Current status and future plans for NeuroTools

Pierre Yger

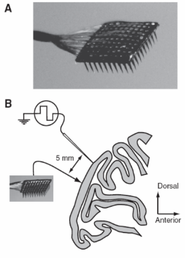
BioEngineering Department, Imperial College, London

March 15, 2012

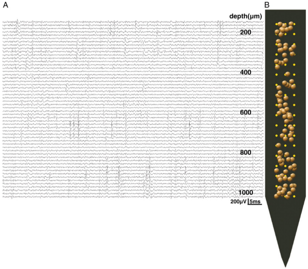
try: reduce(duplication, community)

The curse of the data

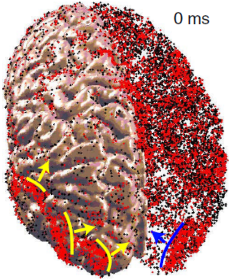
- Simulations and/or multiple recordings are nowadays common.
- Hundreds, thousands, even hundreds of thousands recordings.
- More and more complex analysis handling those massive data.



[Smith *et al*, 2008]



[Blanche *et al*, 2005]



[Izhikevich *et al*, 2007]

Analysis workflows

Direct consequence of this complexity:

→ Analysis/Workflows has to be standardised

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Solutions:

Simplify reuse of code by new tools/methods (svn, documentation, tests, well-defined API) and common format

The current status of NeuroTools

NeuroTools was initiated during the FACETS projects, aiming to:

1. increase the productivity of modellers by automating, simplifying, and establishing best-practices for common tasks
2. increase the productivity of the modelling community by reducing code duplication
3. increase the reliability of the tools, leveraging Linus's law: *"given enough eyeballs, all bugs are shallow"*

Current Status:

Still not 'stable', not modular enough, should be simplified.

The need for a common format

Some Simulators

- Brian *brian.di.ens.fr/*
- Catacomb *www.catcmb.org*
- CSIM *www.lsm.tugraz.at/csim*
- GENESIS *www.genesis-sim.org*
- Matlab *www.mathworks.com*
- Mvaspike *mvaspike.gforge.inria.fr*
- Neosim *www.neurogems.org/neosim2*
- NEST *www.nest-initiative.org*
- NEURON *www.neuron.yale.edu*
- Neurospaces *neurospaces.sourceforge.net*
- SpikeNET *www.spikenet-technology.com*
- SPLIT
- Topographica *topographica.org*
- Your home made one
- ...

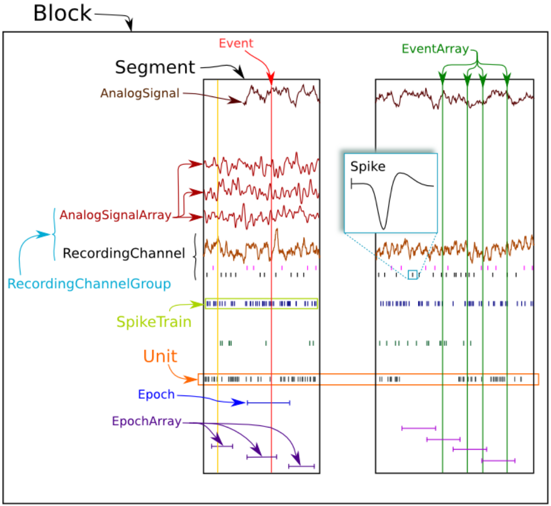
Some Analysis tools

- Spike Train Analysis Toolkit *neuroanalysis.org/toolkit/intro.html*
- Spike Toolbox *www.ini.uzh.ch/d̃ylan/spike_toolbox*
- MEA-Tools *material.brainworks.uni-freiburg.de*
- Spike train analysis software *www.blki.hu/s̃zucs/OS3.html*
- NeuroExplorer *www.adinstruments.com*
- Spike Train Analysis with R (STAR) *sites.google.com/site/spiketrainanalysiswithr/*
- OpenElectrophy *http://neuralensemble.org/trac/OpenElectrophy*
- FIND *http://find.bccn.uni-freiburg.de/*
- Your home made one
- ...

try: reduce(duplication, community)

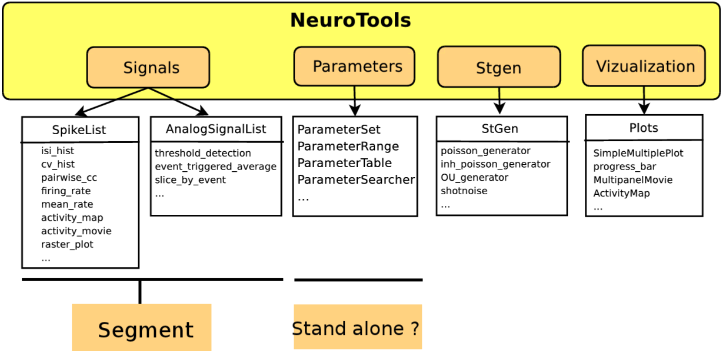
neo: the chosen one

- generic container
- extensible
- r/w common formats
- handle quantities
- match various needs
  - real recordings
  - simulations
- link with OpenElectrophy
- (wait for tomorrow)



Neo 0.2 architecture

The NeuroTools Structure

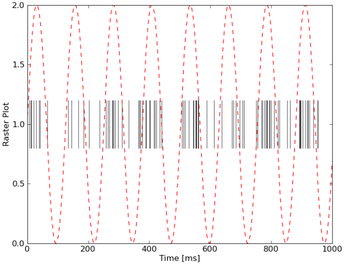


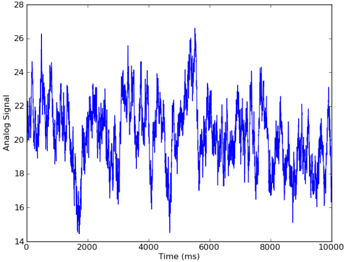
- Particular attention on documentation, to make functions usable
- Tests tend to be systematic (currently $>$ 80% of coverage)

NeuroTools.stgen

Efficient generation of time varying signals

- (in)homogeneous poisson/gamma processes
- Orstein Ulbeck processes
- Shot noise
- ...





`NeuroTools.parameters`

Deal with the parameter mess in simulations

- Good practice to separate the parameters from the model itself.
- At least, parameters should be in a separate section of a file.

Advantages

→ Helps version control, as model vs parameter changes can be conceptually separated

→ Make it easier to track a simulation project, since the parameter sets can be stored in a database, displayed in a GUI, etc.

→ Consolidate the reproducibility of the results (alternatives: `sumatra`)

The ParameterSet class

ParameterSet objects may be created from a dict:

```
>> sim_params = ParameterSet({'dt': 0.11, 'tstop': 1000.0})
```

They may be nested:

```
>> I_params = ParameterSet({'tau_m': 15.0, 'cm': 0.75})
>> network_params = ParameterSet({
...                'excitatory_cells': E_params,
...                'inhibitory_cells': I_params})
>> P = ParameterSet({'sim': sim_params,
...                'network': network_params},
...                label="my_params")
```

Parameter spaces

```
>> P = ParameterSpace({
...         'cm': 1.0,
...         'tau_m': ParameterRange([10.0, 15.0, 20.0])
... })
>>  for p in P.iter_inner():
...     print p
...
{'tau_m': 10.0, 'cm': 1.0}
{'tau_m': 15.0, 'cm': 1.0}
{'tau_m': 20.0, 'cm': 1.0}
```

Parameter distributions

```
>> P = ParameterSpace({
...         'cm': 1.0,
...         'tau_m': NormalDist(mean=12.0, std=5.0)
... })
>>  for p in P.realize_dists(2):
...   print p
...
{'tau_m': 20.237970275471028, 'cm': 1.0}
{'tau_m': 10.068110582245506, 'cm': 1.0}
```

NeuroTools.signals

try: reduce(duplication, community)

Dealing with event signals:

- `SpikeTrain`
- `SpikeList`

And with analog signals

- `AnalogSignal`
- `AnalogSignalList`
  - `MembraneTraceList`
  - `CurrentTraceList`
  - `ConductanceTraceList`

→ All merged into a single class `Segment` to match the `neo` syntax

The SpikeTrain objects

Object to handle the spikes produced by one cell during $[t_{\text{start}}, t_{\text{stop}}]$

- `duration()`, `time_slice()`, `time_offset()`
- `isi()`, `mean_rate()`, `cv_isi()`
- `raster_plot()`
- `time_histogram()`, `psth()`
- `distance_victorpurpura()`, `distance_kreuz(()`
- `merge()`
- ...

→ Distances should be separated
→ Functions instead of methods for less code duplication

The SpikeList class

object to handle the spikes produced by several cells during $[t_{\mathrm{start}}, t_{\mathrm{stop}}]$

- More or less a dictionnary of SpikeTrains
- Cells have unique id
- They could be aranged on a grid for graphical purpose

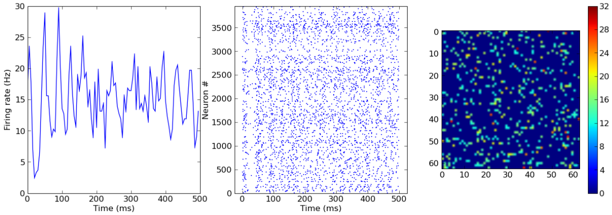
```
>> spikes = SpikeList(data, id_list=range(10000), t_start=0,
      t_stop=500, dims=[100,100])
>> spikes[245].mean_rate()
```

The `SpikeList` class

- All `SpikeTrain` functions can be called
- Easy way of slicing, either by id, time or even by user-defined conditions.
- Easy way of building `SpikeTrain` from your own fileformats
- Pairs generators to average functions over custom-defined pairs:
  - `pairwise_cc()`, `pairwise_pearson_corrcoeff()`, ...
- Graphical functions: `raster_plot()`, activity maps and movies for 2D SpikeList, ...

The SpikeList class

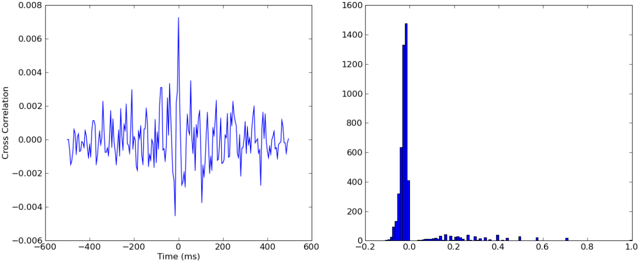

```
>> all_spikes = load_spikelist('data.gdf', t_start=0, t_stop=500,
                                                   dims=[65,65])
>> ids        = all_spikes.select_ids('cell.mean_rate() > 10')
>> my_spikes  = all_spikes.id_slice(ids)
>> my_spikes.firing_rate(time_bin=5, display=subplot(131))
>> my_spikes.raster_plot(1000, display=subplot(132))
>> my_spikes.activity_map(display=subplot(133))
```



The SpikeList class

Pairs Selectors: `Random`, `Auto`, `DistantDependent`, ...

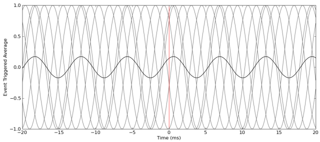
```
>> pairs = RandomPairs(all_spikes, all_spikes, no_silent=True)
>> spikes.pairwise_cc(5000, pairs, time_bin=5)
>> x = spikes.pairwise_pearson_corrcoeff(5000, pairs, time_bin=5)
>> hist(x, 100)
```



The `AnalogSignal(List)` class

Object to handle analog signals produced during $[t_{\text{start}}, t_{\text{stop}}]$, with sampling time dt.

- `duration()`, `time_slice()`, `time_offset()`
- `threshold_detection`, `event_triggered_average()`
- `slice_by_events()`
- ...




```
>> signal = sin(arange(0, 1000, 0.1))
>> x = AnalogSignal(signal, dt=0.1)
>> spk = SpikeTrain(arange(0,1000,100))
>> x.event_triggered_average(spk,
    average=False, t_min=20, t_max=20)
```

New syntax

After the CodeJam, we should have:

```
>> data = neo.PyNNNumpyIO("simulation.npy")
>> data.read_segment()
>> mean_rate(data)
>> psth(data, events=[10, 250, 350])
>> subdata = data.time_slice(2000, 5000)
>> raster_plot(subdata)
```

Further extensions

- Consolidate the `NeuroTools` structure:
  - Simplify the API
  - Finish the transition towards `Segment` objects
  - Clarify all dependencies and simplify the addition of extra functions.
  - Have a look around (nibabel/nipy fMRI community)
- Add more sophisticated analysis functions:
  - More sharing and reuse of code
  - Gain in confidence and correctness
- Enlarge the community

Questions ?

To give a try: `http://www.neuralensemble.org`
Download, install, play, and contribute !

Contributors

Daniel Bruederle, Andrew Davison, Samuel Garcia, Jens Kremkow, Eilif Muller, Laurent Perrinet, Michael Schmuker