

---

# **LFPy Homepage**

***Release 2.2.4***

**LFPy-team**

**Feb 12, 2022**



# CONTENTS

<b>1</b>	<b>Contents</b>	<b>3</b>
1.1	LFPy	3
1.1.1	Summary	3
1.1.2	Latest changes	3
1.1.3	Usage	3
1.1.4	Code status	4
1.1.5	Conda-forge status	4
1.1.6	Information	5
1.1.7	Citing LFPy	5
1.1.8	Tutorial slides on LFPy	6
1.1.9	Related projects	6
1.1.10	Requirements	6
1.1.11	Installation	7
1.1.12	Uninstall	8
1.1.13	Docker	8
1.1.14	HTML Documentation	9
1.1.15	Physical units in LFPy	9
1.2	Module LFPy	9
1.3	Cell classes	11
1.3.1	class Cell	11
1.3.2	class TemplateCell	22
1.3.3	class NetworkCell	33
1.4	Point processes	44
1.4.1	class PointProcess	44
1.4.2	class Synapse	45
1.4.3	class StimIntElectrode	46
1.5	Networks	48
1.5.1	class Network	48
1.5.2	class NetworkPopulation	52
1.6	Forward models	53
1.6.1	class CurrentDipoleMoment	53
1.6.2	class PointSourcePotential	54
1.6.3	class LineSourcePotential	56
1.6.4	class RecExtElectrode	58
1.6.5	class RecMEAElectrode	63
1.6.6	class OneSphereVolumeConductor	67
1.7	Current Dipole Moment forward models	70
1.7.1	class InfiniteVolumeConductor	70
1.7.2	class FourSphereVolumeConductor	72
1.7.3	class NYHeadModel	75

1.7.4	class <code>InfiniteHomogeneousVolCondMEG</code> . . . . .	76
1.7.5	class <code>SphericallySymmetricVolCondMEG</code> . . . . .	80
1.8	Current Source Density (CSD) . . . . .	83
1.8.1	class <code>LaminarCurrentSourceDensity</code> . . . . .	83
1.8.2	class <code>VolumetricCurrentSourceDensity</code> . . . . .	84
1.9	Misc. . . . .	86
1.9.1	submodule <code>lfpcalc</code> . . . . .	86
1.9.2	submodule <code>tools</code> . . . . .	86
1.9.3	submodule <code>alias_method</code> . . . . .	87
1.9.4	submodule <code>inputgenerators</code> . . . . .	87
<b>2</b>	<b>Indices and tables</b>	<b>89</b>
	<b>Bibliography</b>	<b>91</b>
	<b>Python Module Index</b>	<b>93</b>
	<b>Index</b>	<b>95</b>



(Looking for the old LFPy v1.\* documentation? Follow [link](#))



## CONTENTS

### 1.1 LFPy

#### 1.1.1 Summary

LFPy is a Python module for calculation of extracellular potentials from multicompartment neuron models. It relies on the NEURON simulator (<http://www.neuron.yale.edu/neuron>) and uses the Python interface (<http://www.frontiersin.org/neuroinformatics/10.3389/neuro.11.001.2009/abstract>) it provides.

#### 1.1.2 Latest changes

Just updated LFPy? Please check the latest release notes: <https://github.com/LFPy/LFPy/releases>

#### 1.1.3 Usage

A basic simulation of extracellular potentials of a multicompartment neuron model set up with LFPy:

```
>>> # import modules
>>> import LFPy
>>> from LFPy import Cell, Synapse, LineSourcePotential
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> # create Cell
>>> cell = Cell(morphology=''.join(LFPy.__path__ +
>>>                                ['/test/ball_and_sticks.hoc']),
>>>              passive=True, # NEURON 'pas' mechanism
>>>              tstop=100, # ms
>>>              )
>>> # create Synapse
>>> synapse = Synapse(cell=cell,
>>>                    idx=cell.get_idx("soma[0]"), # soma segment index
>>>                    syntype='Exp2Syn', # two-exponential synapse
>>>                    weight=0.005, # max conductance (uS)
>>>                    e=0, # reversal potential (mV)
>>>                    tau1=0.5, # rise time constant
>>>                    tau2=5., # decay time constant
>>>                    record_current=True, # record synapse current
>>>                    )
```

(continues on next page)

(continued from previous page)

```
>>> synapse.set_spike_times(np.array([20., 40])) # set activation times
>>> # create extracellular predictor
>>> lsp = LineSourcePotential(cell=cell,
>>>                             x=np.zeros(11) + 10, # x-coordinates of contacts ( $\mu\text{m}$ )
>>>                             y=np.zeros(11), # y-coordinates
>>>                             z=np.arange(11)*20, # z-coordinates
>>>                             sigma=0.3, # extracellular conductivity (S/m)
>>>                             )
>>> # execute simulation
>>> cell.simulate(probes=[lsp]) # compute measurements at run time
>>> # plot results
>>> fig, axes = plt.subplots(3, 1, sharex=True, figsize=(12, 8))
>>> axes[0].plot(cell.tvec, synapse.i)
>>> axes[0].set_ylabel('i_syn (nA)')
>>> axes[1].plot(cell.tvec, cell.somav)
>>> axes[1].set_ylabel('V_soma (nA)')
>>> axes[2].pcolormesh(cell.tvec, lsp.z, lsp.data, shading='auto')
>>> axes[2].set_ylabel('z ( $\mu\text{m}$ )')
>>> axes[2].set_xlabel('t (ms)')
```

You can now test some LFPy examples online without installation:

### 1.1.4 Code status

### 1.1.5 Conda-forge status



### 1.1.6 Information

LFPy provides a set of easy-to-use Python classes for setting up your model, running your simulations and calculating the extracellular potentials arising from activity in your model neuron. If you have a model working in NEURON ([www.neuron.yale.edu](http://www.neuron.yale.edu)) already, it is likely that it can be adapted to work with LFPy.

The extracellular potentials are calculated from transmembrane currents in multi-compartment neuron models using the line-source method (Holt & Koch, J Comp Neurosci 1999), but a simpler point-source method is also available. The calculations assume that the neuron are surrounded by an infinite extracellular medium with homogeneous and frequency independent conductivity, and compartments are assumed to be at least at a minimal distance from the electrode (which can be specified by the user). For more information on the biophysics underlying the numerical framework used see this coming book chapter:

- K.H. Pettersen, H. Linden, A.M. Dale and G.T. Einevoll: Extracellular spikes and current-source density, in *Handbook of Neural Activity Measurement*, edited by R. Brette and A. Destexhe, Cambridge, to appear (preprint PDF, 5.7MB <http://www.csc.kth.se/~helinden/PettersenLindenDaleEinevoll-BookChapter-revised.pdf>)

The first release of LFPy (v1.x) was mainly designed for simulation extracellular potentials of single neurons, described in our paper on the package in Frontiers in Neuroinformatics entitled “LFPy: A tool for biophysical simulation of extracellular potentials generated by detailed model neurons”. The article can be found at <https://dx.doi.org/10.3389/fninf.2013.00041>. Since version 2 (LFPy v2.x), the tool also facilitates simulations of extracellular potentials and current dipole moment from ongoing activity in recurrently connected networks of multicompartment neurons, prediction of EEG scalp surface potentials, MEG scalp surface magnetic fields, as described in the publication “Multimodal modeling of neural network activity: computing LFP, ECoG, EEG and MEG signals with LFPy2.0” by Espen Hagen, Solveig Naess, Torbjørn V Ness, Gaute T Einevoll, found at <https://dx.doi.org/10.3389/fninf.2018.00092>.

### 1.1.7 Citing LFPy

- LFPy v2.x: Hagen E, Næss S, Ness TV and Einevoll GT (2018) Multimodal Modeling of Neural Network Activity: Computing LFP, ECoG, EEG, and MEG Signals With LFPy 2.0. Front. Neuroinform. 12:92. doi: 10.3389/fninf.2018.00092. <https://dx.doi.org/10.3389/fninf.2018.00092>
- LFPy v1.x: Linden H, Hagen E, Leski S, Norheim ES, Pettersen KH and Einevoll GT (2013). LFPy: A tool for biophysical simulation of extracellular potentials generated by detailed model neurons. Front. Neuroinform. 7:41. doi: 10.3389/fninf.2013.00041. <https://dx.doi.org/10.3389/fninf.2013.00041>

LFPy was developed in the Computational Neuroscience Group, Department of Mathematical Sciences and Technology (<http://www.nmbu.no/imt>), at the Norwegian University of Life Sciences (<http://www.nmbu.no>), in collaboration with the Laboratory of Neuroinformatics (<http://www.nencki.gov.pl/en/laboratory-of-neuroinformatics>), Nencki Institute of Experimental Biology (<http://www.nencki.gov.pl>), Warsaw, Poland. The effort was supported by International Neuroinformatics Coordinating Facility (<http://incf.org>), the Research Council of Norway (<http://www.forskningssradet.no/english>) (eScience, NevroNor), EU-FP7 (BrainScaleS, <http://www.brainscales.org>), the European Union Horizon 2020 Framework Programme for Research and Innovation under Specific Grant Agreement No. 785907 and No. 945539 [Human Brain Project (HBP) SGA2, SGA3 and EBRAINS].

For updated information on LFPy and online documentation, see the LFPy homepage (<http://lfp.readthedocs.io>).

### 1.1.8 Tutorial slides on LFPy

- Slides for OCNS 2019 meeting tutorial T8: Biophysical modeling of extracellular potentials (using LFPy) hosted in Barcelona, Spain on LFPy:
- Older tutorial slides can be found at <https://github.com/LFPy/LFPy.github.io/tree/master/downloads>

### 1.1.9 Related projects

LFPy has been used extensively in ongoing and published work, and may be a required dependency by the publicly available Python modules:

- ViSAPy - Virtual Spiking Activity in Python (<https://github.com/espenhgn/ViSAPy>, <http://software.incf.org/software/visapy>), as described in Hagen, E., et al. (2015), J Neurosci Meth, DOI:10.1016/j.jneumeth.2015.01.029
- ViMEAPy that can be used to incorporate heterogeneous conductivity in calculations of extracellular potentials with LFPy (<https://bitbucket.org/torbnness/vimeapy>, <http://software.incf.org/software/vimeapy>). ViMEAPy and it's application is described in Ness, T. V., et al. (2015), Neuroinform, DOI:10.1007/s12021-015-9265-6.
- hybridLFPy - biophysics-based hybrid scheme for calculating the local field potential (LFP) of spiking activity in simplified point-neuron network models (<https://github.com/INM-6/hybridLFPy>), as described in Hagen, E. and Dahmen, D., et al. (2016), Cereb Cortex, DOI:10.1093/cercor/bhw237
- MEArec - Fast and customizable simulation of extracellular recordings on Multi-Electrode-Arrays (<https://github.com/alejoe91/MEArec>) as described in Buccino, A.P., Einevoll, G.T. MEArec: A Fast and Customizable Testbench Simulator for Ground-truth Extracellular Spiking Activity. Neuroinform (2020). <https://doi.org/10.1007/s12021-020-09467-7>

### 1.1.10 Requirements

Dependencies should normally be automatically installed. For manual preinstallation of dependencies, the following packages are needed:

- Python modules numpy, scipy, matplotlib, h5py, mpi4py
- MEAutility (<https://github.com/alejoe91/MEAutility>)
- LFPykit (<https://github.com/LFPy/LFPykit>)
- NEURON (from <http://www.neuron.yale.edu>) and corresponding Python module. The following should execute without error in a Python console:

```
>>> import neuron
>>> neuron.test()
```

- Cython (C-extensions for python, <http://cython.org>) to speed up simulations of extracellular fields

### 1.1.11 Installation

There are few options to install LFPy:

1. From the Python Package Index with only local access using pip:

```
$ pip install LFPy --user
```

as sudoer (in general not recommended as system Python files may be overwritten):

```
$ sudo pip install LFPy
```

Upgrading LFPy from the Python package index (without attempts at upgrading dependencies):

```
$ pip install --upgrade --no-deps LFPy --user
```

LFPy release candidates can be installed as:

```
$ pip install --pre --index-url https://test.pypi.org/simple/ --extra-index-url ↵
↵https://pypi.org/simple LFPy --user
```

2. From the Python Package Index with only local access using easy\_install:

```
$ easy_install --user LFPy
```

As sudoer:

```
$ sudo easy_install LFPy
```

3. From source:

```
$ tar -xzf LFPy-x.x.tar.gz
$ cd LFPy-x.x
$ (sudo) python setup.py develop (--user)
```

4. Development version from the GitHub repository:

```
$ git clone https://github.com/LFPy/LFPy.git
$ cd LFPy
$ (sudo) pip install -r requirements.txt (--user) # install dependencies
$ (sudo) python setup.py develop (--user)
```

5. Anaconda Python (<https://www.anaconda.com>, macos/linux only):

Add the conda-forge (<https://conda-forge.org>) as channel:

```
$ conda config --add channels conda-forge
$ conda config --set channel_priority strict # suggested
```

Create a new conda environment with LFPy and activate it:

```
$ conda create -n lfp python=3 pip lfp # creates new Python 3.x conda ↵
↵environment named lfp with pip and LFPy and their dependencies
$ conda activate lfp # activate the lfp environment
$ python -c "import LFPy; LFPy.run_tests()" # check that installation is working
```

LFPy can also be installed in existing conda environments if the dependency tree is solvable:

```
$ conda activate <environment>
$ conda install lfpypy # installs LFPy and its dependencies in the current conda
environment
```

### 1.1.12 Uninstall

To remove installed LFPy files it should suffice to issue (repeat until no more LFPy files are found):

```
$ (sudo) pip uninstall LFPy
```

In case LFPy was installed using conda in an environment, it can be uninstalled by issuing:

```
$ conda uninstall lfpypy
```

### 1.1.13 Docker

We provide a Docker (<https://www.docker.com>) container recipe file with LFPy. To get started, install Docker and issue either:

```
# build Dockerfile from GitHub
$ docker build -t lfpypy https://raw.githubusercontent.com/LFPy/LFPy/master/Dockerfile
$ docker run -it -p 5000:5000 lfpypy:latest
```

or

```
# build local Dockerfile (obtained by cloning repo, checkout branch etc.)
$ docker build -t lfpypy - < Dockerfile
$ docker run -it -p 5000:5000 lfpypy:latest
```

If the docker file should fail for some reason it is possible to store the build log and avoid build caches by issuing

```
$ docker build --no-cache --progress=plain -t lfpypy - < Dockerfile 2>&1 | tee lfpypy.log
```

If the build is successful, the `--mount` option can be used to mount a folder on the host to a target folder as:

```
$ docker run --mount type=bind,source="$(pwd)",target=/opt -it -p 5000:5000 lfpypy
```

which mounts the present working directory (`$(pwd)`) to the `/opt` directory of the container. Try mounting the LFPy source directory for example (by setting `source="<path-to-LFPy>"`). Various LFPy example files can then be found in the folder `/opt/LFPy/examples/` when the container is running.

Jupyter notebook servers running from within the container can be accessed after invoking them by issuing:

```
$ cd /opt/LFPy/examples/
$ jupyter-notebook --ip 0.0.0.0 --port=5000 --no-browser --allow-root
```

and opening the resulting URL in a browser on the host computer, similar to: <http://127.0.0.1:5000/?token=dcf8f859f859740fc858c568bdd5b015e0cf15bfc2c5b0c1>

### 1.1.14 HTML Documentation

To generate the html documentation also hosted at <https://lfp.py.rtd.io> using Sphinx, issue from the LFPy source code directory:

```
$ cd doc
$ make html
```

The main html file is in `_build/html/index.html`. `m2r2`, `Numpydoc` and the Sphinx `ReadTheDocs` theme may be needed:

```
$ pip install m2r2 --user
$ pip install numpydoc --user
$ pip install sphinx-rtd-theme --user
```

### 1.1.15 Physical units in LFPy

Physical units follow the NEURON conventions found [here](#). The units in LFPy for given quantities are:

Quantity	Symbol	Unit
Spatial dimensions	x,y,z,d	[m]
Potential	v, Phi,	[mV]
Reversal potential	E	[mV]
Current	i	[nA]
Membrane capacitance	c_m	[F/cm2]
Conductance	g	[S/cm2]
Synaptic conductance	g	[μS]
Extracellular conductivity	sigma,	[S/m]
Current dipole moment	P	[nA μm]
Magnetic field	H	[nA/μm]
Magnetic permeability	μ, mu	[T m/A]
Current Source Density	CSD	[nA/μm3]

Note: resistance, conductance and capacitance are usually specific values, i.e per membrane area (lowercase `r_m`, `g`, `c_m`) Depending on the mechanism files, some may use different units altogether, but this should be taken care of internally by NEURON.

## 1.2 Module LFPy

Initialization of LFPy, a Python module for simulating extracellular potentials.

Group of Computational Neuroscience, Department of Mathematical Sciences and Technology, Norwegian University of Life Sciences.

Copyright (C) 2012 Computational Neuroscience Group, NMBU.

This program is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

**Classes**

- **Cell** - object built on top of NEURON representing biological neuron
- **TemplateCell** - Similar to **Cell**, but for models using cell templates
- **NetworkCell** - Similar to **TemplateCell** with some attributes and methods for spike communication between parallel RANKs
- **PointProcess** - Parent class of **Synapse** and **StimIntElectrode**
- **Synapse** - Convenience class for inserting synapses onto **Cell** objects
- **StimIntElectrode** - Convenience class for inserting stimulating electrodes into **Cell** objects
- **Network** - Class for creating distributed populations of cells and handling connections between cells in populations
- **NetworkPopulation** - Class representing group of **Cell** objects distributed across MPI RANKs
- **RecExtElectrode** - Class for setup of simulations of extracellular potentials
- **RecMEAElectrode** - Class for setup of simulations of in vitro (slice) extracellular potentials
- **PointSourcePotential** - Base forward-model for extracellular potentials assuming point current sources in conductive media
- **LineSourcePotential** - Base forward-model for extracellular potentials assuming line current sources in conductive media
- **OneSphereVolumeConductor** - For computing extracellular potentials within and outside a homogeneous sphere
- **CurrentDipoleMoment** - For computing the current dipole moment,
- **FourSphereVolumeConductor** - For computing extracellular potentials in four-sphere head model (brain, CSF, skull, scalp)
- **InfiniteVolumeConductor** - To compute extracellular potentials with current dipoles in infinite volume conductor
- **MEG** - Class for computing magnetic field from current dipole moment

**Modules**

- **lfpcalc** - Misc. functions used by **RecExtElectrode** class
- **tools** - Some convenient functions
- **inputgenerators** - Functions for synaptic input time generation
- **eegmegcalc** - Classes for calculating current dipole moment vector **P** and **P\_tot** from currents and distances.
- **run\_simulations** - Functions to run NEURON simulations

## 1.3 Cell classes

### 1.3.1 class Cell

```
class LFPy.Cell(morphology, v_init=-70.0, Ra=None, cm=None, passive=False, passive_parameters=None,
                extracellular=False, tstart=0.0, tstop=100.0, dt=0.0625, nsecs_method='lambda100',
                lambda_f=100.0, d_lambda=0.1, max_nsecs_length=None, delete_sections=True,
                custom_code=None, custom_fun=None, custom_fun_args=None, pt3d=False, celsius=None,
                verbose=False, **kwargs)
```

Bases: object

The main cell class used in LFPy.

#### Parameters

**morphology: str or neuron.h.SectionList** File path of morphology on format that NEURON can understand (w. file ending .hoc, .asc, .swc or .xml), or neuron.h.SectionList instance filled with references to neuron.h.Section instances.

**v\_init: float** Initial membrane potential. Defaults to -70 mV.

**Ra: float or None** Axial resistance. Defaults to None (unit Ohm\*cm)

**cm: float** Membrane capacitance. Defaults to None (unit uF/cm2)

**passive: bool** Passive mechanisms are initialized if True. Defaults to False

**passive\_parameters: dict** parameter dictionary with values for the passive membrane mechanism in NEURON ('pas'). The dictionary must contain keys 'g\_pas' [S/cm^2] and 'e\_pas' [mV], like the default: passive\_parameters=dict(g\_pas=0.001, e\_pas=-70)

**extracellular: bool** Switch for NEURON's extracellular mechanism. Defaults to False

**dt: float** simulation timestep. Defaults to 2^-4 ms

**tstart: float** Initialization time for simulation <= 0 ms. Defaults to 0.

**tstop: float** Stop time for simulation > 0 ms. Defaults to 100 ms.

**nsecs\_method: 'lambda100' or 'lambda\_f' or 'fixed\_length' or None** nseg rule, used by NEURON to determine number of compartments. Defaults to 'lambda100'

**max\_nsecs\_length: float or None** Maximum segment length for method 'fixed\_length'. Defaults to None

**lambda\_f: float** AC frequency for method 'lambda\_f'. Defaults to 100. (Hz)

**d\_lambda: float** Parameter for d\_lambda rule. Defaults to 0.1

**delete\_sections: bool** Delete pre-existing section-references. Defaults to True

**custom\_code: list or None** List of model-specific code files ([.py/.hoc]). Defaults to None

**custom\_fun: list or None** List of model-specific functions with args. Defaults to None

**custom\_fun\_args: list or None** List of args passed to custom\_fun functions. Defaults to None

**pt3d: bool** Use pt3d-info of the cell geometries switch. Defaults to False

**celsius: float or None** Temperature in celsius. If nothing is specified here or in custom code it is 6.3 celcius

**verbose: bool** Verbose output switch. Defaults to False

See also:

*TemplateCell*

*NetworkCell*

## Examples

Simple example of how to use the Cell class with a passive-circuit morphology (modify morphology path accordingly):

```
>>> import os
>>> import LFPy
>>> cellParameters = {
>>>     'morphology': os.path.join('examples', 'morphologies',
>>>                                'L5_Mainen96_LFPy.hoc'),
>>>     'v_init': -65.,
>>>     'cm': 1.0,
>>>     'Ra': 150,
>>>     'passive': True,
>>>     'passive_parameters': {'g_pas': 1./30000, 'e_pas': -65},
>>>     'dt': 2**-3,
>>>     'tstart': 0,
>>>     'tstop': 50,
>>> }
>>> cell = LFPy.Cell(**cellParameters)
>>> cell.simulate()
>>> print(cell.somav)
```

**cellpickler**(*filename*, *pickler*=<built-in function dump>)

Save data in cell to filename, using cPickle. It will however destroy any neuron.h objects upon saving, as c-objects cannot be pickled

### Parameters

**filename:** str Where to save cell

### Returns

None or pickle

## Examples

```
>>> # To save a cell, issue:
>>> cell.cellpickler('cell.cpickle')
>>> # To load this cell again in another session:
>>> import cPickle
>>> with file('cell.cpickle', 'rb') as f:
>>>     cell = cPickle.load(f)
```

**chiral\_morphology**(*axis*='x')

Mirror the morphology around given axis, (default x-axis), useful to introduce more heterogeneities in morphology shapes

### Parameters

**axis:** str 'x' or 'y' or 'z'



**distort\_geometry**(*factor=0.0, axis='z', nu=0.0*)

Distorts cellular morphology with a relative factor along a chosen axis preserving Poisson's ratio. A ratio  $nu=0.5$  assumes incompressible and isotropic media that embeds the cell. A ratio  $nu=0$  will only affect geometry along the chosen axis. A ratio  $nu=-1$  will isometrically scale the neuron geometry along each axis. This method does not affect the underlying cable properties of the cell, only predictions of extracellular measurements (by affecting the relative locations of sources representing the compartments).

**Parameters**

**factor:** **float** relative compression/stretching factor of morphology. Default is 0 (no compression/stretching). Positive values implies a compression along the chosen axis.

**axis:** **str** which axis to apply compression/stretching. Default is "z".

**nu:** **float** Poisson's ratio. Ratio between axial and transversal compression/stretching. Default is 0.

**enable\_extracellular\_stimulation**(*electrode, t\_ext=None, n=1, model='inf'*)

Enable extracellular stimulation with NEURON's *extracellular* mechanism. Extracellular potentials are computed from electrode currents using the point-source approximation. If *model* is 'inf' (default), potentials are computed as ( $r_i$  is the position of a compartment  $i$ ,  $r_n$  is the position of an electrode  $n$ ,  $\sigma$  is the conductivity of the medium):

$$V_e(r_i) = \sum_n \frac{I_n}{4\pi\sigma|r_i - r_n|}$$

If *model* is 'semi', the method of images is used:

$$V_e(r_i) = \sum_n \frac{I_n}{2\pi\sigma|r_i - r_n|}$$

**Parameters**

**electrode:** **RecExtElectrode** Electrode object with stimulating currents

**t\_ext:** **np.ndarray or list** Time in ms corresponding to step changes in the provided currents. If None, currents are assumed to have the same time steps as the NEURON simulation.

**n:** **int** Points per electrode for spatial averaging

**model:** **str** 'inf' or 'semi'. If 'inf' the medium is assumed to be infinite and homogeneous. If 'semi', the method of images is used.

**Returns**

**v\_ext:** **np.ndarray** Computed extracellular potentials at cell mid points

**get\_axial\_currents\_from\_vmem**(*timepoints=None*)

Compute axial currents from cell sim: get current magnitude, distance vectors and position vectors.

**Parameters**

**timepoints:** **ndarray, dtype=int** array of timepoints in simulation at which you want to compute the axial currents. Defaults to False. If not given, all simulation timesteps will be included.

**Returns**

**i\_axial:** **ndarray, dtype=float** Shape ((cell.totnsegs-1)\*2, len(timepoints)) array of axial current magnitudes  $I$  in units of (nA) in cell at all timesteps in timepoints, or at all timesteps of the simulation if timepoints=None. Contains two current magnitudes per segment, (except for the root segment): 1) the current from the mid point of the segment to the segment start point, and 2) the current from the segment start point to the mid point of the parent segment.

**d\_vectors: ndarray, dtype=float** Shape (3, (cell.totnsegs-1)\*2) array of distance vectors traveled by each axial current in `i_axial` in units of ( $\mu\text{m}$ ). The indices of the first axis, correspond to the first axis of `i_axial` and `pos_vectors`.

**pos\_vectors: ndarray, dtype=float** Shape ((cell.totnsegs-1)\*2, 3) array of position vectors pointing to the mid point of each axial current in `i_axial` in units of ( $\mu\text{m}$ ). The indices of the first axis, correspond to the first axis of `i_axial` and `d_vectors`.

#### Raises

**AttributeError** Raises an exception if the `cell.vmem` attribute cannot be found

#### `get_axial_resistance()`

Return NEURON axial resistance for all cell compartments.

#### Returns

**ri\_list: ndarray, dtype=float** Shape (cell.totnsegs, ) array containing `neuron.h.ri(seg.x)` in units of (MOhm) for all segments in cell calculated using the `neuron.h.ri(seg.x)` method. `neuron.h.ri(seg.x)` returns the axial resistance from the middle of the segment to the middle of the parent segment. Note: If `seg` is the first segment in a section, i.e. the parent segment belongs to a different section or there is no parent section, then `neuron.h.ri(seg.x)` returns the axial resistance from the middle of the segment to the node connecting the segment to the parent section (or a ghost node if there is no parent)

#### `get_closest_idx(x=0.0, y=0.0, z=0.0, section='allsec')`

Get the index number of a segment in specified section which midpoint is closest to the coordinates defined by the user

#### Parameters

**x: float** x-coordinate

**y: float** y-coordinate

**z: float** z-coordinate

**section: str** String matching a section-name. Defaults to 'allsec'.

#### Returns

**int** segment index

#### `get_dict_of_children_idx()`

Return dictionary with children segment indices for all sections.

#### Returns

**children\_dict: dictionary** Dictionary containing a list for each section, with the segment index of all the section's children. The dictionary is needed to find the sibling of a segment.

#### `get_dict_parent_connections()`

Return dictionary with parent connection point for all sections.

#### Returns

**connection\_dict: dictionary** Dictionary containing a float in range [0, 1] for each section in cell. The float gives the location on the parent segment to which the section is connected. The dictionary is needed for computing axial currents.

#### `get_idx(section='allsec', z_min=- inf, z_max=inf)`

Returns compartment idx of segments from sections with names that match the pattern defined in input section on interval [`z_min`, `z_max`].

#### Parameters

**section:** **str** Any entry in cell.allsecnames or just 'allsec'.

**z\_min:** **float** Depth filter. Specify minimum z-position

**z\_max:** **float** Depth filter. Specify maximum z-position

#### Returns

**ndarray, dtype=int** segment indices

### Examples

```
>>> idx = cell.get_idx(section='allsec')
>>> print(idx)
>>> idx = cell.get_idx(section=['soma', 'dend', 'apic'])
>>> print(idx)
```

**get\_idx\_children**(parent='soma[0]')

Get the idx of parent's children sections, i.e. compartments ids of sections connected to parent-argument

#### Parameters

**parent:** **str** name-pattern matching a sectionname. Defaults to "soma[0]"

#### Returns

**ndarray, dtype=int**

**get\_idx\_name**(idx=array([0]))

Return NEURON convention name of segments with index idx. The returned argument is an array of tuples with corresponding segment idx, section name, and position along the section, like; [(0, 'neuron.h.soma[0]', 0.5),]

#### Parameters

**idx:** **ndarray, dtype int** segment indices, must be between 0 and cell.totnsegs

#### Returns

**ndarray, dtype=object** tuples with section names of segments

**get\_idx\_parent\_children**(parent='soma[0]')

Get all idx of segments of parent and children sections, i.e. segment idx of sections connected to parent-argument, and also of the parent segments

#### Parameters

**parent:** **str** name-pattern matching a sectionname. Defaults to "soma[0]"

#### Returns

**ndarray, dtype=int**

**get\_idx\_polygons**(projection=('x', 'z'))

For each segment idx in cell create a polygon in the plane determined by the projection kwarg (default ('x', 'z')), that can be visualized using plt.fill() or mpl.collections.PolyCollection

#### Parameters

**projection:** **tuple of strings** Determining projection. Defaults to ('x', 'z')

#### Returns

**polygons:** **list** list of (ndarray, ndarray) tuples giving the trajectory of each section

## Examples

```
>>> from matplotlib.collections import PolyCollection
>>> import matplotlib.pyplot as plt
>>> cell = LFPy.Cell(morphology='PATH/TO/MORPHOLOGY')
>>> zips = []
>>> for x, z in cell.get_idx_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                           edgecolors='none',
>>>                           facecolors='gray')
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.add_collection(polycol)
>>> ax.axis(ax.axis('equal'))
>>> plt.show()
```

**get\_intersegment\_distance**(*idx0=0, idx1=0*)

Return the Euclidean distance between midpoints of two segments.

### Parameters

**idx0:** int

**idx1:** int

### Returns

**float** distance ( $\mu\text{m}$ ).

**get\_intersegment\_vector**(*idx0=0, idx1=0*)

Return the distance between midpoints of two segments with index *idx0* and *idx1*. The argument returned is a list [x, y, z], where  $x = \text{self.x}[\text{idx1}].\text{mean}(\text{axis}=-1) - \text{self.x}[\text{idx0}].\text{mean}(\text{axis}=-1)$  etc.

### Parameters

**idx0:** int

**idx1:** int

### Returns

**list of floats** distance between midpoints along x,y,z axis in  $\mu\text{m}$

**get\_multi\_current\_dipole\_moments**(*timepoints=None*)

Return 3D current dipole moment vector and middle position vector from each axial current in space.

### Parameters

**timepoints:** ndarray, dtype=int or None array of timepoints at which you want to compute the current dipole moments. Defaults to None. If not given, all simulation timesteps will be included.

### Returns

**multi\_dipoles:** ndarray, dtype = float Shape (n\_axial\_currents, 3, n\_timepoints) array containing the x-,y-,z-components of the current dipole moment from each axial current in cell, at all timepoints. The number of axial currents,  $n\_axial\_currents = (\text{cell.totnsegs}-1) * 2$  and the number of timepoints,  $n\_timepoints = \text{cell.tvec.size}$ . The current dipole moments are given in units of (nA  $\mu\text{m}$ ).

**pos\_axial:** ndarray, dtype = float Shape (n\_axial\_currents, 3) array containing the x-, y-, and z-components giving the mid position in space of each multi\_dipole in units of ( $\mu\text{m}$ ).

## Examples

Get all current dipole moments and positions from all axial currents in a single neuron simulation:

```
>>> import LFPy
>>> import numpy as np
>>> cell = LFPy.Cell('PATH/TO/MORPHOLOGY', extracellular=False)
>>> syn = LFPy.Synapse(cell, idx=cell.get_closest_idx(0,0,1000),
>>>                    syntype='ExpSyn', e=0., tau=1., weight=0.001)
>>> syn.set_spike_times(np.mgrid[20:100:20])
>>> cell.simulate(rec_vmem=True, rec_imem=False)
>>> timepoints = np.array([1,2,3,4])
>>> multi_dipoles, dipole_locs = cell.get_multi_current_dipole_moments(
>>>     timepoints=timepoints)
```

**get\_pt3d\_polygons**(projection=('x', 'z'))

For each section create a polygon in the plane determined by keyword argument projection=('x', 'z'), that can be visualized using e.g., plt.fill()

### Parameters

**projection:** tuple of strings Determining projection. Defaults to ('x', 'z')

### Returns

**list** list of (x, z) tuples giving the trajectory of each section that can be plotted using PolyCollection

## Examples

```
>>> from matplotlib.collections import PolyCollection
>>> import matplotlib.pyplot as plt
>>> cell = LFPy.Cell(morphology='PATH/TO/MORPHOLOGY')
>>> zips = []
>>> for x, z in cell.get_pt3d_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                          edgecolors='none',
>>>                          facecolors='gray')
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.add_collection(polycol)
>>> ax.axis(ax.axis('equal'))
>>> plt.show()
```

**get\_rand\_idx\_area\_and\_distribution\_norm**(section='allsec', nidx=1, z\_min=-1000000.0, z\_max=1000000.0, fun=<scipy.stats.\_continuous\_distns.norm\_gen object>, funargs={'loc': 0, 'scale': 100}, funweights=None)

Return nidx segment indices in section with random probability normalized to the membrane area of each segment multiplied by the value of the probability density function of “fun”, a function in the scipy.stats module with corresponding function arguments in “funargs” on the interval [z\_min, z\_max]

**Parameters**

**section: str** string matching a section name

**nidx: int** number of random indices

**z\_min: float** lower depth interval

**z\_max: float** upper depth interval

**fun: function or str, or iterable of function or str** if function a scipy.stats method, if str, must be method in scipy.stats module with the same name (like 'norm'), if iterable (list, tuple, numpy.array) of function or str some probability distribution in scipy.stats module

**funargs: dict or iterable** iterable (list, tuple, numpy.array) of dict, arguments to fun.pdf method (e.g., w. keys 'loc' and 'scale')

**funweights: None or iterable** iterable (list, tuple, numpy.array) of floats, scaling of each individual fun (i.e., introduces layer specificity)

**Examples**

```
>>> import LFPy
>>> import numpy as np
>>> import scipy.stats as ss
>>> import matplotlib.pyplot as plt
>>> from os.path import join
>>> cell = LFPy.Cell(morphology=join('cells', 'cells', 'j4a.hoc'))
>>> cell.set_rotation(x=4.99, y=-4.33, z=3.14)
>>> idx = cell.get_rand_idx_area_and_distribution_norm(
>>>     nidx=10000, fun=ss.norm, funargs=dict(loc=0, scale=200))
>>> bins = np.arange(-30, 120)*10
>>> plt.hist(cell.zmid[idx], bins=bins, alpha=0.5)
>>> plt.show()
```

**get\_rand\_idx\_area\_norm**(section='allsec', nidx=1, z\_min=- 1000000.0, z\_max=1000000.0)

Return nidx segment indices in section with random probability normalized to the membrane area of segment on interval [z\_min, z\_max]

**Parameters**

**section: str** String matching a section-name

**nidx: int** Number of random indices

**z\_min: float** Depth filter

**z\_max: float** Depth filter

**Returns**

**ndarray, dtype=int** segment indices

**get\_rand\_prob\_area\_norm**(section='allsec', z\_min=- 10000, z\_max=10000)

Return the probability (0-1) for synaptic coupling on segments in section sum(prob)=1 over all segments in section. Probability normalized by area.

**Parameters**

**section: str** string matching a section-name. Defaults to 'allsec'

**z\_min: float** depth filter

**z\_max: float** depth filter

#### Returns

**ndarray, dtype=float**

**get\_rand\_prob\_area\_norm\_from\_idx**(*idx=array([0])*)

Return the normalized probability (0-1) for synaptic coupling on segments in *idx*-array. Normalised probability determined by area of segments.

#### Parameters

**idx: ndarray, dtype=int.** array of segment indices

#### Returns

**ndarray, dtype=float**

**insert\_v\_ext**(*v\_ext, t\_ext*)

Set external extracellular potential around cell. Playback of some extracellular potential *v\_ext* on each cell.totnseg compartments. Assumes that the “extracellular”-mechanism is inserted on each compartment. Can be used to study ephaptic effects and similar. The inputs will be copied and attached to the cell object as *cell.v\_ext*, *cell.t\_ext*, and converted to (list of) *neuron.h.Vector* types, to allow playback into each compartment *e\_extracellular* reference. Can not be deleted prior to running *cell.simulate()*

#### Parameters

**v\_ext: ndarray** Numpy array of size *cell.totnsegs* x *t\_ext.size*, unit mV

**t\_ext: ndarray** Time vector of *v\_ext* in ms

### Examples

```
>>> import LFPy
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> #create cell
>>> cell = LFPy.Cell(morphology='morphologies/example_morphology.hoc',
>>>                  passive=True)
>>> #time vector and extracellular field for every segment:
>>> t_ext = np.arange(cell.tstop / cell.dt + 1) * cell.dt
>>> v_ext = np.random.rand(cell.totnsegs, t_ext.size)-0.5
>>> #insert potentials and record response:
>>> cell.insert_v_ext(v_ext, t_ext)
>>> cell.simulate(rec_imem=True, rec_vmem=True)
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(311)
>>> ax2 = fig.add_subplot(312)
>>> ax3 = fig.add_subplot(313)
>>> eim = ax1.matshow(np.array(cell.v_ext), cmap='spectral')
>>> cb1 = fig.colorbar(eim, ax=ax1)
>>> cb1.set_label('v_ext')
>>> ax1.axis(ax1.axis('tight'))
>>> iim = ax2.matshow(cell.imem, cmap='spectral')
>>> cb2 = fig.colorbar(iim, ax=ax2)
>>> cb2.set_label('imem')
>>> ax2.axis(ax2.axis('tight'))
>>> vim = ax3.matshow(cell.vmem, cmap='spectral')
```

(continues on next page)

(continued from previous page)

```
>>> ax3.axis(ax3.axis('tight'))
>>> cb3 = fig.colorbar(vim, ax=ax3)
>>> cb3.set_label('vmem')
>>> ax3.set_xlabel('tstep')
>>> plt.show()
```

**set\_point\_process**(*idx, pptype, record\_current=False, record\_potential=False, \*\*kwargs*)Insert pptype-electrode type pointprocess on segment numbered *idx* on cell object**Parameters****idx: int** Index of compartment where point process is inserted**pptype: str** Type of pointprocess. Examples: SEClamp, VClamp, IClamp, SinIClamp, ChirpIClamp**record\_current: bool** Decides if current is stored**kwargs** Parameters passed on from class StimIntElectrode**Returns****int** index of point process on cell**set\_pos**(*x=0.0, y=0.0, z=0.0*)

Set the cell position. Move the cell geometry so that midpoint of soma section is in (x, y, z). If no soma pos, use the first segment

**Parameters****x: float** x position defaults to 0.0**y: float** y position defaults to 0.0**z: float** z position defaults to 0.0**set\_rotation**(*x=None, y=None, z=None, rotation\_order='xyz'*)Rotate geometry of cell object around the x-, y-, z-axis in the order described by *rotation\_order* parameter.**Parameters****x: float or None** rotation angle in radians. Default: None**y: float or None** rotation angle in radians. Default: None**z: float or None** rotation angle in radians. Default: None**rotation\_order: str** string with 3 elements containing x, y and z e.g. 'xyz', 'zyx'. Default: 'xyz'**Examples**

```
>>> cell = LFPy.Cell(**kwargs)
>>> rotation = {'x': 1.233, 'y': 0.236, 'z': np.pi}
>>> cell.set_rotation(**rotation)
```

**set\_synapse**(*idx, syntype, record\_current=False, record\_potential=False, weight=None, \*\*kwargs*)

Insert synapse on cell segment

**Parameters****idx: int** Index of compartment where synapse is inserted



**syntype:** **str** Type of synapse. Built-in types in NEURON: ExpSyn, Exp2Syn  
**record\_current:** **bool** If True, record synapse current  
**record\_potential:** **bool** If True, record postsynaptic potential seen by the synapse  
**weight:** **float** Strength of synapse  
**kwargs** arguments passed on from class Synapse

#### Returns

**int** index of synapse object on cell

**simulate**(*probes=None, rec\_imem=False, rec\_vmem=False, rec\_ipas=False, rec\_icap=False, rec\_variables=[], variable\_dt=False, atol=0.001, rtol=0.0, to\_memory=True, to\_file=False, file\_name=None, \*\*kwargs*)

This is the main function running the simulation of the NEURON model. Start NEURON simulation and record variables specified by arguments.

#### Parameters

**probes:** **list of** [*obj*], optional] None or list of LFPykit.RecExtElectrode like object instances that each have a public method *get\_transformation\_matrix* returning a matrix that linearly maps each compartments' transmembrane current to corresponding measurement as

$$\mathbf{P} = \mathbf{M}\mathbf{I}$$

**rec\_imem:** **bool** If true, segment membrane currents will be recorded If no electrode argument is given, it is necessary to set *rec\_imem=True* in order to make predictions later on. Units of (nA).

**rec\_vmem:** **bool** Record segment membrane voltages (mV)

**rec\_ipas:** **bool** Record passive segment membrane currents (nA)

**rec\_icap:** **bool** Record capacitive segment membrane currents (nA)

**rec\_variables:** **list** List of segment state variables to record, e.g. *arg=['cai', ]*

**variable\_dt:** **bool** Use NEURON's variable timestep method

**atol:** **float** Absolute local error tolerance for NEURON variable timestep method

**rtol:** **float** Relative local error tolerance for NEURON variable timestep method

**to\_memory:** **bool** Only valid with *probes=[:obj:]*, store measurements as *:obj:.data*

**to\_file:** **bool** Only valid with *probes*, save simulated data in hdf5 file format

**file\_name:** **str** Name of hdf5 file, '.h5' is appended if it doesnt exist

**strip\_hoc\_objects()**

Destroy any NEURON hoc objects in the cell object

### 1.3.2 class TemplateCell

```
class LFPy.TemplateCell(templatefile='LFPyCellTemplate.hoc', templatename='LFPyCellTemplate',  
                        templateargs=None, verbose=False, **kwargs)
```

Bases: [LFPy.cell.Cell](#)

LFPy.Cell like class allowing use of NEURON templates with some limitations.

This takes all the same parameters as the Cell class, but requires three more template related parameters `templatefile`, `templatename` and `templateargs`

#### Parameters

- morphology** [str] path to morphology file
- templatefile** [str] File with cell template definition(s)
- templatename** [str] Cell template-name used for this cell object
- templateargs** [str] Parameters provided to template-definition
- v\_init** [float] Initial membrane potential. Default to -65.
- Ra** [float] axial resistance. Defaults to 150.
- cm** [float] membrane capacitance. Defaults to 1.0
- passive** [bool] Passive mechanisms are initialized if True. Defaults to True
- passive\_parameters** [dict] parameter dictionary with values for the passive membrane mechanism in NEURON ('pas'). The dictionary must contain keys 'g\_pas' and 'e\_pas', like the default: `passive_parameters=dict(g_pas=0.001, e_pas=-70)`
- extracellular** [bool] switch for NEURON's extracellular mechanism. Defaults to False
- dt: float** Simulation time step. Defaults to 2\*\*-4
- tstart** [float] initialization time for simulation <= 0 ms. Defaults to 0.
- tstop** [float] stop time for simulation > 0 ms. Defaults to 100.
- nseg\_method** ['lambda100' or 'lambda\_f' or 'fixed\_length' or None] nseg rule, used by NEURON to determine number of compartments. Defaults to 'lambda100'
- max\_nseg\_length** [float or None] max segment length for method 'fixed\_length'. Defaults to None
- lambda\_f** [int] AC frequency for method 'lambda\_f'. Defaults to 100
- d\_lambda** [float] parameter for d\_lambda rule. Defaults to 0.1
- delete\_sections** [bool] delete pre-existing section-references. Defaults to True
- custom\_code** [list or None] list of model-specific code files ([.py/.hoc]). Defaults to None
- custom\_fun** [list or None] list of model-specific functions with args. Defaults to None
- custom\_fun\_args** [list or None] list of args passed to custom\_fun functions. Defaults to None
- pt3d** [bool] use pt3d-info of the cell geometries switch. Defaults to False
- celsius** [float or None] Temperature in celsius. If nothing is specified here or in custom code it is 6.3 celcius
- verbose** [bool] verbose output switch. Defaults to False

See also:

## Cell

### NetworkCell

## Examples

```

>>> import LFPy
>>> cellParameters = {
>>>     'morphology' : '<path to morphology.hoc>',
>>>     'templatefile' : '<path to template_file.hoc>'
>>>     'templatename' : 'templatename'
>>>     'templateargs' : None
>>>     'v_init' : -65,
>>>     'cm' : 1.0,
>>>     'Ra' : 150,
>>>     'passive' : True,
>>>     'passive_parameters' : {'g_pas' : 0.001, 'e_pas' : -65.},
>>>     'dt' : 2**-3,
>>>     'tstart' : 0,
>>>     'tstop' : 50,
>>> }
>>> cell = LFPy.TemplateCell(**cellParameters)
>>> cell.simulate()

```

**cellpickler**(*filename*, *pickler*=<built-in function dump>)

Save data in cell to filename, using cPickle. It will however destroy any neuron.h objects upon saving, as c-objects cannot be pickled

### Parameters

**filename: str** Where to save cell

### Returns

None or pickle

## Examples

```

>>> # To save a cell, issue:
>>> cell.cellpickler('cell.cpickle')
>>> # To load this cell again in another session:
>>> import cPickle
>>> with file('cell.cpickle', 'rb') as f:
>>>     cell = cPickle.load(f)

```

**chiral\_morphology**(*axis*='x')

Mirror the morphology around given axis, (default x-axis), useful to introduce more heterogeneities in morphology shapes

### Parameters

**axis: str** 'x' or 'y' or 'z'

**distort\_geometry**(*factor*=0.0, *axis*='z', *nu*=0.0)

Distorts cellular morphology with a relative factor along a chosen axis preserving Poisson's ratio. A ratio nu=0.5 assumes incompressible and isotropic media that embeds the cell. A ratio nu=0 will only affect

geometry along the chosen axis. A ratio `nu=-1` will isometrically scale the neuron geometry along each axis. This method does not affect the underlying cable properties of the cell, only predictions of extracellular measurements (by affecting the relative locations of sources representing the compartments).

#### Parameters

**factor: float** relative compression/stretching factor of morphology. Default is 0 (no compression/stretching). Positive values implies a compression along the chosen axis.

**axis: str** which axis to apply compression/stretching. Default is "z".

**nu: float** Poisson's ratio. Ratio between axial and transversal compression/stretching. Default is 0.

**enable\_extracellular\_stimulation**(*electrode, t\_ext=None, n=1, model='inf'*)

Enable extracellular stimulation with NEURON's *extracellular* mechanism. Extracellular potentials are computed from electrode currents using the point-source approximation. If `model` is 'inf' (default), potentials are computed as ( $r_i$  is the position of a compartment  $i$ ,  $r_n$  is the position of an electrode  $n$ ,  $\sigma$  is the conductivity of the medium):

$$V_e(r_i) = \sum_n \frac{I_n}{4\pi\sigma|r_i - r_n|}$$

If `model` is 'semi', the method of images is used:

$$V_e(r_i) = \sum_n \frac{I_n}{2\pi\sigma|r_i - r_n|}$$

#### Parameters

**electrode: RecExtElectrode** Electrode object with stimulating currents

**t\_ext: np.ndarray or list** Time in ms corresponding to step changes in the provided currents. If `None`, currents are assumed to have the same time steps as the NEURON simulation.

**n: int** Points per electrode for spatial averaging

**model: str** 'inf' or 'semi'. If 'inf' the medium is assumed to be infinite and homogeneous. If 'semi', the method of images is used.

#### Returns

**v\_ext: np.ndarray** Computed extracellular potentials at cell mid points

**get\_axial\_currents\_from\_vmem**(*timepoints=None*)

Compute axial currents from cell sim: get current magnitude, distance vectors and position vectors.

#### Parameters

**timepoints: ndarray, dtype=int** array of timepoints in simulation at which you want to compute the axial currents. Defaults to `False`. If not given, all simulation timesteps will be included.

#### Returns

**i\_axial: ndarray, dtype=float** Shape `((cell.totnsegs-1)*2, len(timepoints))` array of axial current magnitudes  $I$  in units of (nA) in cell at all timesteps in `timepoints`, or at all timesteps of the simulation if `timepoints=None`. Contains two current magnitudes per segment, (except for the root segment): 1) the current from the mid point of the segment to the segment start point, and 2) the current from the segment start point to the mid point of the parent segment.

**d\_vectors: ndarray, dtype=float** Shape (3, (cell.totnsegs-1)\*2) array of distance vectors traveled by each axial current in `i_axial` in units of ( $\mu\text{m}$ ). The indices of the first axis, correspond to the first axis of `i_axial` and `pos_vectors`.

**pos\_vectors: ndarray, dtype=float** Shape ((cell.totnsegs-1)\*2, 3) array of position vectors pointing to the mid point of each axial current in `i_axial` in units of ( $\mu\text{m}$ ). The indices of the first axis, correspond to the first axis of `i_axial` and `d_vectors`.

#### Raises

**AttributeError** Raises an exception if the `cell.vmem` attribute cannot be found

#### `get_axial_resistance()`

Return NEURON axial resistance for all cell compartments.

#### Returns

**ri\_list: ndarray, dtype=float** Shape (cell.totnsegs, ) array containing `neuron.h.ri(seg.x)` in units of (MOhm) for all segments in cell calculated using the `neuron.h.ri(seg.x)` method. `neuron.h.ri(seg.x)` returns the axial resistance from the middle of the segment to the middle of the parent segment. Note: If `seg` is the first segment in a section, i.e. the parent segment belongs to a different section or there is no parent section, then `neuron.h.ri(seg.x)` returns the axial resistance from the middle of the segment to the node connecting the segment to the parent section (or a ghost node if there is no parent)

#### `get_closest_idx(x=0.0, y=0.0, z=0.0, section='allsec')`

Get the index number of a segment in specified section which midpoint is closest to the coordinates defined by the user

#### Parameters

**x: float** x-coordinate

**y: float** y-coordinate

**z: float** z-coordinate

**section: str** String matching a section-name. Defaults to 'allsec'.

#### Returns

**int** segment index

#### `get_dict_of_children_idx()`

Return dictionary with children segment indices for all sections.

#### Returns

**children\_dict: dictionary** Dictionary containing a list for each section, with the segment index of all the section's children. The dictionary is needed to find the sibling of a segment.

#### `get_dict_parent_connections()`

Return dictionary with parent connection point for all sections.

#### Returns

**connection\_dict: dictionary** Dictionary containing a float in range [0, 1] for each section in cell. The float gives the location on the parent segment to which the section is connected. The dictionary is needed for computing axial currents.

#### `get_idx(section='allsec', z_min=- inf, z_max=inf)`

Returns compartment idx of segments from sections with names that match the pattern defined in input section on interval [`z_min`, `z_max`].

#### Parameters

**section:** **str** Any entry in cell.allsecnames or just 'allsec'.

**z\_min:** **float** Depth filter. Specify minimum z-position

**z\_max:** **float** Depth filter. Specify maximum z-position

#### Returns

**ndarray, dtype=int** segment indices

### Examples

```
>>> idx = cell.get_idx(section='allsec')
>>> print(idx)
>>> idx = cell.get_idx(section=['soma', 'dend', 'apic'])
>>> print(idx)
```

**get\_idx\_children**(parent='soma[0]')

Get the idx of parent's children sections, i.e. compartments ids of sections connected to parent-argument

#### Parameters

**parent:** **str** name-pattern matching a sectionname. Defaults to "soma[0]"

#### Returns

**ndarray, dtype=int**

**get\_idx\_name**(idx=array([0]))

Return NEURON convention name of segments with index idx. The returned argument is an array of tuples with corresponding segment idx, section name, and position along the section, like; [(0, 'neuron.h.soma[0]', 0.5),]

#### Parameters

**idx:** **ndarray, dtype int** segment indices, must be between 0 and cell.totnsegs

#### Returns

**ndarray, dtype=object** tuples with section names of segments

**get\_idx\_parent\_children**(parent='soma[0]')

Get all idx of segments of parent and children sections, i.e. segment idx of sections connected to parent-argument, and also of the parent segments

#### Parameters

**parent:** **str** name-pattern matching a sectionname. Defaults to "soma[0]"

#### Returns

**ndarray, dtype=int**

**get\_idx\_polygons**(projection=('x', 'z'))

For each segment idx in cell create a polygon in the plane determined by the projection kwarg (default ('x', 'z')), that can be visualized using plt.fill() or mpl.collections.PolyCollection

#### Parameters

**projection:** **tuple of strings** Determining projection. Defaults to ('x', 'z')

#### Returns

**polygons:** **list** list of (ndarray, ndarray) tuples giving the trajectory of each section

## Examples

```
>>> from matplotlib.collections import PolyCollection
>>> import matplotlib.pyplot as plt
>>> cell = LFPy.Cell(morphology='PATH/TO/MORPHOLOGY')
>>> zips = []
>>> for x, z in cell.get_idx_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                           edgecolors='none',
>>>                           facecolors='gray')
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.add_collection(polycol)
>>> ax.axis(ax.axis('equal'))
>>> plt.show()
```

**get\_intersegment\_distance**(*idx0=0, idx1=0*)

Return the Euclidean distance between midpoints of two segments.

### Parameters

**idx0:** int

**idx1:** int

### Returns

**float** distance ( $\mu\text{m}$ ).

**get\_intersegment\_vector**(*idx0=0, idx1=0*)

Return the distance between midpoints of two segments with index *idx0* and *idx1*. The argument returned is a list [x, y, z], where  $x = \text{self.x}[\text{idx1}].\text{mean}(\text{axis}=-1) - \text{self.x}[\text{idx0}].\text{mean}(\text{axis}=-1)$  etc.

### Parameters

**idx0:** int

**idx1:** int

### Returns

**list of floats** distance between midpoints along x,y,z axis in  $\mu\text{m}$

**get\_multi\_current\_dipole\_moments**(*timepoints=None*)

Return 3D current dipole moment vector and middle position vector from each axial current in space.

### Parameters

**timepoints:** ndarray, dtype=int or None array of timepoints at which you want to compute the current dipole moments. Defaults to None. If not given, all simulation timesteps will be included.

### Returns

**multi\_dipoles:** ndarray, dtype = float Shape (n\_axial\_currents, 3, n\_timepoints) array containing the x-,y-,z-components of the current dipole moment from each axial current in cell, at all timepoints. The number of axial currents,  $n\_axial\_currents = (\text{cell.totnsegs}-1) * 2$  and the number of timepoints,  $n\_timepoints = \text{cell.tvec.size}$ . The current dipole moments are given in units of (nA  $\mu\text{m}$ ).

**pos\_axial:** ndarray, dtype = float Shape (n\_axial\_currents, 3) array containing the x-, y-, and z-components giving the mid position in space of each multi\_dipole in units of ( $\mu\text{m}$ ).

## Examples

Get all current dipole moments and positions from all axial currents in a single neuron simulation:

```
>>> import LFPy
>>> import numpy as np
>>> cell = LFPy.Cell('PATH/TO/MORPHOLOGY', extracellular=False)
>>> syn = LFPy.Synapse(cell, idx=cell.get_closest_idx(0,0,1000),
>>>                    syntype='ExpSyn', e=0., tau=1., weight=0.001)
>>> syn.set_spike_times(np.mgrid[20:100:20])
>>> cell.simulate(rec_vmem=True, rec_imem=False)
>>> timepoints = np.array([1,2,3,4])
>>> multi_dipoles, dipole_locs = cell.get_multi_current_dipole_moments(
>>>     timepoints=timepoints)
```

**get\_pt3d\_polygons**(projection=('x', 'z'))

For each section create a polygon in the plane determined by keyword argument projection=('x', 'z'), that can be visualized using e.g., plt.fill()

### Parameters

**projection:** tuple of strings Determining projection. Defaults to ('x', 'z')

### Returns

**list** list of (x, z) tuples giving the trajectory of each section that can be plotted using PolyCollection

## Examples

```
>>> from matplotlib.collections import PolyCollection
>>> import matplotlib.pyplot as plt
>>> cell = LFPy.Cell(morphology='PATH/TO/MORPHOLOGY')
>>> zips = []
>>> for x, z in cell.get_pt3d_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                          edgecolors='none',
>>>                          facecolors='gray')
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.add_collection(polycol)
>>> ax.axis(ax.axis('equal'))
>>> plt.show()
```

**get\_rand\_idx\_area\_and\_distribution\_norm**(section='allsec', nidx=1, z\_min=-1000000.0, z\_max=1000000.0, fun=<scipy.stats.\_continuous\_distns.norm\_gen object>, funargs={'loc': 0, 'scale': 100}, funweights=None)

Return nidx segment indices in section with random probability normalized to the membrane area of each segment multiplied by the value of the probability density function of “fun”, a function in the scipy.stats module with corresponding function arguments in “funargs” on the interval [z\_min, z\_max]



**Parameters****section: str** string matching a section name**nidx: int** number of random indices**z\_min: float** lower depth interval**z\_max: float** upper depth interval**fun: function or str, or iterable of function or str** if function a scipy.stats method, if str, must be method in scipy.stats module with the same name (like 'norm'), if iterable (list, tuple, numpy.array) of function or str some probability distribution in scipy.stats module**funargs: dict or iterable** iterable (list, tuple, numpy.array) of dict, arguments to fun.pdf method (e.g., w. keys 'loc' and 'scale')**funweights: None or iterable** iterable (list, tuple, numpy.array) of floats, scaling of each individual fun (i.e., introduces layer specificity)**Examples**

```

>>> import LFPy
>>> import numpy as np
>>> import scipy.stats as ss
>>> import matplotlib.pyplot as plt
>>> from os.path import join
>>> cell = LFPy.Cell(morphology=join('cells', 'cells', 'j4a.hoc'))
>>> cell.set_rotation(x=4.99, y=-4.33, z=3.14)
>>> idx = cell.get_rand_idx_area_and_distribution_norm(
>>>     nidx=10000, fun=ss.norm, funargs=dict(loc=0, scale=200))
>>> bins = np.arange(-30, 120)*10
>>> plt.hist(cell.zmid[idx], bins=bins, alpha=0.5)
>>> plt.show()

```

**get\_rand\_idx\_area\_norm**(section='allsec', nidx=1, z\_min=- 1000000.0, z\_max=1000000.0)

Return nidx segment indices in section with random probability normalized to the membrane area of segment on interval [z\_min, z\_max]

**Parameters****section: str** String matching a section-name**nidx: int** Number of random indices**z\_min: float** Depth filter**z\_max: float** Depth filter**Returns****ndarray, dtype=int** segment indices**get\_rand\_prob\_area\_norm**(section='allsec', z\_min=- 10000, z\_max=10000)

Return the probability (0-1) for synaptic coupling on segments in section sum(prob)=1 over all segments in section. Probability normalized by area.

**Parameters****section: str** string matching a section-name. Defaults to 'allsec'**z\_min: float** depth filter

**z\_max: float** depth filter

#### Returns

**ndarray, dtype=float**

**get\_rand\_prob\_area\_norm\_from\_idx**(*idx=array([0])*)

Return the normalized probability (0-1) for synaptic coupling on segments in *idx*-array. Normalised probability determined by area of segments.

#### Parameters

**idx: ndarray, dtype=int.** array of segment indices

#### Returns

**ndarray, dtype=float**

**insert\_v\_ext**(*v\_ext, t\_ext*)

Set external extracellular potential around cell. Playback of some extracellular potential *v\_ext* on each cell.totnseg compartments. Assumes that the “extracellular”-mechanism is inserted on each compartment. Can be used to study ephaptic effects and similar. The inputs will be copied and attached to the cell object as *cell.v\_ext*, *cell.t\_ext*, and converted to (list of) *neuron.h.Vector* types, to allow playback into each compartment *e\_extracellular* reference. Can not be deleted prior to running *cell.simulate()*

#### Parameters

**v\_ext: ndarray** Numpy array of size *cell.totnsegs* x *t\_ext.size*, unit mV

**t\_ext: ndarray** Time vector of *v\_ext* in ms

### Examples

```
>>> import LFPy
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> #create cell
>>> cell = LFPy.Cell(morphology='morphologies/example_morphology.hoc',
>>>                  passive=True)
>>> #time vector and extracellular field for every segment:
>>> t_ext = np.arange(cell.tstop / cell.dt + 1) * cell.dt
>>> v_ext = np.random.rand(cell.totnsegs, t_ext.size)-0.5
>>> #insert potentials and record response:
>>> cell.insert_v_ext(v_ext, t_ext)
>>> cell.simulate(rec_imem=True, rec_vmem=True)
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(311)
>>> ax2 = fig.add_subplot(312)
>>> ax3 = fig.add_subplot(313)
>>> eim = ax1.matshow(np.array(cell.v_ext), cmap='spectral')
>>> cb1 = fig.colorbar(eim, ax=ax1)
>>> cb1.set_label('v_ext')
>>> ax1.axis(ax1.axis('tight'))
>>> iim = ax2.matshow(cell.imem, cmap='spectral')
>>> cb2 = fig.colorbar(iim, ax=ax2)
>>> cb2.set_label('imem')
>>> ax2.axis(ax2.axis('tight'))
>>> vim = ax3.matshow(cell.vmem, cmap='spectral')
```

(continues on next page)

(continued from previous page)

```

>>> ax3.axis(ax3.axis('tight'))
>>> cb3 = fig.colorbar(vim, ax=ax3)
>>> cb3.set_label('vmem')
>>> ax3.set_xlabel('tstep')
>>> plt.show()

```

**set\_point\_process**(*idx*, *pptype*, *record\_current=False*, *record\_potential=False*, *\*\*kwargs*)

Insert pptype-electrode type pointprocess on segment numbered *idx* on cell object

#### Parameters

**idx: int** Index of compartment where point process is inserted

**pptype: str** Type of pointprocess. Examples: SEClamp, VClamp, IClamp, SinIClamp, ChirpIClamp

**record\_current: bool** Decides if current is stored

**kwargs** Parameters passed on from class StimIntElectrode

#### Returns

**int** index of point process on cell

**set\_pos**(*x=0.0*, *y=0.0*, *z=0.0*)

Set the cell position. Move the cell geometry so that midpoint of soma section is in (x, y, z). If no soma pos, use the first segment

#### Parameters

**x: float** x position defaults to 0.0

**y: float** y position defaults to 0.0

**z: float** z position defaults to 0.0

**set\_rotation**(*x=None*, *y=None*, *z=None*, *rotation\_order='xyz'*)

Rotate geometry of cell object around the x-, y-, z-axis in the order described by *rotation\_order* parameter.

#### Parameters

**x: float or None** rotation angle in radians. Default: None

**y: float or None** rotation angle in radians. Default: None

**z: float or None** rotation angle in radians. Default: None

**rotation\_order: str** string with 3 elements containing x, y and z e.g. 'xyz', 'zyx'. Default: 'xyz'

### Examples

```

>>> cell = LFPy.Cell(**kwargs)
>>> rotation = {'x': 1.233, 'y': 0.236, 'z': np.pi}
>>> cell.set_rotation(**rotation)

```

**set\_synapse**(*idx*, *syntype*, *record\_current=False*, *record\_potential=False*, *weight=None*, *\*\*kwargs*)

Insert synapse on cell segment

#### Parameters

**idx: int** Index of compartment where synapse is inserted

**syntype: str** Type of synapse. Built-in types in NEURON: ExpSyn, Exp2Syn

**record\_current: bool** If True, record synapse current

**record\_potential: bool** If True, record postsynaptic potential seen by the synapse

**weight: float** Strength of synapse

**kwargs** arguments passed on from class Synapse

### Returns

**int** index of synapse object on cell

**simulate**(*probes=None, rec\_imem=False, rec\_vmem=False, rec\_ipas=False, rec\_icap=False, rec\_variables=[], variable\_dt=False, atol=0.001, rtol=0.0, to\_memory=True, to\_file=False, file\_name=None, \*\*kwargs*)

This is the main function running the simulation of the NEURON model. Start NEURON simulation and record variables specified by arguments.

### Parameters

**probes: list of [obj:, optional]** None or list of LFPykit.RecExtElectrode like object instances that each have a public method *get\_transformation\_matrix* returning a matrix that linearly maps each compartments' transmembrane current to corresponding measurement as

$$\mathbf{P} = \mathbf{M}\mathbf{I}$$

**rec\_imem: bool** If true, segment membrane currents will be recorded If no electrode argument is given, it is necessary to set *rec\_imem=True* in order to make predictions later on. Units of (nA).

**rec\_vmem: bool** Record segment membrane voltages (mV)

**rec\_ipas: bool** Record passive segment membrane currents (nA)

**rec\_icap: bool** Record capacitive segment membrane currents (nA)

**rec\_variables: list** List of segment state variables to record, e.g. *arg=['cai', ]*

**variable\_dt: bool** Use NEURON's variable timestep method

**atol: float** Absolute local error tolerance for NEURON variable timestep method

**rtol: float** Relative local error tolerance for NEURON variable timestep method

**to\_memory: bool** Only valid with *probes=[:obj:]*, store measurements as *:obj:.data*

**to\_file: bool** Only valid with *probes*, save simulated data in hdf5 file format

**file\_name: str** Name of hdf5 file, '.h5' is appended if it doesnt exist

**strip\_hoc\_objects()**

Destroy any NEURON hoc objects in the cell object

### 1.3.3 class NetworkCell

**class** LFPy.NetworkCell(\*\*args)

Bases: *LFPy.templatecell.TemplateCell*

Similar to *LFPy.TemplateCell* with the addition of some attributes and methods allowing for spike communication between parallel RANKs.

This class allow using NEURON templates with some limitations.

This takes all the same parameters as the Cell class, but requires three more template related parameters

#### Parameters

- morphology:** **str** path to morphology file
- templatefile:** **str** File with cell template definition(s)
- templatename:** **str** Cell template-name used for this cell object
- templateargs:** **str** Parameters provided to template-definition
- v\_init:** **float** Initial membrane potential. Default to -65.
- Ra:** **float** axial resistance. Defaults to 150.
- cm:** **float** membrane capacitance. Defaults to 1.0
- passive:** **bool** Passive mechanisms are initialized if True. Defaults to True
- passive\_parameters:** **dict** parameter dictionary with values for the passive membrane mechanism in NEURON ('pas'). The dictionary must contain keys 'g\_pas' and 'e\_pas', like the default: passive\_parameters=dict(g\_pas=0.001, e\_pas=-70)
- extracellular:** **bool** switch for NEURON's extracellular mechanism. Defaults to False
- dt:** **float** Simulation time step. Defaults to 2\*\* -4
- tstart:** **float** initialization time for simulation <= 0 ms. Defaults to 0.
- tstop:** **float** stop time for simulation > 0 ms. Defaults to 100.
- nseg\_method:** **'lambda100' or 'lambda\_f' or 'fixed\_length' or None** nseg rule, used by NEURON to determine number of compartments. Defaults to 'lambda100'
- max\_nseg\_length:** **float or None** max segment length for method 'fixed\_length'. Defaults to None
- lambda\_f:** **int** AC frequency for method 'lambda\_f'. Defaults to 100
- d\_lambda:** **float** parameter for d\_lambda rule. Defaults to 0.1
- delete\_sections:** **bool** delete pre-existing section-references. Defaults to True
- custom\_code:** **list or None** list of model-specific code files ([.py/.hoc]). Defaults to None
- custom\_fun:** **list or None** list of model-specific functions with args. Defaults to None
- custom\_fun\_args:** **list or None** list of args passed to custom\_fun functions. Defaults to None
- pt3d:** **bool** use pt3d-info of the cell geometries switch. Defaults to False
- celsius:** **float or None** Temperature in celsius. If nothing is specified here or in custom code it is 6.3 celcius
- verbose:** **bool** verbose output switch. Defaults to False

See also:

*Cell*

*TemplateCell*

## Examples

```
>>> import LFPy
>>> cellParameters = {
>>>     'morphology': '<path to morphology.hoc>',
>>>     'templatefile': '<path to template_file.hoc>',
>>>     'templatename': 'templatename',
>>>     'templateargs': None,
>>>     'v_init': -65,
>>>     'cm': 1.0,
>>>     'Ra': 150,
>>>     'passive': True,
>>>     'passive_parameters': {'g_pas': 0.001, 'e_pas': -65.},
>>>     'dt': 2**-3,
>>>     'tstart': 0,
>>>     'tstop': 50,
>>> }
>>> cell = LFPy.NetworkCell(**cellParameters)
>>> cell.simulate()
```

**cellpickler**(*filename*, *pickler*=<built-in function dump>)

Save data in cell to filename, using cPickle. It will however destroy any neuron.h objects upon saving, as c-objects cannot be pickled

### Parameters

**filename: str** Where to save cell

### Returns

None or pickle

## Examples

```
>>> # To save a cell, issue:
>>> cell.cellpickler('cell.cpickle')
>>> # To load this cell again in another session:
>>> import cPickle
>>> with file('cell.cpickle', 'rb') as f:
>>>     cell = cPickle.load(f)
```

**chiral\_morphology**(*axis*='x')

Mirror the morphology around given axis, (default x-axis), useful to introduce more heterogeneities in morphology shapes

### Parameters

**axis: str** 'x' or 'y' or 'z'

**create\_spike\_detector**(*target*=None, *threshold*=- 10.0, *weight*=0.0, *delay*=0.0)

Create spike-detecting NetCon object attached to the cell's soma midpoint, but this could be extended to having multiple spike-detection sites. The NetCon object created is attached to the cell's *\_hoc\_sd\_netconlist*

attribute, and will be used by the Network class when creating connections between all presynaptic cells and postsynaptic cells on each local RANK.

#### Parameters

**target:** **None (default) or a NEURON point process**

**threshold:** **float** spike detection threshold

**weight:** **float** connection weight (not used unless target is a point process)

**delay:** **float** connection delay (not used unless target is a point process)

**create\_synapse**(*cell, sec, x=0.5, syntype=ExpSyn(), synparams={'e': 0.0, 'tau': 2.0},  
assert\_syn\_values=False)*

Create synapse object of type syntype on sec(x) of cell and append to list cell.netconsynapses

TODO: Use LFPy.Synapse class if possible.

#### Parameters

**cell:** **object** instantiation of class NetworkCell or similar

**sec:** **neuron.h.Section object**, section reference on cell

**x:** **float in [0, 1]**, relative position along section

**syntype:** **hoc.HocObject** NEURON synapse model reference, e.g., neuron.h.ExpSyn

**synparams:** **dict**

**parameters for syntype, e.g., for neuron.h.ExpSyn we have:** tau: float, synapse time constant e: float, synapse reversal potential

**assert\_syn\_values:** **bool** if True, raise AssertionError if synapse attribute values do not match the values in the synparams dictionary

#### Raises

##### AssertionError

**distort\_geometry**(*factor=0.0, axis='z', nu=0.0*)

Distorts cellular morphology with a relative factor along a chosen axis preserving Poisson's ratio. A ratio nu=0.5 assumes incompressible and isotropic media that embeds the cell. A ratio nu=0 will only affect geometry along the chosen axis. A ratio nu=-1 will isometrically scale the neuron geometry along each axis. This method does not affect the underlying cable properties of the cell, only predictions of extracellular measurements (by affecting the relative locations of sources representing the compartments).

#### Parameters

**factor:** **float** relative compression/stretching factor of morphology. Default is 0 (no compression/stretching). Positive values implies a compression along the chosen axis.

**axis:** **str** which axis to apply compression/stretching. Default is "z".

**nu:** **float** Poisson's ratio. Ratio between axial and transversal compression/stretching. Default is 0.

**enable\_extracellular\_stimulation**(*electrode, t\_ext=None, n=1, model='inf'*)

Enable extracellular stimulation with NEURON's *extracellular* mechanism. Extracellular potentials are computed from electrode currents using the point-source approximation. If model is 'inf' (default), potentials are computed as ( $r_i$  is the position of a compartment  $i$ ,  $r_n$  is the position of an electrode  $n$ ,  $\sigma$  is the conductivity of the medium):

$$V_e(r_i) = \sum_n \frac{I_n}{4\pi\sigma|r_i - r_n|}$$

If model is 'semi', the method of images is used:

$$V_e(r_i) = \sum_n \frac{I_n}{2\pi\sigma|r_i - r_n|}$$

#### Parameters

- electrode:** **RecExtElectrode** Electrode object with stimulating currents
- t\_ext:** **np.ndarray or list** Time in ms corresponding to step changes in the provided currents. If None, currents are assumed to have the same time steps as the NEURON simulation.
- n:** **int** Points per electrode for spatial averaging
- model:** **str** 'inf' or 'semi'. If 'inf' the medium is assumed to be infinite and homogeneous. If 'semi', the method of images is used.

#### Returns

- v\_ext:** **np.ndarray** Computed extracellular potentials at cell mid points

#### **get\_axial\_currents\_from\_vmem**(timepoints=None)

Compute axial currents from cell sim: get current magnitude, distance vectors and position vectors.

#### Parameters

- timepoints:** **ndarray, dtype=int** array of timepoints in simulation at which you want to compute the axial currents. Defaults to False. If not given, all simulation timesteps will be included.

#### Returns

- i\_axial:** **ndarray, dtype=float** Shape ((cell.totnsegs-1)\*2, len(timepoints)) array of axial current magnitudes I in units of (nA) in cell at all timesteps in timepoints, or at all timesteps of the simulation if timepoints=None. Contains two current magnitudes per segment, (except for the root segment): 1) the current from the mid point of the segment to the segment start point, and 2) the current from the segment start point to the mid point of the parent segment.
- d\_vectors:** **ndarray, dtype=float** Shape (3, (cell.totnsegs-1)\*2) array of distance vectors traveled by each axial current in i\_axial in units of (μm). The indices of the first axis, correspond to the first axis of i\_axial and pos\_vectors.
- pos\_vectors:** **ndarray, dtype=float** Shape ((cell.totnsegs-1)\*2, 3) array of position vectors pointing to the mid point of each axial current in i\_axial in units of (μm). The indices of the first axis, correspond to the first axis of i\_axial and d\_vectors.

#### Raises

- AttributeError** Raises an exception if the cell.vmem attribute cannot be found

#### **get\_axial\_resistance**()

Return NEURON axial resistance for all cell compartments.

#### Returns

- ri\_list:** **ndarray, dtype=float** Shape (cell.totnsegs, ) array containing neuron.h.ri(seg.x) in units of (MΩ) for all segments in cell calculated using the neuron.h.ri(seg.x) method. neuron.h.ri(seg.x) returns the axial resistance from the middle of the segment to the middle of the parent segment. Note: If seg is the first segment in a section, i.e. the parent segment belongs to a different section or there is no parent section, then neuron.h.ri(seg.x) returns the axial resistance from the middle of the segment to the node connecting the segment to the parent section (or a ghost node if there is no parent)



**get\_closest\_idx**(*x=0.0, y=0.0, z=0.0, section='allsec'*)

Get the index number of a segment in specified section which midpoint is closest to the coordinates defined by the user

**Parameters**

**x: float** x-coordinate  
**y: float** y-coordinate  
**z: float** z-coordinate  
**section: str** String matching a section-name. Defaults to 'allsec'.

**Returns**

**int** segment index

**get\_dict\_of\_children\_idx**()

Return dictionary with children segment indices for all sections.

**Returns**

**children\_dict: dictionary** Dictionary containing a list for each section, with the segment index of all the section's children. The dictionary is needed to find the sibling of a segment.

**get\_dict\_parent\_connections**()

Return dictionary with parent connection point for all sections.

**Returns**

**connection\_dict: dictionary** Dictionary containing a float in range [0, 1] for each section in cell. The float gives the location on the parent segment to which the section is connected. The dictionary is needed for computing axial currents.

**get\_idx**(*section='allsec', z\_min=- inf, z\_max=inf*)

Returns compartment idx of segments from sections with names that match the pattern defined in input section on interval [z\_min, z\_max].

**Parameters**

**section: str** Any entry in cell.allsecnames or just 'allsec'.  
**z\_min: float** Depth filter. Specify minimum z-position  
**z\_max: float** Depth filter. Specify maximum z-position

**Returns**

**ndarray, dtype=int** segment indices

**Examples**

```
>>> idx = cell.get_idx(section='allsec')
>>> print(idx)
>>> idx = cell.get_idx(section=['soma', 'dend', 'apic'])
>>> print(idx)
```

**get\_idx\_children**(*parent='soma[0]'*)

Get the idx of parent's children sections, i.e. compartments ids of sections connected to parent-argument

**Parameters**

**parent: str** name-pattern matching a sectionname. Defaults to "soma[0]"

**Returns****ndarray, dtype=int****get\_idx\_name**(*idx=array([0])*)

Return NEURON convention name of segments with index *idx*. The returned argument is an array of tuples with corresponding segment *idx*, section name, and position along the section, like; [(0, 'neuron.h.soma[0]', 0.5),]

**Parameters****idx: ndarray, dtype int** segment indices, must be between 0 and cell.totnsegs**Returns****ndarray, dtype=object** tuples with section names of segments**get\_idx\_parent\_children**(*parent='soma[0]'*)

Get all *idx* of segments of parent and children sections, i.e. segment *idx* of sections connected to parent-argument, and also of the parent segments

**Parameters****parent: str** name-pattern matching a sectionname. Defaults to "soma[0]"**Returns****ndarray, dtype=int****get\_idx\_polygons**(*projection=('x', 'z')*)

For each segment *idx* in cell create a polygon in the plane determined by the projection kwarg (default ('x', 'z')), that can be visualized using `plt.fill()` or `mpl.collections.PolyCollection`

**Parameters****projection: tuple of strings** Determining projection. Defaults to ('x', 'z')**Returns****polygons: list** list of (ndarray, ndarray) tuples giving the trajectory of each section**Examples**

```
>>> from matplotlib.collections import PolyCollection
>>> import matplotlib.pyplot as plt
>>> cell = LFPy.Cell(morphology='PATH/TO/MORPHOLOGY')
>>> zips = []
>>> for x, z in cell.get_idx_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                           edgecolors='none',
>>>                           facecolors='gray')
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.add_collection(polycol)
>>> ax.axis(ax.axis('equal'))
>>> plt.show()
```

**get\_intersegment\_distance**(*idx0=0, idx1=0*)

Return the Euclidean distance between midpoints of two segments.

**Parameters****idx0: int****idx1: int****Returns****float** distance ( $\mu\text{m}$ ).**get\_intersegment\_vector**(*idx0=0, idx1=0*)

Return the distance between midpoints of two segments with index *idx0* and *idx1*. The argument returned is a list [x, y, z], where  $x = \text{self.x}[\text{idx1}].\text{mean}(\text{axis}=-1) - \text{self.x}[\text{idx0}].\text{mean}(\text{axis}=-1)$  etc.

**Parameters****idx0: int****idx1: int****Returns****list of floats** distance between midpoints along x,y,z axis in  $\mu\text{m}$ **get\_multi\_current\_dipole\_moments**(*timepoints=None*)

Return 3D current dipole moment vector and middle position vector from each axial current in space.

**Parameters**

**timepoints: ndarray, dtype=int or None** array of timepoints at which you want to compute the current dipole moments. Defaults to None. If not given, all simulation timesteps will be included.

**Returns**

**multi\_dipoles: ndarray, dtype = float** Shape (n\_axial\_currents, 3, n\_timepoints) array containing the x-,y-,z-components of the current dipole moment from each axial current in cell, at all timepoints. The number of axial currents,  $n\_axial\_currents = (\text{cell.totnsegs}-1) * 2$  and the number of timepoints,  $n\_timepoints = \text{cell.tvec.size}$ . The current dipole moments are given in units of (nA  $\mu\text{m}$ ).

**pos\_axial: ndarray, dtype = float** Shape (n\_axial\_currents, 3) array containing the x-, y-, and z-components giving the mid position in space of each multi\_dipole in units of ( $\mu\text{m}$ ).

**Examples**

Get all current dipole moments and positions from all axial currents in a single neuron simulation:

```
>>> import LFPy
>>> import numpy as np
>>> cell = LFPy.Cell('PATH/TO/MORPHOLOGY', extracellular=False)
>>> syn = LFPy.Synapse(cell, idx=cell.get_closest_idx(0,0,1000),
>>>                    syntype='ExpSyn', e=0., tau=1., weight=0.001)
>>> syn.set_spike_times(np.mgrid[20:100:20])
>>> cell.simulate(rec_vmem=True, rec_imem=False)
>>> timepoints = np.array([1,2,3,4])
>>> multi_dipoles, dipole_locs = cell.get_multi_current_dipole_moments(
>>>     timepoints=timepoints)
```

**get\_pt3d\_polygons**(*projection*=('x', 'z'))

For each section create a polygon in the plane determined by keyword argument *projection*=('x', 'z'), that can be visualized using e.g., `plt.fill()`

#### Parameters

**projection:** **tuple of strings** Determining projection. Defaults to ('x', 'z')

#### Returns

**list** list of (x, z) tuples giving the trajectory of each section that can be plotted using PolyCollection

#### Examples

```
>>> from matplotlib.collections import PolyCollection
>>> import matplotlib.pyplot as plt
>>> cell = LFPy.Cell(morphology='PATH/TO/MORPHOLOGY')
>>> zips = []
>>> for x, z in cell.get_pt3d_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                           edgecolors='none',
>>>                           facecolors='gray')
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.add_collection(polycol)
>>> ax.axis(ax.axis('equal'))
>>> plt.show()
```

**get\_rand\_idx\_area\_and\_distribution\_norm**(*section*='allsec', *nidx*=1, *z\_min*=-1000000.0, *z\_max*=1000000.0, *fun*=<scipy.stats.\_continuous\_distns.norm\_gen object>, *funargs*={'loc': 0, 'scale': 100}, *funweights*=None)

Return *nidx* segment indices in section with random probability normalized to the membrane area of each segment multiplied by the value of the probability density function of “fun”, a function in the `scipy.stats` module with corresponding function arguments in “funargs” on the interval [*z\_min*, *z\_max*]

#### Parameters

**section:** **str** string matching a section name

**nidx:** **int** number of random indices

**z\_min:** **float** lower depth interval

**z\_max:** **float** upper depth interval

**fun:** **function or str, or iterable of function or str** if function a `scipy.stats` method, if str, must be method in `scipy.stats` module with the same name (like ‘norm’), if iterable (list, tuple, `numpy.array`) of function or str some probability distribution in `scipy.stats` module

**funargs:** **dict or iterable** iterable (list, tuple, `numpy.array`) of dict, arguments to `fun.pdf` method (e.g., w. keys ‘loc’ and ‘scale’)

**funweights:** **None or iterable** iterable (list, tuple, `numpy.array`) of floats, scaling of each individual fun (i.e., introduces layer specificity)

## Examples

```
>>> import LFPy
>>> import numpy as np
>>> import scipy.stats as ss
>>> import matplotlib.pyplot as plt
>>> from os.path import join
>>> cell = LFPy.Cell(morphology=join('cells', 'cells', 'j4a.hoc'))
>>> cell.set_rotation(x=4.99, y=-4.33, z=3.14)
>>> idx = cell.get_rand_idx_area_and_distribution_norm(
    nidx=10000, fun=ss.norm, funargs=dict(loc=0, scale=200))
>>> bins = np.arange(-30, 120)*10
>>> plt.hist(cell.zmid[idx], bins=bins, alpha=0.5)
>>> plt.show()
```

**get\_rand\_idx\_area\_norm**(section='allsec', nidx=1, z\_min=- 1000000.0, z\_max=1000000.0)

Return nidx segment indices in section with random probability normalized to the membrane area of segment on interval [z\_min, z\_max]

### Parameters

**section:** str String matching a section-name

**nidx:** int Number of random indices

**z\_min:** float Depth filter

**z\_max:** float Depth filter

### Returns

ndarray, dtype=int segment indices

**get\_rand\_prob\_area\_norm**(section='allsec', z\_min=- 10000, z\_max=10000)

Return the probability (0-1) for synaptic coupling on segments in section sum(prob)=1 over all segments in section. Probability normalized by area.

### Parameters

**section:** str string matching a section-name. Defaults to 'allsec'

**z\_min:** float depth filter

**z\_max:** float depth filter

### Returns

ndarray, dtype=float

**get\_rand\_prob\_area\_norm\_from\_idx**(idx=array([0]))

Return the normalized probability (0-1) for synaptic coupling on segments in idx-array. Normalised probability determined by area of segments.

### Parameters

**idx:** ndarray, dtype=int. array of segment indices

### Returns

ndarray, dtype=float

**insert\_v\_ext**(v\_ext, t\_ext)

Set external extracellular potential around cell. Playback of some extracellular potential v\_ext on each cell.totnseg compartments. Assumes that the “extracellular”-mechanism is inserted on each compartment.

Can be used to study ephaptic effects and similar. The inputs will be copied and attached to the cell object as `cell.v_ext`, `cell.t_ext`, and converted to (list of) `neuron.h.Vector` types, to allow playback into each compartment `e_extracellular` reference. Can not be deleted prior to running `cell.simulate()`

### Parameters

**v\_ext:** `ndarray` Numpy array of size `cell.totnsegs x t_ext.size`, unit mV

**t\_ext:** `ndarray` Time vector of `v_ext` in ms

### Examples

```
>>> import LFPy
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> #create cell
>>> cell = LFPy.Cell(morphology='morphologies/example_morphology.hoc',
>>>                  passive=True)
>>> #time vector and extracellular field for every segment:
>>> t_ext = np.arange(cell.tstop / cell.dt + 1) * cell.dt
>>> v_ext = np.random.rand(cell.totnsegs, t_ext.size) - 0.5
>>> #insert potentials and record response:
>>> cell.insert_v_ext(v_ext, t_ext)
>>> cell.simulate(rec_imem=True, rec_vmem=True)
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(311)
>>> ax2 = fig.add_subplot(312)
>>> ax3 = fig.add_subplot(313)
>>> eim = ax1.matshow(np.array(cell.v_ext), cmap='spectral')
>>> cb1 = fig.colorbar(eim, ax=ax1)
>>> cb1.set_label('v_ext')
>>> ax1.axis(ax1.axis('tight'))
>>> iim = ax2.matshow(cell.imem, cmap='spectral')
>>> cb2 = fig.colorbar(iim, ax=ax2)
>>> cb2.set_label('imem')
>>> ax2.axis(ax2.axis('tight'))
>>> vim = ax3.matshow(cell.vmem, cmap='spectral')
>>> ax3.axis(ax3.axis('tight'))
>>> cb3 = fig.colorbar(vim, ax=ax3)
>>> cb3.set_label('vmem')
>>> ax3.set_xlabel('tstep')
>>> plt.show()
```

**set\_point\_process**(*idx*, *pptype*, *record\_current=False*, *record\_potential=False*, *\*\*kwargs*)

Insert *pptype*-electrode type pointprocess on segment numbered *idx* on cell object

### Parameters

**idx:** `int` Index of compartment where point process is inserted

**pptype:** `str` Type of pointprocess. Examples: SEClamp, VClamp, IClamp, SinIClamp, ChirpIClamp

**record\_current:** `bool` Decides if current is stored

**kwargs** Parameters passed on from class `StimIntElectrode`

**Returns**

**int** index of point process on cell

**set\_pos**(*x=0.0, y=0.0, z=0.0*)

Set the cell position. Move the cell geometry so that midpoint of soma section is in (x, y, z). If no soma pos, use the first segment

**Parameters**

**x: float** x position defaults to 0.0

**y: float** y position defaults to 0.0

**z: float** z position defaults to 0.0

**set\_rotation**(*x=None, y=None, z=None, rotation\_order='xyz'*)

Rotate geometry of cell object around the x-, y-, z-axis in the order described by rotation\_order parameter.

**Parameters**

**x: float or None** rotation angle in radians. Default: None

**y: float or None** rotation angle in radians. Default: None

**z: float or None** rotation angle in radians. Default: None

**rotation\_order: str** string with 3 elements containing x, y and z e.g. 'xyz', 'zyx'. Default: 'xyz'

**Examples**

```
>>> cell = LFPy.Cell(**kwargs)
>>> rotation = {'x': 1.233, 'y': 0.236, 'z': np.pi}
>>> cell.set_rotation(**rotation)
```

**set\_synapse**(*idx, syntype, record\_current=False, record\_potential=False, weight=None, \*\*kwargs*)

Insert synapse on cell segment

**Parameters**

**idx: int** Index of compartment where synapse is inserted

**syntype: str** Type of synapse. Built-in types in NEURON: ExpSyn, Exp2Syn

**record\_current: bool** If True, record synapse current

**record\_potential: bool** If True, record postsynaptic potential seen by the synapse

**weight: float** Strength of synapse

**kwargs** arguments passed on from class Synapse

**Returns**

**int** index of synapse object on cell

**simulate**(*probes=None, rec\_imem=False, rec\_vmem=False, rec\_ipas=False, rec\_icap=False, rec\_variables=[], variable\_dt=False, atol=0.001, rtol=0.0, to\_memory=True, to\_file=False, file\_name=None, \*\*kwargs*)

This is the main function running the simulation of the NEURON model. Start NEURON simulation and record variables specified by arguments.

**Parameters**

**probes:** list of [obj:, optional] None or list of LFPykit.RecExtElectrode like object instances that each have a public method *get\_transformation\_matrix* returning a matrix that linearly maps each compartments' transmembrane current to corresponding measurement as

$$P = MI$$

**rec\_imem:** bool If true, segment membrane currents will be recorded If no electrode argument is given, it is necessary to set rec\_imem=True in order to make predictions later on. Units of (nA).

**rec\_vmem:** bool Record segment membrane voltages (mV)

**rec\_ipas:** bool Record passive segment membrane currents (nA)

**rec\_icap:** bool Record capacitive segment membrane currents (nA)

**rec\_variables:** list List of segment state variables to record, e.g. arg=['cai', ]

**variable\_dt:** bool Use NEURON's variable timestep method

**atol:** float Absolute local error tolerance for NEURON variable timestep method

**rtol:** float Relative local error tolerance for NEURON variable timestep method

**to\_memory:** bool Only valid with probes=[:obj:], store measurements as *:obj:.data*

**to\_file:** bool Only valid with probes, save simulated data in hdf5 file format

**file\_name:** str Name of hdf5 file, '.h5' is appended if it doesnt exist

**strip\_hoc\_objects()**

Destroy any NEURON hoc objects in the cell object

## 1.4 Point processes

### 1.4.1 class PointProcess

**class** LFPy.**PointProcess**(*cell, idx, record\_current=False, record\_potential=False, \*\*kwargs*)

Bases: object

Parent class of Synapse, StimIntElectrode. Created in order to import and set some shared variables and extract Cartesian coordinates of segments

#### Parameters

**cell:** obj LFPy.Cell object

**idx:** int index of segment

**record\_current:** bool Must be set to True for recording of pointprocess currents

**record\_potential:** bool Must be set to True for recording potential of pointprocess target idx

**kwargs:** pointprocess specific variables passed on to cell/neuron

See also:

[\*Synapse\*](#)

[\*StimIntElectrode\*](#)



**update\_pos(*cell*)**  
 Extract coordinates of point-process

## 1.4.2 class Synapse

**class** LFPy.Synapse(*cell, idx, syntype, record\_current=False, record\_potential=False, \*\*kwargs*)  
 Bases: *LFPy.pointprocess.PointProcess*

The synapse class, pointprocesses that spawn membrane currents. See <http://www.neuron.yale.edu/neuron/static/docs/help/neuron/neuron/mech.html#pointprocesses> for details, or corresponding mod-files.

This class is meant to be used with synaptic mechanisms, giving rise to currents that will be part of the membrane currents at times governed by the methods *set\_spike\_times* or *set\_spike\_times\_w\_netstim*.

### Parameters

**cell:** *obj* LFPy.Cell or LFPy.TemplateCell instance to receive synapptic input  
**idx:** *int* Cell index where the synaptic input arrives  
**syntype:** *str* Type of synapse, such as 'ExpSyn', 'Exp2Syn', 'AlphaSynapse'  
**record\_current:** *bool* If True, record synapse to <synapse>.i in units of nA  
**\*\*kwargs** Additional arguments to be passed on to NEURON in *Cell.set\_synapse*

See also:

*StimIntElectrode*

### Examples

```
>>> import pylab as pl
>>> pl.interactive(1)
>>> import LFPy
>>> import os
>>> cellParameters = {
>>>     'morphology': os.path.join('examples', 'morphologies',
>>>                                'L5_Mainen96_LFPy.hoc'),
>>>     'passive': True,
>>>     'tstop': 50,
>>> }
>>> cell = LFPy.Cell(**cellParameters)

>>> synapseParameters = {
>>>     'idx': cell.get_closest_idx(x=0, y=0, z=800),
>>>     'e': 0,                                     # reversal potential
>>>     'syntype': 'ExpSyn',                         # synapse type
>>>     'tau': 2,                                    # syn. time constant
>>>     'weight': 0.01,                             # syn. weight
>>>     'record_current': True                       # syn. current record
>>> }
>>> synapse = LFPy.Synapse(cell, **synapseParameters)
>>> synapse.set_spike_times(pl.array([10, 15, 20, 25]))
>>> cell.simulate()
```

```
>>> pl.subplot(211)
>>> pl.plot(cell.tvec, synapse.i)
>>> pl.title('Synapse current (nA)')
>>> pl.subplot(212)
>>> pl.plot(cell.tvec, cell.somav)
>>> pl.title('Somatic potential (mV)')
```

**collect\_current**(*cell*)

Collect synapse current. Sets <synapse>.i

**Parameters**

**cell:** LFPy.Cell like object

**collect\_potential**(*cell*)

Collect membrane potential of segment with synapse. Sets <synapse>.v

**Parameters**

**cell:** LFPy.Cell like object

**set\_spike\_times**(*sptimes=array([], dtype=float64)*)

Set the spike times explicitly using numpy arrays

**Parameters**

**ndarray, dtype=float** Sequence of synapse activation times

**set\_spike\_times\_w\_netstim**(*noise=1.0, start=0.0, number=1000.0, interval=10.0, seed=1234.0*)

Generate a train of pre-synaptic stimulus times by setting up the neuron NetStim object associated with this synapse

**Parameters**

**noise: float in range [0, 1]** Fractional randomness, from deterministic to intervals that drawn from negexp distribution (Poisson spiketimes).

**start: float** ms, (most likely) start time of first spike

**number: int** (average) number of spikes

**interval: float** ms, (mean) time between spikes

**seed: float** Random seed value

### 1.4.3 class StimIntElectrode

**class** LFPy.StimIntElectrode(*cell, idx, pptype='SEClamp', record\_current=False, record\_potential=False, \*\*kwargs*)

Bases: [LFPy.pointprocess.PointProcess](#)

Class for NEURON point processes representing electrode currents, such as VClamp, SEClamp and ICLamp.

Membrane currents will no longer sum to zero if these mechanisms are used, as the equivalent circuit is akin to a current input to the compartment from a far away extracellular location (“ground”), not immediately from the surface to the inside of the compartment as with transmembrane currents.

Refer to NEURON documentation @ [neuron.yale.edu](http://neuron.yale.edu) for keyword arguments or class documentation in Python issuing e.g.

`help(neuron.h.VClamp)`

Will insert pptype on cell-instance, pass the corresponding kwargs onto cell.set\_point\_process.

#### Parameters

**cell:** obj

*LFPy.Cell* or *LFPy.TemplateCell* instance to receive Stimulation electrode input

**idx:** int Cell segment index where the stimulation electrode is placed

**pptype:** str Type of point process. Built-in examples: VClamp, SEClamp and IClamp. Defaults to 'SEClamp'.

**record\_current:** bool Decides if current is recorded

**record\_potential:** bool switch for recording the potential on postsynaptic segment index

**\*\*kwargs** Additional arguments to be passed on to NEURON in *cell.set\_point\_process*

See also:

[Synapse](#)

#### Examples

```
>>> import pylab as pl
>>> pl.ion()
>>> import os
>>> import LFPy
>>> # define a list of different electrode implementations from NEURON
>>> pointprocesses = [
>>>     {
>>>         'idx': 0,
>>>         'record_current': True,
>>>         'pptype': 'IClamp',
>>>         'amp': 1,
>>>         'dur': 20,
>>>         'delay': 10,
>>>     },
>>>     {
>>>         'idx': 0,
>>>         'record_current': True,
>>>         'pptype': 'VClamp',
>>>         'amp': [-70, 0, -70],
>>>         'dur': [10, 20, 10],
>>>     },
>>>     {
>>>         'idx': 0,
>>>         'record_current': True,
>>>         'pptype': 'SEClamp',
>>>         'dur1': 10,
>>>         'amp1': -70,
>>>         'dur2': 20,
>>>         'amp2': 0,
>>>         'dur3': 10,
>>>         'amp3': -70,
>>>     },
>>> ]
```

(continues on next page)

(continued from previous page)

```

>>> ]
>>> # create a cell instance for each electrode
>>> fig, axes = plt.subplots(2, 1, sharex=True)
>>> for pointprocess in pointprocesses:
>>>     cell = LFPy.Cell(morphology=os.path.join('examples',
>>>                                             'morphologies',
>>>                                             'L5_Mainen96_LFPy.hoc'),
>>>                     passive=True)
>>>     stimulus = LFPy.StimIntElectrode(cell, **pointprocess)
>>>     cell.simulate()
>>>     axes[0].plot(cell.tvec, stimulus.i, label=pointprocess['pptype'])
>>>     axes[0].legend(loc='best')
>>>     axes[0].set_title('Stimulus currents (nA)')
>>>     axes[1].plot(cell.tvec, cell.somav, label=pointprocess['pptype'])
>>>     axes[1].legend(loc='best')
>>>     axes[1].set_title('Somatic potential (mV)')

```

**collect\_current**(cell)

Fetch electrode current. Sets `<stimintelectrode>.i`

**Parameters**

**cell:** LFPy.Cell like object

**collect\_potential**(cell)

Collect membrane potential of segment with PointProcess. Sets `<stimintelectrode>.v`

**Parameters**

**cell:** LFPy.Cell like object

## 1.5 Networks

### 1.5.1 class Network

**class** LFPy.**Network**(dt=0.1, tstart=0.0, tstop=1000.0, v\_init=-65.0, celsius=6.3,  
OUTPUTPATH='example\_parallel\_network', verbose=False)

Bases: object

Network class, creating distributed populations of cells of type Cell and handling connections between cells in the respective populations.

**Parameters**

**dt:** float Simulation timestep size

**tstart:** float Start time of simulation

**tstop:** float End time of simulation

**v\_init:** float Membrane potential set at first timestep across all cells

**celsius:** float Global control of temperature, affect channel kinetics. It will also be forced when creating the different Cell objects, as LFPy.Cell and LFPy.TemplateCell also accept the same keyword argument.

**verbose:** bool if True, print out misc. messages

```
connect(pre, post, connectivity, syntype=ExpSyn(), synparams={'e': 0.0, 'tau': 2.0}, weightfun=<built-in
method normal of numpy.random.mtrand.RandomState object>, weightargs={'loc': 0.1, 'scale':
0.01}, minweight=0, delayfun=<scipy.stats._continuous_distns.truncnorm_gen object>,
delayargs={'a': 0.3, 'b': inf, 'loc': 2, 'scale': 0.2}, mindelay=None,
multapsefun=<scipy.stats._continuous_distns.truncnorm_gen object>, multapseargs={'a': -3.0, 'b':
6.0, 'loc': 4, 'scale': 1}, syn_pos_args={'fun': [<scipy.stats._continuous_distns.norm_gen object>,
<scipy.stats._continuous_distns.norm_gen object>], 'funargs': [{'loc': 0, 'scale': 100}, {'loc': 0,
'scale': 100}], 'funweights': [0.5, 0.5], 'section': ['soma', 'dend', 'apic'], 'z_max': 1000000.0,
'z_min': -1000000.0}, save_connections=False)
```

Connect presynaptic cells to postsynaptic cells. Connections are drawn from presynaptic cells to postsynaptic cells, hence connectivity array must only be specified for postsynaptic units existing on this RANK.

### Parameters

**pre:** **str** presynaptic population name

**post:** **str** postsynaptic population name

**connectivity:** **ndarray / (scipy.sparse array)** boolean connectivity matrix between pre and post.

**syntype:** **hoc.HocObject** reference to NEURON synapse mechanism, e.g., `neuron.h.ExpSyn`

**synparams:** **dict** dictionary of parameters for synapse mechanism, keys 'e', 'tau' etc.

**weightfun:** **function** function used to draw weights from a `numpy.random` distribution

**weightargs:** **dict** parameters passed to `weightfun`

**minweight:** **float**, minimum weight in units of nS

**delayfun:** **function** function used to draw delays from a subclass of `scipy.stats.rv_continuous` or `numpy.random` distribution

**delayargs:** **dict** parameters passed to `delayfun`

**mindelay:** **float**, minimum delay in multiples of `dt`. Ignored if `delayfun` is an inherited from `scipy.stats.rv_continuous`

**multapsefun:** **function or None** function reference, e.g., `scipy.stats.rv_continuous` used to draw a number of synapses for a cell-to-cell connection. If `None`, draw only one connection

**multapseargs:** **dict** arguments passed to `multapsefun`

**syn\_pos\_args:** **dict** arguments passed to inherited `LFPy.Cell` method `NetworkCell.get_rand_idx_area_and_distribution_norm` to find synapse locations.

**save\_connections:** **bool** if `True` (default `False`), save instantiated connections to HDF5 file `Network.OUTPUTPATH/synapse_connections.h5` as dataset `<pre>:<post>` using a structured `ndarray` with `dtype`

```
[('gid_pre'), ('gid', 'i8'), ('weight', 'f8'), ('delay', 'f8'),
('sec', 'U64'), ('sec.x', 'f8'),
('x', 'f8'), ('y', 'f8'), ('z', 'f8')],
```

where `gid_pre` is presynaptic cell id, `gid` is postsynaptic cell id, `weight` connection weight, `delay` connection delay, `sec` section name, `sec.x` relative location on section, and `x`, `y`, `z` the corresponding midpoint coordinates of the target compartment.

### Returns

**list** Length 2 list with ndarrays [conncount, syncount] with numbers of instantiated connections and synapses.

#### Raises

**DeprecationWarning** if `delayfun` is not a subclass of `scipy.stats.rv_continuous`

**create\_population**(*CWD=None, CELLPATH=None, Cell=<class 'LFPy.network.NetworkCell'>, POP\_SIZE=4, name='L5PC', cell\_args=None, pop\_args=None, rotation\_args=None*)  
Create and append a distributed POP\_SIZE-sized population of cells of type `Cell` with the corresponding name. Cell-object references, gids on this RANK, population size POP\_SIZE and names will be added to the lists `Network.gids`, `Network.cells`, `Network.sizes` and `Network.names`, respectively

#### Parameters

**CWD: path** Current working directory

**CELLPATH: path** Relative path from CWD to source files for cell model (morphology, hoc routines etc.)

**Cell: class** class defining a Cell-like object, see class `NetworkCell`

**POP\_SIZE: int** number of cells in population

**name: str** population name reference

**cell\_args: dict** keys and values for Cell object

**pop\_args: dict** keys and values for `Network.draw_rand_pos` assigning cell positions

**rotation\_arg: dict** default cell rotations around x and y axis on the form { 'x': np.pi/2, 'y': 0 }. Can only have the keys 'x' and 'y'. Cells are randomly rotated around z-axis using the `Cell.set_rotation` method.

**enable\_extracellular\_stimulation**(*electrode, t\_ext=None, n=1, model='inf'*)

Enable extracellular stimulation with NEURON's *extracellular* mechanism. Extracellular potentials are computed from electrode currents using the point-source approximation. If `model` is 'inf' (default), potentials are computed as ( $r_i$  is the position of a compartment  $i$ ,  $r_n$  is the position of an electrode  $n$ ,  $\sigma$  is the conductivity of the medium):

$$V_e(r_i) = \sum_n \frac{I_n}{4\pi\sigma|r_i - r_n|}$$

If `model` is 'semi', the method of images is used:

$$V_e(r_i) = \sum_n \frac{I_n}{2\pi\sigma|r_i - r_n|}$$

#### Parameters

**electrode: RecExtElectrode** Electrode object with stimulating currents

**t\_ext: np.ndarray or list** Time in ms corresponding to step changes in the provided currents. If None, currents are assumed to have the same time steps as the NEURON simulation.

**n: int** Points per electrode for spatial averaging

**model: str** 'inf' or 'semi'. If 'inf' the medium is assumed to be infinite and homogeneous. If 'semi', the method of images is used.

#### Returns

**v\_ext: dict of np.ndarrays** Computed extracellular potentials at cell mid points for each cell of the network's populations. Formatted as `v_ext = {'pop1': np.ndarray[cell, cell_seg, t_ext]}`

**get\_connectivity\_rand**(*pre*='L5PC', *post*='L5PC', *connprob*=0.2)

Dummy function creating a (boolean) cell to cell connectivity matrix between pre and postsynaptic populations.

Connections are drawn randomly between presynaptic cell gids in population 'pre' and postsynaptic cell gids in 'post' on this RANK with a fixed connection probability. self-connections are disabled if presynaptic and postsynaptic populations are the same.

#### Parameters

**pre:** str presynaptic population name

**post:** str postsynaptic population name

**connprob:** float in [0, 1] connection probability, connections are drawn on random

#### Returns

**ndarray, dtype bool** *n\_pre* x *n\_post* array of connections between *n\_pre* presynaptic neurons and *n\_post* postsynaptic neurons on this RANK. Entries with True denotes a connection.

**simulate**(*probes*=None, *rec\_imem*=False, *rec\_vmem*=False, *rec\_ipas*=False, *rec\_icap*=False, *rec\_isyn*=False, *rec\_vmmsyn*=False, *rec\_istim*=False, *rec\_pop\_contributions*=False, *rec\_variables*=[], *variable\_dt*=False, *atol*=0.001, *to\_memory*=True, *to\_file*=False, *file\_name*='OUTPUT.h5', \*\*kwargs)

This is the main function running the simulation of the network model.

#### Parameters

**probes:** list of [obj:, optional] None or list of LFPykit.RecExtElectrode like object instances that each have a public method *get\_transformation\_matrix* returning a matrix that linearly maps each compartments' transmembrane current to corresponding measurement as

$$P = MI$$

**rec\_imem:** bool If true, segment membrane currents will be recorded If no electrode argument is given, it is necessary to set *rec\_imem*=True in order to calculate LFP later on. Units of (nA).

**rec\_vmem:** bool record segment membrane voltages (mV)

**rec\_ipas:** bool record passive segment membrane currents (nA)

**rec\_icap:** bool record capacitive segment membrane currents (nA)

**rec\_isyn:** bool record synaptic currents of from Synapse class (nA)

**rec\_vmmsyn:** bool record membrane voltage of segments with Synapse (mV)

**rec\_istim:** bool record currents of StimIntraElectrode (nA)

**rec\_pop\_contributions:** bool If True, compute and return single-population contributions to the extracellular potential during simulation time

**rec\_variables:** list of str variables to record, i.e arg=['cai', ]

**variable\_dt:** boolean use variable timestep in NEURON. Can not be combined with *to\_file*

**atol:** float absolute tolerance used with NEURON variable timestep

**to\_memory:** bool Simulate to memory. Only valid with *probes*=[<probe>, ...], which store measurements to -> <probe>.data

**to\_file:** bool only valid with *probes*=[<probe>, ...], saves measurement in hdf5 file format.

**file\_name: str** If to\_file is True, file which measurements will be written to. The file format is HDF5, default is "OUTPUT.h5", put in folder Network.OUTPUTPATH

**\*\*kwargs: keyword argument dict values passed along to function**

`__run_simulation_with_probes()`, containing some or all of the boolean flags: *use\_ipas*, *use\_icap*, *use\_isyn* (defaulting to *False*).

#### Returns

**events** Dictionary with keys *times* and *gids*, where values are ndarrays with detected spikes and global neuron identifiers

#### Raises

**Exception** if *CVode().use\_fast\_imem()* method not found

**AssertionError** if *rec\_pop\_contributions==True* and *probes==None*

## 1.5.2 class NetworkPopulation

```
class LFPy.NetworkPopulation(CWD=None, CELLPATH=None, first_gid=0, Cell=<class
    'LFPy.network.NetworkCell'>, POP_SIZE=4, name='L5PC', cell_args=None,
    pop_args=None, rotation_args=None,
    OUTPUTPATH='example_parallel_network')
```

Bases: object

NetworkPopulation class representing a group of Cell objects distributed across RANKs.

#### Parameters

**CWD: path or None** Current working directory

**CELLPATH: path or None** Relative path from CWD to source files for cell model (morphology, hoc routines etc.)

**first\_gid: int** The global identifier of the first cell created in this population instance. The first\_gid in the first population created should be 0 and cannot exist in previously created NetworkPopulation instances

**Cell: class** class defining a Cell object, see class NetworkCell above

**POP\_SIZE: int** number of cells in population

**name: str** population name reference

**cell\_args: dict** keys and values for Cell object

**pop\_args: dict** keys and values for Network.draw\_rand\_pos assigning cell positions

**rotation\_arg: dict** default cell rotations around x and y axis on the form { 'x': np.pi/2, 'y': 0 }. Can only have the keys 'x' and 'y'. Cells are randomly rotated around z-axis using the Cell.set\_rotation() method.

**OUTPUTPATH: str** path to output file destination

**draw\_rand\_pos(POP\_SIZE, radius, loc, scale, cap=None)**

Draw some random location for POP\_SIZE cells within radius radius, at mean depth loc and standard deviation scale.

Returned argument is a list of dicts [{ 'x', 'y', 'z' },].

#### Parameters

**POP\_SIZE: int** Population size



**radius: float** Radius of population.

**loc: float** expected mean depth of somas of population.

**scale: float** expected standard deviation of depth of somas of population.

**cap: None, float or length to list of floats** if float, cap distribution between [loc-cap, loc+cap), if list, cap distribution between [loc-cap[0], loc+cap[1]]

#### Returns

**soma\_pos: list** List of dicts of len POP\_SIZE where dict have keys x, y, z specifying xyz-coordinates of cell at list entry *i*.

## 1.6 Forward models

### 1.6.1 class CurrentDipoleMoment

**class** LFPy.CurrentDipoleMoment(*cell*)

Bases: `lfpypykit.models.LinearModel`

`LinearModel` subclass that defines a 2D linear response matrix **M** between transmembrane current array **I** (nA) of a multicompartment neuron model and the corresponding current dipole moment **P** (nA μm) [1] as

$$\mathbf{P} = \mathbf{M}\mathbf{I}$$

The current **I** is an ndarray of shape (n\_seg, n\_tsteps) with unit (nA), and the rows of **P** represent the x-, y- and z-components of the current dipole moment for every time step.

The current dipole moment can be used to compute distal measures of neural activity such as the EEG and MEG using `lfpypykit.eegmegcalc.FourSphereVolumeConductor` or `lfpypykit.eegmegcalc.MEG`, respectively

#### Parameters

**cell: object** `CellGeometry` instance or similar.

See also:

`LinearModel`

`eegmegcalc.FourSphereVolumeConductor`

`eegmegcalc.MEG`

`eegmegcalc.NYHeadModel`

#### References

[1]

## Examples

Compute the current dipole moment of a 3-compartment neuron model:

```
>>> import numpy as np
>>> from lfpykit import CellGeometry, CurrentDipoleMoment
>>> n_seg = 3
>>> cell = CellGeometry(x=np.array([[0.]*2]*n_seg),
                        y=np.array([[0.]*2]*n_seg),
                        z=np.array([[1.*x, 1.*(x+1)]
                                   for x in range(n_seg)]),
                        d=np.array([1.]*n_seg))
>>> cdm = CurrentDipoleMoment(cell)
>>> M = cdm.get_transformation_matrix()
>>> imem = np.array([[-1., 1.],
                    [0., 0.],
                    [1., -1.]])
>>> P = M@imem
>>> P
array([[ 0.,  0.],
       [ 0.,  0.],
       [ 2., -2.]])
```

### get\_transformation\_matrix()

Get linear response matrix

#### Returns

**response\_matrix:** ndarray shape (3, n\_seg) ndarray

#### Raises

**AttributeError** if cell is None

## 1.6.2 class PointSourcePotential

**class** LFPy.PointSourcePotential(*cell, x, y, z, sigma=0.3*)

Bases: lfpykit.models.LinearModel

LinearModel subclass that defines a 2D linear response matrix **M** between transmembrane current array **I** (nA) of a multicompartment neuron model and the corresponding extracellular electric potential **V<sub>ex</sub>** (mV) as

$$\mathbf{V}_{ex} = \mathbf{M}\mathbf{I}$$

The current **I** is an ndarray of shape (n\_seg, n\_tsteps) with unit (nA), and each row indexed by *j* of **V<sub>ex</sub>** represents the electric potential at each measurement site for every time step.

The elements of **M** are computed as

$$M_{ji} = 1/(4\pi\sigma|\mathbf{r}_i - \mathbf{r}_j|)$$

where  $\sigma$  is the electric conductivity of the extracellular medium,  $\mathbf{r}_i$  the midpoint coordinate of segment *i* and  $\mathbf{r}_j$  the coordinate of measurement site *j* [1], [2].

Assumptions:

- the extracellular conductivity  $\sigma$  is infinite, homogeneous, frequency independent (linear) and isotropic.

- each segment is treated as a point source located at the midpoint between its start and end point coordinate.
- each measurement site  $\mathbf{r}_j = (x_j, y_j, z_j)$  is treated as a point.
- $|\mathbf{r}_i - \mathbf{r}_j| \geq d_i/2$ , where  $d_i$  is the segment diameter.

#### Parameters

**cell:** object CellGeometry instance or similar.  
**x:** ndarray of floats x-position of measurement sites ( $\mu\text{m}$ )  
**y:** ndarray of floats y-position of measurement sites ( $\mu\text{m}$ )  
**z:** ndarray of floats z-position of measurement sites ( $\mu\text{m}$ )  
**sigma:** float > 0 scalar extracellular conductivity (S/m)

See also:

**LinearModel**

*LineSourcePotential*

*RecExtElectrode*

#### References

[1], [2]

#### Examples

Compute the current dipole moment of a 3-compartment neuron model:

```
>>> import numpy as np
>>> from lfpykit import CellGeometry, PointSourcePotential
>>> n_seg = 3
>>> cell = CellGeometry(x=np.array([[0.]*2]*n_seg),
                        y=np.array([[0.]*2]*n_seg),
                        z=np.array([[10.*x, 10.*(x+1)]
                                   for x in range(n_seg)]),
                        d=np.array([1.]*n_seg))
>>> psp = PointSourcePotential(cell,
                              x=np.ones(10)*10,
                              y=np.zeros(10),
                              z=np.arange(10)*10,
                              sigma=0.3)
>>> M = psp.get_transformation_matrix()
>>> imem = np.array([[-1., 1.],
                    [0., 0.],
                    [1., -1.]])
>>> V_ex = M @ imem
>>> V_ex
array([[ -0.01387397,  0.01387397],
       [-0.00901154,  0.00901154],
       [ 0.00901154, -0.00901154],
```

(continues on next page)

(continued from previous page)

```
[ 0.01387397, -0.01387397],
[ 0.00742668, -0.00742668],
[ 0.00409718, -0.00409718],
[ 0.00254212, -0.00254212],
[ 0.00172082, -0.00172082],
[ 0.00123933, -0.00123933],
[ 0.00093413, -0.00093413]])
```

**get\_transformation\_matrix()**

Get linear response matrix

**Returns****response\_matrix:** ndarray shape (n\_coords, n\_seg) ndarray**Raises****AttributeError** if cell is None

### 1.6.3 class LineSourcePotential

**class** LFPy.LineSourcePotential(*cell, x, y, z, sigma=0.3*)

Bases: lfpypykit.models.LinearModel

**LinearModel** subclass that defines a 2D linear response matrix **M** between transmembrane current array **I** (nA) of a multicompartment neuron model and the corresponding extracellular electric potential  $V_{ex}$  (mV) as

$$V_{ex} = \mathbf{M}\mathbf{I}$$

The current **I** is an ndarray of shape (n\_seg, n\_tsteps) with unit (nA), and each row indexed by *j* of  $V_{ex}$  represents the electric potential at each measurement site for every time step.

The elements of **M** are computed as

$$M_{ji} = \frac{1}{4\pi\sigma L_i} \log \left| \frac{\sqrt{h_{ji}^2 + r_{ji}^2} - h_{ji}}{\sqrt{l_{ji}^2 + r_{ji}^2} - l_{ji}} \right|$$

Segment length is denoted  $L_i$ , perpendicular distance from the electrode point contact to the axis of the line segment is denoted  $r_{ji}$ , longitudinal distance measured from the start of the segment is denoted  $h_{ji}$ , and longitudinal distance from the other end of the segment is denoted  $l_{ji} = L_i + h_{ji}$  [1], [2].

Assumptions:

- the extracellular conductivity  $\sigma$  is infinite, homogeneous, frequency independent (linear) and isotropic
- each segment is treated as a straight line source with homogeneous current density between its start and end point coordinate
- each measurement site  $\mathbf{r}_j = (x_j, y_j, z_j)$  is treated as a point
- The minimum distance to a line source is set equal to segment radius.

**Parameters****cell:** object CellGeometry instance or similar.**x:** ndarray of floats x-position of measurement sites ( $\mu\text{m}$ )

**y: ndarray of floats** y-position of measurement sites ( $\mu\text{m}$ )  
**z: ndarray of floats** z-position of measurement sites ( $\mu\text{m}$ )  
**sigma: float > 0** scalar extracellular conductivity (S/m)

See also:

**LinearModel**

*PointSourcePotential*

*RecExtElectrode*

## References

[1], [2]

## Examples

Compute the current dipole moment of a 3-compartment neuron model:

```
>>> import numpy as np
>>> from lfpykit import CellGeometry, LineSourcePotential
>>> n_seg = 3
>>> cell = CellGeometry(x=np.array([[0.]*2]*n_seg),
                        y=np.array([[0.]*2]*n_seg),
                        z=np.array([[10.*x, 10.*(x+1)]
                                   for x in range(n_seg)]),
                        d=np.array([1.]*n_seg))
>>> lsp = LineSourcePotential(cell,
                             x=np.ones(10)*10,
                             y=np.zeros(10),
                             z=np.arange(10)*10,
                             sigma=0.3)
>>> M = lsp.get_transformation_matrix()
>>> imem = np.array([[ -1.,  1.],
                    [ 0.,  0.],
                    [ 1., -1.]])
>>> V_ex = M @ imem
>>> V_ex
array([[ -0.01343699,  0.01343699],
       [ -0.0084647 ,  0.0084647 ],
       [  0.0084647 , -0.0084647 ],
       [  0.01343699, -0.01343699],
       [  0.00758627, -0.00758627],
       [  0.00416681, -0.00416681],
       [  0.002571 , -0.002571 ],
       [  0.00173439, -0.00173439],
       [  0.00124645, -0.00124645],
       [  0.0009382 , -0.0009382 ]])
```

**get\_transformation\_matrix()**

Get linear response matrix

**Returns****response\_matrix:** ndarray shape (n\_coords, n\_seg) ndarray**Raises****AttributeError** if cell is None

### 1.6.4 class RecExtElectrode

```
class LFPy.RecExtElectrode(cell, sigma=0.3, probe=None, x=None, y=None, z=None, N=None, r=None,
                           n=None, contact_shape='circle', method='linesource', verbose=False,
                           seedvalue=None, **kwargs)
```

Bases: lfpypykit.models.LinearModel

class RecExtElectrode

Main class that represents an extracellular electric recording devices such as a laminar probe.

This class is a `LinearModel` subclass that defines a 2D linear response matrix  $\mathbf{M}$  between transmembrane current array  $\mathbf{I}$  (nA) of a multicompartment neuron model and the corresponding extracellular electric potential  $\mathbf{V}_{ex}$  (mV) as

$$\mathbf{V}_{ex} = \mathbf{M}\mathbf{I}$$

The current  $\mathbf{I}$  is an ndarray of shape (n\_seg, n\_tsteps) with unit (nA), and each row indexed by  $j$  of  $\mathbf{V}_{ex}$  represents the electric potential at each measurement site for every time step.

The class differ from `PointSourcePotential` and `LineSourcePotential` by:

- supporting anisotropic volume conductors [1]
- supporting probe geometry specifications using `MEAutility` (<https://meautility.readthedocs.io/en/latest/>, <https://github.com/alejoe91/MEAutility>).
- supporting electrode contact points with finite extents [2], [3]
- switching between point- and linesources, and a combined method that assumes that the root element at segment index 0 is spherical.

**Parameters****cell:** object CellGeometry instance or similar.

**sigma:** float or list/ndarray of floats extracellular conductivity in units of (S/m). A scalar value implies an isotropic extracellular conductivity. If a length 3 list or array of floats is provided, these values corresponds to an anisotropic conductor with conductivities  $[\sigma_x, \sigma_y, \sigma_z]$ .

**probe:** MEAutility MEA object or None MEAutility probe object**x, y, z:** ndarray coordinates or same length arrays of coordinates in units of ( $\mu\text{m}$ ).

**N:** None or list of lists Normal vectors  $[x, y, z]$  of each circular electrode contact surface, default None

**r:** float radius of each contact surface, default None ( $\mu\text{m}$ )

**n:** int if N is not None and  $r > 0$ , the number of discrete points used to compute the n-point average potential on each circular contact point.

**contact\_shape:** str 'circle'/'square' (default 'circle') defines the contact point shape If 'circle' r is the radius, if 'square' r is the side length

**method:** `str` switch between the assumption of 'linesource', 'pointsource', 'root\_as\_point' to represent each compartment when computing extracellular potentials

**verbose:** `bool` Flag for verbose output, i.e., print more information

**seedvalue:** `int` random seed when finding random position on contact with  $r > 0$

**\*\*kwargs:** Additional keyword arguments parsed to `RecExtElectrode.lfp_method()` which is determined by `method` parameter.

See also:

`LinearModel`

`PointSourcePotential`

`LineSourcePotential`

## References

[1], [2], [3]

## Examples

Mock cell geometry and transmembrane currents:

```
>>> import numpy as np
>>> from lfpykit import CellGeometry, RecExtElectrode
>>> # cell geometry with three segments (μm)
>>> cell = CellGeometry(x=np.array([[0, 0], [0, 0], [0, 0]]),
>>>                      y=np.array([[0, 0], [0, 0], [0, 0]]),
>>>                      z=np.array([[0, 10], [10, 20], [20, 30]]),
>>>                      d=np.array([1, 1, 1]))
>>> # transmembrane currents, three time steps (nA)
>>> I_m = np.array([[0., -1., 1.], [-1., 1., 0.], [1., 0., -1.]])
>>> # electrode locations (μm)
>>> r = np.array([[28.24653166, 8.97563241, 18.9492774, 3.47296614,
>>>                  1.20517729, 9.59849603, 21.91956616, 29.84686727,
>>>                  4.41045505, 3.61146625],
>>>                [24.4954352, 24.04977922, 22.41262238, 10.09702942,
>>>                  3.28610789, 23.50277637, 8.14044367, 4.46909208,
>>>                  10.93270117, 24.94698813],
>>>                [19.16644585, 15.20196335, 18.08924828, 24.22864702,
>>>                  5.85216751, 14.8231048, 24.72666694, 17.77573431,
>>>                  29.34508292, 9.28381892]])
>>> # instantiate electrode, get linear response matrix
>>> el = RecExtElectrode(cell=cell, x=r[0, :], y=r[1, :], z=r[2, :],
>>>                      sigma=0.3,
>>>                      method='pointsource')
>>> M = el.get_transformation_matrix()
>>> # compute extracellular potential
>>> M @ I_m
array([[ -4.11657148e-05,   4.16621950e-04,  -3.75456235e-04],
       [ -6.79014892e-04,   7.30256301e-04,  -5.12414088e-05],
```

(continues on next page)

(continued from previous page)

```

[-1.90930536e-04, 7.34007655e-04, -5.43077119e-04],
[ 5.98270144e-03, 6.73490846e-03, -1.27176099e-02],
[-1.34547752e-02, -4.65520036e-02, 6.00067788e-02],
[-7.49957880e-04, 7.03763787e-04, 4.61940938e-05],
[ 8.69330232e-04, 1.80346156e-03, -2.67279180e-03],
[-2.04546513e-04, 6.58419628e-04, -4.53873115e-04],
[ 6.82640209e-03, 4.47953560e-03, -1.13059377e-02],
[-1.33289553e-03, -1.11818140e-04, 1.44471367e-03]])

```

Compute extracellular potentials after simulating and storage of transmembrane currents with the LFPy.Cell class:

```

>>> import os
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> import LFPy
>>> from lfpykit import CellGeometry, RecExtElectrode
>>>
>>> cellParameters = {
>>>     'morphology': os.path.join(LFPy.__path__[0], 'test',
>>>                               'ball_and_sticks.hoc'),
>>>     'v_init': -65,                # initial voltage
>>>     'cm': 1.0,                   # membrane capacitance
>>>     'Ra': 150,                   # axial resistivity
>>>     'passive': True,             # insert passive channels
>>>     'passive_parameters': {"g_pas": 1./3E4,
>>>                             "e_pas": -65}, # passive params
>>>     'dt': 2**-4,                 # simulation time res
>>>     'tstart': 0.,                # start t of simulation
>>>     'tstop': 50.,               # end t of simulation
>>> }
>>> cell = LFPy.Cell(**cellParameters)
>>>
>>> synapseParameters = {
>>>     'idx': cell.get_closest_idx(x=0, y=0, z=800), # segment
>>>     'e': 0,                                     # reversal potential
>>>     'syntype': 'ExpSyn',                        # synapse type
>>>     'tau': 2,                                   # syn. time constant
>>>     'weight': 0.01,                             # syn. weight
>>>     'record_current': True                      # syn. current record
>>> }
>>> synapse = LFPy.Synapse(cell, **synapseParameters)
>>> synapse.set_spike_times(np.array([10., 15., 20., 25.]))
>>>
>>> cell.simulate(rec_imem=True)
>>>
>>> N = np.empty((16, 3))
>>> for i in range(N.shape[0]): N[i,] = [1, 0, 0] # normal vectors
>>> electrodeParameters = {                      # parameters for RecExtElectrode class
>>>     'sigma': 0.3,                            # Extracellular potential
>>>     'x': np.zeros(16)+25,                    # Coordinates of electrode contacts
>>>     'y': np.zeros(16),

```

(continues on next page)



(continued from previous page)

```

>>> 'z': np.linspace(-500,1000,16),
>>> 'n': 20,
>>> 'r': 10,
>>> 'N': N,
>>> }
>>> electrode = RecExtElectrode(cell, **electrodeParameters)
>>> M = electrode.get_transformation_matrix()
>>> V_ex = M @ cell.imem
>>> plt.matshow(V_ex)
>>> plt.colorbar()
>>> plt.axis('tight')
>>> plt.show()

```

Compute extracellular potentials during simulation:

```

>>> import os
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> import LFPy
>>> from lfpykit import CellGeometry, RecExtElectrode
>>>
>>> cellParameters = {
>>>     'morphology': os.path.join(LFPy.__path__[0], 'test',
>>>                                 'ball_and_sticks.hoc'),
>>>     'v_init': -65,                    # initial voltage
>>>     'cm': 1.0,                        # membrane capacitance
>>>     'Ra': 150,                        # axial resistivity
>>>     'passive': True,                  # insert passive channels
>>>     'passive_parameters': {"g_pas": 1./3E4,
>>>                             "e_pas": -65}, # passive params
>>>     'dt': 2**-4,                      # simulation time res
>>>     'tstart': 0.,                     # start t of simulation
>>>     'tstop': 50.,                     # end t of simulation
>>> }
>>> cell = LFPy.Cell(**cellParameters)
>>>
>>> synapseParameters = {
>>>     'idx': cell.get_closest_idx(x=0, y=0, z=800), # compartment
>>>     'e': 0,                                     # reversal potential
>>>     'syntype': 'ExpSyn',                         # synapse type
>>>     'tau': 2,                                    # syn. time constant
>>>     'weight': 0.01,                              # syn. weight
>>>     'record_current': True                       # syn. current record
>>> }
>>> synapse = LFPy.Synapse(cell, **synapseParameters)
>>> synapse.set_spike_times(np.array([10., 15., 20., 25.]))
>>>
>>> N = np.empty((16, 3))
>>> for i in range(N.shape[0]): N[i,] = [1, 0, 0] #normal vec. of contacts
>>> electrodeParameters = {                      # parameters for RecExtElectrode class
>>>     'sigma': 0.3,                            # Extracellular potential
>>>     'x': np.zeros(16)+25,                    # Coordinates of electrode contacts

```

(continues on next page)

(continued from previous page)

```

>>> 'y': np.zeros(16),
>>> 'z': np.linspace(-500,1000,16),
>>> 'n': 20,
>>> 'r': 10,
>>> 'N': N,
>>> }
>>> electrode = RecExtElectrode(cell, **electrodeParameters)
>>> cell.simulate(probes=[electrode])
>>> plt.matshow(electrode.data)
>>> plt.colorbar()
>>> plt.axis('tight')
>>> plt.show()

```

Use MEAutility to to handle probes

```

>>> import os
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> import MEAutility as mu
>>> import LFPy
>>> from lfpykit import CellGeometry, RecExtElectrode
>>>
>>> cellParameters = {
>>>     'morphology': os.path.join(LFPy.__path__[0], 'test',
>>>                               'ball_and_sticks.hoc'),
>>>     'v_init': -65,                    # initial voltage
>>>     'cm': 1.0,                        # membrane capacitance
>>>     'Ra': 150,                        # axial resistivity
>>>     'passive': True,                  # insert passive channels
>>>     'passive_parameters': {"g_pas": 1./3E4,
>>>                             "e_pas": -65}, # passive params
>>>     'dt': 2**-4,                      # simulation time res
>>>     'tstart': 0.,                     # start t of simulation
>>>     'tstop': 50.,                     # end t of simulation
>>> }
>>> cell = LFPy.Cell(**cellParameters)
>>>
>>> synapseParameters = {
>>>     'idx': cell.get_closest_idx(x=0, y=0, z=800), # compartment
>>>     'e': 0,                                     # reversal potential
>>>     'syntype': 'ExpSyn',                        # synapse type
>>>     'tau': 2,                                   # syn. time constant
>>>     'weight': 0.01,                             # syn. weight
>>>     'record_current': True                      # syn. current record
>>> }
>>> synapse = LFPy.Synapse(cell, **synapseParameters)
>>> synapse.set_spike_times(np.array([10., 15., 20., 25.]))
>>>
>>> cell.simulate(rec_imem=True)
>>>
>>> probe = mu.return_mea('Neuropixels-128')
>>> electrode = RecExtElectrode(cell, probe=probe)

```

(continues on next page)

(continued from previous page)

```

>>> V_ex = electrode.get_transformation_matrix() @ cell.imem
>>> mu.plot_mea_recording(V_ex, probe)
>>> plt.axis('tight')
>>> plt.show()

```

**get\_transformation\_matrix()**

Get linear response matrix

**Returns****response\_matrix:** ndarray shape (n\_contacts, n\_seg) ndarray**Raises****AttributeError** if cell is None

### 1.6.5 class RecMEAElectrode

```

class LFPy.RecMEAElectrode(cell, sigma_T=0.3, sigma_S=1.5, sigma_G=0.0, h=300.0, z_shift=0.0, steps=20,
                             probe=None, x=array([0]), y=array([0]), z=array([0]), N=None, r=None,
                             n=None, method='linesource', verbose=False, seedvalue=None,
                             squeeze_cell_factor=None, **kwargs)

```

Bases: [lfpypykit.models.RecExtElectrode](#)

class RecMEAElectrode

Electrode class that represents an extracellular in vitro slice recording as a Microelectrode Array (MEA). Inherits RecExtElectrode class

Illustration:

```

      Above neural tissue (Saline) -> sigma_S
<-----*-----> z = z_shift + h

      Neural Tissue -> sigma_T

      o -> source_pos = [x',y',z']

<-----*-----> z = z_shift + 0
      \-> elec_pos = [x,y,z]

      Below neural tissue (MEA Glass plate) -> sigma_G

```

For further details, see reference [1].

**Parameters****cell:** object GeometryCell instance or similar.**sigma\_T:** float extracellular conductivity of neural tissue in unit (S/m)**sigma\_S:** float conductivity of saline bath that the neural slice is immersed in [1.5] (S/m)**sigma\_G:** float conductivity of MEA glass electrode plate. Most commonly assumed non-conducting [0.0] (S/m)**h:** float, int Thickness in um of neural tissue layer containing current the current sources (i.e., in vitro slice or cortex)

**z\_shift: float, int** Height in  $\mu\text{m}$  of neural tissue layer bottom. If e.g., top of neural tissue layer should be  $z=0$ , use  $z\_shift=-h$ . Defaults to  $z\_shift = 0$ , so that the neural tissue layer extends from  $z=0$  to  $z=h$ .

**squeeze\_cell\_factor: float or None** Factor to squeeze the cell in the  $z$ -direction. This is needed for large cells that are thicker than the slice, since no part of the cell is allowed to be outside the slice. The squeeze is done after the neural simulation, and therefore does not affect neuronal simulation, only calculation of extracellular potentials.

**probe: MEAUtility MEA object or None** MEAUtility probe object

**x, y, z: np.ndarray** coordinates or arrays of coordinates in units of ( $\mu\text{m}$ ). Must be same length

**N: None or list of lists** Normal vectors  $[x, y, z]$  of each circular electrode contact surface, default None

**r: float** radius of each contact surface, default None

**n: int** if N is not None and  $r > 0$ , the number of discrete points used to compute the  $n$ -point average potential on each circular contact point.

**contact\_shape: str** 'circle'/'square' (default 'circle') defines the contact point shape. If 'circle'  $r$  is the radius, if 'square'  $r$  is the side length

**method: str** switch between the assumption of 'linesource', 'pointsource', 'root\_as\_point' to represent each compartment when computing extracellular potentials

**verbose: bool** Flag for verbose output, i.e., print more information

**seedvalue: int** random seed when finding random position on contact with  $r > 0$

See also:

**LinearModel**

[\*PointSourcePotential\*](#)

[\*LineSourcePotential\*](#)

[\*RecExtElectrode\*](#)

## References

[1]

## Examples

Mock cell geometry and transmembrane currents:

```
>>> import numpy as np
>>> from lfpykit import CellGeometry, RecMEAElectrode
>>> # cell geometry with four segments ( $\mu\text{m}$ )
>>> cell = CellGeometry(
>>>     x=np.array([[0, 10], [10, 20], [20, 30], [30, 40]]),
>>>     y=np.array([[0, 0], [0, 0], [0, 0], [0, 0]]),
>>>     z=np.array([[0, 0], [0, 0], [0, 0], [0, 0]]) + 10,
>>>     d=np.array([1, 1, 1, 1]))
>>> # transmembrane currents, three time steps (nA)
>>> I_m = np.array([[0.25, -1., 1.]
```

(continues on next page)

(continued from previous page)

```

>>>         [-1., 1., -0.25],
>>>         [1., -0.25, -1.],
>>>         [-0.25, 0.25, 0.25]])
>>> # electrode locations (μm)
>>> r = np.stack([np.arange(10)*4 + 2, np.zeros(10), np.zeros(10)])
>>> # instantiate electrode, get linear response matrix
>>> el = RecMEAElectrode(cell=cell,
>>>                        sigma_T=0.3, sigma_S=1.5, sigma_G=0.0,
>>>                        x=r[0, ], y=r[1, ], z=r[2, ],
>>>                        method='pointsource')
>>> M = el.get_transformation_matrix()
>>> # compute extracellular potential
>>> M @ I_m
array([[ -0.00233572, -0.01990957,  0.02542055],
       [ -0.00585075, -0.01520865,  0.02254483],
       [ -0.01108601, -0.00243107,  0.01108601],
       [ -0.01294584,  0.01013595, -0.00374823],
       [ -0.00599067,  0.01432711, -0.01709416],
       [  0.00599067,  0.01194602, -0.0266944 ],
       [  0.01294584,  0.00953841, -0.02904238],
       [  0.01108601,  0.00972426, -0.02324134],
       [  0.00585075,  0.01075236, -0.01511768],
       [  0.00233572,  0.01038382, -0.00954429]])

```

See also <LFPy>/examples/example\_MEA.py

```

>>> import os
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> import LFPy
>>> from lfpykit import CellGeometry, RecMEAElectrode
>>>
>>> cellParameters = {
>>>     'morphology': os.path.join(LFPy.__path__[0], 'test',
>>>                                'ball_and_sticks.hoc'),
>>>     'v_init': -65,                    # initial voltage
>>>     'cm': 1.0,                        # membrane capacitance
>>>     'Ra': 150,                        # axial resistivity
>>>     'passive': True,                  # insert passive channels
>>>     'passive_parameters': {"g_pas": 1./3E4,
>>>                             "e_pas": -65}, # passive params
>>>     'dt': 2**-4,                      # simulation time res
>>>     'tstart': 0.,                     # start t of simulation
>>>     'tstop': 50.,                     # end t of simulation
>>> }
>>> cell = LFPy.Cell(**cellParameters)
>>> cell.set_rotation(x=np.pi/2, z=np.pi/2)
>>> cell.set_pos(z=100)
>>> synapseParameters = {
>>>     'idx': cell.get_closest_idx(x=800, y=0, z=100), # segment
>>>     'e': 0,                                         # reversal potential
>>>     'syntype': 'ExpSyn',                           # synapse type

```

(continues on next page)

(continued from previous page)

```

>>>     'tau': 2,                                # syn. time constant
>>>     'weight': 0.01,                          # syn. weight
>>>     'record_current': True                   # syn. current record
>>> }
>>> synapse = LFPy.Synapse(cell, **synapseParameters)
>>> synapse.set_spike_times(np.array([10., 15., 20., 25.]))
>>>
>>> MEA_electrode_parameters = {
>>>     'sigma_T': 0.3,      # extracellular conductivity
>>>     'sigma_G': 0.0,      # MEA glass electrode plate conductivity
>>>     'sigma_S': 1.5,      # Saline bath conductivity
>>>     'x': np.linspace(0, 1200, 16), # 1d vector of positions
>>>     'y': np.zeros(16),
>>>     'z': np.zeros(16),
>>>     "method": "pointsource",
>>>     "h": 300,
>>>     "squeeze_cell_factor": 0.5,
>>> }
>>> cell.simulate(rec_imem=True)
>>>
>>> MEA = RecMEAElectrode(cell, **MEA_electrode_parameters)
>>> V_ext = MEA.get_transformation_matrix() @ lfp_cell.imem
>>>
>>> plt.matshow(V_ext)
>>> plt.colorbar()
>>> plt.axis('tight')
>>> plt.show()

```

**distort\_cell\_geometry**(axis='z', nu=0.0)

Distorts cellular morphology with a relative squeeze\_cell\_factor along a chosen axis preserving Poisson's ratio. A ratio nu=0.5 assumes uncompressible and isotropic media that embeds the cell. A ratio nu=0 will only affect geometry along the chosen axis. A ratio nu=-1 will isometrically scale the neuron geometry along each axis. This method does not affect the underlying cable properties of the cell, only predictions of extracellular measurements (by affecting the relative locations of sources representing the compartments).

**Parameters**

**axis:** str which axis to apply compression/stretching. Default is "z".

**nu:** float Poisson's ratio. Ratio between axial and transversal compression/stretching. Default is 0.

**get\_transformation\_matrix**()

Get linear response matrix

**Returns**

**response\_matrix:** ndarray shape (n\_contacts, n\_seg) ndarray

**Raises**

**AttributeError** if cell is None

### 1.6.6 class OneSphereVolumeConductor

**class** LFPy.OneSphereVolumeConductor(*cell, r, R=10000.0, sigma\_i=0.3, sigma\_o=0.03*)

Bases: lfpypykit.models.LinearModel

Computes extracellular potentials within and outside a spherical volume- conductor model that assumes homogeneous, isotropic, linear (frequency independent) conductivity in and outside the sphere with a radius  $R$ . The conductivity in and outside the sphere must be greater than 0, and the current source(s) must be located within the radius  $R$ .

The implementation is based on the description of electric potentials of point charge in an dielectric sphere embedded in dielectric media [1], which is mathematically equivalent to a current source in conductive media.

This class is a LinearModel subclass that defines a 2D linear response matrix  $\mathbf{M}$  between transmembrane current array  $\mathbf{I}$  (nA) of a multicompartment neuron model and the corresponding extracellular electric potential  $V_{ex}$  (mV) as

$$V_{ex} = \mathbf{M}\mathbf{I}$$

The current  $\mathbf{I}$  is an ndarray of shape (n\_seg, n\_steps) with unit (nA), and each row indexed by  $j$  of  $V_{ex}$  represents the electric potential at each measurement site for every time step.

#### Parameters

- cell:** object or None CellGeometry instance or similar.
- r:** ndarray, dtype=float shape(3, n\_points) observation points in space in spherical coordinates (radius, theta, phi) relative to the center of the sphere.
- R:** float sphere radius ( $\mu\text{m}$ )
- sigma\_i:** float electric conductivity for radius  $r \leq R$  (S/m)
- sigma\_o:** float electric conductivity for radius  $r > R$  (S/m)

#### References

[1]

#### Examples

Compute the potential for a single monopole along the x-axis:

```
>>> # import modules
>>> from lfpypykit import OneSphereVolumeConductor
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> # observation points in spherical coordinates (flattened)
>>> X, Y = np.mgrid[-15000:15100:1000., -15000:15100:1000.]
>>> r = np.array([np.sqrt(X**2 + Y**2).flatten(),
>>>               np.arctan2(Y, X).flatten(),
>>>               np.zeros(X.size)])
>>> # set up class object and compute electric potential in all locations
>>> sphere = OneSphereVolumeConductor(cell=None, r=r, R=10000.,
>>>                                   sigma_i=0.3, sigma_o=0.03)
>>> Phi = sphere.calc_potential(rs=8000, current=1.).reshape(X.shape)
```

(continues on next page)

(continued from previous page)

```
>>> # plot
>>> fig, ax = plt.subplots(1,1)
>>> im=ax.contourf(X, Y, Phi,
>>>                 levels=np.linspace(Phi.min(),
>>>                 np.median(Phi[np.isfinite(Phi)]) * 4, 30))
>>> circle = plt.Circle(xy=(0,0), radius=sphere.R, fc='none', ec='k')
>>> ax.add_patch(circle)
>>> fig.colorbar(im, ax=ax)
>>> plt.show()
```

**calc\_potential**(*rs, current, min\_distance=1.0, n\_max=1000*)

Return the electric potential at observation points for source current as function of time.

**Parameters**

- rs: float** monopole source location along the horizontal x-axis ( $\mu\text{m}$ )
- current: float or ndarray, dtype float** float or shape (n\_tsteps, ) array containing source current (nA)
- min\_distance: None or float** minimum distance between source location and observation point ( $\mu\text{m}$ ) (in order to avoid singularities)
- n\_max: int** Number of elements in polynomial expansion to sum over (see [1]).

**Returns**

- Phi: ndarray** shape (n-points, ) ndarray of floats if I is float like. If I is an 1D ndarray, and shape (n-points, I.size) ndarray is returned. Unit (mV).

**References**

[1]

**get\_transformation\_matrix**(*n\_max=1000*)

Compute linear mapping between transmembrane currents of CellGeometry like object instance and extracellular potential in and outside of sphere.

**Parameters**

- n\_max: int** Number of elements in polynomial expansion to sum over (see [1]).

**Returns**

- ndarray** Shape (n\_points, n\_compartments) mapping between individual segments and extracellular potential in extracellular locations

**Raises**

- AttributeError** if cell is None



## Notes

Each segment is treated as a point source in space. The minimum source to measurement site distance will be set to the diameter of each segment

## References

[1]

## Examples

Compute extracellular potential in one-sphere volume conductor model from LFPy.Cell object:

```
>>> # import modules
>>> import LFPy
>>> from lfpykit import CellGeometry, >>> OneSphereVolumeConductor
>>> import os
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from matplotlib.collections import PolyCollection
>>> # create cell
>>> cell = LFPy.Cell(morphology=os.path.join(LFPy.__path__[0], 'test',
>>>                                         'ball_and_sticks.hoc'),
>>>                  tstop=10.)
>>> cell.set_pos(z=9800.)
>>> # stimulus
>>> syn = LFPy.Synapse(cell, idx=cell.totnsegs-1, syntype='Exp2Syn',
>>>                    weight=0.01)
>>> syn.set_spike_times(np.array([1.]))
>>> # simulate
>>> cell.simulate(rec_imem=True)
>>> # observation points in spherical coordinates (flattened)
>>> X, Z = np.mgrid[-500:501:10., 9500:10501:10.]
>>> Y = np.zeros(X.shape)
>>> r = np.array([np.sqrt(X**2 + Z**2).flatten(),
>>>               np.arccos(Z / np.sqrt(X**2 + Z**2)).flatten(),
>>>               np.arctan2(Y, X).flatten()])
>>> # set up class object and compute mapping between segment currents
>>> # and electric potential in space
>>> sphere = OneSphereVolumeConductor(cell, r=r, R=10000.,
>>>                                   sigma_i=0.3, sigma_o=0.03)
>>> M = sphere.get_transformation_matrix(n_max=1000)
>>> # pick out some time index for the potential and compute potential
>>> ind = cell.tvec==2.
>>> V_ex = (M @ cell.imem)[:, ind].reshape(X.shape)
>>> # plot potential
>>> fig, ax = plt.subplots(1,1)
>>> zips = []
>>> for x, z in cell.get_idx_polygons(projection=('x', 'z')):
>>>     zips.append(list(zip(x, z)))
>>> polycol = PolyCollection(zips,
>>>                          edgecolors='none',
```

(continues on next page)

(continued from previous page)

```

>>>                                     facecolors='gray')
>>> vrange = 1E-3 # limits for color contour plot
>>> im=ax.contour(X, Z, V_ex,
>>>               levels=np.linspace(-vrange, vrange, 41))
>>> circle = plt.Circle(xy=(0,0), radius=sphere.R, fc='none', ec='k')
>>> ax.add_collection(polycol)
>>> ax.add_patch(circle)
>>> ax.axis(ax.axis('equal'))
>>> ax.set_xlim(X.min(), X.max())
>>> ax.set_ylim(Z.min(), Z.max())
>>> fig.colorbar(im, ax=ax)
>>> plt.show()

```

## 1.7 Current Dipole Moment forward models

### 1.7.1 class InfiniteVolumeConductor

**class** LFPy.InfiniteVolumeConductor(*sigma=0.3*)

Bases: lfpypykit.eegmegcalc.InfiniteVolumeConductor

Main class for computing extracellular potentials with current dipole moment  $\mathbf{P}$  in an infinite 3D volume conductor model that assumes homogeneous, isotropic, linear (frequency independent) conductivity  $\sigma$ . The potential  $V$  is computed as [1]:

$$V = \frac{\mathbf{P} \cdot \mathbf{r}}{4\pi\sigma r^3}$$

#### Parameters

**sigma: float** Electrical conductivity in extracellular space in units of (S/cm)

See also:

[\*FourSphereVolumeConductor\*](#)

MEG

#### References

[1]

#### Examples

Computing the potential from dipole moment valid in the far field limit. Theta correspond to the dipole alignment angle from the vertical z-axis:

```

>>> from lfpypykit.eegmegcalc import InfiniteVolumeConductor
>>> import numpy as np
>>> inf_model = InfiniteVolumeConductor(sigma=0.3)
>>> p = np.array([[10.], [10.], [10.]]) # [nA μm]
>>> r = np.array([[1000.], [0.], [5000.]]) # [μm]

```

(continues on next page)

(continued from previous page)

```
>>> inf_model.get_dipole_potential(p, r) # [mV]
array([[1.20049432e-07]])
```

**get\_dipole\_potential(*p*, *r*)**

Return electric potential from current dipole moment *p* in locations *r* relative to dipole

**Parameters**

**p:** **ndarray, dtype=float** Shape (3, n\_timesteps) array containing the x,y,z components of the current dipole moment in units of (nA\*μm) for all timesteps

**r:** **ndarray, dtype=float** Shape (n\_contacts, 3) array containing the displacement vectors from dipole location to measurement location

**Returns**

**potential:** **ndarray, dtype=float** Shape (n\_contacts, n\_timesteps) array containing the electric potential at contact point(s) *r* in units of (mV) for all timesteps of current dipole moment *p*

**get\_multi\_dipole\_potential(*cell*, *electrode\_locs*, *timepoints=None*)**

Return electric potential from multiple current dipoles from cell

The multiple current dipoles corresponds to dipoles computed from all axial currents in a neuron simulation, typically two axial currents per compartment, excluding the root compartment.

**Parameters**

**cell:** LFPy.Cell object

**electrode\_locs:** **ndarray, dtype=float** Shape (n\_contacts, 3) array containing n\_contacts electrode locations in cartesian coordinates in units of [μm]. All *r\_el* in *electrode\_locs* must be placed so that  $|r_{el}|$  is less than or equal to scalp radius and larger than the distance between dipole and sphere center:  $|r_z| < |r_{el}| \leq radii[3]$ .

**timepoints:** **ndarray, dtype=int** array of timepoints at which you want to compute the electric potential. Defaults to None. If not given, all simulation timesteps will be included.

**Returns**

**potential:** **ndarray, dtype=float** Shape (n\_contacts, n\_timesteps) array containing the electric potential at contact point(s) *electrode\_locs* in units of [mV] for all timesteps of neuron simulation

**Examples**

Compute extracellular potential from neuron simulation in four-sphere head model. Instead of simplifying the neural activity to a single dipole, we compute the contribution from every multi dipole from all axial currents in neuron simulation:

```
>>> import LFPy
>>> from lfpykit.eegmegcalc import InfiniteVolumeConductor
>>> import numpy as np
>>> cell = LFPy.Cell('PATH/TO/MORPHOLOGY', extracellular=False)
>>> syn = LFPy.Synapse(cell, idx=cell.get_closest_idx(0,0,100),
>>>                    syntype='ExpSyn', e=0., tau=1., weight=0.001)
>>> syn.set_spike_times(np.mgrid[20:100:20])
>>> cell.simulate(rec_vmem=True, rec_imem=False)
```

(continues on next page)

(continued from previous page)

```

>>> sigma = 0.3
>>> timepoints = np.array([10, 20, 50, 100])
>>> electrode_locs = np.array([[50., -50., 250.]])
>>> MD_INF = InfiniteVolumeConductor(sigma)
>>> phi = MD_INF.get_multi_dipole_potential(cell, electrode_locs,
>>>                                         timepoints = timepoints)

```

**get\_transformation\_matrix(*r*)**

Get linear response matrix mapping current dipole moment in (nA  $\mu\text{m}$ ) to extracellular potential in (mV) at recording sites *r* ( $\mu\text{m}$ )

**Parameters**

**r:** **ndarray, dtype=float** Shape (n\_contacts, 3) array containing the displacement vectors from dipole location to measurement location ( $\mu\text{m}$ )

**Returns**

**response\_matrix:** **ndarray** shape (n\_contacts, 3) ndarray

**1.7.2 class FourSphereVolumeConductor**

**class** LFPy.FourSphereVolumeConductor(*r\_electrodes*, *radii=None*, *sigmas=None*,  
*iter\_factor=2.0202020202020204e-08*)

Bases: lfpypykit.eegmegcalc.FourSphereVolumeConductor

Main class for computing extracellular potentials in a four-sphere volume conductor model that assumes homogeneous, isotropic, linear (frequency independent) conductivity within the inner sphere and outer shells. The conductance outside the outer shell is 0 (air).

This class implements the corrected 4-sphere model described in [1], [2]

**Parameters**

**r\_electrodes:** **ndarray, dtype=float** Shape (n\_contacts, 3) array containing n\_contacts electrode locations in cartesian coordinates in units of ( $\mu\text{m}$ ). All *r\_el* in *r\_electrodes* must be less than or equal to scalp radius and larger than the distance between dipole and sphere center:  $|r_z| < r_{el} \leq radii[3]$ .

**radii:** **list, dtype=float** Len 4 list with the outer radii in units of ( $\mu\text{m}$ ) for the 4 concentric shells in the four-sphere model: brain, csf, skull and scalp, respectively.

**sigmas:** **list, dtype=float** Len 4 list with the electrical conductivity in units of (S/m) of the four shells in the four-sphere model: brain, csf, skull and scalp, respectively.

**iter\_factor:** **float** iteration-stop factor

See also:

[\*InfiniteVolumeConductor\*](#)

MEG

## References

[1], [2]

## Examples

Compute extracellular potential from current dipole moment in four-sphere head model:

```
>>> from lfpypykit.eegmegcalc import FourSphereVolumeConductor
>>> import numpy as np
>>> radii = [79000., 80000., 85000., 90000.] # (μm)
>>> sigmas = [0.3, 1.5, 0.015, 0.3] # (S/m)
>>> r_electrodes = np.array([[0., 0., 90000.], [0., 85000., 0.]]) # (μm)
>>> sphere_model = FourSphereVolumeConductor(r_electrodes, radii,
>>>                                           sigmas)
>>> # current dipole moment
>>> p = np.array([[10.]*10, [10.]*10, [10.]*10]) # 10 timesteps (nA μm)
>>> dipole_location = np.array([0., 0., 78000.]) # (μm)
>>> # compute potential
>>> sphere_model.get_dipole_potential(p, dipole_location) # (mV)
array([[1.06247669e-08, 1.06247669e-08, 1.06247669e-08, 1.06247669e-08,
        1.06247669e-08, 1.06247669e-08, 1.06247669e-08, 1.06247669e-08,
        1.06247669e-08, 1.06247669e-08],
       [2.39290752e-10, 2.39290752e-10, 2.39290752e-10, 2.39290752e-10,
        2.39290752e-10, 2.39290752e-10, 2.39290752e-10, 2.39290752e-10,
        2.39290752e-10, 2.39290752e-10]])
```

### `get_dipole_potential(p, dipole_location)`

Return electric potential from current dipole moment `p` in location `dipole_location` in locations `r_electrodes`

#### Parameters

**p:** `ndarray, dtype=float` Shape (3, `n_timesteps`) array containing the x,y,z components of the current dipole moment in units of (nA\*μm) for all timesteps.

**dipole\_location:** `ndarray, dtype=float` Shape (3, ) array containing the position of the current dipole in cartesian coordinates. Units of (μm).

#### Returns

**potential:** `ndarray, dtype=float` Shape (`n_contacts`, `n_timesteps`) array containing the electric potential at contact point(s) `FourSphereVolumeConductor.rxyz` in units of (mV) for all timesteps of current dipole moment `p`.

### `get_dipole_potential_from_multi_dipoles(cell, timepoints=None)`

Return electric potential from multiple current dipoles from cell.

By multiple current dipoles we mean the dipoles computed from all axial currents in a neuron simulation, typically two axial currents per compartment, except for the root compartment.

#### Parameters

**cell:** LFPy Cell object, `LFPy.Cell`

**timepoints:** `ndarray, dtype=int` array of timepoints at which you want to compute the electric potential. Defaults to None. If not given, all simulation timesteps will be included.

#### Returns

**potential: ndarray, dtype=float** Shape (n\_contacts, n\_timesteps) array containing the electric potential at contact point(s) electrode\_locs in units of [mV] for all timesteps of neuron simulation.

## Examples

Compute extracellular potential from neuron simulation in four-sphere head model. Instead of simplifying the neural activity to a single dipole, we compute the contribution from every multi dipole from all axial currents in neuron simulation:

```
>>> import os
>>> import LFPy
>>> from LFPy import FourSphereVolumeConductor
>>> import numpy as np
>>> cell = LFPy.Cell(os.path.join(LFPy.__path__[0], 'test',
>>>                                'ball_and_sticks.hoc'),
>>>                  v_init=-65, cm=1., Ra=150,
>>>                  passive=True,
>>>                  passive_parameters=dict(g_pas=1/1E4, e_pas=-65))
>>> syn = LFPy.Synapse(cell, idx=cell.get_closest_idx(0,0,100),
>>>                     syntype='ExpSyn', e=0., tau=1., weight=0.001)
>>> syn.set_spike_times(np.mgrid[20:100:20])
>>> cell.simulate(rec_vmem=True, rec_imem=False)
>>> cell.set_pos(0, 0, 78800)
>>> radii = [79000., 80000., 85000., 90000.]
>>> sigmas = [0.3, 1.5, 0.015, 0.3]
>>> r_electrodes = np.array([[0., 0., 90000.]])
>>> MD_4s = FourSphereVolumeConductor(r_electrodes=r_electrodes,
>>>                                    radii=radii,
>>>                                    sigmas=sigmas)
>>> phi = MD_4s.get_dipole_potential_from_multi_dipoles(cell)
```

### **get\_transformation\_matrix**(dipole\_location)

Get linear response matrix mapping current dipole moment in (nA  $\mu\text{m}$ ) located in location **rz** to extracellular potential in (mV) at recording sites **FourSphereVolumeConductor.rxyz** ( $\mu\text{m}$ )

#### Parameters

**dipole\_location: ndarray, dtype=float** Shape (3,) array containing the position of the current dipole in cartesian coordinates. Units of ( $\mu\text{m}$ ).

#### Returns

**response\_matrix: ndarray** shape (n\_contacts, 3) ndarray

### 1.7.3 class NYHeadModel

**class** LFPy.NYHeadModel(*nyhead\_file=None*)

Bases: object

Main class for computing EEG signals from current dipole moment **P** in New York Head Model [1], [2]

Assumes units of nA \*  $\mu\text{m}$  for current dipole moment, and mV for the EEG

#### Parameters

**nyhead\_file: str [optional]** Location of file containing New York Head Model. If empty (or None), it will be looked for in the main LFPykit folder. If not present the user is asked if it should be downloaded from [https://www.parralab.org/nyhead/sa\\_nyhead.mat](https://www.parralab.org/nyhead/sa_nyhead.mat)

See also:

*FourSphereVolumeConductor*

MEG

#### Notes

The original unit of the New York model current dipole moment is (probably?) mA\*m, and the EEG output unit is V. LFPykit's current dipole moments have units nA\* $\mu\text{m}$ , and EEGs from the NYhead model is here recomputed in units of mV.

#### References

[1], [2]

#### Examples

Computing EEG from dipole moment.

```
>>> from lfpypykit.eegmegcalc import NYHeadModel
```

```
>>> nyhead = NYHeadModel()
```

```
>>> nyhead.set_dipole_pos('parietal_lobe') # predefined example location
>>> M = nyhead.get_transformation_matrix()
```

```
>>> # Rotate to be along normal vector of cortex
>>> p = nyhead.rotate_dipole_to_surface_normal([[0.], [0.], [1.]])
>>> eeg = M @ p # (mV)
```

**find\_closest\_electrode()**

Returns minimal distance (mm) and closest electrode idx to dipole location specified in self.dipole\_pos.

**get\_transformation\_matrix()**

Get linear response matrix mapping from current dipole moment (nA  $\mu\text{m}$ ) to EEG signal (mV) at EEG electrodes (n=231)

**Returns**

**response\_matrix:** ndarray shape (231, 3) ndarray

**return\_closest\_idx**(pos)

Returns the index of the closest vertex in the brain to a given position (in mm).

#### Parameters

**pos** [array of length (3)] [x, y, z] of a location in the brain, given in mm, and not in um which is the default position unit in LFPy

#### Returns

——

**idx** [int] Index of the vertex in the brain that is closest to the given location

**rotate\_dipole\_to\_surface\_normal**(p, orig\_ax\_vec=[0, 0, 1])

Returns rotated dipole moment, p\_rot, oriented along the normal vector of the cortex at the dipole location

#### Parameters

**p** [np.ndarray of size (3, num\_timesteps)] Current dipole moment from neural simulation, [p\_x(t), p\_y(t), p\_z(t)]. If z-axis is the depth axis of cortex in the original neural simulation p\_x(t) and p\_y(t) will typically be small, and orig\_ax\_vec = [0, 0, 1].

**orig\_ax\_vec** [np.ndarray or list of length (3)] Original surface vector of cortex in the neural simulation. If depth axis of cortex is the z-axis, orig\_ax\_vec = [0, 0, 1].

#### Returns

**p\_rot** [np.ndarray of size (3, num\_timesteps)] Rotated current dipole moment, oriented along cortex normal vector at the dipole location

## References

See: [https://en.wikipedia.org/wiki/Rotation\\_matrix](https://en.wikipedia.org/wiki/Rotation_matrix) under “Rotation matrix from axis and angle”

**set\_dipole\_pos**(dipole\_pos=None)

Sets the dipole location in the brain

#### Parameters

**dipole\_pos:** None, str or array of length (3) [x, y, z] (mm) Location of the dipole. If no argument is given (or dipole\_pos=None), a location, ‘motorsensory\_cortex’, from self.dipole\_pos\_dict is used. If dipole\_pos is an array of length 3, the closest vertex in the brain will be set as the dipole location.

## 1.7.4 class InfiniteHomogeneousVolCondMEG

**class** LFPy.InfiniteHomogeneousVolCondMEG(sensor\_locations, mu=1.2566370614359173e-06)

Bases: lfpypykit.eegmegcalc.InfiniteHomogeneousVolCondMEG

Basic class for computing magnetic field from current dipole moment. For this purpose we use the Biot-Savart law derived from Maxwell’s equations under the assumption of negligible magnetic induction effects [1]:

$$\mathbf{H} = \frac{\mathbf{p} \times \mathbf{R}}{4\pi R^3}$$

where  $\mathbf{p}$  is the current dipole moment,  $\mathbf{R}$  the vector between dipole source location and measurement location, and  $R = |\mathbf{R}|$



Note that the magnetic field  $\mathbf{H}$  is related to the magnetic field  $\mathbf{B}$  as

$$\mu_0 \mathbf{H} = \mathbf{B} - \mathbf{M}$$

where  $\mu_0$  is the permeability of free space (very close to permeability of biological tissues).  $\mathbf{M}$  denotes material magnetization (also ignored)

#### Parameters

**sensor\_locations:** ndarray, dtype=float shape (n\_locations x 3) array with x,y,z-locations of measurement devices where magnetic field of current dipole moments is calculated. In unit of [ $\mu\text{m}$ ]

**mu:** float Permeability. Default is permeability of vacuum ( $\mu_0 = 4 * \pi * 10^{-7} \text{ T*m/A}$ )

#### Raises

**AssertionError** If dimensionality of sensor\_locations is wrong

See also:

*FourSphereVolumeConductor*

*InfiniteVolumeConductor*

#### References

[1]

#### Examples

Define cell object, create synapse, compute current dipole moment:

```
>>> import LFPy, os, numpy as np, matplotlib.pyplot as plt
>>> from LFPy import InfiniteHomogeneousVolCondMEG as MEG
>>> from LFPy import CurrentDipoleMoment
>>> # create LFPy.Cell object
>>> cell = LFPy.Cell(morphology=os.path.join(LFPy.__path__[0], 'test',
>>>                                         'ball_and_sticks.hoc'),
>>>                  passive=True)
>>> cell.set_pos(0., 0., 0.)
>>> # create single synaptic stimuli at soma (idx=0)
>>> syn = LFPy.Synapse(cell, idx=0, syntype='ExpSyn', weight=0.01, tau=5,
>>>                  record_current=True)
>>> syn.set_spike_times_w_netstim()
>>> # simulate, record current dipole moment
>>> cdm = CurrentDipoleMoment(cell=cell)
>>> cell.simulate(probes=[cdm])
>>> # Compute the dipole location as an average of segment locations
>>> # weighted by membrane area:
>>> dipole_location = (cell.area * np.c_[cell.x.mean(axis=1),
>>>                                     cell.y.mean(axis=1),
>>>                                     cell.z.mean(axis=1)].T
>>>                  / cell.area.sum()).sum(axis=1)
>>> # Define sensor site, instantiate MEG object, get transformation matrix
>>> sensor_locations = np.array([[1E4, 0, 0]])
```

(continues on next page)

(continued from previous page)

```

>>> meg = MEG(sensor_locations)
>>> M = meg.get_transformation_matrix(dipole_location)
>>> # compute the magnetic signal in a single sensor location:
>>> H = M @ cdm.data
>>> # plot output
>>> plt.figure(figsize=(12, 8), dpi=120)
>>> plt.subplot(311)
>>> plt.plot(cell.tvec, cell.somav)
>>> plt.ylabel(r'$V_{soma}$ (mV)')
>>> plt.subplot(312)
>>> plt.plot(cell.tvec, syn.i)
>>> plt.ylabel(r'$I_{syn}$ (nA)')
>>> plt.subplot(313)
>>> plt.plot(cell.tvec, H[0].T)
>>> plt.ylabel(r'$H$ (nA/um)')
>>> plt.xlabel('$t$ (ms)')
>>> plt.legend(['$H_x$', '$H_y$', '$H_z$'])
>>> plt.show()

```

**calculate\_B(*p*, *r\_p*)**

Compute magnetic field **B** from single current dipole **p** localized somewhere in space at **r\_p**.

This function returns the magnetic field **B = H**.

**Parameters**

**p: ndarray, dtype=float** shape (3, n\_timesteps) array with x,y,z-components of current-dipole moment time series data in units of (nA  $\mu\text{m}$ )

**r\_p: ndarray, dtype=float** shape (3, ) array with x,y,z-location of dipole in units of ( $\mu\text{m}$ )

**Returns**

**ndarray, dtype=float** shape (n\_locations x 3 x n\_timesteps) array with x,y,z-components of the magnetic field **B** in units of (nA/ $\mu\text{m}$ )

**calculate\_H(*current\_dipole\_moment*, *dipole\_location*)**

Compute magnetic field **H** from single current-dipole moment localized in an infinite homogeneous volume conductor.

**Parameters**

**current\_dipole\_moment: ndarray, dtype=float** shape (3, n\_timesteps) array with x,y,z-components of current-dipole moment time series data in units of (nA  $\mu\text{m}$ )

**dipole\_location: ndarray, dtype=float** shape (3, ) array with x,y,z-location of dipole in units of ( $\mu\text{m}$ )

**Returns**

**ndarray, dtype=float** shape (n\_locations x 3 x n\_timesteps) array with x,y,z-components of the magnetic field **H** in units of (nA/ $\mu\text{m}$ )

**Raises**

**AssertionError** If dimensionality of *current\_dipole\_moment* and/or *dipole\_location* is wrong

**calculate\_H\_from\_iaxial**(*cell*)

Computes the magnetic field in space from axial currents computed from membrane potential values and axial resistances of multicompartment cells.

See [1] for details on the biophysics governing magnetic fields from axial currents.

**Parameters**

**cell:** **object** LFPy.Cell-like object. Must have attribute `vmem` containing recorded membrane potentials in units of mV

**Returns**

**H:** **ndarray, dtype=float** shape (n\_locations x 3 x n\_timesteps) array with x,y,z-components of the magnetic field **H** in units of (nA/μm)

**References**

[1]

**Examples**

Define cell object, create synapse, compute current dipole moment:

```
>>> import LFPy, os, numpy as np, matplotlib.pyplot as plt
>>> from LFPy import InfiniteHomogeneousVolCondMEG as MEG
>>> cell = LFPy.Cell(morphology=os.path.join(LFPy.__path__[0], 'test',
>>>                                         'ball_and_sticks.hoc'),
>>>                  passive=True)
>>> cell.set_pos(0., 0., 0.)
>>> syn = LFPy.Synapse(cell, idx=0, syntype='ExpSyn', weight=0.01,
>>>                  record_current=True)
>>> syn.set_spike_times_w_netstim()
>>> cell.simulate(rec_vmem=True)
>>> # Instantiate the MEG object, compute and plot the magnetic
>>> # signal in a sensor location:
>>> sensor_locations = np.array([[1E4, 0, 0]])
>>> meg = MEG(sensor_locations)
>>> H = meg.calculate_H_from_iaxial(cell)
>>> plt.subplot(311)
>>> plt.plot(cell.tvec, cell.somav)
>>> plt.subplot(312)
>>> plt.plot(cell.tvec, syn.i)
>>> plt.subplot(313)
>>> plt.plot(cell.tvec, H[0, 1, :]) # y-component
>>> plt.show()
```

**get\_transformation\_matrix**(*dipole\_location*)

Get linear response matrix mapping current dipole moment in (nA μm) located in location `dipole_location` to magnetic field **H** in units of (nA/μm) at `sensor_locations`

**Parameters**

**dipole\_location:** **ndarray, dtype=float** shape (3, ) array with x,y,z-location of dipole in units of (μm)

**Returns**

**response\_matrix:** ndarray shape (n\_contacts, 3, 3) ndarray

### 1.7.5 class SphericallySymmetricVolCondMEG

**class** LFPy.SphericallySymmetricVolCondMEG(*r*, *mu*=1.2566370614359173e-06)

Bases: lfpypykit.eegmegcalc.SphericallySymmetricVolCondMEG

Computes magnetic fields from current dipole in spherically-symmetric volume conductor models.

This class facilitates calculations according to eq. (34) from [1] (see also [2]) defined as:

$$\mathbf{H} = \frac{1}{4\pi} \frac{F \mathbf{p} \times \mathbf{r}_p - (\mathbf{p} \times \mathbf{r}_p \cdot \mathbf{r}) \nabla F}{F^2}, \text{ where}$$

$$F = a(ra + r^2 - \mathbf{r}_p \cdot \mathbf{r}),$$

$$\nabla F = (r^{-1}a^2 + a^{-1}\mathbf{a} \cdot \mathbf{r} + 2a + 2r)\mathbf{r} - (a + 2r + a^{-1}\mathbf{a} \cdot \mathbf{r})\mathbf{r}_p,$$

$$\mathbf{a} = \mathbf{r} - \mathbf{r}_p,$$

$$a = |\mathbf{a}|,$$

$$r = |\mathbf{r}|.$$

Here,  $\mathbf{p}$  is the current dipole moment,  $\mathbf{r}$  the measurement location(s) and  $\mathbf{r}_p$  the current dipole location.

Note that the magnetic field  $\mathbf{H}$  is related to the magnetic field  $\mathbf{B}$  as

$$\mu_0 \mathbf{H} = \mathbf{B} - \mathbf{M},$$

where  $\mu_0$  denotes the permeability of free space (very close to permeability of biological tissues).  $\mathbf{M}$  denotes material magnetization (which is ignored).

#### Parameters

**r:** ndarray sensor locations, shape (*n*, 3) where *n* denotes number of locations, unit [ $\mu\text{m}$ ]

**mu:** float Permeability. Default is permeability of vacuum ( $\mu_0 = 4\pi 10^{-7} \text{ Tm/A}$ )

#### Raises

**AssertionError** If dimensionality of sensor locations *r* is wrong

See also:

[\*InfiniteHomogeneousVolCondMEG\*](#)

#### References

[1], [2]

#### Examples

Compute the magnetic field from a current dipole located

```
>>> import numpy as np
>>> from LFPy import SphericallySymmetricVolCondMEG
>>> p = np.array([[0, 1, 0]]).T # tangential current dipole (nAμm)
>>> r_p = np.array([0, 0, 90000]) # dipole location (μm)
>>> r = np.array([[0, 0, 92000]]) # measurement location (μm)
```

(continues on next page)

(continued from previous page)

```

>>> m = SphericallySymmetricVolCondMEG(r=r)
>>> M = m.get_transformation_matrix(r_p=r_p)
>>> H = M @ p
>>> H # magnetic field (nA/μm)
array([[9.73094081e-09],
       [0.00000000e+00],
       [0.00000000e+00]])

```

**calculate\_B(p, r\_p)**

Compute magnetic field **B** from single current dipole **p** localized somewhere in space at **r\_p**.

This function returns the magnetic field **B = H**.

**Parameters**

**p: ndarray, dtype=float** shape (3, n\_timesteps) array with x,y,z-components of current-dipole moment time series data in units of (nA μm)

**r\_p: ndarray, dtype=float** shape (3, ) array with x,y,z-location of dipole in units of (μm)

**Returns**

**ndarray, dtype=float** shape (n\_locations x 3 x n\_timesteps) array with x,y,z-components of the magnetic field **B** in units of (nA/μm)

**calculate\_H(p, r\_p)**

Compute magnetic field **H** from single current dipole **p** localized somewhere in space at **r\_p**

**Parameters**

**p: ndarray, dtype=float** shape (3, n\_timesteps) array with x,y,z-components of current-dipole moment time series data in units of (nA μm)

**r\_p: ndarray, dtype=float** shape (3, ) array with x,y,z-location of dipole in units of (μm)

**Returns**

**ndarray, dtype=float** shape (n\_locations x 3 x n\_timesteps) array with x,y,z-components of the magnetic field **H** in units of (nA/μm)

**Raises**

**AssertionError** If dimensionality of current\_dipole\_moment **p** and/or dipole\_location **r\_p** is wrong

**calculate\_H\_from\_ixial(cell)**

Computes the magnetic field in space from axial currents computed from membrane potential values and axial resistances of multicompartment cells.

See [1] for details on the biophysics governing magnetic fields from axial currents.

**Parameters**

**cell: object** LFPy.Cell-like object. Must have attribute **vmem** containing recorded membrane potentials in units of mV

**Returns**

**H: ndarray, dtype=float** shape (n\_locations x 3 x n\_timesteps) array with x,y,z-components of the magnetic field **H** in units of (nA/μm)

## References

[1]

## Examples

Define cell object, create synapse, compute current dipole moment:

```
>>> import LFPy, os, numpy as np, matplotlib.pyplot as plt
>>> from LFPy import SphericallySymmetricVolCondMEG as MEG
>>> cell = LFPy.Cell(morphology=os.path.join(LFPy.__path__[0], 'test',
>>>                                         'ball_and_sticks.hoc'),
>>>                  passive=True)
>>> cell.set_pos(0., 0., 0.)
>>> syn = LFPy.Synapse(cell, idx=0, syntype='ExpSyn', weight=0.01,
>>>                  record_current=True)
>>> syn.set_spike_times_w_netstim()
>>> cell.simulate(rec_vmem=True)
>>> # Instantiate the MEG object, compute and plot the magnetic
>>> # signal in a sensor location:
>>> r = np.array([[1E4, 0, 0]])
>>> meg = MEG(r)
>>> H = meg.calculate_H_from_iaxial(cell)
>>> plt.subplot(311)
>>> plt.plot(cell.tvec, cell.somav)
>>> plt.subplot(312)
>>> plt.plot(cell.tvec, syn.i)
>>> plt.subplot(313)
>>> plt.plot(cell.tvec, H[0, 1, :]) # y-component
>>> plt.show()
```

### **get\_transformation\_matrix(*r\_p*)**

Get linear response matrix mapping current dipole moment in (nA  $\mu\text{m}$ ) located in location *r\_p* to magnetic field **H** in units of (nA/ $\mu\text{m}$ ) at sensor locations *r*

#### **Parameters**

**r\_p:** ndarray, dtype=float shape (3, ) array with x,y,z-location of dipole in units of ( $\mu\text{m}$ )

#### **Returns**

**response\_matrix:** ndarray shape (n\_sensors, 3, 3) ndarray

#### **Raises**

**AssertionError** If dipole location *r\_p* has the wrong shape or if its radius is greater than radius to any sensor location in <object>.r

## 1.8 Current Source Density (CSD)

### 1.8.1 class LaminarCurrentSourceDensity

**class** LFPy.LaminarCurrentSourceDensity(*cell*, *z*, *r*)

Bases: lfpypykit.models.LinearModel

Facilitates calculations of the ground truth Current Source Density (CSD) in cylindrical volumes aligned with the z-axis based on [1] and [2].

The implementation assumes piecewise linear current sources similar to LineSourcePotential, and accounts for the fraction of each segment's length within each volume, see Eq. 11 in [2].

This class is a LinearModel subclass that defines a 2D linear response matrix **M** between transmembrane current array **I** (nA) of a multicompartment neuron model and the corresponding CSD **C** (nA/μm<sup>3</sup>) as

$$\mathbf{C} = \mathbf{M}\mathbf{I}$$

The current **I** is an ndarray of shape (n\_seg, n\_steps) with unit (nA), and each row indexed by *j* of **C** represents the CSD in each volume for every time step as the sum of currents divided by the volume.

#### Parameters

**cell:** object or None CellGeometry instance or similar.

**z:** ndarray, dtype=float shape (n\_volumes, 2) array of lower and upper edges of each volume along the z-axis in units of (μm). The lower edge value must be below the upper edge value.

**r:** ndarray, dtype=float shape (n\_volumes, ) array with assumed radius of each cylindrical volume. Each radius must be greater than zero, and in units of (μm)

#### Raises

**AttributeError** inputs *z* and *r* must be ndarrays of correct shape etc.

See also:

**LinearModel**

*VolumetricCurrentSourceDensity*

#### References

[1], [2]

#### Examples

Mock cell geometry and transmembrane currents:

```
>>> import numpy as np
>>> from lfpypykit import CellGeometry, LaminarCurrentSourceDensity
>>> # cell geometry with three segments (μm)
>>> cell = CellGeometry(x=np.array([[0, 0], [0, 0], [0, 0]]),
>>>                      y=np.array([[0, 0], [0, 0], [0, 0]]),
>>>                      z=np.array([[0, 10], [10, 20], [20, 30]]),
>>>                      d=np.array([1, 1, 1]))
>>> # transmembrane currents, three time steps (nA)
```

(continues on next page)

(continued from previous page)

```

>>> I_m = np.array([[0., -1., 1.], [-1., 1., 0.], [1., 0., -1.]])
>>> # define geometry (z - upper and lower boundary; r - radius)
>>> # of cylindrical volumes aligned with the z-axis (μm)
>>> z = np.array([[-10., 0.], [0., 10.], [10., 20.],
>>>               [20., 30.], [30., 40.]])
>>> r = np.array([100., 100., 100., 100., 100.])
>>> # instantiate electrode, get linear response matrix
>>> csd = LaminarCurrentSourceDensity(cell=cell, z=z, r=r)
>>> M = csd.get_transformation_matrix()
>>> # compute current source density [nA/μm³]
>>> M @ I_m
array([[ 0.00000000e+00,  0.00000000e+00,  0.00000000e+00],
       [ 0.00000000e+00, -3.18309886e-06,  3.18309886e-06],
       [-3.18309886e-06,  3.18309886e-06,  0.00000000e+00],
       [ 3.18309886e-06,  0.00000000e+00, -3.18309886e-06],
       [ 0.00000000e+00,  0.00000000e+00,  0.00000000e+00]])

```

**get\_transformation\_matrix()**

Get linear response matrix

**Returns****response\_matrix:** ndarray shape (n\_volumes, n\_seg) ndarray**Raises****AttributeError** if cell is None

## 1.8.2 class VolumetricCurrentSourceDensity

**class** LFPy.VolumetricCurrentSourceDensity(cell, x=None, y=None, z=None, dl=1.0)

Bases: lfpypykit.models.LinearModel

Facilitates calculations of the ground truth Current Source Density (CSD) across 3D volumetric grid with bin edges defined by parameters x, y and z.

The implementation assumes piecewise constant current sources similar to `LineSourcePotential`, and accounts for the fraction of each segment's length within each volume by counting the number of points representing partial segments with max length `dl` divided by the number of partial segments.

This class is a `LinearModel` subclass that defines a 4D linear response matrix **M** of shape (x.size-1, y.size-1, z.size-1, n\_seg) between transmembrane current array **I** (nA) of a multicompartment neuron model and the corresponding CSD **C** (nA/μm³) as

$$\mathbf{C} = \mathbf{M}\mathbf{I}$$

The current **I** is an ndarray of shape (n\_seg, n\_steps) with unit (nA), and each row indexed by *j* of **C** represents the CSD in each bin for every time step as the sum of currents divided by the volume.

**Parameters****cell:** object or None CellGeometry instance or similar.**x, y, z:** ndarray, dtype=float shape (n, ) array of bin edges of each volume along each axis in units of (μm). Must be monotonously increasing.**dl:** float discretization length of compartments before binning (μm). Default=1. Lower values will result in more accurate estimates as each line source gets split into more points.



Raises

See also:

**LinearModel**

*LaminarCurrentSourceDensity*

## Notes

The resulting mapping *M* may be very sparse (i.e, mostly made up by zeros) and can be converted into a sparse array for more efficient multiplication for the same result:

```
>>> import scipy.sparse as ss
>>> M_csc = ss.csc_matrix(M.reshape((-1, M.shape[-1])))
>>> C = M_csc @ I_m
>>> np.all(C.reshape((M.shape[:-1] + (-1,))) == (M @ I_m))
True
```

## Examples

Mock cell geometry and transmembrane currents:

```
>>> import numpy as np
>>> from lfpykit import CellGeometry, VolumetricCurrentSourceDensity
>>> # cell geometry with three segments (μm)
>>> cell = CellGeometry(x=np.array([[0, 0], [0, 0], [0, 0]]),
>>>                      y=np.array([[0, 0], [0, 0], [0, 0]]),
>>>                      z=np.array([[0, 10], [10, 20], [20, 30]]),
>>>                      d=np.array([1, 1, 1]))
>>> # transmembrane currents, three time steps (nA)
>>> I_m = np.array([[0., -1., 1.], [-1., 1., 0.], [1., 0., -1.]])
>>> # instantiate probe, get linear response matrix
>>> csd = VolumetricCurrentSourceDensity(cell=cell,
>>>                                       x=np.linspace(-20, 20, 5),
>>>                                       y=np.linspace(-20, 20, 5),
>>>                                       z=np.linspace(-20, 20, 5), dl=1.)
>>> M = csd.get_transformation_matrix()
>>> # compute current source density [nA/μm3]
>>> M @ I_m
array([[[[ 0.,  0.,  0.],
          [ 0.,  0.,  0.],
          [ 0.,  0.,  0.],
          [ 0.,  0.,  0.]],
        ...
```

**get\_transformation\_matrix()**

Get linear response matrix

Returns

**response\_matrix:** ndarray shape (x.size-1, y.size-1, z.size-1, n\_seg) ndarray

Raises

**AttributeError** if cell is None

## 1.9 Misc.

### 1.9.1 submodule lfpcalc

Copyright (C) 2012 Computational Neuroscience Group, NMBU.

This program is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

### 1.9.2 submodule tools

Copyright (C) 2012 Computational Neuroscience Group, NMBU.

This program is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

`LFPy.tools.load(filename)`

Generic loading of cPickle objects from file

#### Parameters

**filename:** `str` path to pickle file

`LFPy.tools.noise_brown(ncols, nrows=1, weight=1.0, filter=None, filterargs=None)`

Return  $1/f^2$  noise of shape(nrows, ncols) obtained by taking the cumulative sum of gaussian white noise, with rms weight.

If filter is not None, this function will apply the filter coefficients obtained by:

```
>>> b, a = filter(**filterargs)
>>> signal = scipy.signal.lfilter(b, a, signal)
```

#### Parameters

**ncols:** `int`

**nrows:** `int`

**weight:** `float`

**filter:** `None` or `function`

**filterargs:** `**dict` parameters passed to *filter*

### 1.9.3 submodule `alias_method`

`LFPy.alias_method.alias_method(idx, probs, nsyn)`

Alias method for drawing random numbers from a discrete probability distribution. See <http://www.keithschwarz.com/darts-dice-coins/>

#### Parameters

**idx:** `np.ndarray` compartment indices as array of ints  
**probs:** `np.ndarray` compartment areas as array of floats  
**nsyn:** `int` number of randomized compartment indices

#### Returns

**out:** `np.ndarray` integer array of randomly drawn compartment indices

`LFPy.alias_method.alias_setup(probs)`

Set up function for alias method. See <http://www.keithschwarz.com/darts-dice-coins/>

#### Parameters

**probs:** `np.ndarray` float array of compartment areas

#### Returns

**J:** `np.ndarray` array of ints  
**q:** `np.ndarray` array of floats

### 1.9.4 submodule `inputgenerators`

Copyright (C) 2012 Computational Neuroscience Group, NMBU.

This program is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

`LFPy.inputgenerators.get_activation_times_from_distribution(n, tstart=0.0, tstop=1000000.0, distribution=<scipy.stats._continuous_distns.expon_gen object>, rvs_args={'loc': 0, 'scale': 1}, maxiter=1000000.0)`

Construct a length *n* list of ndarrays containing continuously increasing random numbers on the interval [*tstart*, *tstop*], with intervals drawn from a chosen continuous random variable distribution subclassed from `scipy.stats.rv_continuous`, e.g., `scipy.stats.expon` or `scipy.stats.gamma`.

The most likely initial first entry is `tstart + method.rvs(size=inf, **rvs_args).mean()`

#### Parameters

**n:** `int` number of ndarrays in list  
**tstart:** `float` minimum allowed value in ndarrays  
**tstop:** `float` maximum allowed value in ndarrays

**distribution: object** subclass of `scipy.stats.rv_continuous`. Distributions producing negative values should be avoided if continuously increasing values should be obtained, i.e., the probability density function (`distribution.pdf(**rvs_args)`) should be 0 for  $x < 0$ , which is not explicitly tested for.

**rvs\_args: dict** parameters for method.rvs method. If “size” is in dict, then tstop will be ignored, and each ndarray in output list will be `distribution.rvs(**rvs_args).cumsum() + tstart`. If size is not given in dict, then values up to tstop will be included

**maxiter: int** maximum number of iterations

#### Returns

**list of ndarrays** length n list of arrays containing data

#### Raises

**AssertionError** if distribution does not have the ‘rvs’ attribute

**StopIteration** if number of while-loop iterations reaches maxiter

### Examples

Create n sets of activation times with intervals drawn from the exponential distribution, with rate expectation  $\lambda = 10 \text{ s}^{-1}$  (thus  $\text{scale} = 1000 / \lambda$ ). Here we assume output in units of ms

```
>>> from LFPy.inputgenerators import get_activation_times_from_distribution
>>> import scipy.stats as st
>>> import matplotlib.pyplot as plt
>>> times = get_activation_times_from_distribution(n=10, tstart=0.,
>>>                                             tstop=1000.,
>>>                                             distribution=st.expon,
>>>                                             rvs_args=dict(loc=0.,
>>>                                             scale=100.))
```

## INDICES AND TABLES

- `genindex`
- `modindex`
- `search`



## BIBLIOGRAPHY

- [1] H. Linden, K. H. Pettersen, G. T. Einevoll (2010). Intrinsic dendritic filtering gives low-pass power spectra of local field potentials. *J Comput Neurosci*, 29:423–444. DOI: 10.1007/s10827-010-0245-4
- [1] Linden H, Hagen E, Leski S, Norheim ES, Pettersen KH, Einevoll GT (2014) LFPy: a tool for biophysical simulation of extracellular potentials generated by detailed model neurons. *Front. Neuroinform.* 7:41. doi: 10.3389/fninf.2013.00041
- [2] Hagen E, Næss S, Ness TV and Einevoll GT (2018) Multimodal Modeling of Neural Network Activity: Computing LFP, ECoG, EEG, and MEG Signals With LFPy 2.0. *Front. Neuroinform.* 12:92. doi: 10.3389/fninf.2018.00092
- [1] Linden H, Hagen E, Leski S, Norheim ES, Pettersen KH, Einevoll GT (2014) LFPy: a tool for biophysical simulation of extracellular potentials generated by detailed model neurons. *Front. Neuroinform.* 7:41. doi: 10.3389/fninf.2013.00041
- [2] Hagen E, Næss S, Ness TV and Einevoll GT (2018) Multimodal Modeling of Neural Network Activity: Computing LFP, ECoG, EEG, and MEG Signals With LFPy 2.0. *Front. Neuroinform.* 12:92. doi: 10.3389/fninf.2018.00092
- [1] Ness, T. V., Chintaluri, C., Potworowski, J., Leski, S., Glabska, H., Wojcik, D. K., et al. (2015). Modelling and analysis of electrical potentials recorded in microelectrode arrays (MEAs). *Neuroinformatics* 13:403–426. doi: 10.1007/s12021-015-9265-6
- [2] Linden H, Hagen E, Leski S, Norheim ES, Pettersen KH, Einevoll GT (2014) LFPy: a tool for biophysical simulation of extracellular potentials generated by detailed model neurons. *Front. Neuroinform.* 7:41. doi: 10.3389/fninf.2013.00041
- [3] Hagen E, Næss S, Ness TV and Einevoll GT (2018) Multimodal Modeling of Neural Network Activity: Computing LFP, ECoG, EEG, and MEG Signals With LFPy 2.0. *Front. Neuroinform.* 12:92. doi: 10.3389/fninf.2018.00092
- [1] Ness, T. V., Chintaluri, C., Potworowski, J., Leski, S., Glabska, H., Wojcik, D. K., et al. (2015). Modelling and analysis of electrical potentials recorded in microelectrode arrays (MEAs). *Neuroinformatics* 13:403–426. doi: 10.1007/s12021-015-9265-6
- [1] Shaozhong Deng (2008), *Journal of Electrostatics* 66:549-560. DOI: 10.1016/j.elstat.2008.06.003
- [1] Shaozhong Deng (2008), *Journal of Electrostatics* 66:549-560. DOI: 10.1016/j.elstat.2008.06.003
- [1] Shaozhong Deng (2008), *Journal of Electrostatics* 66:549-560. DOI: 10.1016/j.elstat.2008.06.003
- [1] Nunez and Srinivasan, Oxford University Press, 2006
- [1] Næss S, Chintaluri C, Ness TV, Dale AM, Einevoll GT and Wójcik DK (2017) Corrected Four-sphere Head Model for EEG Signals. *Front. Hum. Neurosci.* 11:490. doi: 10.3389/fnhum.2017.00490
- [2] Hagen E, Næss S, Ness TV and Einevoll GT (2018) Multimodal Modeling of Neural Network Activity: Computing LFP, ECoG, EEG, and MEG Signals With LFPy 2.0. *Front. Neuroinform.* 12:92. doi: 10.3389/fninf.2018.00092

- [1] Huang, Parra, Haufe (2016) The New York Head—A precise standardized volume conductor model for EEG source localization and tES targeting. *Neuroimage* 140:150–162. doi: 10.1016/j.neuroimage.2015.12.019
- [2] Naess et al. (2020) Biophysical modeling of the neural origin of EEG and MEG signals. *bioRxiv* 2020.07.01.181875. doi: 10.1101/2020.07.01.181875
- [1] Nunez and Srinivasan, Oxford University Press, 2006
- [1] Blagoev et al. (2007) Modelling the magnetic signature of neuronal tissue. *NeuroImage* 37 (2007) 137–148 DOI: 10.1016/j.neuroimage.2007.04.033
- [1] Hämmäläinen M., et al., *Reviews of Modern Physics*, Vol. 65, No. 2, April 1993.
- [2] Sarvas J., *Phys.Med. Biol.*, 1987, Vol. 32, No 1, 11-22.
- [1] Blagoev et al. (2007) Modelling the magnetic signature of neuronal tissue. *NeuroImage* 37 (2007) 137–148 DOI: 10.1016/j.neuroimage.2007.04.033
- [1] Pettersen KH, Hagen E, Einevoll GT (2008) Estimation of population firing rates and current source densities from laminar electrode recordings. *J Comput Neurosci* (2008) 24:291–313. DOI 10.1007/s10827-007-0056-4
- [2] Hagen E, Fossum JC, Pettersen KH, Alonso JM, Swadlow HA, Einevoll GT (2017) *Journal of Neuroscience*, 37(20):5123-5143. DOI: <https://doi.org/10.1523/JNEUROSCI.2715-16.2017>



## PYTHON MODULE INDEX

|

LFPy, [9](#)

LFPy.alias\_method, [87](#)

LFPy.inputgenerators, [87](#)

LFPy.lfpcalc, [86](#)

LFPy.tools, [86](#)



## A

alias\_method() (in module *LFPy.alias\_method*), 87  
alias\_setup() (in module *LFPy.alias\_method*), 87

## C

calc\_potential() (*LFPy.OneSphereVolumeConductor* method), 68  
calculate\_B() (*LFPy.InfiniteHomogeneousVolCondMEG* method), 78  
calculate\_B() (*LFPy.SphericallySymmetricVolCondMEG* method), 81  
calculate\_H() (*LFPy.InfiniteHomogeneousVolCondMEG* method), 78  
calculate\_H() (*LFPy.SphericallySymmetricVolCondMEG* method), 81  
calculate\_H\_from\_iaxial() (*LFPy.InfiniteHomogeneousVolCondMEG* method), 78  
calculate\_H\_from\_iaxial() (*LFPy.SphericallySymmetricVolCondMEG* method), 81  
Cell (class in *LFPy*), 11  
cellpickler() (*LFPy.Cell* method), 12  
cellpickler() (*LFPy.NetworkCell* method), 34  
cellpickler() (*LFPy.TemplateCell* method), 23  
chiral\_morphology() (*LFPy.Cell* method), 12  
chiral\_morphology() (*LFPy.NetworkCell* method), 34  
chiral\_morphology() (*LFPy.TemplateCell* method), 23  
collect\_current() (*LFPy.StimIntElectrode* method), 48  
collect\_current() (*LFPy.Synapse* method), 46  
collect\_potential() (*LFPy.StimIntElectrode* method), 48  
collect\_potential() (*LFPy.Synapse* method), 46  
connect() (*LFPy.Network* method), 48  
create\_population() (*LFPy.Network* method), 50  
create\_spike\_detector() (*LFPy.NetworkCell* method), 34  
create\_synapse() (*LFPy.NetworkCell* method), 35  
CurrentDipoleMoment (class in *LFPy*), 53

## D

distort\_cell\_geometry() (*LFPy.RecMEAElectrode* method), 66  
distort\_geometry() (*LFPy.Cell* method), 12  
distort\_geometry() (*LFPy.NetworkCell* method), 35  
distort\_geometry() (*LFPy.TemplateCell* method), 23  
draw\_rand\_pos() (*LFPy.NetworkPopulation* method), 52

## E

enable\_extracellular\_stimulation() (*LFPy.Cell* method), 13  
enable\_extracellular\_stimulation() (*LFPy.Network* method), 50  
enable\_extracellular\_stimulation() (*LFPy.NetworkCell* method), 35  
enable\_extracellular\_stimulation() (*LFPy.TemplateCell* method), 24

## F

find\_closest\_electrode() (*LFPy.NYHeadModel* method), 75  
FourSphereVolumeConductor (class in *LFPy*), 72

## G

get\_activation\_times\_from\_distribution() (in module *LFPy.inputgenerators*), 87  
get\_axial\_currents\_from\_vmem() (*LFPy.Cell* method), 13  
get\_axial\_currents\_from\_vmem() (*LFPy.NetworkCell* method), 36  
get\_axial\_currents\_from\_vmem() (*LFPy.TemplateCell* method), 24  
get\_axial\_resistance() (*LFPy.Cell* method), 14  
get\_axial\_resistance() (*LFPy.NetworkCell* method), 36  
get\_axial\_resistance() (*LFPy.TemplateCell* method), 25  
get\_closest\_idx() (*LFPy.Cell* method), 14  
get\_closest\_idx() (*LFPy.NetworkCell* method), 36  
get\_closest\_idx() (*LFPy.TemplateCell* method), 25

`get_connectivity_rand()` (*LFPy.NetworkCell method*), 51

`get_dict_of_children_idx()` (*LFPy.Cell method*), 14

`get_dict_of_children_idx()` (*LFPy.NetworkCell method*), 37

`get_dict_of_children_idx()` (*LFPy.TemplateCell method*), 25

`get_dict_parent_connections()` (*LFPy.Cell method*), 14

`get_dict_parent_connections()` (*LFPy.NetworkCell method*), 37

`get_dict_parent_connections()` (*LFPy.TemplateCell method*), 25

`get_dipole_potential()` (*LFPy.FourSphereVolumeConductor method*), 73

`get_dipole_potential()` (*LFPy.InfiniteVolumeConductor method*), 71

`get_dipole_potential_from_multi_dipoles()` (*LFPy.FourSphereVolumeConductor method*), 73

`get_idx()` (*LFPy.Cell method*), 14

`get_idx()` (*LFPy.NetworkCell method*), 37

`get_idx()` (*LFPy.TemplateCell method*), 25

`get_idx_children()` (*LFPy.Cell method*), 15

`get_idx_children()` (*LFPy.NetworkCell method*), 37

`get_idx_children()` (*LFPy.TemplateCell method*), 26

`get_idx_name()` (*LFPy.Cell method*), 15

`get_idx_name()` (*LFPy.NetworkCell method*), 38

`get_idx_name()` (*LFPy.TemplateCell method*), 26

`get_idx_parent_children()` (*LFPy.Cell method*), 15

`get_idx_parent_children()` (*LFPy.NetworkCell method*), 38

`get_idx_parent_children()` (*LFPy.TemplateCell method*), 26

`get_idx_polygons()` (*LFPy.Cell method*), 15

`get_idx_polygons()` (*LFPy.NetworkCell method*), 38

`get_idx_polygons()` (*LFPy.TemplateCell method*), 26

`get_intersegment_distance()` (*LFPy.Cell method*), 16

`get_intersegment_distance()` (*LFPy.NetworkCell method*), 38

`get_intersegment_distance()` (*LFPy.TemplateCell method*), 27

`get_intersegment_vector()` (*LFPy.Cell method*), 16

`get_intersegment_vector()` (*LFPy.NetworkCell method*), 39

`get_intersegment_vector()` (*LFPy.TemplateCell method*), 27

`get_multi_current_dipole_moments()` (*LFPy.Cell method*), 16

`get_multi_current_dipole_moments()` (*LFPy.NetworkCell method*), 39

`get_multi_current_dipole_moments()` (*LFPy.TemplateCell method*), 27

`get_multi_dipole_potential()` (*LFPy.InfiniteVolumeConductor method*), 71

`get_pt3d_polygons()` (*LFPy.Cell method*), 17

`get_pt3d_polygons()` (*LFPy.NetworkCell method*), 39

`get_pt3d_polygons()` (*LFPy.TemplateCell method*), 28

`get_rand_idx_area_and_distribution_norm()` (*LFPy.Cell method*), 17

`get_rand_idx_area_and_distribution_norm()` (*LFPy.NetworkCell method*), 40

`get_rand_idx_area_and_distribution_norm()` (*LFPy.TemplateCell method*), 28

`get_rand_idx_area_norm()` (*LFPy.Cell method*), 18

`get_rand_idx_area_norm()` (*LFPy.NetworkCell method*), 41

`get_rand_idx_area_norm()` (*LFPy.TemplateCell method*), 29

`get_rand_prob_area_norm()` (*LFPy.Cell method*), 18

`get_rand_prob_area_norm()` (*LFPy.NetworkCell method*), 41

`get_rand_prob_area_norm()` (*LFPy.TemplateCell method*), 29

`get_rand_prob_area_norm_from_idx()` (*LFPy.Cell method*), 19

`get_rand_prob_area_norm_from_idx()` (*LFPy.NetworkCell method*), 41

`get_rand_prob_area_norm_from_idx()` (*LFPy.TemplateCell method*), 30

`get_transformation_matrix()` (*LFPy.CurrentDipoleMoment method*), 54

`get_transformation_matrix()` (*LFPy.FourSphereVolumeConductor method*), 74

`get_transformation_matrix()` (*LFPy.InfiniteHomogeneousVolCondMEG method*), 79

`get_transformation_matrix()` (*LFPy.InfiniteVolumeConductor method*), 72

`get_transformation_matrix()` (*LFPy.LaminarCurrentSourceDensity method*), 84

`get_transformation_matrix()` (*LFPy.LineSourcePotential method*), 57

`get_transformation_matrix()` (*LFPy.NYHeadModel method*), 75

`get_transformation_matrix()` (*LFPy.OneSphereVolumeConductor method*), 68

`get_transformation_matrix()`

(*LFPy.PointSourcePotential* method), 56  
*get\_transformation\_matrix()*  
 (*LFPy.RecExtElectrode* method), 63  
*get\_transformation\_matrix()*  
 (*LFPy.RecMEAElectrode* method), 66  
*get\_transformation\_matrix()*  
 (*LFPy.SphericallySymmetricVolCondMEG*  
*method*), 82  
*get\_transformation\_matrix()*  
 (*LFPy.VolumetricCurrentSourceDensity*  
*method*), 85

## I

*InfiniteHomogeneousVolCondMEG* (class in *LFPy*), 76  
*InfiniteVolumeConductor* (class in *LFPy*), 70  
*insert\_v\_ext()* (*LFPy.Cell* method), 19  
*insert\_v\_ext()* (*LFPy.NetworkCell* method), 41  
*insert\_v\_ext()* (*LFPy.TemplateCell* method), 30

## L

*LaminarCurrentSourceDensity* (class in *LFPy*), 83  
*LFPy*  
 module, 9  
*LFPy.alias\_method*  
 module, 87  
*LFPy.inputgenerators*  
 module, 87  
*LFPy.lfpcalc*  
 module, 86  
*LFPy.tools*  
 module, 86  
*LineSourcePotential* (class in *LFPy*), 56  
*load()* (in module *LFPy.tools*), 86

## M

module  
*LFPy*, 9  
*LFPy.alias\_method*, 87  
*LFPy.inputgenerators*, 87  
*LFPy.lfpcalc*, 86  
*LFPy.tools*, 86

## N

*Network* (class in *LFPy*), 48  
*NetworkCell* (class in *LFPy*), 33  
*NetworkPopulation* (class in *LFPy*), 52  
*noise\_brown()* (in module *LFPy.tools*), 86  
*NYHeadModel* (class in *LFPy*), 75

## O

*OneSphereVolumeConductor* (class in *LFPy*), 67

## P

*PointProcess* (class in *LFPy*), 44

*PointSourcePotential* (class in *LFPy*), 54

## R

*RecExtElectrode* (class in *LFPy*), 58  
*RecMEAElectrode* (class in *LFPy*), 63  
*return\_closest\_idx()* (*LFPy.NYHeadModel*  
*method*), 76  
*rotate\_dipole\_to\_surface\_normal()*  
 (*LFPy.NYHeadModel* method), 76

## S

*set\_dipole\_pos()* (*LFPy.NYHeadModel* method), 76  
*set\_point\_process()* (*LFPy.Cell* method), 20  
*set\_point\_process()* (*LFPy.NetworkCell* method), 42  
*set\_point\_process()* (*LFPy.TemplateCell* method),  
 31  
*set\_pos()* (*LFPy.Cell* method), 20  
*set\_pos()* (*LFPy.NetworkCell* method), 43  
*set\_pos()* (*LFPy.TemplateCell* method), 31  
*set\_rotation()* (*LFPy.Cell* method), 20  
*set\_rotation()* (*LFPy.NetworkCell* method), 43  
*set\_rotation()* (*LFPy.TemplateCell* method), 31  
*set\_spike\_times()* (*LFPy.Synapse* method), 46  
*set\_spike\_times\_w\_netstim()* (*LFPy.Synapse*  
*method*), 46  
*set\_synapse()* (*LFPy.Cell* method), 20  
*set\_synapse()* (*LFPy.NetworkCell* method), 43  
*set\_synapse()* (*LFPy.TemplateCell* method), 31  
*simulate()* (*LFPy.Cell* method), 21  
*simulate()* (*LFPy.Network* method), 51  
*simulate()* (*LFPy.NetworkCell* method), 43  
*simulate()* (*LFPy.TemplateCell* method), 32  
*SphericallySymmetricVolCondMEG* (class in *LFPy*),  
 80  
*StimIntElectrode* (class in *LFPy*), 46  
*strip\_hoc\_objects()* (*LFPy.Cell* method), 21  
*strip\_hoc\_objects()* (*LFPy.NetworkCell* method), 44  
*strip\_hoc\_objects()* (*LFPy.TemplateCell* method),  
 32  
*Synapse* (class in *LFPy*), 45

## T

*TemplateCell* (class in *LFPy*), 22

## U

*update\_pos()* (*LFPy.PointProcess* method), 44

## V

*VolumetricCurrentSourceDensity* (class in *LFPy*),  
 84