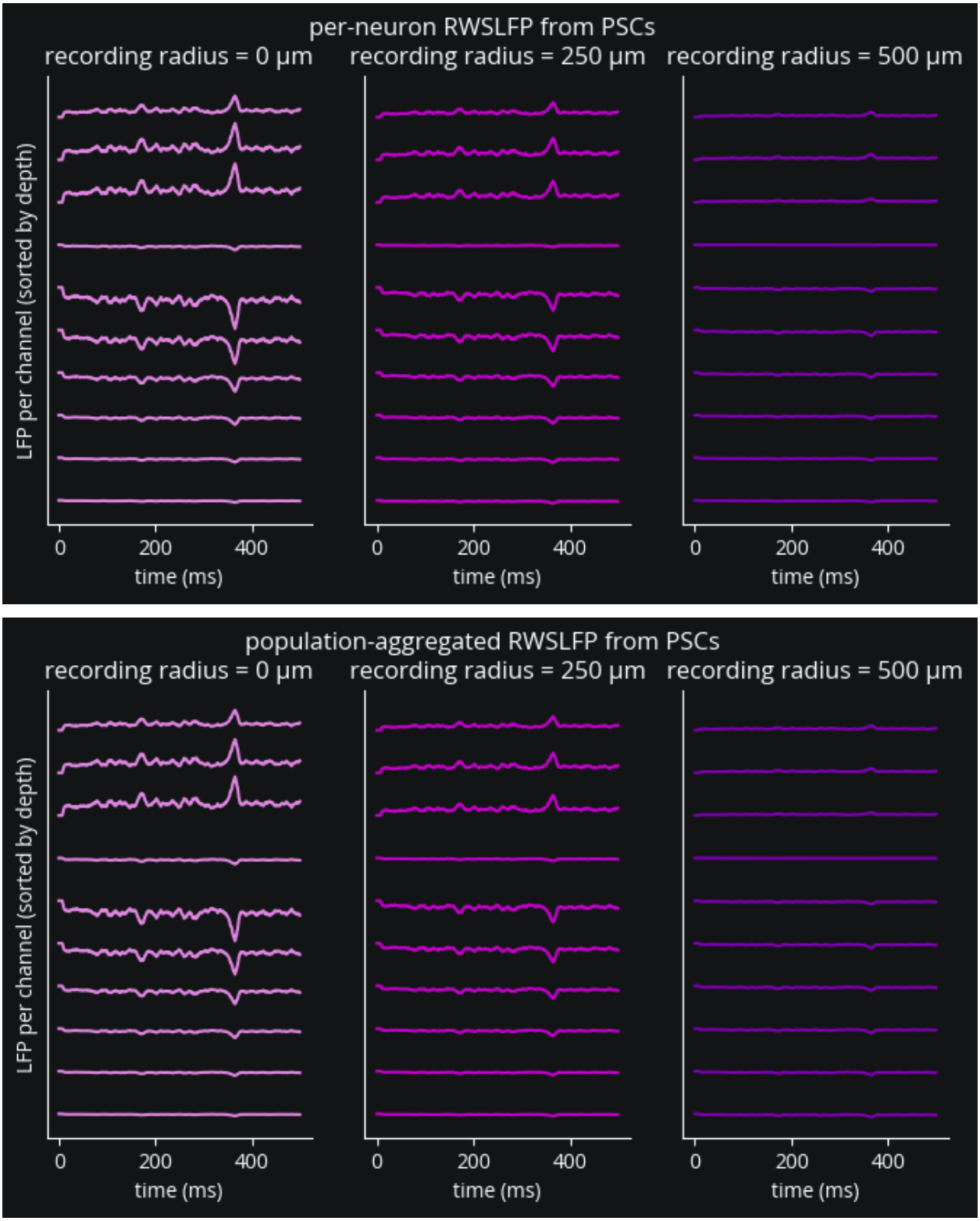
```
        ax.plot(
            t_ms,
            lfp_for_shank + np.arange(n_contacts_per_shank) * 1.1 * np.abs(lfp.max()),
            c=color,
        )
        ax.set(xlabel="time (ms)", yticks=[], title=f"recording radius = {r_rec} µm")

    axs[0].set(ylabel="LFP per channel (sorted by depth)")
    if title:
        fig.suptitle(title)


for signal in probe.signals:
    if isinstance(
        signal,
        (ephys.TKLFPSignal, ephys.RWSLFPSignalFromPSCs, ephys.RWSLFPSignalFromSpikes),
    ):
        lfp = signal.lfp
    else:
        continue
    plot_lfp(signal.t_ms, lfp, title=signal.name)
```




per-neuron RWSLFP from spikes
recording radius = 0 µm
recording radius = 250 µm
recording radius = 500 µm
LFP per channel (sorted by depth)
0
200
400
time (ms)
population-aggregated RWSLFP from spikes
recording radius = 0 µm
recording radius = 250 µm
recording radius = 500 µm
LFP per channel (sorted by depth)
0
200
400
time (ms)



Despite using all the same parameters for the postsynaptic current curves, the `FromSpikes` and `FromPSCs` signals look different. In fact, what we see above matches the WSLFP demo, where the spike convolution signal is somewhat spikier (i.e., with higher peaks the jump at the beginning looks smaller).

6.3 Reference

6.3.1 cleo module

Contains core classes and functions for the Cleo package.

class cleo.**CLSimulator**(*network: Network*)

Bases: *NeoExportable*

The centerpiece of cleo. Integrates simulation components and runs.

Method generated by attrs for class CLSimulator.

devices: set[*InterfaceDevice*]

get_state() → dict

Return current recorder measurements.

Returns
A dictionary of *name*: *state* pairs for all recorders in the simulator.

Return type
dict

inject(*device:* InterfaceDevice, **neuron_groups: NeuronGroup*, ***kwparams: Any*) → *CLSimulator*

Inject InterfaceDevice into the network, connecting to specified neurons.

Calls *connect_to_neuron_group()* for each group with kwparams and adds the device's *brian_objects* to the simulator's *network*.

Parameters
device (*InterfaceDevice*) – Device to inject

Returns
self

Return type
CLSimulator

io_processor: *IOProcessor*

network: Network

The Brian network forming the core model

recorders: dict[str, *Recorder*]

reset(***kwargs*)

Reset the simulator to a neutral state

Restores the Brian Network to where it was when the CLSimulator was last modified (last injection, IO-Processor change). Calls reset() on *devices* and *io_processor*.

run(*duration: Quantity*, ***kwparams*) → None

Run simulation.

Parameters

- **duration** (*brian2 temporal Quantity*) – Length of simulation
- ****kwparams** (*additional arguments passed to brian2.run()*) – level has a default value of 1

set_io_processor(*io_processor:* IOProcessor, *communication_period=None*) → *CLSimulator*

Set simulator IO processor

Will replace any previous IOProcessor so there is only one at a time. A Brian NetworkOperation is created to govern communication between the Network and the IOProcessor.

Parameters
io_processor (IOProcessor) –

Returns
self

Return type
CLSimulator

stimulators: dict[str, *Stimulator*]

to_neo() → Block

Exports simulator data to a Neo Block

Returns
Neo Block containing signals representing each device's data

Return type
neo.core.Block

update_stimulators(*stim_values: dict[str, Any]*) → None

Update stimulators with output from the *IOProcessor*

Parameters
stim_values (*dict*) – {*stimulator_name*: *stim_value*} dictionary with values to update each stimulator.

class cleo.**IOProcessor**(*sample_period_ms: float = 1*)

Bases: ABC

Abstract class for implementing sampling, signal processing and control

This must be implemented by the user with their desired closed-loop use case, though most users will find the LatencyIOProcessor() class more useful, since delay handling is already defined.

Method generated by attrs for class IOProcessor.

abstract get_ctrl_signals(*query_time_ms: float*) → dict

Get per-stimulator control signal from the *IOProcessor*.

Parameters
query_time_ms (*float*) – Current simulation time.

Returns
A {'stimulator_name': ctrl_signal} dictionary for updating stimulators.

Return type
dict

get_intersample_ctrl_signal(*query_time_ms: float*) → dict

Get per-stimulator control signal between samples. I.e., for implementing a time-varying waveform based on parameters from the last sample. Such parameters will need to be stored in the *IOProcessor*.

get_stim_values(*query_time_ms: float*) → dict

abstract is_sampling_now(*time*) → bool

Determines whether the processor will take a sample at this timestep.

Parameters
time (*Brian 2 temporal Unit*) – Current timestep.

Return type
bool

latest_ctrl_signal: dict

The most recent control signal returned by *get_ctrl_signals()*

preprocess_ctrl_signals(*latest_ctrl_signals: dict*, *query_time_ms: float*) → dict

Preprocess control signals as needed to control stimulator waveforms between samples.

I.e., if a control signal defines the frequency of a periodic light stimulus, this function computes the current intensity given the latest frequency and the current time. This is called immediately after *get_ctrl_signals()* and on every timestep to update the stimulator waveform between samples.

This only needs to be implemented when a stimulus that varies between samples is desired. Otherwise, the control signal returned by *get_ctrl_signals()* is used directly. If not all stimulators need this functionality, only return a dict for those that do. The original, unprocessed control signal is used for the others.

Parameters
query_time_ms (*float*) – Current simulation time.

Returns
A {'stimulator_name': value} dictionary for updating stimulators.

Return type
dict

abstract put_state(*state_dict: dict*, *sample_time_ms: float*) → None

Deliver network state to the *IOProcessor*.

Parameters

- **state_dict** (*dict*) – A dictionary of recorder measurements, as returned by *get_state()*
- **sample_time_ms** (*float*) – The current simulation timestep. Essential for simulating control latency and for time-varying control.

reset(***kwargs*) → None

sample_period_ms: float

Determines how frequently the processor takes samples

class cleo.**InterfaceDevice**(*, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: ABC

Base class for devices to be injected into the network

Method generated by attrs for class InterfaceDevice.

add_self_to_plot(*ax: Axes3D*, *axis_scale_unit: Unit*, ***kwargs*) → list[Artist]

Add device to an existing plot

Should only be called by *plot()*.

Parameters

- **ax** (*Axes3D*) – The existing matplotlib Axes object

- **axis_scale_unit** (*Unit*) – The unit used to label axes and define chart limits
- ****kwargs** (*optional*) –

Returns
A list of artists used to render the device. Needed for use in conjunction with *VideoVisualizer*.

Return type
list[Artist]

brian_objects: set

All the Brian objects added to the network by this device. Must be kept up-to-date in *connect_to_neuron_group()* and other functions so that those objects can be automatically added to the network when the device is injected.

abstract connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → None

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

init_for_simulator(*simulator:* CLSimulator) → None

Initialize device for simulator on initial injection.

This function is called only the first time a device is injected into a simulator and performs any operations that are independent of the individual neuron groups it is connected to.

Parameters
simulator (CLSimulator) – simulator being injected into

name: str

Identifier for device, used in sampling, plotting, etc. Name of the class by default. Must be unique among recorders and stimulators

reset(***kwargs*) → None

Reset the device to a neutral state

save_history: bool

Determines whether times and inputs/outputs are recorded. True by default.

For stimulators, this is when *update()* is called. For recorders, it is when *get_state()* is called.

sim: *CLSimulator*

The simulator the device is injected into

update_artists(*artists: list[Artist]*, **args*, ***kwargs*) → list[Artist]

Update the artists used to render the device

Used to set the artists' state at every frame of a video visualization. The current state would be passed in **args* or ***kwargs*

Parameters
artists (*list[Artist]*) – the artists used to render the device originally, i.e., which were returned from the first *add_self_to_plot()* call.

Returns
The artists that were actually updated. Needed for efficient blit rendering, where only updated artists are re-rendered.

Return type
list[Artist]

class cleo.**NeoExportable**

Bases: ABC

Mixin class for classes that can be exported to Neo objects

abstract to_neo() → neo.core.BaseNeo

Return a Neo signal object with the device's data

Returns
Neo object representing exported data

Return type
neo.core.BaseNeo

class cleo.**Recorder**(*, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *InterfaceDevice*

Device for taking measurements of the network.

Method generated by attrs for class Recorder.

abstract get_state() → Any

Return current measurement.

class cleo.**Stimulator**(*default_value: Any = 0*, *, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *InterfaceDevice*, *NeoExportable*

Device for manipulating the network

Method generated by attrs for class Stimulator.

default_value: Any

The default value of the device—used on initialization and on *reset()*

reset(***kwargs*) → None

Reset the stimulator device to a neutral state

t_ms: list[float]

Times stimulator was updated, stored if *save_history*

to_neo()

Return a Neo signal object with the device's data

Returns
Neo object representing exported data

Return type
neo.core.BaseNeo

update(*ctrl_signal*) → None

Set the stimulator value.

By default this sets *value* to `ctrl_signal` and updates saved times and values. You will want to implement this method if your stimulator requires additional logic. Use `super.update(self, value)` to preserve the `self.value` and `save_history` logic

Parameters
ctrl_signal (*any*) – The value the stimulator is to take.

value: Any

The current value of the stimulator device

values: list[Any]

Values taken by the stimulator at each *update()* call, stored if *save_history*

class cleo.**SynapseDevice**(*extra_namespace: dict = _Nothing.NOTHING*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *InterfaceDevice*

Base class for devices that record from/stimulate neurons via a Synapses object with device-specific model. Used for opsin and indicator classes

Method generated by attrs for class SynapseDevice.

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → None

Transfect neuron group with device.

Parameters
neuron_group (*NeuronGroup*) – The neuron group to transform

Keyword Arguments

- **p_expression** (*float*) – Probability (0 <= p <= 1) that a given neuron in the group will express the protein. 1 by default.
- **i_targets** (*array-like*) – Indices of neurons in the group to transfect. recommended for efficiency when stimulating or imaging a small subset of the group. Incompatible with `p_expression`.
- **rho_rel** (*float*) – The expression level, relative to the standard model fit, of the protein. 1 by default. For heterogeneous expression, this would have to be modified in the light-dependent synapse post-injection, e.g., `opsin.syns["neuron_group_name"].rho_rel = ...`
- **[default_name]_var_name** (*str*) – See *required_vars*. Allows for custom variable names.

extra_namespace: dict

Additional items (beyond parameters) to be added to the opto synapse namespace

init_syn_vars(*syn: Synapses*) → None

Initializes appropriate variables in Synapses implementing the model

Also called on *reset()*.

Parameters
syn (*Synapses*) – The synapses object implementing this model

model: str

Basic Brian model equations string.

Should contain a *rho_rel* term reflecting relative expression levels. Will likely also contain special NeuronGroup-dependent symbols such as V_VAR_NAME to be replaced on injection in *modify_model_and_params_for_ng()*.

modify_model_and_params_for_ng(*neuron_group: NeuronGroup*, *injct_params: dict*) → Tuple[Equations, dict]

Adapt model for given neuron group on injection

This enables the specification of variable names differently for each neuron group, allowing for custom names and avoiding conflicts.

Parameters

- **neuron_group** (*NeuronGroup*) – NeuronGroup this opsin model is being connected to
- **injct_params** (*dict*) – kwargs passed in on injection, could contain variable names to plug into the model

Keyword Arguments

model (*str, optional*) – Model to start with, by default that defined for the class. This allows for prior string manipulations before it can be parsed as an *Equations* object.

Returns

A tuple containing an Equations object and a parameter dictionary, constructed from *model* and *params*, respectively, with modified names for use in `synapses`

Return type

Equations, dict

on_pre: str

Model string for `brian2.synapses.synapses.Synapses` reacting to spikes.

property params: dict

Returns a dictionary of parameters for the model

per_ng_unit_replacements: list[Tuple[str, str]]

List of (UNIT_NAME, neuron_group_specific_unit_name) tuples to be substituted in the model string on injection and before checking required variables.

required_vars: list[Tuple[str, Unit]]

Default names of state variables required in the neuron group, along with units, e.g., [('Iopto', amp)].

It is assumed that non-default values can be passed in on injection as a keyword argument `[default_name]_var_name=[non_default_name]` and that these are found in the model string as `[DEFAULT_NAME]_VAR_NAME` before replacement.

reset(***kwargs*)

Reset the device to a neutral state

source_ngs: dict[str, NeuronGroup]

`{target_ng.name: source_ng}` dict of source neuron groups.

The source is the target itself by default or light aggregator neurons for *LightDependent*.

synapses: dict[str, Synapses]

Stores the synapse objects implementing the model, connecting from source (light aggregator neurons or the target group itself) to target neuron groups, of form `{target_ng.name: synapses}`.

6.3.2 cleo.coords module

Contains functions for assigning neuron coordinates and visualizing

cleo.coords.**assign_coords**(*neuron_group: NeuronGroup*, *coords: Quantity*)

Assigns x, y, and z coordinates for neuron group from (n, 3) array

cleo.coords.**assign_coords_grid_rect_prism**(*neuron_group: NeuronGroup*, *xlim: Tuple[float, float]*, *ylim: Tuple[float, float]*, *zlim: Tuple[float, float]*, *shape: Tuple[int, int, int]*, *unit: Unit = mmetre*) → None

Assign grid coordinates to neurons in a rectangular grid

Parameters

- **neuron_group** (*NeuronGroup*) – The neuron group to assign coordinates to
- **xlim** (*Tuple[float, float]*) – xmin, xmax, with no unit
- **ylim** (*Tuple[float, float]*) – ymin, ymax, with no unit
- **zlim** (*Tuple[float, float]*) – zmin, zmax with no unit
- **shape** (*Tuple[int, int, int]*) – n_x, n_y, n_z tuple representing the shape of the resulting grid
- **unit** (*Unit, optional*) – Brian unit determining what scale to use for coordinates, by default mm

Raises

ValueError – When the shape is incompatible with the number of neurons in the group

cleo.coords.**assign_coords_rand_cylinder**(*neuron_group: NeuronGroup*, *xyz_start: Tuple[float, float, float]*, *xyz_end: Tuple[float, float, float]*, *radius: float*, *unit: Unit = mmetre*) → None

Assign random coordinates within a cylinder.

Parameters

- **neuron_group** (*NeuronGroup*) – neurons to assign coordinates to
- **xyz_start** (*Tuple[float, float, float]*) – starting position of cylinder without unit
- **xyz_end** (*Tuple[float, float, float]*) – ending position of cylinder without unit
- **radius** (*float*) – radius of cylinder without unit
- **unit** (*Unit, optional*) – Brian unit to scale other params, by default mm

cleo.coords.**assign_coords_rand_rect_prism**(*neuron_group: NeuronGroup*, *xlim: Tuple[float, float]*, *ylim: Tuple[float, float]*, *zlim: Tuple[float, float]*, *unit: Unit = mmetre*) → None

Assign random coordinates to neurons within a rectangular prism

Parameters

- **neuron_group** (*NeuronGroup*) – neurons to assign coordinates to
- **xlim** (*Tuple[float, float]*) – xmin, xmax without unit
- **ylim** (*Tuple[float, float]*) – ymin, ymax without unit
- **zlim** (*Tuple[float, float]*) – zmin, zmax without unit
- **unit** (*Unit, optional*) – Brian unit to specify scale implied in limits, by default mm

cleo.coords.**assign_coords_uniform_cylinder**(*neuron_group: NeuronGroup*, *xyz_start: Tuple[float, float, float]*, *xyz_end: Tuple[float, float, float]*, *radius: float*, *unit: Unit = mmetre*) → None

Assign uniformly spaced coordinates within a cylinder.

Parameters

- **neuron_group** (*NeuronGroup*) – neurons to assign coordinates to
- **xyz_start** (*Tuple[float, float, float]*) – starting position of cylinder without unit
- **xyz_end** (*Tuple[float, float, float]*) – ending position of cylinder without unit
- **radius** (*float*) – radius of cylinder without unit
- **unit** (*Unit, optional*) – Brian unit to scale other params, by default mm

cleo.coords.**assign_xyz**(*neuron_group: NeuronGroup*, *x: ndarray*, *y: ndarray*, *z: ndarray*, *unit: Unit = mmetre*)

Assign arbitrary coordinates to neuron group.

Parameters

- **neuron_group** (*NeuronGroup*) – neurons to be assigned coordinates
- **x** (*np.ndarray*) – x positions to assign (preferably 1D with no unit)
- **y** (*np.ndarray*) – y positions to assign (preferably 1D with no unit)
- **z** (*np.ndarray*) – z positions to assign (preferably 1D with no unit)
- **unit** (*Unit, optional*) – Brian unit determining what scale to use for coordinates, by default mm

cleo.coords.**concat_coords**(**coords: Quantity*) → Quantity

Combine multiple coordinate Quantity arrays into one

Parameters
***coords** (*Quantity*) – Multiple coordinate n x 3 Quantity arrays to combine

Returns
A single n x 3 combined Quantity array

Return type
Quantity

cleo.coords.**coords_from_ng**(*ng: NeuronGroup*) → Quantity

Get (n, 3) coordinate array from NeuronGroup.

cleo.coords.**coords_from_xyz**(*x: Quantity*, *y: Quantity*, *z: Quantity*) → Quantity

Create (..., 3) coordinate array from x, y, z arrays (with units).

6.3.3 cleo.ephys module

Contains probes, convenience functions for generating electrode array coordinates, signals, spiking, and LFP

class cleo.ephys.**LFPSignalBase**(*, *name: str = _Nothing.NOTHING*)

Bases: *Signal*, *NeoExportable*

Base class for LFP Signals.

Injection kwargs

orientation (*np.ndarray, optional*) – Array of shape (n_neurons, 3) representing which way is "up," that is, towards the surface of the cortex, for each neuron. If a single vector is given, it is taken to be the orientation for all neurons in the group. [0, 0, -1] is the default, meaning the negative z axis is "up."

Method generated by attrs for class Signal.

brian_objects: set

All Brian objects created by the signal. Must be kept up-to-date for automatic injection into the network

lfp: NDArray[Any, Any, Quantity] = _CountingAttr(counter=155, _default=NOTHING, repr=False, eq=True, order=True, hash=None, init=False, on_setattr=None, alias=None, metadata={})

Approximated LFP from every call to `get_state()`. Shape is (n_samples, n_channels). Stored if *save_history* on *probe*

name: str

Unique identifier used to organize probe output. Name of the class by default.

probe: *Probe*

The probe the signal is configured to record for.

t_ms: NDArray[Any, float] = _CountingAttr(counter=154, _default=NOTHING, repr=False, eq=True, order=True, hash=None, init=False, on_setattr=None, alias=None, metadata={})

Times at which LFP is recorded, in ms, stored if *save_history* on *probe*

to_neo() → AnalogSignal

Return a Neo signal object with the device's data

Returns

Neo object representing exported data

Return type

neo.core.BaseNeo

class cleo.ephys.**MultiUnitSpiking**(*r_perfect_detection: Quantity*, *r_half_detection: Quantity*, *cutoff_probability: float = 0.01*, *, *name: str = _Nothing.NOTHING*)

Bases: *Spiking*

Detects (unsorted) spikes per channel.

Method generated by attrs for class MultiUnitSpiking.

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → None

Configure signal to record from specified neuron group

Parameters

neuron_group (*NeuronGroup*) – group to record from

get_state() → tuple[NDArray[None, UInt], NDArray[None, Float], NDArray[None, UInt]]

Return spikes since method was last called (i, t_ms, y)

Returns

(i, t_ms, y) where i is channel (for multi-unit) or neuron (for sorted) spike indices, t_ms is spike times, and y is a spike count vector suitable for control- theoretic uses—i.e., a 0 for every channel/neuron that hasn't spiked and a 1 for a single spike.

Return type

tuple[NDArray[np.uint], NDArray[float], NDArray[np.uint]]

to_neo() → Group

Return a Neo signal object with the device's data

Returns

Neo object representing exported data

Return type

neo.core.BaseNeo

class cleo.ephys.**Probe**(*coords: Quantity*, *signals: list[Signal] = _Nothing.NOTHING*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *Recorder*, *NeoExportable*

Picks up specified signals across an array of electrodes.

Visualization kwargs

- **marker** (*str, optional*) – The marker used to represent each contact. "x" by default.
- **size** (*float, optional*) – The size of each contact marker. 40 by default.
- **color** (*Any, optional*) – The color of contact markers. "xkcd:dark gray" by default.

Method generated by attrs for class Probe.

add_self_to_plot(*ax: Axes3D*, *axis_scale_unit: Unit*, ***kwargs*) → list[Artist]

Add device to an existing plot

Should only be called by *plot()*.

Parameters

- **ax** (*Axes3D*) – The existing matplotlib Axes object
- **axis_scale_unit** (*Unit*) – The unit used to label axes and define chart limits
- ****kwargs** (*optional*) –

Returns

A list of artists used to render the device. Needed for use in conjunction with *VideoVisualizer*.

Return type

list[Artist]

add_signals(**signals: Signal*) → None

Add signals to the probe for recording

Parameters

***signals** (Signal) – signals to add

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams: Any*) → None

Configure probe to record from given neuron group

Will call *Signal.connect_to_neuron_group()* for each signal

Parameters

- **neuron_group** (*NeuronGroup*) – neuron group to connect to, i.e., record from
- ****kwparams** (*Any*) – Passed in to signals' connect functions, needed for some signals

coords: Quantity

Coordinates of n electrodes. Must be an n x 3 array (with unit) where columns represent x, y, and z

get_state() → dict

Get current state from probe, i.e., all signals

Returns
{'signal_name': value} dict with signal states

Return type
dict

property n

Number of electrode contacts in the probe

probe: *Probe*

reset(***kwargs*)

Reset the probe to a neutral state

Calls reset() on each signal

signals: list[*Signal*]

Signals recorded by the probe. Can be added to post-init with *add_signals()*.

to_neo() → Group

Return a Neo signal object with the device's data

Returns
Neo object representing exported data

Return type
neo.core.BaseNeo

property xs: Quantity

x coordinates of recording contacts

Returns
x coordinates represented as a Brian quantity, that is, including units. Should be like a 1D array.

Return type
Quantity

property ys: Quantity

y coordinates of recording contacts

Returns
y coordinates represented as a Brian quantity, that is, including units. Should be like a 1D array.

Return type
Quantity

property zs: Quantity

z coordinates of recording contacts

Returns
z coordinates represented as a Brian quantity, that is, including units. Should be like a 1D array.

Return type
Quantity

class cleo.ephys.**RWSLFPSignalBase**(*amp_func: callable = <function mazzoni15_nrn>*, *pop_aggregate: bool = False*, *wslfp_kwargs: dict = _Nothing.NOTHING*, *lfp_unit: ~brian2.units.fundamentalunits.Unit = 1*, ***, *name: str = _Nothing.NOTHING*)

Bases: *LFPSignalBase*

Base class for *RWSLFPSignalFromSpikes* and *RWSLFPSignalFromPSCs*.

These signals should only be injected into neurons representing pyramidal cells with standard synaptic structure (see Mazzoni, Lindén et al., 2015).

RWSLFP is computed using the wslfp package.

`amp_func` and `pop_aggregate` can be overridden on injection.

Method generated by attrs for class RWSLFPSignalBase.

amp_func: callable

Function to calculate LFP amplitudes, by default `wslfp.mazzoni15_nrn`.

See wslfp documentation for more info.

get_state() → ndarray

Get the signal's current value

pop_aggregate: bool

Whether to aggregate currents across the population (as opposed to neurons having differential contributions to LFP depending on their location). False by default.

reset(***kwargs*) → None

Reset signal to a neutral state

to_neo() → AnalogSignal

Return a Neo signal object with the device's data

Returns
Neo object representing exported data

Return type
neo.core.BaseNeo

wslfp_kwargs: dict

Keyword arguments to pass to the WSLFP calculator, e.g., `alpha`, `tau_ampa_ms`, `tau_gaba_ms```source_coords_are_somata`, `source_dendrite_length_um`, `amp_kwargs`, `strict_boundaries`.

class cleo.ephys.**RWSLFPSignalFromPSCs**(*amp_func: callable = <function mazzoni15_nrn>*, *pop_aggregate: bool = False*, *wslfp_kwargs: dict = _Nothing.NOTHING*, *lfp_unit: ~brian2.units.fundamentalunits.Unit = 1*, ***, *name: str = _Nothing.NOTHING*)

Bases: *RWSLFPSignalBase*

Computes RWSLFP from the currents onto pyramidal cells.

Use this if your model already simulates synaptic current dynamics. `Iampa_var_names` and `Igaba_var_names` are lists of variable names to include and must be passed in as kwargs on injection or else the target neuron group will not contribute to this signal (desirable for interneurons).

RWSLFP refers to the Reference Weighted Sum of synaptic currents LFP proxy from Mazzoni, Lindén et al., 2015.

Injection kwargs

- **Iampa_var_names** (*list[str]*) – List of variable names in the neuron group representing AMPA currents.
- **Igaba_var_names** (*list[str]*) – List of variable names in the neuron group representing GABA currents.

Method generated by attrs for class RWSLFPSignalFromPSCs.

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*)

Configure signal to record from specified neuron group

Parameters
neuron_group (*NeuronGroup*) – group to record from

reset(***kwargs*) → None

Reset signal to a neutral state

class cleo.ephys.**RWSLFPSignalFromSpikes**(*amp_func: callable = <function mazzoni15_nrn>*, *pop_aggregate: bool = False*, *wslfp_kwargs: dict = _Nothing.NOTHING*, *lfp_unit: ~brian2.units.fundamentalunits.Unit = 1*, *tau1_ampa: ~brian2.units.fundamentalunits.Quantity = 2. * msecond*, *tau2_ampa: ~brian2.units.fundamentalunits.Quantity = 0.4 * msecond*, *tau1_gaba: ~brian2.units.fundamentalunits.Quantity = 5. * msecond*, *tau2_gaba: ~brian2.units.fundamentalunits.Quantity = 250. * usecond*, *syn_delay: ~brian2.units.fundamentalunits.Quantity = 1. * msecond*, *I_threshold: float = 0.001*, *weight: str = 'w'*, ***, *name: str = _Nothing.NOTHING*)

Bases: *RWSLFPSignalBase*

Computes RWSLFP from the spikes onto pyramidal cell.

Use this if your model does not simulate synaptic current dynamics directly. The parameters of this class are used to synthesize biexponential synaptic currents using `wslfp.spikes_to_biexp_currents()`. `ampa_syns` and `gaba_syns` are lists of Synapses or SynapticSubgroup objects and must be passed as kwargs on injection, or else this signal will not be recorded for the target neurons (useful for ignoring interneurons). Attributes set on the signal object serve as the default, but can be overridden on injection. Also, in the case that parameters (e.g., `tau1_ampa` or `weight`) vary by synapse, these can be overridden by passing a tuple of the Synapses or SynapticSubgroup object and a dictionary of the parameters to override.

RWSLFP refers to the Reference Weighted Sum of synaptic currents LFP proxy from Mazzoni, Lindén et al., 2015.

Injection kwargs

- **ampa_syns** (*list[Synapses | SynapticSubgroup | tuple[Synapses|SynapticSubgroup, dict]]*) – Synapses or SynapticSubgroup objects representing AMPA synapses (delivering excitatory currents). Or a tuple of the Synapses or SynapticSubgroup object and a dictionary of parameters to override.
- **gaba_syns** (*list[Synapses | SynapticSubgroup | tuple[Synapses|SynapticSubgroup, dict]]*) – Synapses or SynapticSubgroup objects representing GABA synapses (delivering inhibitory currents). Or a tuple of the Synapses or SynapticSubgroup object and a dictionary of parameters to override.
- **weight** (*str | float, optional*) – Name of the weight variable or parameter in the Synapses or SynapticSubgroup objects, or a float in the case of a single weight for all synapses. Default is 'w'.

Method generated by attrs for class RWSLFPSignalFromSpikes.

`I_threshold: float`

Threshold, as a proportion of the peak current, below which spikes' contribution to synaptic currents (and thus LFP) is ignored, by default 1e-3.

`connect_to_neuron_group`(*neuron_group: NeuronGroup*, ***kwparams*)

Configure signal to record from specified neuron group

Parameters
neuron_group (*NeuronGroup*) – group to record from

`syn_delay: Quantity`

The synaptic transmission delay, i.e., between a spike and the onset of the postsynaptic current. 1 ms by default.

`tau1_ampa: Quantity`

The fall time constant of the biexponential current kernel for AMPA synapses. 2 ms by default.

`tau1_gaba: Quantity`

The fall time constant of the biexponential current kernel for GABA synapses. 5 ms by default.

`tau2_ampa: Quantity`

The time constant of subtracted part of the biexponential current kernel for AMPA synapses. 0.4 ms by default.

`tau2_gaba: Quantity`

The time constant of subtracted part of the biexponential current kernel for GABA synapses. 0.25 ms by default.

`weight: str`

Name of the weight variable or parameter in the Synapses or SynapticSubgroup objects. Default is 'w'.

`class cleo.ephys.Signal`(*, *name: str = _Nothing.NOTHING*)

Bases: ABC

Base class representing something an electrode can record

Method generated by attrs for class Signal.

`brian_objects: set`

All Brian objects created by the signal. Must be kept up-to-date for automatic injection into the network

abstract connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*)

Configure signal to record from specified neuron group

Parameters
neuron_group (*NeuronGroup*) – group to record from

abstract get_state() → Any

Get the signal's current value

init_for_probe(*probe: Probe*) → None

Called when attached to a probe.

Ensures signal can access probe and is only attached to one

Parameters
probe (Probe) – Probe to attach to

Raises
ValueError – When signal already attached to another probe

name: str

Unique identifier used to organize probe output. Name of the class by default.

probe: *Probe*

The probe the signal is configured to record for.

reset(***kwargs*) → None

Reset signal to a neutral state

class cleo.ephys.**SortedSpiking**(*r_perfect_detection: Quantity*, *r_half_detection: Quantity*, *cutoff_probability: float = 0.01*, *, *name: str = _Nothing.NOTHING*)

Bases: *Spiking*

Detect spikes identified by neuron indices.

The indices used by the probe do not correspond to those coming from neuron groups, since the probe must consider multiple potential groups and within a group ignores those neurons that are too far away to be easily detected.

Method generated by attrs for class SortedSpiking.

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → None

Configure sorted spiking signal to record from given neuron group

Parameters
neuron_group (*NeuronGroup*) – group to record from

get_state() → tuple[NDArray[None, UInt], NDArray[None, Float], NDArray[None, UInt]]

Return spikes since method was last called (i, t_ms, y)

Returns
(i, t_ms, y) where i is channel (for multi-unit) or neuron (for sorted) spike indices, t_ms is spike times, and y is a spike count vector suitable for control- theoretic uses—i.e., a 0 for every channel/neuron that hasn't spiked and a 1 for a single spike.

Return type
tuple[NDArray[np.uint], NDArray[float], NDArray[np.uint]]

class cleo.ephys.**Spiking**(*r_perfect_detection: Quantity*, *r_half_detection: Quantity*, *cutoff_probability: float = 0.01*, ***, *name: str = _Nothing.NOTHING*)

Bases: *Signal*, *NeoExportable*

Base class for probabilistically detecting spikes

Method generated by attrs for class Spiking.

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → ndarray

Configure signal to record from specified neuron group

Parameters
neuron_group (*NeuronGroup*) – Neuron group to record from

Returns
num_neurons_to_consider x num_channels array of spike detection probabilities, for use in subclasses

Return type
np.ndarray

cutoff_probability: float

Spike detection probability below which neurons will not be considered. For computational efficiency.

abstract get_state() → tuple[NDArray[None, UInt], NDArray[None, Float], NDArray[None, UInt]]

Return spikes since method was last called (i, t_ms, y)

Returns
(i, t_ms, y) where i is channel (for multi-unit) or neuron (for sorted) spike indices, t_ms is spike times, and y is a spike count vector suitable for control- theoretic uses—i.e., a 0 for every channel/neuron that hasn't spiked and a 1 for a single spike.

Return type
tuple[NDArray[np.uint], NDArray[float], NDArray[np.uint]]

i: NDArray[Any, np.uint]

Channel (for multi-unit) or neuron (for sorted) indices of spikes, stored if *save_history* on *probe*

i_probe_by_i_ng: bidict

(neuron_group, i_ng) keys, i_probe values. bidict for converting between neuron group indices and the indices the probe uses

r_half_detection: Quantity

Radius (with Brian unit) within which half of all spikes are detected

r_perfect_detection: Quantity

Radius (with Brian unit) within which all spikes are detected

reset(***kwargs*) → None

Reset signal to a neutral state

t_ms: NDArray[Any, float]

Spike times in ms, stored if *save_history* on *probe*

t_samp_ms: NDArray[Any, float]

Sample times in ms when each spike was recorded, stored if *save_history* on *probe*

to_neo() → Group

Return a Neo signal object with the device's data

Returns
Neo object representing exported data

Return type
neo.core.BaseNeo

class cleo.ephys.**TKLFPSignal**(*uLFP_threshold_uV: float = 0.001*, *lfp_unit: Unit = uvolt*, ***, *name: str = _Nothing.NOTHING*)

Bases: *LFPSignalBase*

Records the Teleńczuk kernel LFP approximation.

Requires `tklfp_type='exc'|'inh'` to specify cell type on injection.

TKLFP is computed from spikes using the tklfp package.

Injection kwargs
tklfp_type (*str*) – Either 'exc' or 'inh' to specify the cell type.

Method generated by attrs for class TKLFPSignal.

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*)

Configure signal to record from specified neuron group

Parameters
neuron_group (*NeuronGroup*) – group to record from

get_state() → ndarray

Get the signal's current value

reset(***kwargs*) → None

Reset signal to a neutral state

uLFP_threshold_uV: float

Threshold, in microvolts, above which the uLFP for a single spike is guaranteed to be considered, by default 1e-3. This determines the buffer length of past spikes, since the uLFP from a long-past spike becomes negligible and is ignored.

cleo.ephys.**linear_shank_coords**(*array_length: Quantity*, *channel_count: int*, *start_location: Quantity = array([0., 0., 0.]) * metre*, *direction: Tuple[float, float, float] = (0, 0, 1)*) → Quantity

Generate coordinates in a linear pattern

Parameters

- **array_length** (*Quantity*) – Distance from the first to the last contact (with a Brian unit)
- **channel_count** (*int*) – Number of coordinates to generate, i.e. electrode contacts
- **start_location** (*Quantity, optional*) – x, y, z coordinate (with unit) for the start of the electrode array, by default (0, 0, 0)*mm
- **direction** (*Tuple[float, float, float], optional*) – x, y, z vector indicating the direction in which the array extends, by default (0, 0, 1), meaning pointing straight down

Returns
channel_count x 3 array of coordinates, where the 3 columns represent x, y, and z

Return type
Quantity

cleo.ephys.**poly2_shank_coords**(*array_length: Quantity*, *channel_count: int*, *intercol_space: Quantity*, *start_location: Quantity = array([0., 0., 0.]) * metre*, *direction: Tuple[float, float, float] = (0, 0, 1)*) → Quantity

Generate NeuroNexus-style Poly2 array coordinates

Poly2 refers to 2 parallel columns with staggered contacts. See https://www.neuronexus.com/products/electrode-arrays/up-to-15-mm-depth for more detail.

Parameters

- **array_length** (*Quantity*) – Length from the beginning to the end of the two-column array, as measured in the center
- **channel_count** (*int*) – Total (not per-column) number of coordinates (recording contacts) desired
- **intercol_space** (*Quantity*) – Distance between columns (with Brian unit)
- **start_location** (*Quantity, optional*) – Where to place the beginning of the array, by default (0, 0, 0)*mm
- **direction** (*Tuple[float, float, float], optional*) – x, y, z vector indicating the direction in which the two columns extend; by default (0, 0, 1), meaning straight down.

Returns
channel_count x 3 array of coordinates, where the 3 columns represent x, y, and z

Return type
Quantity

cleo.ephys.**poly3_shank_coords**(*array_length: Quantity*, *channel_count: int*, *intercol_space: Quantity*, *start_location: Quantity = array([0., 0., 0.]) * metre*, *direction: Tuple[float, float, float] = (0, 0, 1)*) → Quantity

Generate NeuroNexus Poly3-style array coordinates

Poly3 refers to three parallel columns of electrodes. The middle column will be longest if the channel count isn't divisible by three and the side columns will be centered vertically with respect to the middle.

Parameters

- **array_length** (*Quantity*) – Length from beginning to end of the array as measured along the center column
- **channel_count** (*int*) – Total (not per-column) number of coordinates to generate (i.e., electrode contacts)
- **intercol_space** (*Quantity*) – Spacing between columns, with Brian unit
- **start_location** (*Quantity, optional*) – Location of beginning of the array, that is, the first contact in the center column, by default (0, 0, 0)*mm
- **direction** (*Tuple[float, float, float], optional*) – x, y, z vector indicating the direction along which the array extends, by default (0, 0, 1), meaning straight down

Returns
channel_count x 3 array of coordinates, where the 3 columns represent x, y, and z

Return type
Quantity

cleo.ephys.**tetrode_shank_coords**(*array_length: Quantity*, *tetrode_count: int*, *start_location: Quantity = array([0., 0., 0.]) * metre*, *direction: Tuple[float, float, float] = (0, 0, 1)*, *tetrode_width: Quantity = 25. * umetre*) → Quantity

Generate coordinates for a linear array of tetrodes

See https://www.neuronexus.com/products/electrode-arrays/up-to-15-mm-depth to visualize NeuroNexus-style arrays.

Parameters

- **array_length** (*Quantity*) – Distance from the center of the first tetrode to the last (with a Brian unit)
- **tetrode_count** (*int*) – Number of tetrodes desired
- **start_location** (*Quantity, optional*) – Center location of the first tetrode in the array, by default (0, 0, 0)*mm
- **direction** (*Tuple[float, float, float], optional*) – x, y, z vector determining the direction in which the linear array extends, by default (0, 0, 1), meaning straight down.
- **tetrode_width** (*Quantity, optional*) – Distance between contacts in a single tetrode. Not the diagonal distance, but the length of one side of the square. By default 25*umeter, as in NeuroNexus probes.

Returns
(tetrode_count*4) x 3 array of coordinates, where 3 columns represent x, y, and z

Return type
Quantity

cleo.ephys.**tile_coords**(*coords: Quantity*, *num_tiles: int*, *tile_vector: Quantity*) → Quantity

Tile (repeat) coordinates to produce multi-shank/matrix arrays

Parameters

- **coords** (*Quantity*) – The n x 3 coordinates array to tile
- **num_tiles** (*int*) – Number of times to tile (repeat) the coordinates. For example, if you are tiling linear shank coordinates to produce multi-shank coordinates, this would be the desired number of shanks
- **tile_vector** (*Quantity*) – x, y, z array with Brian unit determining both the length and direction of the tiling

Returns
(n * num_tiles) x 3 array of coordinates, where the 3 columns represent x, y, and z

Return type
Quantity

6.3.4 cleo.imaging module

Contains Scope and sensors for two-photon microscopy

class cleo.imaging.**CalBindingActivationModel**(*model: str*)

Bases: object

Base class for modeling calcium binding/activation

Method generated by attrs for class CalBindingActivationModel.

model: str

class cleo.imaging.**CalciumModel**(*model: str*)

Bases: object

Base class for how GECI computes calcium concentration

Must provide variable Ca (molar) in model.

Method generated by attrs for class CalciumModel.

model: str

on_pre: str

class cleo.imaging.**DoubExpCalBindingActivation**(*, *A: float*, *tau_on: Quantity*, *tau_off: Quantity*, *Ca_rest: Quantity*)

Bases: *CalBindingActivationModel*

Double exponential kernel convolution representing CaB binding/activation.

Convolution is implemented via ODEs; see `notebooks/double_exp_conv_as_ode.ipynb` for derivation.

A, *tau_on*, and *tau_off* are the versions with proper scale and units of NAOMi's `ca_amp`, `t_on`, and `t_off`.

Some parameters found here. Fitting code here.

Method generated by attrs for class DoubExpCalBindingActivation.

A: float
amplitude of double exponential kernel

Ca_rest: Quantity
Resting Ca2+ concentration (molar).

init_syn_vars(*syn: Synapses*) → None

model: str

tau_off: Quantity
CaB unbinding/deactivation time constant (sec)

tau_on: Quantity
CaB binding/activation time constant (sec)

class cleo.imaging.**DynamicCalcium**(*, *Ca_rest: Quantity*, *gamma: Quantity*, *B_T: Quantity*, *kappa_S: float*, *dCa_T: Quantity*)

Bases: *CalciumModel*

Simulates intracellular calcium dynamics from spikes. Pieced together from Lütke et al., 2013; Helmchen and Tank, 2015; and Song et al., 2021. (code)

Method generated by attrs for class DynamicCalcium.

B_T: Quantity
total indicator (buffer) concentration (molar)

Ca_rest: Quantity
resting Ca2+ concentration (molar)

dCa_T: Quantity
total Ca2+ concentration increase per spike (molar)

gamma: Quantity

clearance/extrusion rate (1/sec)

init_syn_vars(*syn: Synapses*) → None

kappa_S: float

Ca2+ binding ratio of the endogenous buffer

model: str

from eq 8 in Lütke et al., 2013

on_pre: str

from eq 9 in Lütke et al., 2013

class cleo.imaging.**ExcitationModel**(*model: str*)

Bases: object

Defines exc_factor

Method generated by attrs for class ExcitationModel.

model: str

class cleo.imaging.**GECI**(*extra_namespace: dict = _Nothing.NOTHING*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*, *sigma_noise: float*, *dFF_1AP: float*, *cal_model:* CalciumModel, *bind_act_model:* CalBindingActivationModel, *exc_model:* ExcitationModel, *K_d: Quantity*, *n_H: float*, *dFF_max: float*)

Bases: *Sensor*

GECI model based on Song et al., 2021, with interchangeable components.

See *geci()* for a convenience function for creating GECI models.

As a potentially simpler alternative for future work, see the phenomological S2F model from Zhang et al., 2023. While parameter count looks similar, at least they have parameters fit already, and directly to data, rather than to biophysical processes before the data.

Method generated by attrs for class GECI.

K_d: Quantity

indicator dissociation constant (binding affinity) (molar)

bind_act_model: *CalBindingActivationModel*

cal_model: *CalciumModel*

dFF_max: float

amplitude of Hill equation for conversion from Ca2+ to F/F, Fmax/F0. May be approximated from 'dynamic range' in literature Fmax/Fmin

exc_model: *ExcitationModel*

fluor_model: str

Uses a Hill equation to convert from Ca2+ to F/F, as in Song et al., 2021

get_state() → dict[NeuronGroup, ndarray]

Returns a {neuron_group: fluorescence} dict of dFF values.

init_syn_vars(*syn: Synapses*) → None

Initializes appropriate variables in Synapses implementing the model

Also called on `reset()`.

Parameters
syn (*Synapses*) – The synapses object implementing this model

location: str

cytoplasm or membrane

Type
where sensor is expressed

n_H: float

Hill coefficient for conversion from Ca2+ to F/F

property params: dict

Returns a dictionary of all parameters from model/submodels

class cleo.imaging.**LightExcitation**

Bases: *ExcitationModel*

Models light-dependent excitation (not implemented yet)

Method generated by attrs for class LightExcitation.

model: str

class cleo.imaging.**NullBindingActivation**

Bases: *CalBindingActivationModel*

Doesn't model binding/activation; i.e., goes straight from [Ca2+] to F/F

Method generated by attrs for class NullBindingActivation.

model: str

class cleo.imaging.**NullExcitation**

Bases: *ExcitationModel*

Models excitation as a constant factor

Method generated by attrs for class NullExcitation.

model: str

class cleo.imaging.**PreexistingCalcium**

Bases: *CalciumModel*

Calcium concentration is pre-existing in neuron model

Method generated by attrs for class PreexistingCalcium.

model: str

class cleo.imaging.**Scope**(*sensor: Sensor*, *img_width: Quantity*, *focus_depth: Quantity = None*, *location: Quantity = array([0., 0., 0.]) * metre*, *direction: Quantity = (0, 0, 1)*, *soma_radius: Quantity = 10. * umetre*, *snr_cutoff: float = 1*, *rand_seed: int = None*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *Recorder*

Two-photon microscope.

Injection kwargs

- **rho_rel_generator** (*Callable[[int], NDArray[(Any,), float]], optional*) – A function assigning expression levels. Takes n as an arg, outputs float array. `lambda n: np.ones(n)` by default.
- **focus_depth** (*Quantity, optional*) – The depth of the focal plane, by default that of the scope.
- **soma_radius** (*Quantity, optional*) – The radius of the soma of the neuron, by default that of the scope. Used to compute noise focus factor, since smaller ROIs will have a noisier distribution of fluorescence, averaged over fewer pixels.

Method generated by attrs for class Scope.

add_self_to_plot(*ax: Axes3D*, *axis_scale_unit: Unit*, ***kwargs*) → list[Artist]

Add device to an existing plot

Should only be called by *plot()*.

Parameters

- **ax** (*Axes3D*) – The existing matplotlib Axes object
- **axis_scale_unit** (*Unit*) – The unit used to label axes and define chart limits
- ****kwargs** (*optional*) –

Returns

A list of artists used to render the device. Needed for use in conjunction with *VideoVisualizer*.

Return type

list[Artist]

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → None

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

dFF: list[NDArray[Any, float]]

F/F from every call to *get_state()*. Shape is (n_samples, n_ROIs). Stored if *save_history*

property dFF_1AP: NDArray[Any, Float]

dFF_1AP for all targets, in order injected. Varies with expression levels.

direction: NDArray[3, float]

Direction in which the microscope is pointing. By default straight down (+z direction)

focus_coords_per_injct: list[NDArray[Any, float]]

coordinates on the focal plane of neurons selected from each injection

focus_depth: Quantity

The depth of the focal plane, with distance units

get_state() → NDArray[Any, Float]

Returns a 1D array of F/F values for all targets, in order injected.

Returns
Fluorescence values for all targets

Return type
NDArray[(Any,), float]

i_targets_for_neuron_group(*neuron_group*)

can handle multiple injections into same ng

i_targets_per_injct: list[NDArray[Any, int]]

targets of neurons selected from each injection

img_width: Quantity

The width (diameter) of the (circular) image captured by the microscope. Specified in distance units.

inject_sensor_for_targets(***kwparams*) → None

location: Quantity

Location of the objective lens.

property n: int

Number of imaged ROIs

neuron_groups: list[NeuronGroup]

neuron groups the scope has been injected into, in order of injection

rand_seed: int

reset(***kwargs*) → None

Reset the device to a neutral state

rho_rel_per_injct: list[NDArray[Any, float]]

relative expression levels of neurons selected from each injection

sensor: *Sensor*

property sigma_noise: NDArray[Any, Float]

noise std dev (in terms of F/F) for all targets, in order injected.

sigma_per_injct: list[NDArray[Any, float]]

sigma_noise of neurons selected from each injection

snr_cutoff: float

SNR below which neurons are discarded. Applied only when not focus_depth is not None

soma_radius: Quantity

Assumed radius of neurons, used to compute noise focus factor. Smaller neurons have noisier signals.

t_ms: list[float]

Times at which sensor traces are recorded, in ms, stored if *save_history*

target_neurons_in_plane(*ng*, *focus_depth: Quantity = None*, *soma_radius: Quantity = None*) → tuple[NDArray[Any, Int], NDArray[Any, Float], NDArray[Any, 3, Float]]

calls *target_neurons_in_plane()* with scope parameter defaults. *focus_depth* and *soma_radius* can be overridden here.

Parameters

- **ng** (*NeuronGroup*) – The neuron group to target.
- **focus_depth** (*Quantity*) – The depth of the focal plane, by default that of the microscope.
- **soma_radius** (*Quantity, optional*) – The radius of the soma of the neuron, by default that of the microscope. Used to compute noise focus factor, since smaller ROIs will have a noisier distribution of fluorescence, averaged over fewer pixels.

Returns
A tuple of (i_targets, noise_focus_factor, coords_on_plane)

Return type
Tuple[NDArray[(Any,), int], NDArray[(Any,), float], NDArray[(Any, 3), float]]

`class cleo.imaging.Sensor(`*extra_namespace: dict = _Nothing.NOTHING*, *, *name: str = _Nothing.NOTHING*, *save_history: bool = True*, *sigma_noise: float*, *dFF_1AP: float*, *location: str*`)`

Bases: *SynapseDevice*

Base class for sensors

Method generated by attrs for class Sensor.

dFF_1AP: float
F/F for 1 AP, only used for scope SNR cutoff

property exc_spectrum: list[tuple[float, float]]
Excitation spectrum, alias for `spectrum`

get_state() → dict[NeuronGroup, ndarray]
Returns a {neuron_group: fluorescence} dict of dFF values.

location: str
cytoplasm or membrane

Type
where sensor is expressed

sigma_noise: float
standard deviation of Gaussian noise in F/F measurement

property snr: float
Signal-to-noise ratio for 1 AP

`cleo.imaging.gcamp3(`*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=287. * nmolar*, *n_H=2.52*, *dFF_max=12*, *sigma_noise=0.018571428571428572*, *dFF_1AP=0.039*, *ca_amp=0.05*, *t_on=1*, *t_off=1*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='gcamp3'*, ***kwparams*`)` → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

cleo.imaging.**gcamp6f**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=290. * nmolar*, *n_H=2.7*, *dFF_max=25.2*, *sigma_noise=0.03748181818181818*, *dFF_1AP=0.09775500000000001*, *ca_amp=76.1251*, *t_on=0.8535*, *t_off=98.6173*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='gcamp6f'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

cleo.imaging.**gcamp6rs06**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=0.32 * umolar*, *n_H=3*, *dFF_max=15*, *sigma_noise=0.030227272727272728*, *dFF_1AP=None*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='gcamp6rs06'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

Don't know sigma_noise. Default is the GCaMP6s value.

cleo.imaging.**gcamp6rs09**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=0.52 * umolar*, *n_H=3.2*, *dFF_max=25*, *sigma_noise=0.030227272727272728*, *dFF_1AP=None*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='gcamp6rs09'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

Don't know sigma_noise. Default is the GCaMP6s value.

cleo.imaging.**gcamp6s**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=147. * nmolar*, *n_H=2.45*, *dFF_max=27.2*, *sigma_noise=0.030227272727272728*, *dFF_1AP=0.133*, *ca_amp=54.6943*, *t_on=0.4526*, *t_off=68.5461*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='gcamp6s'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

ca_amp, t_on, and t_off are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, A = ca_amp / (second / 100) and tau_[on|off] = second / t_[on|off].

cleo.imaging.**geci**(*light_dependent: bool*, *doub_exp_conv: bool*, *pre_existing_cal: bool*, ***kwparams*) → *GECI*

Initializes a *GECI* model with given parameters.

Parameters

- **light_dependent** (*bool*) – Whether the indicator is light-dependent.
- **doub_exp_conv** (*bool*) – Whether to use double exponential convolution for binding/activation.
- **pre_existing_cal** (*bool*) – Whether to use calcium concentrations already simulated in the neuron model.
- ****kwparams** – Keyword parameters for *GECI* and sub-models.

Returns
A (LightDependent)GECI model specified submodels and parameters.

Return type
GECI

cleo.imaging.**jgcamp7b**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=82. * nmolar*, *n_H=3.06*, *dFF_max=22.1*, *sigma_noise=0.007556818181818182*, *dFF_1AP=0.61712*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='jgcamp7b'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is None, then we don't have it fit yet.

ca_amp, t_on, and t_off are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, A = ca_amp / (second / 100) and tau_[on|off] = second / t_[on|off].

cleo.imaging.**jgcamp7c**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=298. * nmolar*, *n_H=2.44*, *dFF_max=145.6*, *sigma_noise=0.011788636363636364*, *dFF_1AP=0.24605000000000002*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='jgcamp7c'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is None, then we don't have it fit yet.

ca_amp, t_on, and t_off are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, A = ca_amp / (second / 100) and tau_[on|off] = second / t_[on|off].

cleo.imaging.**jgcamp7f**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=174. * nmolar*, *n_H=2.3*, *dFF_max=30.2*, *sigma_noise=0.021763636363636363*, *dFF_1AP=0.22743000000000002*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='jgcamp7f'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

cleo.imaging.**jgcamp7s**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=68. * nmolar*, *n_H=2.49*, *dFF_max=40.4*, *sigma_noise=0.009975000000000001*, *dFF_1AP=0.65968*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='jgcamp7s'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

cleo.imaging.**ogb1**(*light_dependent=False*, *doub_exp_conv=True*, *pre_existing_cal=False*, *K_d=250. * nmolar*, *n_H=1*, *dFF_max=14*, *sigma_noise=0.030227272727272728*, *dFF_1AP=None*, *ca_amp=None*, *t_on=None*, *t_off=None*, *Ca_rest=50. * nmolar*, *kappa_S=110*, *gamma=292.3 * hertz*, *B_T=200. * umolar*, *dCa_T=7.6 * umolar*, *name='ogb1'*, ***kwparams*) → *GECI*

Returns a (light-dependent) GECI model with specified submodel choices. Default parameters are taken from NAOMi's code (Song et al., 2021) as well as Dana et al., 2019 and Zhang et al., 2023.

Only those parameters used in chosen model components apply. If the default is `None`, then we don't have it fit yet.

`ca_amp`, `t_on`, and `t_off` are given as in NAOMi, but are converted to the proper scale and units for the double exponential convolution model. Namely, `A = ca_amp / (second / 100)` and `tau_[on|off] = second / t_[on|off]`.

Don't know sigma_noise. Default is the GCaMP6s value.

cleo.imaging.**target_neurons_in_plane**(*ng: NeuronGroup*, *scope_focus_depth: Quantity*, *scope_img_width: Quantity*, *scope_location: Quantity = array([0., 0., 0.]) * metre*, *scope_direction: tuple = (0, 0, 1)*, *soma_radius: Quantity = 10. * umetre*, *sensor_location: str = 'cytoplasm'*) → tuple[NDArray[Any, Int], NDArray[Any, Float], NDArray[Any, 3, Float]]

Returns a tuple of (i_targets, noise_focus_factor, coords_on_plane)

Parameters

- **ng** (*NeuronGroup*) – The neuron group to target.
- **scope_focus_depth** (*Quantity*) – The depth of the focal plane of the microscope.
- **scope_img_width** (*Quantity*) – The width of the image captured by the microscope.
- **scope_location** (*Quantity, optional*) – The location of the microscope, by default (0, 0, 0) * mm.

- **scope_direction** (*tuple, optional*) – The direction of the microscope, by default (0, 0, 1).
- **soma_radius** (*Quantity, optional*) – The radius of the soma of the neuron, by default 10 * um. Used to compute noise focus factor, since smaller ROIs will have a noisier distribution of fluorescence, averaged over fewer pixels.
- **sensor_location** (*str, optional*) – The location of the sensor, by default "cytoplasm".

Returns
A tuple of (i_targets, noise_focus_factor, coords_on_plane)

Return type
Tuple[NDArray[(Any,), int], NDArray[(Any,), float], NDArray[(Any, 3), float]]

6.3.5 cleo.ioproc module

Classes and functions for constructing and configuring an *IOProcessor*.

class cleo.ioproc.**ConstantDelay**(*delay_ms: float*)

Bases: *Delay*

Simply adds a constant delay to the computation

Parameters
delay_ms (*float*) – Desired delay in milliseconds

compute()
Compute delay.

class cleo.ioproc.**Delay**

Bases: ABC

Abstract base class for computing delays.

abstract compute() → float
Compute delay.

class cleo.ioproc.**FiringRateEstimator**(*tau_ms: float*, *sample_period_ms: float*, ***kwargs*)

Bases: *ProcessingBlock*

Exponential filter to estimate firing rate.

Requires *sample_time_ms* kwarg when process is called.

Parameters
- **tau_ms** (*float*) – Time constant of filter
- **sample_period_ms** (*float*) – Sampling period in milliseconds

compute_output(*input: NDArray[Any, UInt]*, ***kwargs*) → NDArray[Any, Float]
Estimate firing rate given past and current spikes.

Parameters
input (*NDArray[(n,), np.uint]*) – n-length vector of spike counts

Keyword Arguments
sample_time_ms (*float*) – Time measurement was taken in milliseconds

Returns
n-length vector of firing rates

Return type
NDArray[(n,), float]

class cleo.ioproc.**GaussianDelay**(*loc: float*, *scale: float*)

Bases: *Delay*

Generates normal-distributed delay.

Will return 0 when a negative value is sampled.

Parameters

- **loc** (*float*) – Center of distribution
- **scale** (*float*) – Standard deviation of delay distribution

compute() → float

Compute delay.

class cleo.ioproc.**LatencyIOProcessor**(*sample_period_ms: float = 1*, *sampling: str = 'fixed'*, *processing: str = 'parallel'*)

Bases: *IOProcessor*

IOProcessor capable of delivering stimulation some time after measurement.

Note: It doesn't make much sense to combine parallel computation with "when idle" sampling, because "when idle" sampling only produces one sample at a time to process.

Method generated by attrs for class LatencyIOProcessor.

get_ctrl_signals(*query_time_ms*)

Get per-stimulator control signal from the *IOProcessor*.

Parameters
query_time_ms (*float*) – Current simulation time.

Returns
A {'stimulator_name': ctrl_signal} dictionary for updating stimulators.

Return type
dict

is_sampling_now(*query_time_ms*)

Determines whether the processor will take a sample at this timestep.

Parameters
time (*Brian 2 temporal Unit*) – Current timestep.

Return type
bool

out_buffer: deque[Tuple[dict, float]]

abstract process(*state_dict: dict*, *sample_time_ms: float*) → Tuple[dict, float]

Process network state to generate output to update stimulators.

This is the function the user must implement to define the signal processing pipeline.

Parameters

- **state_dict** (*dict*) – {*recorder_name*: *state*} dictionary from *get_state()*

- **time_ms** (*float*) –

Returns
{'stim_name': *ctrl_signal*} dictionary and output time in milliseconds.

Return type
Tuple[dict, float]

processing: str

"serial" or "parallel".

"parallel" computes the output time by adding the delay for a sample onto the sample time, so if the delay is 2 ms, for example, while the sample period is only 1 ms, some of the processing is happening in parallel. Output order matches input order even if the computed output time for a sample is sooner than that for a previous sample.

"serial" computes the output time by adding the delay for a sample onto the output time of the previous sample, rather than the sampling time. Note this may be of limited utility because it essentially means the *entire* round trip cannot be in parallel at all. More realistic is that simply each block or phase of computation must be serial. If anyone cares enough about this, it will have to be implemented in the future.

Type
Processing scheme

put_state(*state_dict: dict*, *sample_time_ms: float*)

Deliver network state to the `IOProcessor`.

Parameters

- **state_dict** (*dict*) – A dictionary of recorder measurements, as returned by *get_state()*
- **sample_time_ms** (*float*) – The current simulation timestep. Essential for simulating control latency and for time-varying control.

sampling: str

"fixed" or "when idle".

"fixed" sampling means samples are taken on a fixed schedule, with no exceptions.

"when idle" sampling means no samples are taken before the previous sample's output has been delivered. A sample is taken ASAP after an over-period computation: otherwise remains on schedule.

Type
Sampling scheme

t_samp_ms: list[float]

Record of sampling times—each time *put_state()* is called.

class cleo.ioproc.**PIController**(*ref_signal: callable*, *Kp: float*, *Ki: float = 0*, *sample_period_ms: float = 0*, ***kwargs: Any*)

Bases: *ProcessingBlock*

Simple PI controller.

compute_output() requires a `sample_time_ms` keyword argument. Only tested on controlling scalar values, but could be easily adapted to controlling a multi-dimensional state.

Parameters

- **ref_signal** (*callable*) – Must return the target as a function of time in ms
- **Kp** (*float*) – Gain on the proportional error

- **Ki** (*float, optional*) – Gain on the integral error, by default 0
- **sample_period_ms** (*float, optional*) – Rate at which processor takes samples, by default 0. Only used to compute integrated error on first sample

compute_output(*input: float*, ***kwargs*) → float

Compute control input to the system using previously specified gains.

Parameters
input (*Any*) – Current system state

Returns
Control signal

Return type
float

ref_signal: callable[[float], Any]

Callable returning the target as a function of time in ms

class cleo.ioproc.**ProcessingBlock**(***kwargs*)

Bases: ABC

Abstract signal processing stage or control block.

It's important to use *super().__init__(**kwargs)* in the base class to use the parent-class logic here.

Keyword Arguments
delay (Delay) – Delay object which adds to the compute time

Raises
TypeError – When *delay* is not a *Delay* object.

abstract compute_output(*input: Any*, ***kwargs*) → Any

Computes output for given input.

This is where the user will implement the desired functionality of the *ProcessingBlock* without regard for latency.

Parameters

- **input** (*Any*) – Data to be processed. Passed in from *process()*.
- ****kwargs** (*Any*) – optional key-value argument pairs passed from *process()*. Could be used to pass in such values as the IO processor's walltime or the measurement time for time- dependent functions.

Returns
output

Return type
Any

delay: *Delay*

The delay object determining compute latency for the block

process(*input: Any*, *t_in_ms: float*, ***kwargs*) → Tuple[Any, float]

Computes and saves output and output time given input and input time.

The user should implement *compute_output()* for their child classes, which performs the computation itself without regards for timing or saving variables.

Parameters

- **input** (*Any*) – Data to be processed
- **t_in_ms** (*float*) – Time the block receives the input data
- ****kwargs** (*Any*) – Key-value list of arguments passed to *compute_output()*

Returns
output, out time in milliseconds

Return type
Tuple[Any, float]

save_history: bool
Whether to record *t_in_ms*, *t_out_ms*, and *values* with every timestep

t_in_ms: list[float]
The walltime the block received each input. Only recorded if *save_history*

t_out_ms: list[float]
The walltime of each of the block's outputs. Only recorded if *save_history*

values: list[Any]
Each of the block's outputs. Only recorded if *save_history*

class cleo.ioproc.**RecordOnlyProcessor**(*sample_period_ms*, ***kwargs*)
Bases: *LatencyIOProcessor*

Take samples without performing any control.

Use this if all you are doing is recording.

Method generated by attrs for class LatencyIOProcessor.

out_buffer: deque[Tuple[dict, float]]

process(*state_dict: dict*, *sample_time_ms: float*) → Tuple[dict, float]
Process network state to generate output to update stimulators.

This is the function the user must implement to define the signal processing pipeline.

Parameters
- **state_dict** (*dict*) – {*recorder_name*: *state*} dictionary from *get_state()*
- **time_ms** (*float*) –

Returns
{'stim_name': *ctrl_signal*} dictionary and output time in milliseconds.

Return type
Tuple[dict, float]

processing: str
"serial" or "parallel".

"parallel" computes the output time by adding the delay for a sample onto the sample time, so if the delay is 2 ms, for example, while the sample period is only 1 ms, some of the processing is happening in parallel. Output order matches input order even if the computed output time for a sample is sooner than that for a previous sample.

"serial" computes the output time by adding the delay for a sample onto the output time of the previous sample, rather than the sampling time. Note this may be of limited utility because it essentially means the *entire* round trip cannot be in parallel at all. More realistic is that simply each block or phase of computation must be serial. If anyone cares enough about this, it will have to be implemented in the future.

Type
Processing scheme

sampling: str

"fixed" or "when idle".

"fixed" sampling means samples are taken on a fixed schedule, with no exceptions.

"when idle" sampling means no samples are taken before the previous sample's output has been delivered. A sample is taken ASAP after an over-period computation: otherwise remains on schedule.

Type
Sampling scheme

t_samp_ms: list[float]

Record of sampling times—each time `put_state()` is called.

6.3.6 cleo.light module

class cleo.light.**GaussianEllipsoid**(*sigma_axial: Quantity = 18. * umetre*, *sigma_lateral: Quantity = 8. * umetre*)

Bases: *LightModel*

Method generated by attrs for class GaussianEllipsoid.

sigma_axial: Quantity

Standard deviation distance along the focal axis.

Standard deviations estimated by taking point where response is ~60% of peak:

Publication	axial	lateral	measure
Prakash et al., 2012	13 m	7 m	photocurrent
Rickgauer et al., 2014	8 m	4 m	Ca2+ dF/F response
Packer et al., 2015	18 m	8 m	AP probability
Chen et al., 2019	18/11 m	8/? m	AP probability/photocurrent

sigma_lateral: Quantity

Standard deviation distance along the focal plane.

transmittance(*source_coords: Quantity*, *source_dir_uvec: NDArray[Any, 3, Any]*, *target_coords: Quantity*) → NDArray[Any, Any, Float]

Output must be between 0 and 1 with shape (n_sources, n_targets).

viz_params(*coords: Quantity*, *direction: NDArray[Any, 3, Any]*, *T_threshold: float*, *n_points_per_source: int = 4000*, ***kwargs*) → Quantity

Returns info needed for visualization. Output is ((m, n_points_per_source, 3) viz_points array, markersize_um, intensity_scale).

For best-looking results, implementations should scale *markersize_um* and *intensity_scale*.

class cleo.light.**Koehler**(*radius: Quantity*, *zmax: Quantity = 0.5 * mmetre*)

Bases: *LightModel*

Even illumination over a circular area, with no scattering.

Method generated by attrs for class Koehler.

radius: Quantity

The radius of the Köhler beam

transmittance(*source_coords*, *source_dir_uvec*, *target_coords*)

Output must be between 0 and 1 with shape (n_sources, n_targets).

viz_params(*coords*, *direction*, *T_threshold*, *n_points_per_source=4000*, ***kwargs*)

Returns info needed for visualization. Output is ((m, n_points_per_source, 3) viz_points array, markersize_um, intensity_scale).

For best-looking results, implementations should scale *markersize_um* and *intensity_scale*.

zmax: Quantity

The maximum extent of the Köhler beam, 500 m by default (i.e., no thicker than necessary to go through a slice or culture).

class cleo.light.**Light**(*coords=array([0., 0., 0.]) * metre*, *direction: Quantity = (0, 0, 1)*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*, *light_model:* LightModel, *wavelength: Quantity = 0.473 * umetre*, *max_Irr0_mW_per_mm2: float = None*, *max_Irr0_mW_per_mm2_viz: float = None*, *default_value: NDArray[Any, Float] = _Nothing.NOTHING*)

Bases: *Stimulator*

Delivers light to the network for photostimulation and (when implemented) imaging.

Requires neurons to have 3D spatial coordinates already assigned.

Visualization kwargs

- **n_points_per_source** (*int, optional*) – The number of points per light source used to represent light intensity in space. Default varies by *light_model*. Alias `n_points`.
- **T_threshold** (*float, optional*) – The transmittance below which no points are plotted. By default 1e-3.
- **intensity** (*float, optional*) – How bright the light appears, should be between 0 and 1. By default 0.5.
- **rasterized** (*bool, optional*) – Whether to render as rasterized in vector output, True by default. Useful since so many points makes later rendering and editing slow.

Method generated by attrs for class Light.

add_self_to_plot(*ax*, *axis_scale_unit*, ***kwargs*) → list[PathCollection]

Add device to an existing plot

Should only be called by *plot()*.

Parameters

- **ax** (*Axes3D*) – The existing matplotlib Axes object
- **axis_scale_unit** (*Unit*) – The unit used to label axes and define chart limits
- ****kwargs** (*optional*) –

Returns

A list of artists used to render the device. Needed for use in conjunction with *VideoVisualizer*.

Return type

list[Artist]

property color

Color of light

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams: Any*) → None

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

coords: Quantity

(x, y, z) coords with Brian unit specifying where to place the base of the light source, by default (0, 0, 0)*mm. Can also be an nx3 array for multiple sources.

default_value: NDArray[Any, Float]

The default value of the device—used on initialization and on `reset()`

direction: NDArray[Any, 3, Any]

(x, y, z) vector specifying direction in which light source is pointing, by default (0, 0, 1).

Will be converted to unit magnitude.

init_for_simulator(*sim: CLSimulator*) → None

Initialize device for simulator on initial injection.

This function is called only the first time a device is injected into a simulator and performs any operations that are independent of the individual neuron groups it is connected to.

Parameters

simulator (CLSimulator) – simulator being injected into

light_model: *LightModel*

Defines how light is emitted. See *OpticFiber* for an example.

max_Irr0_mW_per_mm2: float

The maximum irradiance the light source can emit.

Usually determined by hardware in a real experiment.

max_Irr0_mW_per_mm2_viz: float

Maximum irradiance for visualization purposes.

i.e., the level at or above which the light appears maximally bright. Only relevant in video visualization.

property n

Number of light sources

property source: Subgroup

Returns the "neuron(s)" representing the light source(s).

to_neo()

Return a Neo signal object with the device's data

Returns

Neo object representing exported data

Return type
neo.core.BaseNeo

transmittance(*target_coords*) → ndarray

Returns *light_model* transmittance given light's coords and direction.

update(*value: float | ndarray*) → None

Set the light intensity, in mW/mm2 (without unit) for 1P excitation or laser power (mW) for 2P excitation (GaussianEllipsoid light model).

Parameters
Irr0_mW_per_mm2 (*float*) – Desired light intensity for light source

update_artists(*artists: list[Artist]*, *value*, **args*, ***kwargs*) → list[Artist]

Update the artists used to render the device

Used to set the artists' state at every frame of a video visualization. The current state would be passed in **args* or ***kwargs*

Parameters
artists (*list[Artist]*) – the artists used to render the device originally, i.e., which were returned from the first *add_self_to_plot()* call.

Returns
The artists that were actually updated. Needed for efficient blit rendering, where only updated artists are re-rendered.

Return type
list[Artist]

wavelength: Quantity

light wavelength with unit (usually nmeter)

class cleo.light.**LightDependent**(*spectrum: list[tuple[float, float]] = _Nothing.NOTHING*, *spectrum_interpolator: ~typing.Callable = <function cubic_interpolator>*)

Bases: object

Mix-in class for opsin and light-dependent indicator. Light-dependent devices are connected to light sources (and vice-versa) on injection via the registry.

We approximate dynamics under multiple wavelengths using a weighted sum of photon fluxes, where the factor indicates the activation relative to the peak-sensitivity wavelength for a equivalent power, which most papers report. When they report the action spectrum for equivalent photon flux instead (see Mager et al, 2018), use *equal_photon_flux_spectrum()*. This weighted sum is an approximation of a nonlinear peak-non-peak wavelength relation; see notebooks/multi_wavelength_model.ipynb for details.

Method generated by attrs for class LightDependent.

epsilon(*lambda_new*) → float

Returns the ε value for a given lambda (in nm) representing the relative sensitivity of the opsin to that wavelength.

property light_agg_ngs

spectrum: list[tuple[float, float]]

List of (wavelength, epsilon) tuples representing the action (opsin) or excitation (indicator) spectrum.

spectrum_interpolator: Callable

Function of signature (lambdas_nm, epsilons, lambda_new_nm) that interpolates the action spectrum data and returns $\varepsilon \in [0, 1]$ for the new wavelength.

class cleo.light.**LightModel**

Bases: ABC

Defines how light propagates given a source location and direction.

Method generated by attrs for class LightModel.

abstract transmittance(*source_coords: Quantity*, *source_direction: NDArray[Any, 3, Any]*, *target_coords: Quantity*) → NDArray[Any, Any, Float]

Output must be between 0 and 1 with shape (n_sources, n_targets).

abstract viz_params(*coords: Quantity*, *direction: NDArray[Any, 3, Any]*, *T_threshold: float*, *n_points_per_source: int = None*, ***kwargs*) → tuple[NDArray[Any, Any, 3, Any], float, float]

Returns info needed for visualization. Output is ((m, n_points_per_source, 3) viz_points array, markersize_um, intensity_scale).

For best-looking results, implementations should scale *markersize_um* and *intensity_scale*.

class cleo.light.**OpticFiber**(*R0: Quantity = 100. * umetre*, *NAfib: float = 0.37*, *K: Quantity = 125. * metre**-1*, *S: Quantity = 7370. * metre**-1*, *ntis: float = 1.36*)

Bases: *LightModel*

Optic fiber light model from Foutz et al., 2012.

Defaults are from paper for 473 nm wavelength.

Method generated by attrs for class OpticFiber.

K: Quantity

absorbance coefficient (wavelength/tissue dependent)

NAfib: float

optical fiber numerical aperture

R0: Quantity

optical fiber radius

S: Quantity

scattering coefficient (wavelength/tissue dependent)

ntis: float

tissue index of refraction (wavelength/tissue dependent)

transmittance(*source_coords: Quantity*, *source_dir_uvec: NDArray[Any, 3, Any]*, *target_coords: Quantity*) → NDArray[Any, Any, Float]

Output must be between 0 and 1 with shape (n_sources, n_targets).

viz_params(*coords: Quantity*, *direction: NDArray[Any, 3, Any]*, *T_threshold: float*, *n_points_per_source: int = 4000*, ***kwargs*) → Quantity

Returns info needed for visualization. Output is ((m, n_points_per_source, 3) viz_points array, markersize_um, intensity_scale).

For best-looking results, implementations should scale *markersize_um* and *intensity_scale*.

cleo.light.**cubic_interpolator**(*lambdas_nm*, *epsilons*, *lambda_new_nm*)

cleo.light.**equal_photon_flux_spectrum**(*spectrum: list[tuple[float, float]]*) → list[tuple[float, float]]

Converts an equival photon flux spectrum to an equal power density spectrum.

cleo.light.**fiber473nm**(*R0=100. * umetre*, *NAfib=0.37*, *K=125. * metre**-1*, *S=7370. * metre**-1*, *ntis=1.36*) → *OpticFiber*

Returns an `OpticFiber` model with parameters for 473 nm light.

Parameters from Foutz et al., 2012.

cleo.light.**linear_interpolator**(*lambdas_nm*, *epsilons*, *lambda_new_nm*)

cleo.light.**plot_spectra**(**ldds: LightDependent*) → tuple[plt.Figure, plt.Axes]

Plots the action/excitation spectra for multiple light-dependent devices.

cleo.light.**tp_light_from_scope**(*scope*, *wavelength=1.06 * umetre*, ***kwargs*) → *Light*

Creates a light object from a scope object with 2P focused laser points at each target.

Parameters

- **scope** (`Scope`) – The scope object containing the laser spots.
- **wavelength** (*`Quantity, optional`*) – The wavelength of the laser, by default 1060 * nmeter.

6.3.7 cleo.opto module

Contains opsin models, light sources, and some parameters

class cleo.opto.**BansalFourStateOpsin**(*extra_namespace: dict = _Nothing.NOTHING*, *spectrum: list[tuple[float, float]] = _Nothing.NOTHING*, *spectrum_interpolator: Callable = <function cubic_interpolator>*, *Gd1: Quantity = 66. * hertz*, *Gd2: Quantity = 10. * hertz*, *Gr0: Quantity = 0.333 * hertz*, *g0: Quantity = 3.2 * nsiemens*, *phim: Quantity = 1.e+22 * metre ** -2 * second ** -1*, *k1: Quantity = 0.4 * khertz*, *k2: Quantity = 120. * hertz*, *Gf0: Quantity = 18. * hertz*, *Gb0: Quantity = 8. * hertz*, *kf: Quantity = 10. * hertz*, *kb: Quantity = 8. * hertz*, *gamma: Quantity = 0.05*, *p: Quantity = 1*, *q: Quantity = 1*, *E: Quantity = 0. * volt*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: `MarkovOpsin`

4-state model from Bansal et al. 2020.

The difference from the PyRhO model is that there is no voltage dependence.

rho_rel is channel density relative to standard model fit; modifying it post-injection allows for heterogeneous opsin expression.

IOPTO_VAR_NAME and V_VAR_NAME are substituted on injection.

Method generated by attrs for class BansalFourStateOpsin.

E: Quantity

Gb0: Quantity

Gd1: Quantity

Gd2: Quantity

Gf0: Quantity

Gr0: Quantity

g0: Quantity

gamma: Quantity

init_syn_vars(*opto_syn: Synapses*) → None

Initializes appropriate variables in Synapses implementing the model

Also called on `reset()`.

Parameters

syn (*Synapses*) – The synapses object implementing this model

k1: Quantity

k2: Quantity

kb: Quantity

kf: Quantity

model: str

Basic Brian model equations string.

Should contain a *rho_rel* term reflecting relative expression levels. Will likely also contain special NeuronGroup-dependent symbols such as V_VAR_NAME to be replaced on injection in `modify_model_and_params_for_ng()`.

p: Quantity

phim: Quantity

q: Quantity

class cleo.opto.**BansalThreeStatePump**(*extra_namespace: dict = _Nothing.NOTHING*, *spectrum: list[tuple[float, float]] = _Nothing.NOTHING*, *spectrum_interpolator: Callable = <function cubic_interpolator>*, *Gd: Quantity = 250. * hertz*, *Gr: Quantity = 50. * hertz*, *ka: Quantity = msecond ** -1*, *p: Quantity = 0.7*, *q: Quantity = 0.1*, *phim: Quantity = 1.2e+24 * metre ** -2 * second ** -1*, *E: Quantity = -0.4 * volt*, *g0: Quantity = 22.34 * nsiemens*, *a: Quantity = 2.e+08 * metre ** -3 * second ** -1 * amp ** -1 * mole*, *b: float = 12*, *vartheta_max: Quantity = 5. * katal / (metre ** 3)*, *kd: Quantity = 16. * mmolar*, *g_Cl: Quantity = 2.3 * nsiemens*, *Cl_out: Quantity = 124. * mmolar*, *Psi0: Quantity = 4.4286 * katal / (metre ** 3)*, *E_Cl0: Quantity = -70. * mvolt*, *vmin: Quantity = -0.4 * volt*, *vmax: Quantity = 50. * mvolt*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: `MarkovOpsin`

3-state model from Bansal et al. 2020. Defaults are for eNpHR3.0.

rho_rel is channel density relative to standard model fit; modifying it post-injection allows for heterogeneous opsin expression.

IOPTO_VAR_NAME and V_VAR_NAME are substituted on injection.

Method generated by attrs for class BansalThreeStatePump.

Cl_out: Quantity

E: Quantity

E_Cl0: Quantity

Gd: Quantity

Gr: Quantity

Psi0: Quantity

a: Quantity

b: float

g0: Quantity

g_Cl: Quantity

init_syn_vars(*opto_syn: Synapses*) → None

Initializes appropriate variables in Synapses implementing the model

Also called on `reset()`.

Parameters

syn (*Synapses*) – The synapses object implementing this model

ka: Quantity

kd: Quantity

model: str

Basic Brian model equations string.

Should contain a *rho_rel* term reflecting relative expression levels. Will likely also contain special NeuronGroup-dependent symbols such as V_VAR_NAME to be replaced on injection in `modify_model_and_params_for_ng()`.

p: Quantity

phim: Quantity

q: Quantity

vartheta_max: Quantity

vmax: Quantity

Needed to avoid jumps in [Cl_in] for EIF neurons

vmin: Quantity

Needed to avoid jumps in [Cl_in] for EIF neurons

class cleo.opto.**FourStateOpsin**(*spectrum: list[tuple[float, float]] = _Nothing.NOTHING*, *spectrum_interpolator: Callable = <function cubic_interpolator>*, *g0: Quantity = 114. * nsiemens*, *gamma: Quantity = 0.00742*, *phim: Quantity = 2.33e+23 * metre ** -2 * second ** -1*, *k1: Quantity = 4.15 * khertz*, *k2: Quantity = 0.868 * khertz*, *p: Quantity = 0.833*, *Gf0: Quantity = 37.3 * hertz*, *kf: Quantity = 58.1 * hertz*, *Gb0: Quantity = 16.1 * hertz*, *kb: Quantity = 63. * hertz*, *q: Quantity = 1.94*, *Gd1: Quantity = 105. * hertz*, *Gd2: Quantity = 13.8 * hertz*, *Gr0: Quantity = 0.33 * hertz*, *E: Quantity = 0. * volt*, *v0: Quantity = 43. * mvolt*, *v1: Quantity = 17.1 * mvolt*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: `MarkovOpsin`

4-state model from PyRhO (Evans et al. 2016).

rho_rel is channel density relative to standard model fit; modifying it post-injection allows for heterogeneous opsin expression.

IOPTO_VAR_NAME and V_VAR_NAME are substituted on injection.

Defaults are for ChR2.

Method generated by attrs for class FourStateOpsin.

E: Quantity

Gb0: Quantity

Gd1: Quantity

Gd2: Quantity

Gf0: Quantity

Gr0: Quantity

extra_namespace: dict[str, Any]

Additional items (beyond parameters) to be added to the opto synapse namespace

g0: Quantity

gamma: Quantity

init_syn_vars(*opto_syn: Synapses*) → None

Initializes appropriate variables in Synapses implementing the model

Also called on `reset()`.

Parameters

syn (*Synapses*) – The synapses object implementing this model

k1: Quantity

k2: Quantity

kb: Quantity

kf: Quantity

model: str

Basic Brian model equations string.

Should contain a *rho_rel* term reflecting relative expression levels. Will likely also contain special NeuronGroup-dependent symbols such as V_VAR_NAME to be replaced on injection in `modify_model_and_params_for_ng()`.

p: Quantity

phim: Quantity

q: Quantity

v0: Quantity

v1: Quantity

class cleo.opto.**Opsin**(*extra_namespace: dict = _Nothing.NOTHING*, *spectrum: list[tuple[float, float]] = _Nothing.NOTHING*, *spectrum_interpolator: Callable = <function cubic_interpolator>*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *LightDependent*, *SynapseDevice*

Base class for opsin model.

Requires that the neuron model has a current term (by default Iopto) which is assumed to be positive (unlike the convention in many opsin modeling papers, where the current is described as negative).

We approximate dynamics under multiple wavelengths using a weighted sum of photon fluxes, where the factor indicates the activation relative to the peak-sensitivy wavelength for an equivalent number of photons (see Mager et al, 2018). This weighted sum is an approximation of a nonlinear peak-non-peak wavelength relation; see `notebooks/multi_wavelength_model.ipynb` for details.

Method generated by attrs for class Opsin.

property action_spectrum

Alias for `light_receptor.spectrum`

class cleo.opto.**ProportionalCurrentOpsin**(*extra_namespace: dict = _Nothing.NOTHING*, *spectrum: list[tuple[float, float]] = _Nothing.NOTHING*, *spectrum_interpolator: Callable = <function cubic_interpolator>*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*, *I_per_Irr: Quantity*)

Bases: *Opsin*

A simple model delivering current proportional to light intensity

Method generated by attrs for class ProportionalCurrentOpsin.

I_per_Irr: Quantity

How much current (in amps or unitless, depending on neuron model) to deliver per mW/mm2.

model: str

Basic Brian model equations string.

Should contain a *rho_rel* term reflecting relative expression levels. Will likely also contain special NeuronGroup-dependent symbols such as V_VAR_NAME to be replaced on injection in `modify_model_and_params_for_ng()`.

required_vars: list[Tuple[str, Unit]]

Default names of state variables required in the neuron group, along with units, e.g., [('Iopto', amp)].

It is assumed that non-default values can be passed in on injection as a keyword argument `[default_name]_var_name=[non_default_name]` and that these are found in the model string as `[DEFAULT_NAME]_VAR_NAME` before replacement.

`cleo.opto.`**`chr2_4s`**`()` → *FourStateOpsin*

Returns a 4-state ChR2 model.

Params taken from try.projectpyrho.org's default 4-state configuration. Action spectrum from Nagel et al., 2003, Fig. 4a, extracted using Plot Digitizer.

Parameters can be changed after initialization but *before injection*.

`cleo.opto.`**`chr2_b4s`**`()` → *BansalFourStateOpsin*

Returns a 4-state ChR2 model.

Params given in Bansal et al., 2020. Action spectrum from Nagel et al., 2003, Fig. 4a, extracted using Plot Digitizer.

Parameters can be changed after initialization but *before injection*.

`cleo.opto.`**`chr2_h134r_4s`**`()` → *BansalFourStateOpsin*

Returns a 4-state ChR2(H134R) model.

Params given in Bansal et al., 2020. Action spectrum is same as for *chr2_4s()*, but blue-shifted 20 nm (I cannot find it directly in the literature).

Parameters can be changed after initialization but *before injection*.

`cleo.opto.`**`chrimson_4s`**`()` → *BansalFourStateOpsin*

Returns a 4-state Chrimson model.

Params given in Bansal et al., 2020. Action spectrum from Mager et al., 2018, Supp. Fig. 1a, extracted using Plot Digitizer.

Parameters can be changed after initialization but *before injection*.

`cleo.opto.`**`enphr3_3s`**`()`

Returns a 3-state model of eNpHR3, a chloride pump.

Params given in Bansal et al., 2020. Action spectrum from Gradinaru et al., 2010, Figure 3F, extracted using Plot Digitizer.

`cleo.opto.`**`gtacr2_4s`**`()` → *BansalFourStateOpsin*

Returns a 4-state model of GtACR2, an anion channel.

Params given in Bansal et al., 2020. Action spectra from Govorunova et al., 2015, Fig. 1f, extracted using Plot Digitizer.

Parameters can be changed after initialization but *before injection*.

`cleo.opto.`**`vfchrimson_4s`**`()` → *BansalFourStateOpsin*

Returns a 4-state vf-Chrimson model.

Params given in Bansal et al., 2020. Action spectrum from Mager et al., 2018, Supp. Fig. 1a, extracted using Plot Digitizer.

Parameters can be changed after initialization but *before injection*.

6.3.8 cleo.recorders module

Contains basic recorders.

class cleo.recorders.**GroundTruthSpikeRecorder**(*, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *Recorder*

Reports the number of spikes seen since last queried for each neuron.

This amounts effectively to the number of spikes per control period. Note: this will only work for one neuron group at the moment.

Method generated by attrs for class GroundTruthSpikeRecorder.

connect_to_neuron_group(*neuron_group*)

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

get_state() → NDArray[Any, UInt]

Returns
n_neurons-length array with spike counts over the latest control period.

Return type
NDArray[(n_neurons,), np.uint]

neuron_group: NeuronGroup

class cleo.recorders.**RateRecorder**(*i: int*, *, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *Recorder*

Records firing rate from a single neuron.

Firing rate comes from Brian's PopulationRateMonitor

Method generated by attrs for class RateRecorder.

connect_to_neuron_group(*neuron_group*)

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

get_state()

Return current measurement.

i: **int**

index of neuron to record

mon: PopulationRateMonitor

class cleo.recorders.**VoltageRecorder**(*voltage_var_name: str = 'v'*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *Recorder*

Records the voltage of a single neuron group.

Method generated by attrs for class VoltageRecorder.

connect_to_neuron_group(*neuron_group*)

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

get_state() → Quantity

Returns
Current voltage of target neuron group

Return type
Quantity

mon: StateMonitor

voltage_var_name: **str**

Name of variable representing membrane voltage

6.3.9 cleo.registry module

Code for orchestrating inter-device interactions.

This should only be relevant for developers, not users, as this code is used under the hood when interacting devices are injected (e.g., light and opsin).

class cleo.registry.**DeviceInteractionRegistry**(*sim:* CLSimulator)

Bases: `object`

Facilitates the creation and maintenance of 'neurons' and 'synapses' implementing many-to-many light-opsin/indicator relationships

Method generated by attrs for class DeviceInteractionRegistry.

brian_objects: **set**

Stores all Brian objects created (and injected into the network) by this registry

connect_light_to_ldd_for_ng(*light:* Light, *ldd:* LightDependent, *ng: NeuronGroup*) → None

Connects a light to a light-dependent device for a given neuron group.

Parameters

- **light** (Light) – Light being injected
- **ldd** (LightDependent) – Light-dependent device the light will affect

- **ng** (*NeuronGroup*) – Neurons affected by the light-dependent device

Raises

ValueError – if the connection has already been made

connections: set[Tuple['Light', 'LightDependent', NeuronGroup]]

Set of (light, light-dependent device, neuron group) tuples representing previously created connections.

init_register_light(*light:* Light) → Subgroup

Creates neurons for the light source, if they don't already exist

ldds_for_ng: dict[NeuronGroup, set['LightDependent']]

Maps neuron group to the light-dependent devices injected into it

light_prop_model = '\n T : 1\n epsilon : 1\n Ephoton : joule\n Irr_post = epsilon * T * Irr0_pre : watt/meter2 (summed)\n phi_post = Irr_post / Ephoton : 1/second/meter**2 (summed)\n '**

Model used in light propagation synapses

light_prop_syns: dict[Tuple['LightDependent', NeuronGroup], Synapses]

Maps (light-dependent device, neuron group) to the synapses implementing light propagation

light_source_ng: NeuronGroup

Represents ALL light sources (multiple devices)

lights_for_ng: dict[NeuronGroup, set['Light']]

Maps neuron group to the lights injected into it

register(*device:* InterfaceDevice, *ng: NeuronGroup*) → None

Registers a device injection with the registry.

Parameters

- **device** (InterfaceDevice) – Device being injected
- **ng** (*NeuronGroup*) – Neurons being injected into

register_ldd(*ldd:* LightDependent, *ng: NeuronGroup*)

Connects lights previously injected into this neuron group to this light-dependent device

register_light(*light:* Light, *ng: NeuronGroup*)

Connects light to light-dependent devices already injected into this neuron group

sim: *CLSimulator*

source_for_light(*light:* Light) → Subgroup

Returns the subgroup representing the given light source

subgroup_idx_for_light: dict['Light', slice]

Maps light to its indices in the *light_source_ng*

cleo.registry.**registries: dict['CLSimulator', *DeviceInteractionRegistry*] = {}**

Maps simulator to its registry

cleo.registry.**registry_for_sim**(*sim:* CLSimulator) → *DeviceInteractionRegistry*

Returns the registry for the given simulator

6.3.10 cleo.stimulators module

Contains basic stimulators.

class cleo.stimulators.**StateVariableSetter**(*default_value: Any = 0*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*, *variable_to_ctrl: str*, *unit: Unit*)

Bases: *Stimulator*

Sets the given state variable of target neuron groups.

Method generated by attrs for class StateVariableSetter.

connect_to_neuron_group(*neuron_group*)

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

neuron_groups: list[NeuronGroup]

unit: Unit

will be used in *update()*

Type
Unit of controlled variable

update(*ctrl_signal: float*) → None

Set state variable of target neuron groups

Parameters
ctrl_signal (*float*) – Value to update variable to, without unit. The unit provided on initialization is automatically multiplied.

variable_to_ctrl: str

Name of state variable to control

6.3.11 cleo.utilities module

Assorted utilities for developers.

cleo.utilities.**add_to_neo_segment**(*segment: Segment*, **objects: DataObject*)

Conveniently adds multiple objects to a segment.

Taken from neo.core.group.Group.

cleo.utilities.**analog_signal**(*t_ms*, *values_no_unit*, *units=''*) → BaseSignal

cleo.utilities.**brian_safe_name**(*name: str*) → str

cleo.utilities.**get_orth_vectors_for_V**(*V*)

For nx3 block of row vectors V, return nx3 W1, W2 orthogonal vector blocks

cleo.utilities.**modify_model_with_eqs**(*neuron_group*, *eqs_to_add*)

Adapted from _create_variables() from neurongroup.py from Brian2 source code v2.3.0.2

cleo.utilities.**normalize_coords**(*coords: Quantity*) → Quantity

Normalize coordinates to unit vectors.

cleo.utilities.**rng = Generator(PCG64) at 0x7F8C141917E0**

supposed to be the central random number generator, but not yet used everywhere

cleo.utilities.**style_plots_for_docs**(*dark=True*)

cleo.utilities.**style_plots_for_paper**()

cleo.utilities.**times_are_regular**(*times*)

cleo.utilities.**uniform_cylinder_rz**(*n*, *rmax*, *zmax*)

uniformly fills a cylinder with radius rmax and height zmax with n points.

Does so by generating a Fibonacci spiral cylinder by rotating around axis and up and down cylinder simultaneously, using different angle steps.

cleo.utilities.**unit_safe_append**(*q1: Quantity*, *q2: Quantity*, *axis=0*)

cleo.utilities.**wavelength_to_rgb**(*wavelength_nm*, *gamma=0.8*) → tuple[float, float, float]

taken from http://www.noah.org/wiki/Wavelength_to_RGB_in_Python This converts a given wavelength of light to an approximate RGB color value. The wavelength must be given in nanometers in the range from 380 nm through 750 nm (789 THz through 400 THz).

Based on code by Dan Bruton http://www.physics.sfasu.edu/astro/color/spectra.html

cleo.utilities.**xyz_from_rz**(*rs*, *thetas*, *zs*, *xyz_start*, *xyz_end*)

Convert from cylindrical to Cartesian coordinates.

6.3.12 cleo.viz module

Tools for visualizing models and simulations

class cleo.viz.**VideoVisualizer**(*devices: Iterable[*InterfaceDevice | *Tuple[*InterfaceDevice*, dict]] = _Nothing.NOTHING*, *dt: Quantity = 1. * msecond*, ***, *name: str = _Nothing.NOTHING*, *save_history: bool = True*)

Bases: *InterfaceDevice*

Device for visualizing a simulation.

Must be injected after all other devices and before the simulation is run.

Method generated by attrs for class VideoVisualizer.

ax: Axes

connect_to_neuron_group(*neuron_group: NeuronGroup*, ***kwparams*) → None

Connect device to given *neuron_group*.

If your device introduces any objects which Brian must keep track of, such as a NeuronGroup, Synapses, or Monitor, make sure to add these to *brian_objects*.

Parameters

- **neuron_group** (*NeuronGroup*) –
- ****kwparams** (*optional*) – Passed from *inject*

devices: `Iterable[InterfaceDevice | Tuple[InterfaceDevice, dict]]`

list of devices or (device, vis_kwargs) tuples to include in the plot, just as in the *plot()* function, by default "all", which will include all recorders and stimulators currently injected when this visualizer is injected into the simulator.

dt: `Quantity`

length of each frame—that is, every `dt` the visualizer takes a snapshot of the network, by default 1*ms

fig: `Figure`

generate_Animation(*plotargs: dict*, *slowdown_factor: float = 10*, ***figargs: Any*) → Animation

Create a matplotlib Animation object from the recorded simulation

Parameters

- **plotargs** (*dict*) – dictionary of arguments as taken by *plot()*. can include *xlim*, *ylim*, *zlim*, *colors*, *axis_scale_unit*, *invert_z*, and/or *scatterargs*. neuron groups and devices are automatically added and ***figargs* are specified separately.
- **slowdown_factor** (*float, optional*) – how much slower the animation will be rendered, as a multiple of real-time, by by default 10
- ****figargs** (*Any, optional*) – keyword arguments passed to plt.figure(), such as figsize

Returns

An Animation object capturing the desired visualization. See matplotlib's docs for saving and rendering options.

Return type

matplotlib.animation.Animation

init_for_simulator(*simulator:* CLSimulator)

Initialize device for simulator on initial injection.

This function is called only the first time a device is injected into a simulator and performs any operations that are independent of the individual neuron groups it is connected to.

Parameters

simulator (CLSimulator) – simulator being injected into

neuron_groups: `list[NeuronGroup]`

cleo.viz.**plot**(**neuron_groups: NeuronGroup*, *xlim: Tuple[float, float] = None*, *ylim: Tuple[float, float] = None*, *zlim: Tuple[float, float] = None*, *colors: Iterable = None*, *axis_scale_unit: Unit = umetre*, *devices: Iterable[*InterfaceDevice | *Tuple[*InterfaceDevice*, dict]] = []*, *invert_z: bool = True*, *scatterargs: dict = {}*, *sim:* CLSimulator *= None*, ***figargs: Any*) → None

Visualize neurons and interface devices

Parameters

- **xlim** (*Tuple[float, float], optional*) – xlim for plot, determined automatically by default
- **ylim** (*Tuple[float, float], optional*) – ylim for plot, determined automatically by default
- **zlim** (*Tuple[float, float], optional*) – zlim for plot, determined automatically by default
- **colors** (*Iterable, optional*) – colors, one for each neuron group, automatically determined by default

- **axis_scale_unit** (*Unit, optional*) – Brian unit to scale lim params, by default mm
- **devices** (*Iterable[Union[InterfaceDevice, Tuple[InterfaceDevice, dict]]], optional*) – devices to add to the plot or (device, kwargs) tuples. *add_self_to_plot()* is called for each, using the kwargs dict if given. By default []
- **invert_z** (*bool, optional*) – whether to invert z-axis, by default True to reflect the convention that +z represents depth from cortex surface
- **scatterargs** (*dict, optional*) – arguments passed to plt.scatter() for each neuron group, such as marker
- **sim** (*CLSimulator, optional*) – Optional shortcut to include all neuron groups and devices
- ****figargs** (*Any, optional*) – keyword arguments passed to plt.figure(), such as figsize

Raises

ValueError – When neuron group doesn't have x, y, and z already defined

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