NNGT Documentation

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User Documentation

CHAPTER 1

Overview

The Neural Network Growth and Topology (NNGT) module provides tools to grow and study detailed biological networks by interfacing efficient graph libraries with highly distributed activity simulators.

Main classes

NNGT uses four main classes:

`Graph` provides a simple implementation over graphs objects from graph libraries (namely the addition of a name, management of detailed nodes and connection properties, and simple access to basic graph measurements).

`SpatialGraph` a Graph embedded in space (neurons have positions and connections are associated to a distance)

`Network` provides more detailed characteristics to emulate biological neural networks, such as classes of inhibitory and excitatory neurons, synaptic properties...

`SpatialNetwork` combines spatial embedding and biological properties

Generation of graphs

Structured connectivity: connectivity between the nodes can be chosen from various well-known graph models

Populations: populations of neurons are distributed afterwards on the structured connectivity, and can be set to respect various constraints (for instance a given fraction of inhibitory neurons and synapses)

Synaptic properties: synaptic weights and delays can be set from various distributions or correlated to edge properties

Interacting with NEST

The generated graphs can be used to easily create complex networks using the NEST simulator, on which you can then simulate their activity.

CHAPTER 2

The docs

Installation

Dependencies

This package depends on several libraries (the number varies according to which modules you want to use).

Basic dependencies

Regardless of your needs, the following libraries are required:

- numpy
- scipy
- graph_tool
- or igraph
- or networkx

Additionnal dependencies

- matplotlib (optional but will limit the functionalities if not present)
- *peewee* for database features

Note: If they are not present on your computer, *pip* will directly try to install the three first libraries, however:

- lapack is necessary for *scipy* and *pip* cannot install it on its own
- you will have to install the graph library yourself (only *networkx* can be installed directly using *pip*)

Simple install

Linux

Install the requirements (through `aptitude` or `apt-get` on debian/ubuntu/mint, `pacman` and `yaourt` on arch-based distributions, or your *.rpm* manager on fedora. Otherwise you can also install the latest versions via *pip*:

```
sudo pip install numpy scipy matplotlib networkx
```

Under most linux distributions, the simplest way is to install pip and git, then simply type into a terminal:

```
sudo pip install git+https://github.com/Silmathoron/NNGT.git
```

Mac

I recommend using Macports with which you can install all required features to use *NEST* and *NNGT* with *graph-tool*. The following command lines are used with *python 2.7* since it is what people are used to but I recommend using version *3.5* or higher (replace all 27/2.7 by 35/3.5).

```
sudo port select gcc mp-gcc5 && sudo port install gsl +gcc5 && sudo port install␣
↪autoconf automake libtool && sudo port install python27 pip && sudo port select␣
↪python python27 && sudo port install py27-cython && sudo port select cython␣
↪cython27 && sudo port install py27-numpy py27-scipy py27-matplotlib py27-ipython &&␣
↪sudo port select ipython ipython-2.7 && sudo port install py-graph-tool gtk3
```

Windows

It's the same as linux for windows users once you've installed Python and *pip*, but NEST won't work anyway...

Note: *igraph* can be installed on windows if you need something faster than *networkx*.

Local install

If you want to modify the library more easily, you can also install it locally, then simply add it to your `PYTHONPATH` environment variable:

```
cd && mkdir .nngt-install
cd .nngt-install
git clone https://github.com/Silmathoron/NNGT.git .
git submodule init
git submodule update
nano .bash_profile
```

Then add:

```
export PYTHONPATH="/path/to/your/home/.nngt-install/src/:PYTHONPATH"
```

In order to update your local repository to keep it up to date, you will need to run the two following commands:

```
git pull origin master
git submodule update --remote --merge
```

Configuration

The configuration file is created in `~/.nngt/nngt.conf` after you first run `import nngt` in *python*. Here is the default file:

```
#-------------------------#
# NNGT configuration file #
#-------------------------#

version = 0.7

#-------------------------
## default graph library ------------------------------------------------------
#-------------------------

# (choose among "graph-tool", "igraph", "networkx")

graph_library = graph-tool


#---------------------
## Try to load NEST? -----------------------------------------------------------
#---------------------

load_nest = True


#----------------------
## Matplotlib backend ----------------------------------------------------------
#----------------------

# Uncomment and choose among your available backends.
# See http://matplotlib.org/faq/usage_faq.html#what-is-a-backend for details

#mpl_backend = Qt5Agg

# use TeX rendering for axis labels
use_tex = False

# color library either matplotlib or seaborn
color_lib = matplotlib

# palette to use
palette = Set1


#-----------------------------
## Settings for database    -------------------------------------------------
#-----------------------------

use_database = False

# use a database (if False, results will be stored in CSV files)
db_to_file = False
#db_folder = ~/.nngt/database

# database url or temporary database used if use_database = False
# example of real database url: db_url = mysql://user:password@host:port/my_db
```

```
db_url = mysql:///nngt_db


#------------------------------
## Settings for data logging --------------------------------------------------
#------------------------------

# which messages are printed? (see logging module levels:
# https://docs.python.org/2/library/logging.html#levels)
# set to WARNING or above to remove the messages on import
log_level = INFO

# write log to file?
log_to_file = False
# if True, write to default folder '~/.nngt/log'
#log_folder = ~/.nngt/log


#-----------------------------
## Multithreaded algorithms ---------------------------------------------------
#-----------------------------

# C++ algorithms using OpenMP are compiled and imported using Cython if True,
# otherwise regular numpy/scipy algorithms are used (equivalent for one thread)

multithreading = False
```

It can be necessary to modify this file to use the desired graph library, but mostly to correct problems with GTK and matplotlib (if the *plot* module complains, try `Gtk3Agg` and `Qt4Agg`).

Using NEST

If you want to simulate activities on your complex networks, NNGT can directly interact with the NEST simulator to implement the network inside *PyNEST*. For this, you will need to install NEST with Python bindings, which requires:

- the python headers (*python-dev* package on debian-based distribs)
- *autoconf*
- *automake*
- *libtool*
- *libltdl*
- *libncurses*
- *readlines*
- *gsl* (the GNU Scientific Library) for many neuronal models

Introduction

Yet another graph library?

It is not ;)

This library is based on existing graph libraries (such as graph_tool, igraph, networkx, and possibly soon SNAP) and acts as a convenient interface to build various networks from efficient and verified algorithms.

Moreover, it also acts as an interface between those graph libraries and the NEST simulator.

For users that are in a hurry, you can go directly to the Tutorial section. Specific examples are also detailed in the following sections:

Graph generation

Principle

In order to keep the code as generic and easy to maintain as possible, the generation of graphs or networks is divided in several steps:

- **Structured connectivity:** a simple graph is generated as an assembly of nodes and edges, without any biological properties. This allows us to implement known graph-theoretical algorithms in a straightforward fashion.
- **Populations:** detailed properties can be implemented, such as inhibitory synapses and separation of the neurons into inhibitory and excitatory populations – these can be done while respecting user-defined constraints.
- **Synaptic properties:** eventually, synaptic properties such as weight/strength and delays can be added to the network.

Modularity

The library as been designed so that these various operations can be realized in any order!

Juste to get work on a topological graph/network:

1. Create graph class
2. Connect
3. Set connection weights (optional)
4. Spatialize (optional)
5. Set types (optional: to use with NEST)

To work on a really spatially embedded graph/network:

1. Create spatial graph/network
2. Connect (can depend on positions)
3. Set connection weights (optional, can depend on positions)
4. Set types (optional)

Or to model a complex neural network in NEST:

1. Create spatial network (with space and neuron types)
2. Connect (can depend on types and positions)
3. Set connection weights and types (optional, can depend on types and positions)

Setting weights

The weights can be either user-defined or generated by one of the available distributions (MAKE A REF). User-defined weights are generated via:

- a list of edges
- a list of weights

Pre-defined distributions require the following variables:

- a distribution name ("constant", "gaussian"...)
- a dictionary containing the distribution properties
- an optional attribute for distributions that are correlated to another (e.g. the distances between neurons)
- a optional value defining the variance of the Gaussian noise that should be applied on the weights

There are several ways of settings the weights of a graph which depend on the time at which you assign them.

At graph creation You can define the weights by entering a `weight_prop` argument to the constructor; this should be a dictionary containing at least the name of the weight distribution: `{"distrib": "distribution_name"}`. If entered, this will be stored as a graph property and used to assign the weights whenever new edges are created unless you specifically assign rules for those new edges' weights.

At any given time You can use the `Connections` class to set the weights of a `graph` explicitely by using:

```
>>> nngt.Connections.weights(graph, elist=edges_to_weigh, distrib="distrib_of_
↪choice", ...)
```

Examples

```
import nngt
import nngt.generation as ng
```

Simple generation

```
num_nodes = 1000
degree = 25

# random graphs
g1 = ng.erdos_renyi(num_nodes, avg_deg=degree)
g2 = ng.erdos_renyi(num_nodes, avg_deg=degree, directed=False)  # the same graph
                                                                 # but undirected

# 2-step generation of a scale-free with Gaussian weight distribution

w = {
    "distribution": "gaussian",
    "distrib_prop": {"avg": 60., "std":5.}
}
g3 = nngt.Graph(num_nodes, weights=w)
ng.random_scale_free(2.2, 2.9, from_graph=g3)

# same in 1 step
g4 = ng.random_scale_free(2.2, 2.9, nodes=num_nodes, weights=w)
```

Networks composed of heterogeneous groups

```
num_nodes = 1000


'''
Make the population
'''

# two groups of neurons
g1 = nngt.NeuralGroup(500)   # neurons 0 to 499
g2 = nngt.NeuralGroup(500)   # neurons 500 to 999

# make population (without NEST models)
pop = nngt.NeuralPop.from_groups(
    (g1, g2), ("left", "right"), with_models=False)

# create network from this population
net = nngt.Network(population=pop)


'''
Connect the groups
'''

# inter-groups (Erdos-Renyi)
prop_er1 = {"density": 0.005}
ng.connect_neural_groups(net, "left", "right", "erdos_renyi", prop_er1)

# intra-groups (Newman-Watts)
prop_nw = {
    "coord_nb": 20,
    "proba_shortcut": 0.1
}

ng.connect_neural_groups(net, "left", "left", "newman_watts", prop_nw)
ng.connect_neural_groups(net, "right", "right", "newman_watts", prop_nw)
```

Use with NEST

Generating a network with excitatory and inhibitory neurons:

```
# 800 excitatory neurons, 200 inhibitory
net = nngt.Network.ei_network(num_nodes, ei_ratio=0.2)

'''
Connect the populations.
'''
# exc -> inhib (Erdos-Renyi)
prop_er1 = {"density": 0.035}
ng.connect_neural_types(net, 1, -1, "erdos_renyi", prop_er1)

# exc -> exc (Newmann-Watts)
prop_nw = {
    "coord_nb": 10,
    "proba_shortcut": 0.1
}
ng.connect_neural_types(net, 1, 1, "newman_watts", prop_nw)

# inhib -> exc (Random scale-free)
prop_rsf = {
    "in_exp": 2.1,
    "out_exp": 2.6,
    "density": 0.2
}
ng.connect_neural_types(net, -1, 1, "random_scale_free", prop_rsf)

# inhib -> inhib (Erdos-Renyi)
prop_er2 = { "density": 0.04 }
ng.connect_neural_types(net, -1, -1, "erdos_renyi", prop_er2)
```

Send the network to NEST:

```
import nest
from nngt.simulation import monitor_groups, plot_activity, set_poisson_input

'''
Prepare the network and devices.
'''
# send to NEST,
gids = net.to_nest()
# excite
set_poisson_input(gids, rate=100000.)
# record
groups = [key for key in net.population]
recorder, record = monitor_groups(groups, net)

'''
Simulate and plot.
'''
simtime = 100.
nest.Simulate(simtime)

plot_activity(
    recorder, record, network=net, show=True, hist=False,
    limits=(0,simtime))
```

Advanced examples

Receptor ports in NEST

Some models, such as multisynaptic neurons, or advanced models incorporating various neurotransmitters use an additional information, called `"port"` to identify the synapse that will be used by the `nest.Connect` method. These models can also be used with NNGT by telling the `NeuralGroup` which type of port the neuron should try to bind to.

NB: the port is specified in the **source** neuron and declares which synapse of the **target** neuron is concerned.

```
'''
Build a network with two populations:
* excitatory (80%)
* inhibitory (20%)
```

```
'''
num_neurons = 50   # number of neurons
avg_degree  = 20   # average number of neighbours
std_degree  = 3    # deviation for the Gaussian graph

# parameters
neuron_model = "ht_neuron"      # hill-tononi model
exc_syn = {'receptor_type': 1}  # 1 is 'AMPA' in this model
inh_syn = {'receptor_type': 3}  # 3 is 'GABA_A' in this model

pop = nngt.NeuralPop.exc_and_inhib(
    num_neurons, en_model=neuron_model, in_model=neuron_model,
    es_param=exc_syn, is_param=inh_syn)

# create the network and send it to NEST
w_prop = {"distribution": "gaussian", "avg": 1., "std": .2}
net = nngt.generation.gaussian_degree(
    avg_degree, std_degree, population=pop, weights=w_prop)

'''
Send to NEST and set excitation and recorders
'''
import nest
from nngt.simulation import monitor_groups, plot_activity, set_noise

gids = net.to_nest()

# add noise to the excitatory neurons
excs = list(pop["excitatory"].nest_gids)
set_noise(excs, 10., 2.)

# record
groups = [key for key in net.population]
recorder, record = monitor_groups(groups, net)

'''
Simulate and plot.
'''
simtime = 2000.
nest.Simulate(simtime)

plot_activity(
    recorder, record, network=net, show=True, hist=False,
    limits=(0, simtime))
```

Properties of graph components

Warning: This section is not up to date anymore!

Components

In the graph libraries used by NNGT, the main components of a graph are *nodes* (also called *vertices* in graph theory), which correspond to *neurons* in neural networks, and *edges*, which link *nodes* and correspond to synaptic connections between neurons in biology.

The library supposes for now that nodes/neurons and edges/synapses are always added and never removed. Because of this, we can attribute indices to the nodes and the edges which will be directly related to the order in which they have been created (the first node will have index 0, .

Node properties

If you are just working with basic graphs (for instance looking at the influence of topology with purely excitatory networks), then your nodes do not need to have properties. This is the same if you consider only the average effect of inhibitory neurons by including inhibitory connections between the neurons but not a clear distinction between populations of purely excitatory and purely inhibitory neurons. To model more realistic networks, however, you might want to define these two types of populations and connect them in specific ways.

Two types of node properties

In the library, there is a difference between:

- spatial properties (the positions of the neurons), which are stored in a specific `numpy.array`,
- biological/group properties, which define assemblies of nodes sharing common properties, and are stored inside a `NeuralPop` object.

Biological/group properties

Note: All biological/group properties are stored in a `NeuralPop` object inside a *`Network`* instance (let us call it `graph` in this example); this attribute can be accessed using `graph.population`. `NeuralPop` objects can also be created from a *`Graph`* or *`SpatialGraph`* but they will not be stored inside the object.

The `NeuralPop` class allows you to define specific groups of neurons (described by a `NeuralGroup`). Once these populations are defined, you can constrain the connections between those populations. If the connectivity already exists, you can use the `GroupProperties` class to create a population with groups that respect specific constraints.

Warning: The implementation of this library has been optimized for generating an arbitrary number of neural populations where neurons share common properties; this implies that accessing the properties of one specific neuron will take O(N) operations, where N is the number of neurons. This might change in the future if such operations are judged useful enough.

Edge properties

In the library, there is a difference between the (synaptic) weights and types (excitatory or inhibitory) and the other biological properties (delays, synaptic models and synaptic parameters). This is because the weights and types are directly involved in many measurements in graph theory and are therefore directly stored inside the *`GraphObject`*.

Activity analysis

Principle

The interesting fact about having a link between the graph and the simulation is that you can easily analyze the activity be taking into account what you know from the graph structure.

Sorted rasters

Rater plots can be sorted depending on some specific node property, e.g. the degree or the betweenness:

```
import nest

import nngt
from nngt.simulation import monitor_nodes, plot_activity

pop = nngt.NeuralPop.uniform(1000, neuron_model="aeif_psc_alpha")
net = nngt.generation.gaussian_degree(100, 20, population=pop)

nodes = net.to_nest()
recorders, recordables = monitor_nodes(nodes)
simtime = 1000.
nest.Simulate(simtime)

fignums = plot_activity(
    recorders, recordables, network=net, show=True, hist=False,
    limits=(0.,simtime), sort="in-degree")
```

Activity properties

NNGT can also be used to analyze the general properties of a raster.

Either from a .gdf file containing the raster data

```
import nngt
from nngt.simulation import analyze_raster

a = analyze_raster("path/to/raster.gdf")
print(a.phases)
print(a.properties)
```

Or from a spike detector gid `sd`:

```
a = analyze_raster(sd)
```

Simulation module

Module to interact easily with the NEST simulator. It allows to:

- build a NEST network from *`Network`* or *`SpatialNetwork`* objects,
- monitor the activity of the network (taking neural groups into account)
- plot the activity while separating the behaviours of predefined neural groups

Content

nngt.simulation.ActivityRecord(spike_data, ...)	Class to record the properties of the simulated activity.
nngt.simulation.activity_types(...[, ...])	Analyze the spiking pattern of a neural network.
nngt.simulation.analyze_raster([raster, ...])	Return the activity types for a given raster.
nngt.simulation.get_nest_adjacency([...])	Get the adjacency matrix describing a NEST network.
nngt.simulation.get_recording(network, record)	Return the evolution of some recorded values for each neuron.
nngt.simulation.make_nest_network(network[, ...])	Create a new network which will be filled with neurons and connector objects to reproduce the topology from the initial network.
nngt.simulation.monitor_groups(group_names, ...)	Monitoring the activity of nodes in the network.
nngt.simulation.monitor_nodes(gids[, ...])	Monitoring the activity of nodes in the network.
nngt.simulation.plot_activity([...])	Plot the monitored activity.
nngt.simulation.randomize_neural_states(...)	Randomize the neural states according to the instructions.
nngt.simulation.raster_plot(times, senders)	Plotting routine that constructs a raster plot along with an optional histogram.
nngt.simulation.reproducible_weights(...[, ...])	Find the values of the connection weights that will give PSP responses of *min_weight* and *max_weight* in mV.
nngt.simulation.save_spikes(filename[, ...])	Plot the monitored activity.
nngt.simulation.set_minis(network, base_rate)	Mimick spontaneous release of neurotransmitters, called spontaneous PSCs or "minis".
nngt.simulation.set_noise(gids, mean, std)	Submit neurons to a current white noise.
nngt.simulation.set_poisson_input(gids, rate)	Submit neurons to a Poissonian rate of spikes.
nngt.simulation.set_step_currents(gids, ...)	Set step-current excitations

Details

Main functions to send `Network` instances to NEST, as well as helper functions to excite or record the network activity.

class `nngt.simulation.`**`ActivityRecord`**(*spike_data*, *phases*, *properties*, *parameters=None*)

Class to record the properties of the simulated activity.

Initialize the instance using *spike_data* (store proxy to an optional *network*) and compute the properties of provided data.

Parameters

- **spike_data** (*2D array*) – Array of shape (num_spikes, 2), containing the senders on the 1st row and the times on the 2nd row.
- **phases** (*dict*) – Limits of the different phases in the simulated period.
- **properties** (*dict*) – Values of the different properties of the activity (e.g. "firing_rate", "IBI"...).
- **parameters** (*dict, optional (default: None)*) – Parameters used to compute the phases.

Note: The firing rate is computed as num_spikes / total simulation time, the period is the sum of an IBI and a bursting period.

data
Returns the (N, 2) array of (senders, spike times).

phases
Return the phases detected –

- "bursting" for periods of high activity where a large fraction of the network is recruited.
- "quiescent" for periods of low activity
- "mixed" for firing rate in between "quiescent" and "bursting".
- "localized" for periods of high activity but where only a small fraction of the network is recruited.

Note: See *parameters* for details on the conditions used to differenciate these phases.

properties
Returns the properties of the activity. Contains the following entries:

- "firing_rate": average value in Hz for 1 neuron in the network.
- "bursting": True if there were bursts of activity detected.
- "burst_duration", "IBI", "ISI", and "period" in ms, if "bursting" is True.
- "SpB" (Spikes per Burst): average number of spikes per neuron during a burst.

simplify()

`nngt.simulation.`**activity_types**(*spike_detector*, *limits*, *network=None*, *phase_coeff=(0.5*, *10.0)*, *mbis=0.5*, *mfb=0.2*, *mflb=0.05*, *skip_bursts=0*, *simplify=False*, *fignums=[]*, *show=False*)
Analyze the spiking pattern of a neural network.

@todo: think about inserting t=0. and t=simtime at the beginning and at the end of `times`.

Parameters

- **spike_detector** (*NEST node(s) (tuple or list of tuples)*) – The recording device that monitored the network's spikes.
- **limits** (*tuple of floats*) – Time limits of the simulation region which should be studied (in ms).
- **network** (*Network*, optional (default: None)) – Neural network that was analyzed
- **phase_coeff** (*tuple of floats, optional (default: (0.2, 5.))*) – A phase is considered *bursting' when the interspike between all spikes that compose it is smaller than ''phase_coeff[0] / avg_rate'* (where `avg_rate` is the average firing rate), *quiescent' when it is greater that ''phase_coeff[1] / avg_rate'*, 'mixed' otherwise.
- **mbis** (*float, optional (default: 0.5)*) – Maximum interspike interval allowed for two spikes to be considered in the same burst (in ms).
- **mfb** (*float, optional (default: 0.2)*) – Minimal fraction of the neurons that should participate for a burst to be validated (i.e. if the interspike is smaller that the limit BUT the number of participating neurons is too small, the phase will be considered as *localized*).
- **mflb** (*float, optional (default: 0.05)*) – Minimal fraction of the neurons that should participate for a local burst to be validated (i.e. if the interspike is smaller that the limit BUT the number of participating neurons is too small, the phase will be considered as *mixed*).

- **skip_bursts** (*int, optional (default: 0)*) – Skip the *skip_bursts* first bursts to consider only the permanent regime.
- **simplify** (*bool, optional (default: False)*) – If `True`, *mixed* phases that are contiguous to a burst are incorporated to it.
- **return_steps** (*bool, optional (default: False)*) – If `True`, a second dictionary, *phases_steps* will also be returned. @todo: not implemented yet
- **fignums** (*list, optional (default: [])*) – Indices of figures on which the periods can be drawn.
- **show** (*bool, optional (default: False)*) – Whether the figures should be displayed.

Note: Effects of *skip_bursts* and *limits[0]* are cumulative: the *limits[0]* first milliseconds are ignored, then the *skip_bursts* first bursts of the remaining activity are ignored.

Returns **phases** (*dict*) – Dictionary containing the time intervals (in ms) for all four phases (*bursting', 'quiescent', 'mixed', and 'localized*) as lists. E.g: `phases["bursting"]` could give `[[123.5,334.2], [857.1,1000.6]]`.

`nngt.simulation.`**`analyze_raster`**(*raster=None*, *limits=None*, *network=None*, *phase_coeff=(0.5, 10.0)*, *mbis=0.5*, *mfb=0.2*, *mflb=0.05*, *skip_bursts=0*, *skip_ms=0.0*, *simplify=False*, *fignums=[]*, *show=False*)

Return the activity types for a given raster.

Parameters

- **raster** (*array-like or str*) – Either an array containing the ids of the spiking neurons and the corresponding time, or the path to a NEST .gdf recording.
- **limits** (*tuple of floats*) – Time limits of the simulation regrion which should be studied (in ms).
- **network** (`Network`, optional (default: None)) – Network on which the recorded activity was simulated.
- **phase_coeff** (*tuple of floats, optional (default: (0.2, 5.))*) – A phase is considered *bursting' when the interspike between all spikes that compose it is smaller than ``phase_coeff[0] / avg_rate`* (where `avg_rate` is the average firing rate), *quiescent' when it is greater that ``phase_coeff[1] / avg_rate`*, 'mixed' otherwise.
- **mbis** (*float, optional (default: 0.5)*) – Maximum interspike interval allowed for two spikes to be considered in the same burst (in ms).
- **mfb** (*float, optional (default: 0.2)*) – Minimal fraction of the neurons that should participate for a burst to be validated (i.e. if the interspike is smaller that the limit BUT the number of participating neurons is too small, the phase will be considered as *localized*).
- **mflb** (*float, optional (default: 0.05)*) – Minimal fraction of the neurons that should participate for a local burst to be validated (i.e. if the interspike is smaller that the limit BUT the number of participating neurons is too small, the phase will be considered as *mixed*).
- **skip_bursts** (*int, optional (default: 0)*) – Skip the *skip_bursts* first bursts to consider only the permanent regime.
- **simplify** (*bool, optional (default: False)*) – If `True`, *mixed* phases that are contiguous to a burst are incorporated to it.
- **fignums** (*list, optional (default: [])*) – Indices of figures on which the periods can be drawn.

- **show** (*bool, optional (default: False)*) – Whether the figures should be displayed.

Note: Effects of *skip_bursts* and *limits[0]* are cumulative: the *limits[0]* first milliseconds are ignored, then the *skip_bursts* first bursts of the remaining activity are ignored.

Returns activity (*ActivityRecord*) – Object containing the phases and the properties of the activity from these phases.

`nngt.simulation.`**`get_recording`**(*network*, *record*, *recorder=None*, *nodes=None*)

Return the evolution of some recorded values for each neuron.

Parameters

- **network** (`nngt.Network`) – Network for which the activity was simulated.
- **record** (*str or list*) – Name of the record(s) to obtain.
- **recorder** (*tuple of ints, optional (default: all multimeters)*) – GID of the "spike_detector" objects recording the network activity.
- **nodes** (*array-like, optional (default: all nodes)*) – NNGT ids of the nodes for which the recording should be returned.

Returns values (*dict of dict of arrays*) – Dictionary containing, for each *record*, an M array with the recorded values for n-th neuron is stored under entry *n* (integer). A *times* entry is also added; it should be the same size for all records, otherwise an error will be raised.

Examples

After the creation of a `Network` called `net`, use the following code:

```
import nest

rec, _ = monitor_nodes(
    net.nest_gid, "multimeter", {"record_from": ["V_m"]}, net)
nest.Simulate(100.)
recording = nngt.simulation.get_recording(net, "V_m")

# access the membrane potential of first neuron + the times
V_m   = recording["V_m"][0]
times = recording["times"]
```

`nngt.simulation.`**`make_nest_network`**(*network*, *use_weights=True*)

Create a new network which will be filled with neurons and connector objects to reproduce the topology from the initial network.

Parameters

- **network** (`nngt.Network` or `nngt.SpatialNetwork`) – the network we want to reproduce in NEST.
- **use_weights** (*bool, optional (default: True)*) – Whether to use the network weights or default ones (value: 10.).

Returns gids (*tuple (nodes in NEST)*) – GIDs of the neurons in the network.

`nngt.simulation.`**`get_nest_adjacency`**(*id_converter=None*)

Get the adjacency matrix describing a NEST network.

Parameters **id_converter** (*dict, optional (default: None)*) – A dictionary which maps NEST gids to the desired neurons ids.

Returns **mat_adj** (`lil_matrix`) – Adjacency matrix of the network.

`nngt.simulation.`**`reproducible_weights`**(*weights*, *neuron_model*, *di_param={}*, *timestep=0.05*, *simtime=50.0*, *num_bins=1000*, *log=False*)

Find the values of the connection weights that will give PSP responses of *min_weight* and *max_weight* in mV.

Parameters

- **weights** (*list of floats*) – Exact desired synaptic weights.
- **neuron_model** (*string*) – Name of the model used.
- **di_param** (*dict, optional (default: {})*) – Parameters of the model, default parameters if not supplied.
- **timestep** (*float, optional (default: 0.01)*) – Timestep of the simulation in ms.
- **simtime** (*float, optional (default: 10.)*) – Simulation time in ms (default: 10).
- **num_bins** (*int, optional (default: 10000)*) – Number of bins used to discretize the exact synaptic weights.
- **log** (*bool, optional (default: False)*) – Whether bins should use a logarithmic scale.

Note: If the parameters used are not the default ones, they MUST be provided, otherwise the resulting weights will likely be WRONG.

`nngt.simulation.`**`monitor_groups`**(*group_names*, *network*, *nest_recorder=None*, *params=None*)

Monitoring the activity of nodes in the network.

Parameters

- **group_name** (*list of strings*) – Names of the groups that should be recorded.
- **network** (*`Network`* or subclass) – Network which population will be used to differentiate groups.
- **nest_recorder** (*strings or list, optional (default: "spike_detector"0)*) – Device(s) to monitor the network.
- **params** (dict or list of, optional (default: *{}*)) – Dictionarie(s) containing the parameters for each recorder (see NEST documentation for details).

Returns

- **recorders** (*tuple*) – Tuple of the recorders' gids
- **recordables** (*tuple*) – Tuple of the recordables' names.

`nngt.simulation.`**`monitor_nodes`**(*gids*, *nest_recorder=None*, *params=None*, *network=None*)

Monitoring the activity of nodes in the network.

Parameters

- **gids** (*tuple of ints or list of tuples*) – GIDs of the neurons in the NEST subnetwork; either one list per recorder if they should monitor different neurons or a unique list which will be monitored by all devices.
- **nest_recorder** (*strings or list, optional (default: "spike_detector")*) – Device(s) to monitor the network.

- **params** (dict or list of, optional (default: *{}*)) – Dictionarie(s) containing the parameters for each recorder (see NEST documentation for details).
- **network** (`Network` or subclass, optional (default: None)) – Network which population will be used to differentiate groups.

Returns

- **recorders** (*tuple*) – Tuple of the recorders' gids
- **recordables** (*tuple*) – Tuple of the recordables' names.

`nngt.simulation.`**`randomize_neural_states`**(*network*, *instructions*, *groups=None*, *make_nest=False*)

Randomize the neural states according to the instructions.

Parameters

- **network** (`Network` subclass instance) – Network that will be simulated.
- **instructions** (*dict*) – Variables to initialize. Allowed keys are "V_m" and "w". Values are 3-tuples of type `("distrib_name", double, double)`.
- **groups** (list of `NeuralGroup`, optional (default: None)) – If provided, only the neurons belonging to these groups will have their properties randomized.
- **make_nest** (*bool, optional (default: False)*) – If `True` and network has not been converted to NEST, automatically generate the network, else raises an exception.

Example

```
instructions = {
    "V_m": ("uniform", -80., -60.),
    "w": ("normal", 50., 5.)
}
```

`nngt.simulation.`**`save_spikes`**(*filename*, *recorder=None*, *network=None*, ***kwargs*)

Plot the monitored activity.

New in version 0.7.

Parameters

- **filename** (*str*) – Path to the file where the activity should be saved.
- **recorder** (*tuple or list of tuples, optional (default: None)*) – The NEST gids of the recording devices. If None, then all existing "spike_detector"s are used.
- **network** (`Network` or subclass, optional (default: None)) – Network which activity will be monitored.
- ****kwargs** (see `numpy.savetxt()`)

`nngt.simulation.`**`set_minis`**(*network*, *base_rate*, *weight_fraction=0.4*, *nodes=None*, *gids=None*, *syn_model='static_synapse'*, *syn_params=None*)

Mimick spontaneous release of neurotransmitters, called spontaneous PSCs or "minis". These minis consists in only a fraction of the usual strength of a spike- triggered PSC and can be modeled by a Poisson process. This Poisson process occurs independently at every synapse of a neuron, so a neuron receiving k inputs will be subjected to these events with a rate $k * \lambda$, where λ is the base rate.

Changed in version 0.7: Added *nodes*, *syn_model* and *syn_param*.

Parameters

- **network** (`Network` object) – Network on which the minis should be simulated.
- **base_rate** (*float*) – Rate for the Poisson process on one synapse (λ).
- **weight_fraction** (*float, optional (default: 0.4)*) – Fraction of a spike-triggered PSC that will be released by a mini.
- **nodes** (*array-like, optional (default: all nodes)*) – NNGT ids of the neurons that should be subjected to minis.
- **gids** (*array-like container ids, optional (default: all neurons)*) – NEST gids of the neurons that should be subjected to minis.
- **syn_model** (*str, optional (default: 'static_synapse')*) – NEST model for the synapse.
- **syn_params** (*dict, optional (default: None)*) – Parameters of the synapse.

Note: *nodes* and *gids* are uncompatible, only one one the two arguments can be used in any given call to *set_minis*.

When using this function, make sure that the synapses you use are the same as the synapses the neurons are receiving, otherwise the weights will not be correctly tuned. This is especially true when using STDP.

`nngt.simulation.`**`set_noise`**(*gids*, *mean*, *std*)

Submit neurons to a current white noise. @todo: check how NEST handles the $\sqrt{t}$ in the standard dev.

Parameters

- **gids** (*tuple*) – NEST gids of the target neurons.
- **mean** (*float*) – Mean current value.
- **std** (*float*) – Standard deviation of the current

Returns **noise** (*tuple*) – The NEST gid of the noise_generator.

`nngt.simulation.`**`set_poisson_input`**(*gids*, *rate*)

Submit neurons to a Poissonian rate of spikes.

Parameters

- **gids** (*tuple*) – NEST gids of the target neurons.
- **rate** (*float*) – Rate of the spike train.

Returns **poisson_input** (*tuple*) – The NEST gid of the poisson_generator.

`nngt.simulation.`**`set_step_currents`**(*gids*, *times*, *currents*)

Set step-current excitations

Parameters

- **gids** (*tuple*) – NEST gids of the target neurons.
- **times** (list or `numpy.ndarray`) – List of the times where the current will change (by default the current generator is initiated at I=0. for t=0.)
- **currents** (list or `numpy.ndarray`) – List of the new current value after the associated time value in *times*.

Returns **noise** (*tuple*) – The NEST gid of the noise_generator.

`nngt.simulation.`**`plot_activity`**(*gid_recorder=None*, *record=None*, *network=None*, *gids=None*, *show=False*, *limits=None*, *hist=True*, *title=None*, *label=None*, *sort=None*, *average=False*, *normalize=1.0*, *decimate=None*)

Plot the monitored activity.

Parameters

- **gid_recorder** (*tuple or list of tuples, optional (default: None)*) – The gids of the recording devices. If None, then all existing "spike_detector"s are used.
- **record** (*tuple or list, optional (default: None)*) – List of the monitored variables for each device. If *gid_recorder* is None, record can also be None and only spikes are considered.
- **network** (`Network` or subclass, optional (default: None)) – Network which activity will be monitored.
- **gids** (*tuple, optional (default: None)*) – NEST gids of the neurons which should be monitored.
- **show** (*bool, optional (default: False)*) – Whether to show the plot right away or to wait for the next plt.show().
- **hist** (*bool, optional (default: True)*) – Whether to display the histogram when plotting spikes rasters.
- **limits** (*tuple, optional (default: None)*) – Time limits of the plot (if not specified, times of first and last spike for raster plots).
- **title** (*str, optional (default: None)*) – Title of the plot.
- **fignum** (*int, optional (default: None)*) – Plot the activity on an existing figure (from `figure.number`).
- **label** (*str or list, optional (default: None)*) – Add labels to the plot (one per recorder).
- **sort** (*str or list, optional (default: None)*) – Sort neurons using a topological property ("in-degree", "out-degree", "total-degree" or "betweenness"), an activity-related property ("firing_rate") or a user-defined list of sorted neuron ids. Sorting is performed by increasing value of the *sort* property from bottom to top inside each group.
- **normalize** (*float or list, optional (default: None)*) – Normalize the recorded results by a given float. If a list is provided, there should be one entry per voltmeter or multimeter in the recorders. If the recording was done through *monitor_groups*, the population can be passed to normalize the data by the nuber of nodes in each group.
- **decimate** (*int or list of ints, optional (default: None)*) – Represent only a fraction of the spiking neurons; only one neuron in *decimate* will be represented (e.g. setting *decimate* to 5 will lead to only 20% of the neurons being represented). If a list is provided, it must have one entry per NeuralGroup in the population.

Warning: Sorting with "firing_rate" only works if NEST gids form a continuous integer range.

Returns **lines** (list of lists of `matplotlib.lines.Line2D`) – Lines containing the data that was plotted, grouped by figure.

`nngt.simulation.`**`raster_plot`**(*times*, *senders*, *limits=None*, *title='Spike raster'*, *hist=False*, *num_bins=1000*, *color='b'*, *decimate=None*, *fignum=None*, *label=None*, *show=True*, *sort=None*, *sort_attribute=None*, *network=None*)

Plotting routine that constructs a raster plot along with an optional histogram.

Parameters

- **times** (list or `numpy.ndarray`) – Spike times.
- **senders** (list or `numpy.ndarray`) – Index for the spiking neuron for each time in *times*.
- **limits** (*tuple, optional (default: None)*) – Time limits of the plot (if not specified, times of first and last spike).
- **title** (*string, optional (default: 'Spike raster')*) – Title of the raster plot.
- **hist** (*bool, optional (default: True)*) – Whether to plot the raster's histogram.
- **num_bins** (*int, optional (default: 1000)*) – Number of bins for the histogram.
- **color** (*string or float, optional (default: 'b')*) – Color of the plot lines and markers.
- **decimate** (*int, optional (default: None)*) – Represent only a fraction of the spiking neurons; only one neuron in *decimate* will be represented (e.g. setting *decimate* to 10 will lead to only 10% of the neurons being represented).
- **fignum** (*int, optional (default: None)*) – Id of another raster plot to which the new data should be added.
- **label** (*str, optional (default: None)*) – Label the current data.
- **show** (*bool, optional (default: True)*) – Whether to show the plot right away or to wait for the next plt.show().

Returns **lines** (list of `matplotlib.lines.Line2D`) – Lines containing the data that was plotted.

Multithreading

Principle

The NNGT package provides the possibility to use multithreaded algorithms to generate networks. This feature means that the computation is distributed on several CPUs and can be useful for:

- machines with several cores but low frequency
- generation functions requiring large amounts of computation
- very large graphs

However, the multithreading part concerns only the generation of the edges; if a graph library such as `graph-tool`, `igraph`, or `networkx` is used, the building process of the graph object will be taken care of by this library. Since this process is not multithreaded, obtaining the graph object can be much longer than the actual generation process.

Use

Setting multithreading

Multithreading in NNGT can be set via

```
>>> nngt.set_config({"multithreading": True, "omp": num_omp_threads})
```

and you can then switch it off using

```
>>> nngt.set_config("multithreading", False)
```

This will automatically switch between the standard and multithreaded algorithms for graph generation.

Random seeds for multithreading

@Todo

Graph-tool caveat

The `graph-tool` library also provides some multithreading capabilities, using

```
>>> graph_tool.openmp_set_num_threads(num_omp_threads)
```

However, this sets the number of OpenMP threads session-wide, which means that **it will interfere with the ''NEST'' setup!** Hence, if you are working with both `NEST` and `graph-tool`, **you have to use the same number of OpenMP threads in both libraries**.

To prevent bad surprises as much as possible, NNGT will raise an error if a value of `"omp"` is provided, which differs from the current NEST configuration. Regardless of this precaution, keeping only one value for the number of threads and using it consistently throughout the code is strongly advised.

Note: This library provides many tools which will (or not) be loaded on startup depending on the python packages available on your computer. The default behaviour of those tools is set in the *~/.nngt/nngt.conf* file (see Configuration). Moreover, to see all potential messages related to the import of those tools, you can use the logging function of NNGT, either by setting the *log_level* value to *INFO*, or by setting *log_to_file* to True, and having a look at the log file in *~/.nngt/log/*.

Description

The graph objects

Neural networks are described by four graph classes which inherit from the main class of the chosen graph library (`gt.Graph`, `igraph.Graph` or `networkx.DiGraph`):

- *`Graph`*: base for simple topological graphs with no spatial structure, nor biological properties
- *`SpatialGraph`*: subclass for spatial graphs without biological properties
- *`Network`*: subclass for topological graphs with biological properties (to interact with NEST)
- *`SpatialNetwork`*: subclass with spatial and biological properties (to interact with NEST)

Using these objects, the user can access to the topological structure of the network (including the connections' type – inhibitory or excitatory – and its weight, which is always positive)

Warning: This object should never be directly modified through the initial library's methods but always using those of NNGT. If, for some reason, you should directly use the methods from the graph library on the object, make sure they do not modify its structure; any modification performed from a method other than those of *`Graph`* subclasses will lead to undefined behaviour!

Additional properties

Nodes/neurons are defined by a unique index which can be used to access their properties and those of the connections between them.

The graph objects can have other attributes, such as:

- `shape` for *`SpatialGraph`* and *`SpatialNetwork`*, which describes the spatial delimitations of the neurons' environment (e.g. many *in vitro* culture are contained in circular dishes),
- `population`, for *`Network`*, which contains informations on the various groups of neurons that exist in the network (for instance inhibitory and excitatory neurons can be grouped together),
- `connections` which stores the informations about the synaptic connections between the neurons.

Graph-theoretical models

Several classical graphs are efficiently implemented and the generation procedures are detailed in the documentation.

Main module

For more details regarding the main classes, see:

Graph classes

class `nngt.`**`Graph`**(*nodes=0*, *name='Graph'*, *weighted=True*, *directed=True*, *from_graph=None*, ***kwargs*)

The basic graph class, which inherits from a library class such as `gt.Graph`, `networkx.DiGraph`, or *igraph.Graph*.

The objects provides several functions to easily access some basic properties.

Initialize Graph instance

Parameters

- **nodes** (*int, optional (default: 0)*) – Number of nodes in the graph.
- **name** (*string, optional (default: "Graph")*) – The name of this *`Graph`* instance.
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weight properties.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or undirected.
- **from_graph** (*`GraphObject`*, optional) – An optional *`GraphObject`* to serve as base.
- **kwargs** (*optional keywords arguments*) – Optional arguments that can be passed to the graph, e.g. a dict containing information on the synaptic weights (`weights={"distribution": "constant", "value": 2.3}` which is equivalent to `weights=2.3`), the synaptic *delays*, or a `type` information.

Returns **self** (*`Graph`*)

`attributes`(*edge=None*, *name=None*)

Attributes of the graph's edges.

Parameters

- **edge** (tuple, optional (default: `None`)) – Edge whose attribute should be displayed.

- **name** (str, optional (default: `None`)) – Name of the desired attribute.

Returns

- *List containing the names of the graph's attributes (synaptic weights,*
- delays...) if *edge* is `None`, else a `dict` containing the
- attributes of the edge (or the value of attribute *name* if it is not
- `None`).

`copy``()`
Returns a deepcopy of the current *`Graph`* instance

`eattr_class`
alias of `_GtEProperty`

`edge_id``(`*edge*`)`
Return the ID a given edge or a list of edges in the graph. Raises an error if the edge is not in the graph or if one of the vertices in the edge is nonexistent.

Parameters **edge** (*2-tuple or array of edges*) – Edge descriptor (source, target).

Returns **index** (*int or array of ints*) – Index of the given *edge*.

`edges_array`
Edges of the graph, sorted by order of creation, as an array of 2-tuple.

`edges_attributes`
Access edge attributes

New in version 0.7.

static `from_file``(`*filename*, *fmt='auto'*, *separator=' '*, *secondary=';'*, *attributes=None*, *notifier='@'*, *ignore='#'*, *from_string=False*`)`
Import a saved graph from a file. @todo: implement population and shape loading, implement gml, dot, xml, gt

Parameters

- **filename** (*str*) – The path to the file.
- **fmt** (*str, optional (default: "neighbour")*) – The format used to save the graph. Supported formats are: "neighbour" (neighbour list, default if format cannot be deduced automatically), "ssp" (scipy.sparse), "edge_list" (list of all the edges in the graph, one edge per line, represented by a `source target`-pair), "gml" (gml format, default if *filename* ends with '.gml'), "graphml" (graphml format, default if *filename* ends with '.graphml' or '.xml'), "dot" (dot format, default if *filename* ends with '.dot'), "gt" (only when using *graph_tool'<http://graph-tool.skewed.de/>_ as library, detected if 'filename* ends with '.gt').
- **separator** (*str, optional (default " ")*) – separator used to separate inputs in the case of custom formats (namely "neighbour" and "edge_list")
- **secondary** (*str, optional (default: ";")*) – Secondary separator used to separate attributes in the case of custom formats.
- **attributes** (*list, optional (default: [])*) – List of names for the attributes present in the file. If a *notifier* is present in the file, names will be deduced from it; otherwise the attributes will be numbered.
- **notifier** (*str, optional (default: "@")*) – Symbol specifying the following as meaningfull information. Relevant information is formatted `@info_name=info_value`, where `info_name` is in ("attributes", "directed", "name", "size") and associated

info_value``s are of type (``list, bool, str, int). Additional notifiers are @type=SpatialGraph/Network/ SpatialNetwork, which must be followed by the relevant notifiers among @shape, @population, and @graph.

- **from_string** (*bool, optional (default: False)*) – Load from a string instead of a file.

Returns graph (*Graph* or subclass) – Loaded graph.

classmethod **`from_matrix`**(*matrix*, *weighted=True*, *directed=True*)
Creates a *Graph* from a `scipy.sparse` matrix or a dense matrix.

Parameters

- **matrix** (`scipy.sparse` matrix or `numpy.array`) – Adjacency matrix.
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weight properties.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or undirected.

Returns *Graph*

`get_attribute_type`(*attribute_name*)
Return the type of an attribute

`get_betweenness`(*btype='both'*, *use_weights=False*)
Betweenness centrality sequence of all nodes and edges.

Parameters

- **btype** (str, optional (default: `"both"`)) – Type of betweenness to return (`"edge"`, `"node"`-betweenness, or `"both"`).
- **use_weights** (*bool, optional (default: False)*) – Whether to use weighted (True) or simple degrees (False).

Returns

- **node_betweenness** (`numpy.array`) – Betweenness of the nodes (if *btype* is `"node"` or `"both"`).
- **edge_betweenness** (`numpy.array`) – Betweenness of the edges (if *btype* is `"edge"` or `"both"`).

`get_degrees`(*deg_type='total'*, *node_list=None*, *use_weights=False*)
Degree sequence of all the nodes.

Parameters

- **deg_type** (*string, optional (default: "total")*) – Degree type (among 'in', 'out' or 'total').
- **node_list** (*list, optional (default: None)*) – List of the nodes which degree should be returned
- **use_weights** (*bool, optional (default: False)*) – Whether to use weighted (True) or simple degrees (False).

Returns `numpy.array` or None (if an invalid type is asked).

`get_delays`()
Returns the delay adjacency matrix as a `scipy.sparse.lil_matrix` if delays are present; else raises an error.

`get_density`()
Density of the graph: $\frac{E}{N^2}$, where E is the number of edges and N the number of nodes.

get_graph_type()
Return the type of the graph (see nngt.generation)

get_name()
Get the name of the graph

get_weights()
Returns the weighted adjacency matrix as a `scipy.sparse.lil_matrix`.

graph_id
Unique `int` identifying the instance.

is_directed()
Whether the graph is directed or not

is_network()
Whether the graph is a subclass of *Network* (i.e. if it has a *NeuralPop* attribute).

is_spatial()
Whether the graph is embedded in space (i.e. if it has a *Shape* attribute). Returns `True` is the graph is a subclass of *SpatialGraph*.

is_weighted()
Whether the edges have weights

static **make_network**(*graph*, *neural_pop*, *copy=False*, ***kwargs*)
Turn a *Graph* object into a *Network*, or a *SpatialGraph* into a *SpatialNetwork*.

Parameters

- **graph** (*Graph* or *SpatialGraph*) – Graph to convert
- **neural_pop** (*NeuralPop*) – Population to associate to the new *Network*
- **copy** (bool, optional (default: `False`)) – Whether the operation should be made in-place on the object or if a new object should be returned.

Notes

In-place operation that directly converts the original graph if *copy* is `False`, else returns the copied *Graph* turned into a *Network*.

static **make_spatial**(*graph*, *shape=None*, *positions=None*, *copy=False*)
Turn a *Graph* object into a *SpatialGraph*, or a *Network* into a *SpatialNetwork*.

Parameters

- **graph** (*Graph* or *SpatialGraph*) – Graph to convert.
- **shape** (*Shape*, optional (default: None)) – Shape to associate to the new *SpatialGraph*.
- **positions** (*(N, 2) array*) – Positions, in a 2D space, of the N neurons.
- **copy** (bool, optional (default: `False`)) – Whether the operation should be made in-place on the object or if a new object should be returned.

Notes

In-place operation that directly converts the original graph if *copy* is `False`, else returns the copied *Graph* turned into a *SpatialGraph*. The *shape* argument can be skipped if *positions* are given; in that case, the neurons will be embedded in a rectangle that contains them all.

name
Name of the graph.

nattr_class
alias of `_GtNProperty`

neighbours (*node*, *mode='all'*)
Return the neighbours of *node*.

Parameters

- **node** (*int*) – Index of the node of interest.
- **mode** (*string, optional (default: "all")*) – Type of neighbours that will be returned: "all" returns all the neighbours regardless of directionality, "in" returns the in-neighbours (also called predecessors) and "out" retruns the out-neighbours (or successors).

Returns **neighbours** (*tuple*) – The neighbours of *node*.

new_edge (*source*, *target*, *attributes=None*, *ignore=False*)
Adding a connection to the graph, with optional properties.

Parameters

- **source** (`int/node`) – Source node.
- **target** (`int/node`) – Target node.
- **attributes** (`dict`, optional (default: `{}`)) – Dictionary containing optional edge properties. If the graph is weighted, defaults to `{"weight": 1.}`, the unit weight for the connection (synaptic strength in NEST).
- **ignore** (*bool, optional (default: False)*) – If set to True, ignore attempts to add an existing edge, otherwise raises an error.

Returns *The new connection.*

new_edge_attribute (*name*, *value_type*, *values=None*, *val=None*)
Create a new attribute for the edges.

New in version 0.7.

Parameters

- **name** (*str*) – The name of the new attribute.
- **value_type** (*str*) – Type of the attribute, among 'int', 'double', 'string'
- **values** (*array, optional (default: None)*) – Values with which the edge attribute should be initialized. (must have one entry per node in the graph)
- **val** (*int, float or str , optional (default: None)*) – Identical value for all edges.

new_edges (*edge_list*, *attributes=None*)
Add a list of edges to the graph.

Warning: This function currently does not check for duplicate edges!

Parameters

- **edge_list** (*list of 2-tuples or np.array of shape (edge_nb, 2)*) – List of the edges that should be added as tuples (source, target)

- **attributes** (`dict`, optional (default: `{}`)) – Dictionary containing optional edge properties. If the graph is weighted, defaults to `{"weight": ones}`, where `ones` is an array the same length as the *edge_list* containing a unit weight for each connection (synaptic strength in NEST).
- **@todo** (*add example, check the edges for self-loops and multiple edges*)

`new_node`(*n=1*, *ntype=1*, *attributes=None*, *value_types=None*)
Adding a node to the graph, with optional properties.

Parameters

- **n** (*int, optional (default: 1)*) – Number of nodes to add.
- **ntype** (*int, optional (default: 1)*) – Type of neuron (1 for excitatory, -1 for inhibitory)
- **attributes** (*dict, optional (default: None)*) – Dictionary containing the attributes of the nodes.
- **value_types** (*dict, optional (default: None)*) – Dict of the *attributes* types, necessary only if the *attributes* do not exist yet.

Returns *The node or a tuple of the nodes created.*

`new_node_attribute`(*name*, *value_type*, *values=None*, *val=None*)
Create a new attribute for the nodes.

New in version 0.7.

Parameters

- **name** (*str*) – The name of the new attribute.
- **value_type** (*str*) – Type of the attribute, among 'int', 'double', 'string'
- **values** (*array, optional (default: None)*) – Values with which the node attribute should be initialized. (must have one entry per node in the graph)
- **val** (*int, float or str , optional (default: None)*) – Identical value for all nodes.

`nodes_attributes`
Access node attributes

New in version 0.7.

classmethod `num_graphs`()
Returns the number of alive instances.

`set_delays`(*delay=None*, *elist=None*, *distribution=None*, *parameters=None*, *noise_scale=None*)
Set the delay for spike propagation between neurons. ..todo :: take elist into account in Connections.delays

Parameters

- **delay** (float or class:*numpy.array*, optional (default: None)) – Value or list of delays (for user defined delays).
- **elist** (class:*numpy.array*, optional (default: None)) – List of the edges (for user defined delays).
- **distribution** (class:*string*, optional (default: None)) – Type of distribution (choose among "constant", "uniform", "gaussian", "lognormal", "lin_corr", "log_corr").
- **parameters** (*dict, optional (default: {})*) – Dictionary containing the properties of the delay distribution.

- **noise_scale** (class:*int*, optional (default: None)) – Scale of the multiplicative Gaussian noise that should be applied on the delays.

`set_edge_attribute` (*attribute*, *values=None*, *val=None*, *value_type=None*, *edges=None*)
Set attributes to the connections between neurons.

> **Warning:** The special "type" attribute cannot be modified when using graphs that inherit from the `Network` class. This is because for biological networks, neurons make only one kind of synapse, which is determined by the `nngt.NeuralGroup` they belong to.

Parameters

- **attribute** (*str*) – The name of the attribute.
- **value_type** (*str*) – Type of the attribute, among 'int', 'double', 'string'
- **values** (*array, optional (default: None)*) – Values with which the edge attribute should be initialized. (must have one entry per node in the graph)
- **val** (*int, float or str , optional (default: None)*) – Identical value for all edges.
- **value_type** (*str, optional (default: None)*) – Type of the attribute, among 'int', 'double', 'string'. Only used if the attribute does not exist and must be created.
- **edges** (*list of edges or array of shape (E, 2), optional (default: all)*) – Edges whose attributes should be set. Others will remain unchanged.

`set_name` (*name='‘*)
set graph name

`set_types` (*syn_type*, *nodes=None*, *fraction=None*)
Set the synaptic/connection types.

> **Warning:** The special "type" attribute cannot be modified when using graphs that inherit from the `Network` class. This is because for biological networks, neurons make only one kind of synapse, which is determined by the `nngt.NeuralGroup` they belong to.

Parameters

- **syn_type** (*int or string*) – Type of the connection among 'excitatory' (also *1*) or 'inhibitory' (also *-1*).
- **nodes** (int, float or list, optional (default: *None*)) – If *nodes* is an int, number of nodes of the required type that will be created in the graph (all connections from inhibitory nodes are inhibitory); if it is a float, ratio of *syn_type* nodes in the graph; if it is a list, ids of the *syn_type* nodes.
- **fraction** (float, optional (default: *None*)) – Fraction of the selected edges that will be set as *syn_type* (if *nodes* is not *None*, it is the fraction of the specified nodes' edges, otherwise it is the fraction of all edges in the graph).

Returns **t_list** (`numpy.ndarray`) – List of the types in an order that matches the *edges* attribute of the graph.

`set_weights` (*weight=None*, *elist=None*, *distribution=None*, *parameters=None*, *noise_scale=None*)
Set the synaptic weights.

..todo :: take elist into account in Connections.weights

Parameters

- **weight** (float or class:*numpy.array*, optional (default: None)) – Value or list of the weights (for user defined weights).
- **elist** (class:*numpy.array*, optional (default: None)) – List of the edges (for user defined weights).
- **distribution** (class:*string*, optional (default: None)) – Type of distribution (choose among "constant", "uniform", "gaussian", "lognormal", "lin_corr", "log_corr").
- **parameters** (*dict, optional (default: {})*) – Dictionary containing the properties of the weight distribution.
- **noise_scale** (class:*int*, optional (default: None)) – Scale of the multiplicative Gaussian noise that should be applied on the weights.

`to_file`(*filename*, *fmt='auto'*, *separator=' '*, *secondary=';'*, *attributes=None*, *notifier='@'*)
Save graph to file; options detailed below.

See also:

`nngt.lib.save_to_file()` function for options.

`type`
Type of the graph.

class `nngt.`**`SpatialGraph`**(*nodes=0*, *name='Graph'*, *weighted=True*, *directed=True*, *from_graph=None*, *shape=None*, *positions=None*, ***kwargs*)
The detailed class that inherits from `Graph` and implements additional properties to describe spatial graphs (i.e. graph where the structure is embedded in space.

Initialize SpatialClass instance. .. todo:: see what we do with the from_graph argument

Parameters

- **nodes** (*int, optional (default: 0)*) – Number of nodes in the graph.
- **name** (*string, optional (default: "Graph")*) – The name of this `Graph` instance.
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weight properties.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or undirected.
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment (None leads to a square of side 1 cm)
- **positions** (`numpy.array` (N, 2), optional (default: None)) – Positions of the neurons; if not specified and *nodes* is not 0, then neurons will be reparted at random inside the `Shape` object of the instance.
- ****kwargs** (keyword arguments for `Graph` or) – `Shape` if no shape was given.

Returns **self** (`SpatialGraph`)

`get_positions`(*neurons=None*)
Returns the neurons' positions as a (N, 2) array.

Parameters **neurons** (*int or array-like, optional (default: all neurons)*) – List of the neurons for which the position should be returned.

`shape`

class `nngt.`**`Network`**(*name='Network'*, *weighted=True*, *directed=True*, *from_graph=None*, *population=None*, ***kwargs*)

The detailed class that inherits from `Graph` and implements additional properties to describe various biological functions and interact with the NEST simulator.

Initializes `Network` instance.

Parameters

- **nodes** (*int, optional (default: 0)*) – Number of nodes in the graph.
- **name** (*string, optional (default: "Graph")*) – The name of this `Graph` instance.
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weight properties.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or undirected.
- **from_graph** (`GraphObject`, optional (default: None)) – An optional `GraphObject` to serve as base.
- **population** (`nngt.NeuralPop`, (default: None)) – An object containing the neural groups and their properties: model(s) to use in NEST to simulate the neurons as well as their parameters.

Returns **self** (`Network`)

classmethod **`ei_network`**(*size*, *ei_ratio=0.2*, *en_model='aeif_cond_alpha'*, *en_param=None*, *es_model='static_synapse'*, *es_param=None*, *in_model='aeif_cond_alpha'*, *in_param=None*, *is_model='static_synapse'*, *is_param=None*, ***kwargs*)

Generate a network containing a population of two neural groups: inhibitory and excitatory neurons.

Parameters

- **size** (*int*) – Number of neurons in the network.
- **ei_ratio** (*double, optional (default: 0.2)*) – Ratio of inhibitory neurons: $\frac{N_i}{N_e+N_i}$.
- **en_model** (*string, optional (default: 'aeif_cond_alpha')*) – Nest model for the excitatory neuron.
- **en_param** (*dict, optional (default: {})*) – Dictionary of parameters for the the excitatory neuron.
- **es_model** (*string, optional (default: 'static_synapse')*) – NEST model for the excitatory synapse.
- **es_param** (*dict, optional (default: {})*) – Dictionary containing the excitatory synaptic parameters.
- **in_model** (*string, optional (default: 'aeif_cond_alpha')*) – Nest model for the inhibitory neuron.
- **in_param** (*dict, optional (default: {})*) – Dictionary of parameters for the the inhibitory neuron.
- **is_model** (*string, optional (default: 'static_synapse')*) – NEST model for the inhibitory synapse.
- **is_param** (*dict, optional (default: {})*) – Dictionary containing the inhibitory synaptic parameters.

Returns **net** (`Network` or subclass) – Network of disconnected excitatory and inhibitory neurons.

classmethod `from_gids`(*gids*, *get_connections=True*, *get_params=False*, *neuron_model='aeif_cond_alpha'*, *neuron_param=None*, *syn_model='static_synapse'*, *syn_param=None*, ***kwargs*)

Generate a network from gids.

> **Warning:** Unless *get_connections* and *get_params* is True, or if your population is homogeneous and you provide the required information, the information contained by the network and its *population* attribute will be erroneous! To prevent conflicts the `to_nest()` function is not available. If you know what you are doing, you should be able to find a workaround...

Parameters

- **gids** (*array-like*) – Ids of the neurons in NEST or simply user specified ids.
- **get_params** (*bool, optional (default: True)*) – Whether the parameters should be obtained from NEST (can be very slow).
- **neuron_model** (*string, optional (default: None)*) – Name of the NEST neural model to use when simulating the activity.
- **neuron_param** (*dict, optional (default: {})*) – Dictionary containing the neural parameters; the default value will make NEST use the default parameters of the model.
- **syn_model** (*string, optional (default: 'static_synapse')*) – NEST synaptic model to use when simulating the activity.
- **syn_param** (*dict, optional (default: {})*) – Dictionary containing the synaptic parameters; the default value will make NEST use the default parameters of the model.

Returns **net** (`Network` or subclass) – Uniform network of disconnected neurons.

`get_neuron_type`(*neuron_ids*)

Return the type of the neurons (+1 for excitatory, -1 for inhibitory).

Parameters **neuron_ids** (*int or tuple*) – NEST gids.

Returns **ids** (*int or tuple*) – Ids in the network. Same type as the requested *gids* type.

`id_from_nest_gid`(*gids*)

Return the ids of the nodes in the `nngt.Network` instance from the corresponding NEST gids.

Parameters **gids** (*int or tuple*) – NEST gids.

Returns **ids** (*int or tuple*) – Ids in the network. Same type as the requested *gids* type.

`nest_gid`

`neuron_properties`(*idx_neuron*)

Properties of a neuron in the graph.

Parameters **idx_neuron** (*int*) – Index of a neuron in the graph.

Returns *dict of the neuron's properties.*

classmethod `num_networks`()

Returns the number of alive instances.

`population`

`NeuralPop` that divides the neurons into groups with specific properties.

`set_types`(*syn_type*, *nodes=None*, *fraction=None*)

to_nest (*use_weights=True*)
Send the network to NEST.

See also:

make_nest_network() for parameters

classmethod uniform_network (*size, neuron_model='aeif_cond_alpha', neuron_param=None, syn_model='static_synapse', syn_param=None, **kwargs*)
Generate a network containing only one type of neurons.

Parameters

- **size** (*int*) – Number of neurons in the network.
- **neuron_model** (*string, optional (default: 'aief_cond_alpha')*) – Name of the NEST neural model to use when simulating the activity.
- **neuron_param** (*dict, optional (default: {})*) – Dictionary containing the neural parameters; the default value will make NEST use the default parameters of the model.
- **syn_model** (*string, optional (default: 'static_synapse')*) – NEST synaptic model to use when simulating the activity.
- **syn_param** (*dict, optional (default: {})*) – Dictionary containing the synaptic parameters; the default value will make NEST use the default parameters of the model.

Returns **net** (*Network* or subclass) – Uniform network of disconnected neurons.

class nngt.**SpatialNetwork** (*population, name='Graph', weighted=True, directed=True, shape=None, from_graph=None, positions=None, **kwargs*)
Class that inherits from *Network* and *SpatialGraph* to provide a detailed description of a real neural network in space, i.e. with positions and biological properties to interact with NEST.

Initialize Graph instance

Parameters

- **name** (*string, optional (default: "Graph")*) – The name of this *Graph* instance.
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weight properties.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or undirected.
- **shape** (*Shape*, optional (default: None)) – Shape of the neurons' environment (None leads to a square of side 1 cm)
- **positions** (`numpy.array`, optional (default: None)) – Positions of the neurons; if not specified and *nodes* != 0, then neurons will be reparted at random inside the *Shape* object of the instance.
- **population** (class:~*nngt.NeuralPop*, optional (default: None)) – Population from which the network will be built.

Returns **self** (*SpatialNetwork*)

set_types (*syn_type, nodes=None, fraction=None*)

Main functions

nngt.**generate** (*di_instructions, **kwargs*)
Generate a *Graph* or one of its subclasses from a `dict` containing all the relevant informations.

Parameters di_instructions (`dict`) – Dictionary containing the instructions to generate the graph. It must have at least `"graph_type"` in its keys, with a value among `"distance_rule"`, `"erdos_renyi"`, `"fixed_degree"`, `"newman_watts"`, `"price_scale_free"`, `"random_scale_free"`. Depending on the type, *di_instructions* should also contain at least all non-optional arguments of the generator function.

See also:

generation

`nngt.`**`get_config`**(*key=None*)

Get the NNGT configuration as a dictionary.

`nngt.`**`load_from_file`**(*filename*, *fmt='neighbour'*, *separator=' '*, *secondary=';'*, *attributes=[]*, *notifier='@'*, *ignore='#'*)

Load the main properties (edges, attributes...) from a file.

Warning: To import a graph directly from a file, use the `from_file()` classmethod.

Parameters

- **filename** (*str*) – The path to the file.
- **fmt** (*str, optional (default: "neighbour")*) – The format used to save the graph. Supported formats are: "neighbour" (neighbour list, default if format cannot be deduced automatically), "ssp" (scipy.sparse), "edge_list" (list of all the edges in the graph, one edge per line, represented by a `source target`-pair), "gml" (gml format, default if *filename* ends with '.gml'), "graphml" (graphml format, default if *filename* ends with '.graphml' or '.xml'), "dot" (dot format, default if *filename* ends with '.dot'), "gt" (only when using *graph_tool'<http://graph-tool.skewed.de/>_ as library, detected if 'filename* ends with '.gt').
- **separator** (*str, optional (default " ")*) – separator used to separate inputs in the case of custom formats (namely "neighbour" and "edge_list")
- **secondary** (*str, optional (default: ";")*) – Secondary separator used to separate attributes in the case of custom formats.
- **attributes** (*list, optional (default: [])*) – List of names for the attributes present in the file. If a *notifier* is present in the file, names will be deduced from it; otherwise the attributes will be numbered.
- **notifier** (*str, optional (default: "@")*) – Symbol specifying the following as meaningfull information. Relevant information are formatted `@info_name=info_value`, where `info_name` is in ("attributes", "directed", "name", "size") and associated ``info_value``s are of type (``list``, `bool`, `str`, `int`). Additional notifiers are `@type=SpatialGraph/Network/SpatialNetwork`, which must be followed by the relevant notifiers among `@shape`, `@population`, and `@graph`.
- **ignore** (*str, optional (default: "#")*) – Ignore lines starting with the *ignore* string.

Returns

- **edges** (*list of 2-tuples*) – Edges of the graph.
- **di_attributes** (*dict*) – Dictionary containing the attribute name as key and its value as a list sorted in the same order as *edges*.
- **pop** (`NeuralPop`) – Population (`None` if not present in the file).

- **shape** (`Shape`) – Shape of the graph (`None` if not present in the file).
- **positions** (*array-like of shape (N, d)*) – The positions of the neurons (`None` if not present in the file).

`nngt.save_to_file`(*graph*, *filename*, *fmt='auto'*, *separator=' '*, *secondary=';'*, *attributes=None*, *notifier='@'*)

Save a graph to file. @todo: implement population and shape saving, implement gml, dot, xml, gt

Parameters

- **graph** (`Graph` or subclass) – Graph to save.
- **filename** (*str*) – The path to the file.
- **fmt** (*str, optional (default: "auto")*) – The format used to save the graph. Supported formats are: "neighbour" (neighbour list, default if format cannot be deduced automatically), "ssp" (scipy.sparse), "edge_list" (list of all the edges in the graph, one edge per line, represented by a `source target`-pair), "gml" (gml format, default if *filename* ends with '.gml'), "graphml" (graphml format, default if *filename* ends with '.graphml' or '.xml'), "dot" (dot format, default if *filename* ends with '.dot'), "gt" (only when using *graph_tool'<http://graph-tool.skewed.de/>_ as library, detected if 'filename* ends with '.gt').
- **separator** (*str, optional (default " ")*) – separator used to separate inputs in the case of custom formats (namely "neighbour" and "edge_list")
- **secondary** (*str, optional (default: ";")*) – Secondary separator used to separate attributes in the case of custom formats.
- **attributes** (list, optional (default: `None`)) – List of names for the edge attributes present in the graph that will be saved to disk; by default (`None`), all attributes will be saved.
- **notifier** (*str, optional (default: "@")*) – Symbol specifying the following as meaningfull information. Relevant information are formatted `@info_name=info_value`, with `info_name` in ("attributes", "attr_types", "directed", "name", "size"). Additional notifiers are `@type=SpatialGraph/Network/SpatialNetwork`, which are followed by the relevant notifiers among `@shape`, `@population`, and `@graph` to separate the sections.
- **.. warning ::** – For now, all formats lead to dataloss if your graph is a subclass of `SpatialGraph` or `Network` (the `Shape` and `NeuralPop` attributes will not be saved).
- **.. note ::** – Positions are saved as bytes by `numpy.nparray.tostring()`

`nngt.seed`(*seed=None*)

Seed the random generator used by NNGT (i.e. the numpy *RandomState*: for details, see `numpy.random.RandomState`).

Parameters **seed** (*int or array_like, optional*) – Seed for *RandomState*. Must be convertible to 32 bit unsigned integers.

`nngt.set_config`(*config*, *value=None*)

Set NNGT's configuration.

Parameters

- **config** (*dict or str*) – Either a full configuration dictionary or one key to be set together with its associated value.
- **value** (*object, optional (default: None)*) – Value associated to *config* if *config* is a key.

Examples

```
>>> nngt.set_config({'multithreading': True, 'omp': 4})
>>> nngt.set_config('multithreading', False)
```

Note: See the config file *nngt/nngt.conf.default* or *~/.nngt/nngt.conf* for details about your configuration.

See also:

get_config()

`nngt.`**`use_library`**(*library*, *reloading=True*)

Allows the user to switch to a specific graph library.

Parameters

- **library** (*string*) – Name of a graph library among ‘graph_tool’, ‘igraph’, ‘networkx’.
- **reload_moduleing** (*bool, optional (default: True)*) – Whether the graph objects should be reload_moduleed (this should always be set to True except when NNGT is first initiated!)

Side classes

class `nngt.`**`GroupProperty`**(*size*, *constraints={}*, *neuron_model=None*, *neuron_param={}*, *syn_model=None*, *syn_param={}*)

Class defining the properties needed to create groups of neurons from an existing `GraphClass` or one of its subclasses.

Variables

- ***size*** – `int` Size of the group.
- **`constraints`** – `dict`, optional (default: {}) Constraints to respect when building the `NeuralGroup` .
- ***neuron_model*** – `string`, optional (default: None) name of the model to use when simulating the activity of this group.
- **`neuron_param`** – `dict`, optional (default: {}) the parameters to use (if they differ from the model’s defaults)

Create a new instance of GroupProperties.

Notes

The constraints can be chosen among:

- “avg_deg”, “min_deg”, “max_deg” (`int`) to constrain the total degree of the nodes
- “avg/min/max_in_deg”, “avg/min/max_out_deg”, to work with the in/out-degrees
- “avg/min/max_betw” (`double`) to constrain the betweenness centrality
- “in_shape” (*`nngt.geometry.Shape`*) to chose neurons inside a given spatial region

Examples

```
>>> di_constrain = { "avg_deg": 10, "min_betw": 0.001 }
>>> group_prop = GroupProperties(200, constraints=di_constrain)
```

class `nngt.`**`NeuralGroup`**(*nodes=None*, *ntype=1*, *model=None*, *neuron_param=None*, *syn_model=None*, *syn_param=None*)

Class defining groups of neurons.

Variables

- ***`ids`*** – `list` of `int` the ids of the neurons in this group.
- **`neuron_type`** – `int` the default is `1` for excitatory neurons; `-1` is for interneurons
- **`model`** – `string`, optional (default: None) the name of the model to use when simulating the activity of this group
- **`neuron_param`** – `dict`, optional (default: {}) the parameters to use (if they differ from the model's defaults)

Note: By default, synapses are registered as `"static_synapse"` in NEST; because of this, only the `neuron_model` attribute is checked by the `has_model` function.

Warning: Equality between `` NeuralGroup`s only compares the neuronal and synaptic ``model` `` and `param` attributes, i.e. groups differing only by their `ids` will register as equal.

Create a group of neurons (empty group is default, but it is not a valid object for most use cases).

Parameters

- **nodes** (*int or array-like, optional (default: None)*) – Desired size of the group or, a posteriori, NNGT indices of the neurons in an existing graph.
- **ntype** (*int, optional (default: 1)*) – Type of the neurons (1 for excitatory, -1 for inhibitory).
- **model** (*str, optional (default: None)*) – NEST model for the neuron.
- **neuron_param** (*dict, optional (default: model defaults)*) – Dictionary containing the parameters associated to the NEST model.
- **syn_model** (*str, optional (default: "static_synapse")*) – NEST model for the incoming synapses.
- **syn_param** (*dict, optional (default: model defaults)*) – Dictionary containing the parameters associated to the NEST model.

Returns A new `NeuralGroup` instance.

`has_model`

`ids`

`nest_gids`

`neuron_model`

`properties`

size

class `nngt.`**NeuralPop**(*size*, *parent=None*, *with_models=True*, ***kwargs*)

The basic class that contains groups of neurons and their properties.

Variables ***has_models*** – `bool`, `True` if every group has a `model` attribute.

Initialize NeuralPop instance

Parameters

- **size** (*int*) – Number of neurons that the population will contain.
- **parent** (*Network*, optional (default: None)) – Network associated to this population.
- **with_models** (`bool`) – whether the population's groups contain models to use in NEST
- ****kwargs** (`dict`)

Returns **pop** (*NeuralPop* object.)

add_to_group(*group_name*, *ids*)

classmethod copy(*pop*)

Copy an existing NeuralPop

create_group(*name*, *neurons*, *ntype=1*, *neuron_model=None*, *neuron_param=None*, *syn_model='static_synapse'*, *syn_param=None*)

Create a new groupe from given properties.

Parameters

- **name** (*str*) – Name of the group.
- **neurons** (*array-like*) – List of the neurons indices.
- **ntype** (*int, optional (default: 1)*) – Type of the neurons : 1 for excitatory, -1 for inhibitory.
- **neuron_model** (*str, optional (default: None)*) – Name of a neuron model in NEST.
- **neuron_param** (*dict, optional (default: None)*) – Parameters for *neuron_model* in the NEST simulator. If None, default parameters will be used.
- **syn_model** (*str, optional (default: "static_synapse")*) – Name of a synapse model in NEST.
- **syn_param** (*dict, optional (default: None)*) – Parameters for *syn_model* in the NEST simulator. If None, default parameters will be used.

classmethod exc_and_inhib(*size*, *iratio=0.2*, *en_model='aeif_cond_alpha'*, *en_param=None*, *es_model='static_synapse'*, *es_param=None*, *in_model='aeif_cond_alpha'*, *in_param=None*, *is_model='static_synapse'*, *is_param=None*, *parent=None*)

Make a NeuralPop with a given ratio of inhibitory and excitatory neurons.

classmethod from_groups(*groups*, *names=None*, *parent=None*, *with_models=True*)

Make a NeuralPop object from a (list of) *NeuralGroup* object(s).

Parameters

- **groups** (list of *NeuralGroup* objects) – Groups that will be used to form the population.
- **names** (*list of str, optional (default: None)*) – Names that can be used as keys to retreive a specific group. If not provided, keys will be the position of the group in *groups*, stored as a string. In this case, the first group in a population named *pop* will be retreived by either *pop[0]* or *pop['0']*.

- **parent** (*Graph*, optional (default: None)) – Parent if the population is created from an exiting graph.

Note: If the population is not generated from an existing *Graph* and the groups do not contain explicit ids, then the ids will be generated upon population creation: the first group, of size N0, will be associated the indices 0 to N0 - 1, the second group (size N1), will get N0 to N0 + N1 - 1, etc.

classmethod `from_network`(*graph*, **args*)
Make a NeuralPop object from a network. The groups of neurons are determined using instructions from an arbitrary number of `GroupProperties`.

`get_group`(*neurons*, *numbers=False*)
Return the group of the neurons.

Parameters

- **neurons** (*int or array-like*) – IDs of the neurons for which the group should be returned.
- **numbers** (*bool, optional (default: False)*) – Whether the group identifier should be returned as a number; if `False`, the group names are returned.

`get_param`(*groups=None*, *neurons=None*, *element='neuron'*)
Return the *element* (neuron or synapse) parameters for neurons or groups of neurons in the population.

Parameters

- **groups** (`str`, `int` or array-like, optional (default: `None`)) – Names or numbers of the groups for which the neural properties should be returned.
- **neurons** (int or array-like, optional (default: `None`)) – IDs of the neurons for which parameters should be returned.
- **element** (`list` of `str`, optional (default: `"neuron"`)) – Element for which the parameters should be returned (either `"neuron"` or `"synapse"`).

Returns **param** (`list`) – List of all dictionaries with the elements' parameters.

`has_models`

`is_valid`

`set_model`(*model*, *group=None*)
Set the groups' models.

Parameters

- **model** (*dict*) – Dictionary containing the model type as key ("neuron" or "synapse") and the model name as value (e.g. {"neuron": "iaf_neuron"}).
- **group** (*list of strings, optional (default: None)*) – List of strings containing the names of the groups which models should be updated.

Note: By default, synapses are registered as "static_synapse"s in NEST; because of this, only the `neuron_model` attribute is checked by the `has_models` function: it will answer `True` if all groups have a 'non-None' `neuron_model` attribute.

Warning: No check is performed on the validity of the models, which means that errors will only be detected when building the graph in NEST.

`set_param`(*param*, *group=None*)
Set the groups' parameters.

Parameters

- **param** (*dict*) – Dictionary containing the model type as key ("neuron" or "synapse") and the model parameter as value (e.g. {"neuron": {"C_m": 125.}}).
- **group** (*list of strings, optional (default: None)*) – List of strings containing the names of the groups which models should be updated.
- **.. warning::** – No check is performed on the validity of the parameters, which means that errors will only be detected when building the graph in NEST.

`size`

classmethod `uniform`(*size*, *neuron_model='aeif_cond_alpha'*, *neuron_param=None*, *syn_model='static_synapse'*, *syn_param=None*, *parent=None*)
Make a NeuralPop of identical neurons

NNGT

Package aimed at facilitating the analysis of Neural Networks Growth and Topology.

The library mainly provides algorithms for

1. generating networks
2. analyzing their activity
3. studying the graph theoretical properties of those networks

Available modules

analysis Tools to study graph topology and neuronal activity.

core Where the main classes are coded; however, most useful classes and methods for users are loaded at the main level (*nngt*) when the library is imported, so *nngt.core* should generally not be used.

generation Functions to generate specific networks.

geometry Tools to work on metric graphs (see PyNCulture).

io Tools for input/output operations.

lib Basic functions used by several most other modules.

simulation Tools to provide complex network generation with NEST and help analyze the influence of the network structure on neuronal activity.

plot plot data or graphs using matplotlib and graph_tool.

Units

Functions related to spatial embedding of networks are using micrometers (um) as default unit; other units from the metric system can also be provided:

- *mm* for milimeters
- *cm* centimeters

- *dm* for decimeters
- *m* for meters

Main classes and functions

`nngt.Graph`([nodes, name, weighted, ...])	The basic graph class, which inherits from a library class such as `gt.Graph`, `networkx.DiGraph`, or *igraph.Graph*.
`nngt.GroupProperty`(size[, constraints, ...])	Class defining the properties needed to create groups of neurons from an existing `GraphClass` or one of its subclasses.
`nngt.Network`([name, weighted, directed, ...])	The detailed class that inherits from `Graph` and implements additional properties to describe various biological functions and interact with the NEST simulator.
`nngt.NeuralGroup`([nodes, ntype, model, ...])	Class defining groups of neurons.
`nngt.NeuralPop`(size[, parent, with_models])	The basic class that contains groups of neurons and their properties.
`nngt.SpatialGraph`([nodes, name, weighted, ...])	The detailed class that inherits from `Graph` and implements additional properties to describe spatial graphs (i.e.
`nngt.SpatialNetwork`(population[, name, ...])	Class that inherits from `Network` and `SpatialGraph` to provide a detailed description of a real neural network in space, i.e.
`nngt.generate`(di_instructions, **kwargs)	Generate a `Graph` or one of its subclasses from a `dict` containing all the relevant informations.
`nngt.get_config`([key])	Get the NNGT configuration as a dictionary.
`nngt.load_from_file`(filename[, fmt, ...])	Load the main properties (edges, attributes...) from a file.
`nngt.save_to_file`(graph, filename[, fmt, ...])	Save a graph to file.
`nngt.seed`([seed])	Seed the random generator used by NNGT (i.e.
`nngt.set_config`(config[, value])	Set NNGT's configuration.
`nngt.use_library`(library[, reloading])	Allows the user to switch to a specific graph library.

Analysis module

Tools to analyze neuronal networks, using either their topological properties, their activity, or more importantly, taking both into account.

Content

`nngt.analysis.adjacency_matrix`(graph[, ...])	Adjacency matrix of the graph.
`nngt.analysis.assortativity`(graph[, deg_type])	Assortativity of the graph.
`nngt.analysis.bayesian_blocks`(t[, x, sigma, ...])	Bayesian Blocks Implementation
`nngt.analysis.betweenness_distrib`(graph[, ...])	Betweenness distribution of a graph.
`nngt.analysis.binning`(x[, bins, log])	Binning function providing automatic binning using Bayesian blocks in addition to standard linear and logarithmic uniform bins.

Continued on next page

Table 2.3 – continued from previous page

nngt.analysis.closeness(graph[, nodes, ...])	Return the closeness centrality for each node in *nodes*.
nngt.analysis.clustering(graph)	Global clustering coefficient of the graph.
nngt.analysis.degree_distrib(graph[, ...])	Degree distribution of a graph.
nngt.analysis.diameter(graph)	Pseudo-diameter of the graph
nngt.analysis.get_b2([network, ...])	Return the B2 coefficient for the neurons.
nngt.analysis.get_firing_rate([network, ...])	Return the average firing rate for the neurons.
nngt.analysis.get_spikes([recorder, ...])	Return a 2D sparse matrix, where:
nngt.analysis.local_clustering(graph[, nodes])	Local clustering coefficient of the nodes.
nngt.analysis.node_attributes(network, ...)	Return node *attributes* for a set of *nodes*.
nngt.analysis.num_iedges(graph)	Returns the number of inhibitory connections.
nngt.analysis.num_scc(graph[, listing])	Returns the number of strongly connected components (SCCs).
nngt.analysis.num_wcc(graph[, listing])	Connected components if the directivity of the edges is ignored.
nngt.analysis.reciprocity(graph)	Graph reciprocity, defined as $E^{\leftrightarrow}/E$, where $E^{\leftrightarrow}$ and E are, respectively, the number of bidirectional edges and the total number of edges in the graph.
nngt.analysis.spectral_radius(graph[, ...])	Spectral radius of the graph, defined as the eigenvalue of greatest module.
nngt.analysis.subgraph_centrality(graph[, ...])	Subgraph centrality, accordign to [Estrada2005], for each node in the graph.
nngt.analysis.total_firing_rate([network, ...])	Computes the total firing rate of the network from the spike times.
nngt.analysis.transitivity(graph)	Same as *nngt.analysis.clustering()* (for networkx users)

Details

nngt.analysis.**bayesian_blocks**(*t*, *x=None*, *sigma=None*, *fitness='events'*, ***kwargs*)

Bayesian Blocks Implementation

This is a flexible implementation of the Bayesian Blocks algorithm described in Scargle 2012[1]

New in version 0.7.

Parameters

- **t** (*array_like*) – data times (one dimensional, length N)
- **x** (*array_like (optional)*) – data values
- **sigma** (*array_like or float (optional)*) – data errors
- **fitness** (*str or object*) – the fitness function to use. If a string, the following options are supported:
  - **'events'** [binned or unbinned event data] extra arguments are *p0*, which gives the false alarm probability to compute the prior, or *gamma* which gives the slope of the prior on the number of bins.
  - **'regular_events'** [non-overlapping events measured at multiples] of a fundamental tick rate, *dt*, which must be specified as an additional argument. The prior can be specified through *gamma*, which gives the slope of the prior on the number of bins.

[1] Scargle, J *et al.* (2012) http://adsabs.harvard.edu/abs/2012arXiv1207.5578S

  – **'measures'** [fitness for a measured sequence with Gaussian errors] The prior can be specified using *gamma*, which gives the slope of the prior on the number of bins. If *gamma* is not specified, then a simulation-derived prior will be used.

  Alternatively, the fitness can be a user-specified object of type derived from the FitnessFunc class.

Returns **edges** (*ndarray*) – array containing the (N+1) bin edges

Examples

Event data:

```
>>> t = np.random.normal(size=100)
>>> bins = bayesian_blocks(t, fitness='events', p0=0.01)
```

Event data with repeats:

```
>>> t = np.random.normal(size=100)
>>> t[80:] = t[:20]
>>> bins = bayesian_blocks(t, fitness='events', p0=0.01)
```

Regular event data:

```
>>> dt = 0.01
>>> t = dt * np.arange(1000)
>>> x = np.zeros(len(t))
>>> x[np.random.randint(0, len(t), len(t) / 10)] = 1
>>> bins = bayesian_blocks(t, fitness='regular_events', dt=dt, gamma=0.9)
```

Measured point data with errors:

```
>>> t = 100 * np.random.random(100)
>>> x = np.exp(-0.5 * (t - 50) ** 2)
>>> sigma = 0.1
>>> x_obs = np.random.normal(x, sigma)
>>> bins = bayesian_blocks(t, fitness='measures')
```

References

See also:

`astroML.plotting.hist()` histogram plotting function which can make use of bayesian blocks.

`nngt.analysis.`**`adjacency_matrix`**(*graph*, *types=True*, *weights=True*)
Adjacency matrix of the graph.

Parameters

- **graph** (`Graph` or subclass) – Network to analyze.
- **types** (*bool, optional (default: True)*) – Whether the excitatory/inhibitory type of the connnections should be considered (only if the weighing factor is the synaptic strength).
- **weights** (*bool or string, optional (default: True)*) – Whether weights should be taken into account; if True, then connections are weighed by their synaptic strength, if False, then a

binary matrix is returned, if *weights* is a string, then the ponderation is the correponding value of the edge attribute (e.g. "distance" will return an adjacency matrix where each connection is multiplied by its length).

Returns a `csr_matrix`.

`nngt.analysis.`**`assortativity`**(*graph*, *deg_type='total'*)

Assortativity of the graph.

Parameters

- **graph** (`Graph` or subclass) – Network to analyze.
- **deg_type** (*string, optional (default: 'total')*) – Type of degree to take into account (among 'in', 'out' or 'total').

Returns *a float quantifying the graph assortativity.*

`nngt.analysis.`**`betweenness_distrib`**(*graph*, *use_weights=True*, *nodes=None*, *num_nbins='bayes'*, *num_ebins='bayes'*, *log=False*)

Betweenness distribution of a graph.

Changed in version 0.7.

Inclusion of automatic binning.

Parameters

- **graph** (`Graph` or subclass) – the graph to analyze.
- **use_weights** (*bool, optional (default: True)*) – use weighted degrees (do not take the sign into account : all weights are positive).
- **nodes** (*list or numpy.array of ints, optional (default: all nodes)*) – Restrict the distribution to a set of nodes (only impacts the node attribute).
- **log** (*bool, optional (default: False)*) – use log-spaced bins.
- **num_bins** (*int, list or str, optional (default: 'bayes')*) – Any of the automatic methodes from `numpy.histogram()`, or 'bayes' will provide automatic bin optimization. Otherwise, an int for the number of bins can be provided, or the direct bins list.

Returns

- **ncounts** (`numpy.array`) – number of nodes in each bin
- **nbetw** (`numpy.array`) – bins for node betweenness
- **ecounts** (`numpy.array`) – number of edges in each bin
- **ebetw** (`numpy.array`) – bins for edge betweenness

`nngt.analysis.`**`binning`**(*x*, *bins='bayes'*, *log=False*)

Binning function providing automatic binning using Bayesian blocks in addition to standard linear and logarithmic uniform bins.

New in version 0.7.

Parameters

- **x** (*array-like*) – Array of data to be histogrammed
- **bins** (*int, list or 'auto', optional (default: 'bayes')*) – If *bins* is 'bayes', in use bayesian blocks for dynamic bin widths; if it is an int, the interval will be separated into
- **log** (*bool, optional (default: False)*) – Whether the bins should be evenly spaced on a logarithmic scale.

`nngt.analysis.`**`closeness`**(*graph*, *nodes=None*, *use_weights=False*)

Return the closeness centrality for each node in *nodes*.

Parameters

- **graph** (*Graph* object) – Graph to analyze.
- **nodes** (*array-like container with node ids, optional (default = all nodes)*) – Nodes for which the local clustering coefficient should be computed.
- **use_weights** (*bool, optional (default: False)*) – Whether weighted closeness should be used.

`nngt.analysis.`**`clustering`**(*graph*)

Global clustering coefficient of the graph. Defined as:

$$c = 3 \times \frac{\text{triangles}}{\text{connected triples}}$$

`nngt.analysis.`**`degree_distrib`**(*graph*, *deg_type='total'*, *node_list=None*, *use_weights=False*, *log=False*, *num_bins='bayes'*)

Degree distribution of a graph.

Changed in version 0.7.

Inclusion of automatic binning.

Parameters

- **graph** (*Graph* or subclass) – the graph to analyze.
- **deg_type** (*string, optional (default: "total")*) – type of degree to consider ("in", "out", or "total").
- **node_list** (*list or numpy.array of ints, optional (default: None)*) – Restrict the distribution to a set of nodes (default: all nodes).
- **use_weights** (*bool, optional (default: False)*) – use weighted degrees (do not take the sign into account: all weights are positive).
- **log** (*bool, optional (default: False)*) – use log-spaced bins.
- **num_bins** (*int, list or str, optional (default: 'bayes')*) – Any of the automatic methodes from `numpy.histogram()`, or 'bayes' will provide automatic bin optimization. Otherwise, an int for the number of bins can be provided, or the direct bins list.

See also:

`numpy.histogram()`, *`binning()`*

Returns

- **counts** (`numpy.array`) – number of nodes in each bin
- **deg** (`numpy.array`) – bins

`nngt.analysis.`**`diameter`**(*graph*)

Pseudo-diameter of the graph

@todo: weighted diameter

`nngt.analysis.`**`local_clustering`**(*graph*, *nodes=None*)

Local clustering coefficient of the nodes. Defined as

$$c_i = 3 \times \frac{\text{triangles}}{\text{connected triples}}$$

Parameters

- **graph** (`Graph` object) – Graph to analyze.
- **nodes** (*array-like container with node ids, optional (default = all nodes)*) – Nodes for which the local clustering coefficient should be computed.

`nngt.analysis.`**`node_attributes`**(*network*, *attributes*, *nodes=None*, *data=None*)

Return node *attributes* for a set of *nodes*.

Parameters

- **network** (`Graph`) – The graph where the *nodes* belong.
- **attributes** (*str or list*) – Attributes which should be returned, among: * "betweenness" * "clustering" * "in-degree", "out-degree", "total-degree" * "subgraph_centrality"
- **nodes** (*list, optional (default: all nodes)*) – Nodes for which the attributes should be returned.
- **data** (`numpy.array` of shape (N, 2), optional (default: None)) – Potential data on the spike events; if not None, it must contain the sender ids on the first column and the spike times on the second.

Returns **values** (*array-like or dict*) – Returns the attributes, either as an array if only one attribute is required (*attributes* is a `str`) or as a `dict` of arrays.

`nngt.analysis.`**`num_iedges`**(*graph*)

Returns the number of inhibitory connections.

`nngt.analysis.`**`num_scc`**(*graph*, *listing=False*)

Returns the number of strongly connected components (SCCs). SCC are ensembles where all contained nodes can reach any other node in the ensemble using the directed edges.

See also:

`num_wcc()`

`nngt.analysis.`**`num_wcc`**(*graph*, *listing=False*)

Connected components if the directivity of the edges is ignored. (i.e. all edges are considered bidirectional).

See also:

`num_scc()`

`nngt.analysis.`**`reciprocity`**(*graph*)

Graph reciprocity, defined as $E^{\leftrightarrow}/E$, where $E^{\leftrightarrow}$ and E are, respectively, the number of bidirectional edges and the total number of edges in the graph.

Returns *a float quantifying the reciprocity.*

`nngt.analysis.`**`spectral_radius`**(*graph*, *typed=True*, *weighted=True*)

Spectral radius of the graph, defined as the eigenvalue of greatest module.

Parameters

- **graph** (`Graph` or subclass) – Network to analyze.
- **typed** (*bool, optional (default: True)*) – Whether the excitatory/inhibitory type of the connnections should be considered.
- **weighted** (*bool, optional (default: True)*) – Whether the weights should be taken into account.

Returns *the spectral radius as a float.*

`nngt.analysis.`**`subgraph_centrality`**(*graph*, *weights=True*, *normalize='max_centrality'*)

Subgraph centrality, accordign to [Estrada2005], for each node in the graph.

[Estrada2005]: Ernesto Estrada and Juan A. Rodríguez-Velázquez, Subgraph centrality in complex networks, PHYSICAL REVIEW E 71, 056103 (2005), available on ArXiv.

Parameters

- **graph** (*`Graph`* or subclass) – Network to analyze.
- **weights** (*bool or string, optional (default: True)*) – Whether weights should be taken into account; if True, then connections are weighed by their synaptic strength, if False, then a binary matrix is returned, if *weights* is a string, then the ponderation is the correponding value of the edge attribute (e.g. "distance" will return an adjacency matrix where each connection is multiplied by its length).
- **normalize** (*str, optional (default: "max_centrality")*) – Whether the centrality should be normalized. Accepted normalizations are "max_eigenvalue" and "max_centrality"; the first rescales the adjacency matrix by the its largest eigenvalue before taking the exponential, the second sets the maximum centrality to one.

Returns **centralities** (`numpy.ndarray`) – The subgraph centrality of each node.

`nngt.analysis.`**`transitivity`**(*graph*)

Same as *`nngt.analysis.clustering()`* (for networkx users)

`nngt.analysis.`**`get_b2`**(*network=None*, *spike_detector=None*, *data=None*, *nodes=None*)

Return the B2 coefficient for the neurons.

Parameters

- **network** (*`nngt.Network`*, optional (default: None)) – Network for which the activity was simulated.
- **spike_detector** (*tuple of ints, optional (default: spike detectors)*) – GID of the "spike_detector" objects recording the network activity.
- **data** (*array-like of shape (N, 2), optionale (default: None)*) – Array containing the spikes data (first line must contain the NEST GID of the neuron that fired, second line must contain the associated spike time).
- **nodes** (*array-like, optional (default: all neurons)*) – NNGT ids of the nodes for which the B2 should be computed.

Returns **b2** (*array-like*) – B2 coefficient for each neuron in *nodes*.

`nngt.analysis.`**`get_firing_rate`**(*network=None*, *spike_detector=None*, *data=None*, *nodes=None*)

Return the average firing rate for the neurons.

Parameters

- **network** (*`nngt.Network`*, optional (default: None)) – Network for which the activity was simulated.
- **spike_detector** (*tuple of ints, optional (default: spike detectors)*) – GID of the "spike_detector" objects recording the network activity.
- **data** (`numpy.array` of shape (N, 2), optionale (default: None)) – Array containing the spikes data (first line must contain the NEST GID of the neuron that fired, second line must contain the associated spike time).
- **nodes** (*array-like, optional (default: all nodes)*) – NNGT ids of the nodes for which the B2 should be computed.

Returns **fr** (*array-like*) – Firing rate for each neuron in *nodes*.

`nngt.analysis.`**`get_spikes`**(*recorder=None*, *spike_times=None*, *senders=None*)

Return a 2D sparse matrix, where:

- each row i contains the spikes of neuron i
- each column j contains the times of the jth spike for all neurons

Parameters

- **recorder** (*tuple, optional (default: None)*) – Tuple of NEST gids, where the first one should point to the spike_detector which recorded the spikes.
- **spike_times** (*array-like, optional (default: None)*) – If *recorder* is not provided, the spikes' data can be passed directly through their *spike_times* and the associated *senders*.
- **senders** (*array-like, optional (default: None)*) – *senders[i]* corresponds to the neuron which fired at *spike_times[i]*.

Example

```
>>> get_spikes()
```

```
>>> get_spikes(recorder)
```

```
>>> times = [1.5, 2.68, 125.6]
>>> neuron_ids = [12, 0, 65]
>>> get_spikes(spike_times=times, senders=neuron_ids)
```

Note: This function supposes that neuron GIDs for a continuous set of integers. If no arguments are passed to the function, the first spike_recorder available in NEST will be used.

Returns

- *CSR matrix containing the spikes sorted by neuron (rows) and time*
- *(columns).*

`nngt.analysis.`**`total_firing_rate`**(*network=None*, *spike_detector=None*, *data=None*, *kernel_center=0.0*, *kernel_std=30.0*, *resolution=None*, *cut_gaussian=5.0*)

Computes the total firing rate of the network from the spike times. Firing rate is obtained as the convolution of the spikes with a Gaussian kernel characterized by a standard deviation and a temporal shift.

New in version 0.7.

Parameters

- **network** (`nngt.Network`, optional (default: None)) – Network for which the activity was simulated.
- **spike_detector** (*tuple of ints, optional (default: spike detectors)*) – GID of the "spike_detector" objects recording the network activity.

- **data** (`numpy.array` of shape (N, 2), optionale (default: None)) – Array containing the spikes data (first line must contain the NEST GID of the neuron that fired, second line must contain the associated spike time).
- **kernel_center** (*float, optional (default: 0.)*) – Temporal shift of the Gaussian kernel, in ms.
- **kernel_std** (*float, optional (default: 30.)*) – Characteristic width of the Gaussian kernel (standard deviation) in ms.
- **resolution** (float or array, optional (default: *0.1*kernel_std*)) – The resolution at which the firing rate values will be computed. Choosing a value smaller than *kernel_std* is strongly advised. If resolution is an array, it will be considered as the times were the firing rate should be computed.
- **cut_gaussian** (*float, optional (default: 5.)*) – Range over which the Gaussian will be computed. By default, we consider the 5-sigma range. Decreasing this value will increase speed at the cost of lower fidelity; increasing it with increase the fidelity at the cost of speed.

Returns

- **fr** (*array-like*) – The firing rate in Hz.
- **times** (*array-like*) – The times associated to the firing rate values.

Core module

Core classes and functions. Most of them are not visible in the module as they are directly loaded at `nngt` level.

Content

class `nngt.core.`**`Connections`**

The basic class that computes the properties of the connections between neurons for graphs.

static **`delays`**(*graph=None*, *dlist=None*, *elist=None*, *distribution='constant'*, *parameters=None*, *noise_scale=None*)

Compute the delays of the neuronal connections.

Parameters

- **graph** (class:~*nngt.Graph* or subclass) – Graph the nodes belong to.
- **dlist** (class:*numpy.array*, optional (default: None)) – List of user-defined delays).
- **elist** (class:*numpy.array*, optional (default: None)) – List of the edges which value should be updated.
- **distribution** (class:*string*, optional (default: "constant")) – Type of distribution (choose among "constant", "uniform", "lognormal", "gaussian", "user_def", "lin_corr", "log_corr").
- **parameters** (class:*dict*, optional (default: {})) – Dictionary containing the distribution parameters.
- **noise_scale** (class:*int*, optional (default: None)) – Scale of the multiplicative Gaussian noise that should be applied on the weights.

Returns **new_delays** (class:*scipy.sparse.lil_matrix*) – A sparse matrix containing *ONLY* the newly-computed weights.

static `distances` (*graph*, *elist=None*, *pos=None*, *dlist=None*, *overwrite=False*)

Compute the distances between connected nodes in the graph. Try to add only the new distances to the graph. If they overlap with previously computed distances, recomputes everything.

Parameters

- **graph** (class:*~nngt.Graph* or subclass) – Graph the nodes belong to.
- **elist** (class:*numpy.array*, optional (default: None)) – List of the edges.
- **pos** (class:*numpy.array*, optional (default: None)) – Positions of the nodes; note that if *graph* has a "position" attribute, *pos* will not be taken into account.
- **dlist** (class:*numpy.array*, optional (default: None)) – List of distances (for user-defined distances)

Returns **new_dist** (class:*numpy.array*) – Array containing *ONLY* the newly-computed distances.

static `types` (*graph*, *inhib_nodes=None*, *inhib_frac=None*)

@todo

Define the type of a set of neurons. If no arguments are given, all edges will be set as excitatory.

Parameters

- **graph** (`Graph` or subclass) – Graph on which edge types will be created.
- **inhib_nodes** (int, float or list, optional (default: *None*)) – If *inhib_nodes* is an int, number of inhibitory nodes in the graph (all connections from inhibitory nodes are inhibitory); if it is a float, ratio of inhibitory nodes in the graph; if it is a list, ids of the inhibitory nodes.
- **inhib_frac** (float, optional (default: *None*)) – Fraction of the selected edges that will be set as refractory (if *inhib_nodes* is not *None*, it is the fraction of the nodes' edges that will become inhibitory, otherwise it is the fraction of all the edges in the graph).

Returns **t_list** (`ndarray`) – List of the edges' types.

static `weights` (*graph=None*, *elist=None*, *wlist=None*, *distribution='constant'*, *parameters={}*, *noise_scale=None*)

Compute the weights of the graph's edges. @todo: take elist into account

Parameters

- **graph** (class:*~nngt.Graph* or subclass) – Graph the nodes belong to.
- **elist** (class:*numpy.array*, optional (default: None)) – List of the edges (for user defined weights).
- **wlist** (class:*numpy.array*, optional (default: None)) – List of the weights (for user defined weights).
- **distribution** (class:*string*, optional (default: "constant")) – Type of distribution (choose among "constant", "uniform", "lognormal", "gaussian", "user_def", "lin_corr", "log_corr").
- **parameters** (class:*dict*, optional (default: {})) – Dictionary containing the distribution parameters.
- **noise_scale** (class:*int*, optional (default: None)) – Scale of the multiplicative Gaussian noise that should be applied on the weights.

Returns **new_weights** (class:*scipy.sparse.lil_matrix*) – A sparse matrix containing *ONLY* the newly-computed weights.

nngt.core.**GraphObject**

Graph object (reference to one of the main libraries' wrapper

alias of `_GtGraph`

Generation module

Functions that generates the underlying connectivity of graphs, as well as the synaptic properties (weight/strength and delay).

Content

nngt.generation.connect_neural_groups(...)	Function to connect excitatory and inhibitory population with a given graph model.
nngt.generation.connect_neural_types(...)	Function to connect excitatory and inhibitory population with a given graph model.
nngt.generation.distance_rule(scale[, rule, ...])	Create a graph using a 2D distance rule to create the connection between neurons.
nngt.generation.erdos_renyi([density, ...])	Generate a random graph as defined by Erdos and Renyi but with a reciprocity that can be chosen.
nngt.generation.fixed_degree(degree[, ...])	Generate a random graph with constant in- or out-degree.
nngt.generation.gaussian_degree(avg, std[, ...])	Generate a random graph with constant in- or out-degree.
nngt.generation.newman_watts(coord_nb, ...)	Generate a small-world graph using the Newman-Watts algorithm.
nngt.generation.price_scale_free(m[, c, ...])	@todo
nngt.generation.random_scale_free(in_exp, ...)	Generate a free-scale graph of given reciprocity and otherwise devoid of correlations.

Details

nngt.generation.**connect_neural_groups**(*network*, *source_groups*, *target_groups*, *graph_model*, *model_param*)

Function to connect excitatory and inhibitory population with a given graph model.

@todo make the modifications for only a set of edges

Parameters

- **network** (`Network` or `SpatialNetwork`) – The network to connect.
- **source_groups** (*str or tuple*) – Names of the source groups (which contain the pre-synaptic neurons)
- **target_groups** (*str or tuple*) – Names of the target groups (which contain the post-synaptic neurons)
- **graph_model** (*string*) – The name of the connectivity model (among "erdos_renyi", "random_scale_free", "price_scale_free", and "newman_watts").
- **model_param** (*dict*) – Dictionary containing the model parameters (the keys are the keywords of the associated generation function — see above).

`nngt.generation.`**`connect_neural_types`**(*network*, *source_type*, *target_type*, *graph_model*, *model_param*)

Function to connect excitatory and inhibitory population with a given graph model.

@todo make the modifications for only a set of edges

Parameters

- **network** (`Network` or `SpatialNetwork`) – The network to connect.
- **source_type** (*int*) – The type of source neurons (`1` for excitatory, `-1` for inhibitory neurons).
- **source_type** (*int*) – The type of target neurons.
- **graph_model** (*string*) – The name of the connectivity model (among "erdos_renyi", "random_scale_free", "price_scale_free", and "newman_watts").
- **model_param** (*dict*) – Dictionary containing the model parameters (the keys are the keywords of the associated generation function — see above).

`nngt.generation.`**`distance_rule`**(*scale*, *rule='exp'*, *shape=None*, *neuron_density=1000.0*, *nodes=0*, *density=-1.0*, *edges=-1*, *avg_deg=-1.0*, *unit='um'*, *weighted=True*, *directed=True*, *multigraph=False*, *name='DR'*, *positions=None*, *population=None*, *from_graph=None*, ***kwargs*)

Create a graph using a 2D distance rule to create the connection between neurons. Available rules are linear and exponential.

Parameters

- **scale** (*float*) – Characteristic scale for the distance rule. E.g for linear distance- rule, $P(i,j) \propto (1-d_{ij}/scale))$, whereas for the exponential distance-rule, $P(i,j) \propto e^{-d_{ij}/scale}$.
- **rule** (*string, optional (default: 'exp')*) – Rule that will be apply to draw the connections between neurons. Choose among "exp" (exponential), "lin" (linear), "power" (power-law, not implemented yet).
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment. If not specified, a square will be created with the appropriate dimensions for the number of neurons and the neuron spatial density.
- **neuron_density** (*float, optional (default: 1000.)*) – Density of neurons in space ($neurons \cdot mm^{-2}$).
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **density** (*double, optional (default: 0.1)*) – Structural density given by *edges* / (*nodes* * *nodes*).
- **edges** (*int (optional)*) – The number of edges between the nodes
- **avg_deg** (*double, optional*) – Average degree of the neurons given by *edges* / *nodes*.
- **unit** (*string (default: 'um')*) – Unit for the length $scale$ among 'um' (μm), 'mm', 'cm', 'dm', 'm'.
- **weighted** (*bool, optional (default: True)*) – @todo Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or not.
- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes.
- **name** (*string, optional (default: "DR")*) – Name of the created graph.

- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D (N, 2) or 3D (N, 3) shaped array containing the positions of the neurons in space.
- **population** (*`NeuralPop`*, optional (default: None)) – Population of neurons defining their biological properties (to create a *`Network`*).
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

`nngt.generation.`**`erdos_renyi`**(*density=-1.0, nodes=0, edges=-1, avg_deg=-1.0, reciprocity=-1.0, weighted=True, directed=True, multigraph=False, name='ER', shape=None, positions=None, population=None, from_graph=None, **kwargs*)

Generate a random graph as defined by Erdos and Renyi but with a reciprocity that can be chosen.

Parameters

- **density** (*double, optional (default: -1.)*) – Structural density given by *edges / nodes*^{2}. It is also the probability for each possible edge in the graph to exist.
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **edges** (*int (optional)*) – The number of edges between the nodes
- **avg_deg** (*double, optional*) – Average degree of the neurons given by *edges / nodes*.
- **reciprocity** (*double, optional (default: -1 to let it free)*) – Fraction of edges that are bidirectional (only for directed graphs – undirected graphs have a reciprocity of 1 by definition)
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or not.
- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes.
- **name** (*string, optional (default: "ER")*) – Name of the created graph.
- **shape** (*`Shape`*, optional (default: None)) – Shape of the neurons' environment.
- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D or 3D array containing the positions of the neurons in space.
- **population** (*`NeuralPop`*, optional (default: None)) – Population of neurons defining their biological properties (to create a *`Network`*).
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

Returns **graph_er** (*`Graph`*, or subclass) – A new generated graph or the modified *from_graph*.

Note: *nodes* is required unless *from_graph* or *population* is provided. If an *from_graph* is provided, all preexistant edges in the object will be deleted before the new connectivity is implemented.

`nngt.generation.`**`fixed_degree`**(*degree, degree_type='in', nodes=0, reciprocity=-1.0, weighted=True, directed=True, multigraph=False, name='FD', shape=None, positions=None, population=None, from_graph=None, **kwargs*)

Generate a random graph with constant in- or out-degree.

Parameters

- **degree** (*int*) – The value of the constant degree.

- **degree_type** (*str, optional (default: 'in')*) – The type of the fixed degree, among `'in'`, `'out'` or `'total'`.

  @todo *'total'* not implemented yet.
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **reciprocity** (*double, optional (default: -1 to let it free)*) – @todo: not implemented yet. Fraction of edges that are bidirectional (only for directed graphs – undirected graphs have a reciprocity of 1 by definition)
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – @todo: only for directed graphs for now. Whether the graph is directed or not.
- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes.
- **name** (*string, optional (default: "ER")*) – Name of the created graph.
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment.
- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D or 3D array containing the positions of the neurons in space.
- **population** (`NeuralPop`, optional (default: None)) – Population of neurons defining their biological properties (to create a `Network`).
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

Note: *nodes* is required unless *from_graph* or *population* is provided. If an *from_graph* is provided, all preexistant edges in the object will be deleted before the new connectivity is implemented.

Returns **graph_fd** (`Graph`, or subclass) – A new generated graph or the modified *from_graph*.

`nngt.generation.`**`gaussian_degree`**(*avg*, *std*, *degree_type='in'*, *nodes=0*, *reciprocity=-1.0*, *weighted=True*, *directed=True*, *multigraph=False*, *name='GD'*, *shape=None*, *positions=None*, *population=None*, *from_graph=None*, ***kwargs*)

Generate a random graph with constant in- or out-degree. @todo: adapt it for undirected graphs!

Parameters

- **avg** (*float*) – The value of the average degree.
- **std** (*float*) – The standard deviation of the Gaussian distribution.
- **degree_type** (*str, optional (default: 'in')*) – The type of the fixed degree, among 'in', 'out' or 'total' @todo: Implement 'total' degree
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **reciprocity** (*double, optional (default: -1 to let it free)*) – @todo: not implemented yet. Fraction of edges that are bidirectional (only for directed graphs – undirected graphs have a reciprocity of 1 by definition)
- **weighted** (*bool, optional (default: True)*) – Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – @todo: only for directed graphs for now. Whether the graph is directed or not.

- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes.
- **name** (*string, optional (default: "ER")*) – Name of the created graph.
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment.
- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D or 3D array containing the positions of the neurons in space.
- **population** (`NeuralPop`, optional (default: None)) – Population of neurons defining their biological properties (to create a `Network`).
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

Returns **graph_gd** (`Graph`, or subclass) – A new generated graph or the modified *from_graph*.

Note: *nodes* is required unless *from_graph* or *population* is provided. If an *from_graph* is provided, all preexistant edges in the object will be deleted before the new connectivity is implemented.

`nngt.generation.`**`random_scale_free`**(*in_exp, out_exp, nodes=0, density=0.1, edges=-1, avg_deg=-1, reciprocity=0.0, weighted=True, directed=True, multigraph=False, name='RandomSF', shape=None, positions=None, population=None, from_graph=None, **kwargs*)

Generate a free-scale graph of given reciprocity and otherwise devoid of correlations.

Parameters

- **in_exp** (*float*) – Absolute value of the in-degree exponent γ_i, such that $p(k_i) \propto k_i^{-\gamma_i}$
- **out_exp** (*float*) – Absolute value of the out-degree exponent γ_o, such that $p(k_o) \propto k_o^{-\gamma_o}$
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **density** (*double, optional (default: 0.1)*) – Structural density given by *edges / (nodes*nodes)*.
- **edges** (*int (optional)*) – The number of edges between the nodes
- **avg_deg** (*double, optional*) – Average degree of the neurons given by *edges / nodes*.
- **weighted** (*bool, optional (default: True)*) – @todo Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or not.
- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes. can contain multiple edges between two
- **name** (*string, optional (default: "ER")*) – Name of the created graph.
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment.
- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D or 3D array containing the positions of the neurons in space.
- **population** (`NeuralPop`, optional (default: None)) – Population of neurons defining their biological properties (to create a `Network`)
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

Returns **graph_fs** (`Graph`)

Note: As reciprocity increases, requested values of *in_exp* and *out_exp* will be less and less respected as the distribution will converge to a common exponent $\gamma = (\gamma_i + \gamma_o)/2$. Parameter *nodes* is required unless *from_graph* or *population* is provided.

`nngt.generation.`**`price_scale_free`**(*m*, *c=None*, *gamma=1*, *nodes=0*, *weighted=True*, *directed=True*, *seed_graph=None*, *multigraph=False*, *name='PriceSF'*, *shape=None*, *positions=None*, *population=None*, *from_graph=None*, ***kwargs*)

@todo make the algorithm.

Generate a Price graph model (Barabasi-Albert if undirected).

Parameters

- **m** (*int*) – The number of edges each new node will make.
- **c** (*double*) – Constant added to the probability of a vertex receiving an edge.
- **gamma** (*double*) – Preferential attachment power.
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **weighted** (*bool, optional (default: True)*) –

  @todo Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or not.
- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes.
- **name** (*string, optional (default: "ER")*) – Name of the created graph.
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment
- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D or 3D array containing the positions of the neurons in space.
- **population** (`NeuralPop`, optional (default: None)) – Population of neurons defining their biological properties (to create a `Network`).
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

Returns **graph_price** (`Graph` or subclass.)

Note: *nodes* is required unless *from_graph* or *population* is provided.

`nngt.generation.`**`newman_watts`**(*coord_nb*, *proba_shortcut*, *nodes=0*, *weighted=True*, *directed=True*, *multigraph=False*, *name='NW'*, *shape=None*, *positions=None*, *population=None*, *from_graph=None*, ***kwargs*)

Generate a small-world graph using the Newman-Watts algorithm.

@todo generate the edges of a circular graph to not replace the graph of the *from_graph* and implement chosen reciprocity.

Parameters

- **coord_nb** (*int*) – The number of neighbours for each node on the initial topological lattice.

- **proba_shortcut** (*double*) – Probability of adding a new random (shortcut) edge for each existing edge on the initial lattice.
- **nodes** (*int, optional (default: None)*) – The number of nodes in the graph.
- **density** (*double, optional (default: 0.1)*) – Structural density given by *edges* / (*nodes`*`nodes*).
- **edges** (*int (optional)*) – The number of edges between the nodes
- **avg_deg** (*double, optional*) – Average degree of the neurons given by *edges* / *nodes*.
- **weighted** (*bool, optional (default: True)*) – @todo Whether the graph edges have weights.
- **directed** (*bool, optional (default: True)*) – Whether the graph is directed or not.
- **multigraph** (*bool, optional (default: False)*) – Whether the graph can contain multiple edges between two nodes.
- **name** (*string, optional (default: "ER")*) – Name of the created graph.
- **shape** (`Shape`, optional (default: None)) – Shape of the neurons' environment
- **positions** (`numpy.ndarray`, optional (default: None)) – A 2D or 3D array containing the positions of the neurons in space.
- **population** (`NeuralPop`, optional (default: None)) – Population of neurons defining their biological properties (to create a `Network`).
- **from_graph** (`Graph` or subclass, optional (default: None)) – Initial graph whose nodes are to be connected.

Returns **graph_nw** (`Graph` or subclass)

Note: *nodes* is required unless *from_graph* or *population* is provided.

Geometry module

This module is a direct copy of the SENeC package PyNCulture. Therefore, in the examples below, you will have to import `nngt` instead of `PyNCulture` and replace `pnc` by `nngt.geometry`.

Overview

`nngt.geometry.Shape`	alias of `BackupShape`
`nngt.geometry.culture_from_file`(filename[, ...])	Generate a culture from an SVG or DXF file.
`nngt.geometry.plot_shape`(shape[, axis, m, ...])	Plot a shape (set the *axis* aspect to 1 to respect the proportions).

Principle

Module dedicated to the description of the spatial boundaries of neuronal cultures. This allows for the generation of neuronal networks that are embedded in space.

The shapely library is used to generate and deal with the spatial environment of the neurons.

Examples

Basic features

The module provides a backup Shape object, which can be used with only the *numpy* and *scipy* libraries. It allows for the generation of simple rectangle, disk and ellipse shapes.

```
import matplotlib.pyplot as plt

import PyNCulture as pnc


fig, ax = plt.subplots()

''' Choose a shape (uncomment the desired line) '''
culture = pnc.Shape.rectangle(15, 20, (5, 0))
# culture = pnc.Shape.disk(20, (5, 0))
# culture = pnc.Shape.ellipse((20, 5), (5, 0))

''' Generate the neurons inside '''
pos = culture.seed_neurons(neurons=1000, xmax=0., ymax=0.)

''' Plot '''
pnc.plot_shape(culture, ax)
ax.scatter(pos[:, 0], pos[:, 1], s=2, zorder=2)

plt.show()
```

All these features are of course still available with the more advanced Shape object which inherits from shapely.geometry.Polygon.

Complex shapes from files

```
import matplotlib.pyplot as plt

import PyNCulture as pnc


''' Choose a file '''
culture_file = "culture_from_filled_polygons.svg"
# culture_file = "culture_with_holes.svg"
# culture_file = "culture.dxf"

shapes = None

if culture_file.endswith(".dxf"):
    shapes = pnc.shapes_from_dxf(culture_file)
else:
    shapes = pnc.shapes_from_svg(culture_file)

''' Plot the shapes '''
fig, ax = plt.subplots()
plt.title("shapes")

for shape in shapes:
    pnc.plot_shape(shape, ax)
```

```
''' Make a culture '''
fig2, ax2 = plt.subplots()
plt.title("culture")

culture = pnc.culture_from_file(culture_file)

pnc.plot_shape(culture, ax2)

''' Add neurons '''
fig3, ax3 = plt.subplots()
plt.title("culture with neurons")

culture_bis = pnc.culture_from_file(culture_file)
pos = culture_bis.seed_neurons(neurons=1000, xmax=0)

pnc.plot_shape(culture_bis, ax3)
ax3.scatter(pos[:, 0], pos[:, 1], s=2, zorder=3)

plt.show()
```

Content

`nngt.geometry.`**`Shape`**
alias of `BackupShape`

`nngt.geometry.`**`plot_shape`**(*shape*, *axis=None*, *m=''*, *mc='#999999'*, *fc='#8888ff'*, *ec='#444444'*, *alpha=0.5*, ***kwargs*)
Plot a shape (set the *axis* aspect to 1 to respect the proportions).

Parameters

- **shape** (*Shape*) – Shape to plot.
- **axis** (`matplotlib.axes.Axes` instance, optional (default: None)) – Axis on which the shape should be plotted. By default, a new figure is created.
- **m** (*str, optional (default: invisible)*) – Marker to plot the shape's vertices, matplotlib syntax.
- **mc** (*str, optional (default: "#999999")*) – Color of the markers.
- **fc** (*str, optional (default: "#8888ff")*) – Color of the shape's interior.
- **ec** (*str, optional (default: "#444444")*) – Color of the shape's edges.
- **alpha** (*float, optional (default: 0.5)*) – Opacity of the shape's interior.
- **kwargs** (keywords arguments for `matplotlib.patches.PathPatch`)

Lib module

Tools for the other modules.

Warning: These tools have been designed primarily for internal use throughout the library and often work only in very specific situations (e.g. `find_idx_nearest()` works only on sorted arrays), so make sure you read their doc carefully before using them.

Content

nngt.lib.InvalidArgument	Error raised when an argument is invalid.
nngt.lib.delta_distrib([graph, elist, num, ...])	Delta distribution for edge attributes.
nngt.lib.find_idx_nearest(array, values)	Find the indices of the nearest elements of *values* in a sorted *array*.
nngt.lib.gaussian_distrib(graph[, elist, ...])	Gaussian distribution for edge attributes.
nngt.lib.lin_correlated_distrib(graph[, ...])	
nngt.lib.log_correlated_distrib(graph[, ...])	
nngt.lib.lognormal_distrib(graph[, elist, ...])	
nngt.lib.nonstring_container(obj)	Returns true for any iterable which is not a string or byte sequence.
nngt.lib.not_implemented(*args, **kwargs)	
nngt.lib.seed([seed])	Seed the random generator used by NNGT (i.e.
nngt.lib.uniform_distrib(graph[, elist, ...])	Uniform distribution for edge attributes.
nngt.lib.valid_gen_arguments(func)	

Details

Various tools for random number generation, array searching and type testing.

nngt.lib.**delta_distrib**(*graph=None*, *elist=None*, *num=None*, *value=1.0*, ***kwargs*)

Delta distribution for edge attributes.

Parameters

- **graph** (*Graph* or subclass) – Graph for which an edge attribute will be generated.
- **elist** (*@todo*)
- **value** (*float, optional (default: 1.)*) – Value of the delta distribution.
- **Returns** (numpy.ndarray) – Attribute value for each edge in *graph*.

nngt.lib.**find_idx_nearest**(*array*, *values*)

Find the indices of the nearest elements of *values* in a sorted *array*.

Warning: Both `array` and `values` should be *numpy.array* objects and *array* MUST be sorted in increasing order.

Parameters

- **array** (*reference list or np.ndarray*)
- **values** (double, list or array of values to find in *array*)

Returns **idx** (int or array representing the index of the closest value in *array*)

nngt.lib.**gaussian_distrib**(*graph*, *elist=None*, *num=None*, *avg=1.0*, *std=0.2*, ***kwargs*)

Gaussian distribution for edge attributes.

Parameters

- **graph** (*Graph* or subclass) – Graph for which an edge attribute will be generated.
- **elist** (*@todo*)

- **avg** (*float, optional (default: 0.)*) – Average of the Gaussian distribution.
- **std** (*float, optional (default: 1.5)*) – Standard deviation of the Gaussian distribution.
- **Returns** (`numpy.ndarray`) – Attribute value for each edge in *graph*.

exception `nngt.lib.`**`InvalidArgument`**

Error raised when an argument is invalid.

`nngt.lib.`**`lin_correlated_distrib`**(*graph*, *elist=None*, *correl_attribute='betweenness'*, *noise_scale=None*, *lower=0.0*, *upper=2.0*, ***kwargs*)

`nngt.lib.`**`log_correlated_distrib`**(*graph*, *elist=None*, *correl_attribute='betweenness'*, *noise_scale=None*, *lower=0.0*, *upper=2.0*, ***kwargs*)

`nngt.lib.`**`lognormal_distrib`**(*graph*, *elist=None*, *num=None*, *position=1.0*, *scale=0.2*, ***kwargs*)

`nngt.lib.`**`nonstring_container`**(*obj*)

Returns true for any iterable which is not a string or byte sequence.

`nngt.lib.`**`uniform_distrib`**(*graph*, *elist=None*, *num=None*, *lower=0.0*, *upper=1.5*, ***kwargs*)

Uniform distribution for edge attributes.

Parameters

- **graph** (`Graph` or subclass) – Graph for which an edge attribute will be generated.
- **elist** (*@todo*)
- **lower** (*float, optional (default: 0.)*) – Min value of the uniform distribution.
- **upper** (*float, optional (default: 1.5)*) – Max value of the uniform distribution.
- **Returns** (`numpy.ndarray`) – Attribute value for each edge in *graph*.

Plot module

Functions for plotting graphs and graph properties.

Content

`nngt.plot.betweenness_distribution`(network)	Plotting the betweenness distribution of a graph.
`nngt.plot.compare_population_attributes`(...)	Compare node *attributes* between two sets of nodes.
`nngt.plot.correlation_to_attribute`(network, ...)	For each node plot the value of *reference_attributes* against each of the *other_attributes* to check for correlations.
`nngt.plot.degree_distribution`(network[, ...])	Plotting the degree distribution of a graph.
`nngt.plot.draw_network`(network[, nsize, ...])	Draw a given graph/network.
`nngt.plot.node_attributes_distribution`(...)	Return node *attributes* for a set of *nodes*.
`nngt.plot.palette`(numbers)	

Details

This modules provides the following features:

- plotting the distribution of some attribute over the graph
- basic graph plotting
- animation of some recorded activity

`nngt.plot.`**`Animation2d`**

`nngt.plot.`**`AnimationNetwork`**

`nngt.plot.`**`draw_network`**(*network*, *nsize='total-degree'*, *ncolor='group'*, *nshape='o'*, *nborder_color='k'*, *nborder_width=0.5*, *esize=1.0*, *ecolor='k'*, *max_nsize=5.0*, *max_esize=2.0*, *threshold=0.5*, *decimate=None*, *spatial=True*, *size=(600, 600)*, *xlims=None*, *ylims=None*, *dpi=75*, *axis=None*, *show=False*, ***kwargs*)

Draw a given graph/network.

Parameters

- **network** (`Graph` or subclass) – The graph/network to plot.
- **nsize** (*float, array of float or string, optional (default: "total-degree")*) – Size of the nodes as a percentage of the canvas length. Otherwise, it can be a string that correlates the size to a node attribute among "in/out/total-degree", or "betweenness".
- **ncolor** (*float, array of floats or string, optional (default: 0.5)*) – Color of the nodes; if a float in [0, 1], position of the color in the current palette, otherwise a string that correlates the color to a node attribute among "in/out/total-degree", "betweenness" or "group".
- **nshape** (*char or array of chars, optional (default: "o")*) – Shape of the nodes (see Matplotlib markers).
- **nborder_color** (*char, float or array, optional (default: "k")*) – Color of the node's border using predefined Matplotlib colors). or floats in [0, 1] defining the position in the palette.
- **nborder_width** (*float or array of floats, optional (default: 0.5)*) – Width of the border in percent of canvas size.
- **esize** (*float, str, or array of floats, optional (default: 0.5)*) – Width of the edges in percent of canvas length. Available string values are "betweenness" and "weight".
- **ecolor** (*char, float or array, optional (default: "k")*) – Edge color.
- **max_esize** (*float, optional (default: 5.)*) – If a custom property is entered as *esize*, this normalizes the edge width between 0. and *max_esize*.
- **decimate** (*int, optional (default: keep all connections)*) – Plot only one connection every *decimate*.
- **spatial** (*bool, optional (default: True)*) – If True, use the neurons' positions to draw them.
- **size** (*tuple of ints, optional (default: (600,600))*) – (width, height) tuple for the canvas size (in px).
- **dpi** (*int, optional (default: 75)*) – Resolution (dot per inch).

`nngt.plot.`**`palette`**(*numbers*)

`nngt.plot.`**`degree_distribution`**(*network*, *deg_type='total'*, *nodes=None*, *num_bins='doane'*, *use_weights=False*, *logx=False*, *logy=False*, *axis=None*, *axis_num=None*, *colors=None*, *norm=False*, *show=False*, ***kwargs*)

Plotting the degree distribution of a graph.

Parameters

- **graph** (`Graph` or subclass) – The graph to analyze.
- **deg_type** (*string or N-tuple, optional (default: "total")*) – Type of degree to consider ("in", "out", or "total")

- **nodes** (*list or numpy.array of ints, optional (default: all nodes)*) – Restrict the distribution to a set of nodes.
- **num_bins** (*int or N-tuple, optional (default: 'auto'):*) – Number of bins used to sample the distribution. Defaults to unsupervised Bayesian blocks method.
- **use_weights** (*bool, optional (default: False)*) – Use weighted degrees (do not take the sign into account : only the magnitude of the weights is considered).
- **logx** (*bool, optional (default: False)*) – Use log-spaced bins.
- **logy** (*bool, optional (default: False)*) – Use logscale for the degree count.
- **axis** (`matplotlib.axes.Axes` instance, optional (default: new one)) – Axis which should be used to plot the histogram, if None, a new one is created.
- **show** (*bool, optional (default: True)*) – Show the Figure right away if True, else keep it warm for later use.
- ****kwargs** (keyword arguments for `matplotlib.axes.Axes.bar()`.)

`nngt.plot.`**`betweenness_distribution`**(*network*, *btype='both'*, *use_weights=True*, *nodes=None*, *logx=False*, *logy=False*, *num_nbins='auto'*, *num_ebins=None*, *axes=None*, *colors=None*, *norm=False*, *show=True*, ***kwargs*)

Plotting the betweenness distribution of a graph.

Parameters

- **graph** (`Graph` or subclass) – the graph to analyze.
- **btype** (*string, optional (default: "both")*) – type of betweenness to display ("node", "edge" or "both")
- **use_weights** (*bool, optional (default: True)*) – use weighted degrees (do not take the sign into account : all weights are positive).
- **nodes** (*list or numpy.array of ints, optional (default: all nodes)*) – Restrict the distribution to a set of nodes (taken into account only for the node attribute).
- **logx** (*bool, optional (default: False)*) – use log-spaced bins.
- **logy** (*bool, optional (default: False)*) – use logscale for the degree count.
- **num_nbins** (*int or 'auto', optional (default: 'auto'):*) – Number of bins used to sample the node distribution. Defaults to unsupervised Bayesian blocks method.
- **num_ebins** (*int or 'auto', optional (default: None):*) – Number of bins used to sample the edge distribution. Defaults to *max(num_edges / 500., 10)* ('auto' method will be slow).
- **axes** (list of `matplotlib.axis.Axis`, optional (default: new ones)) – Axes which should be used to plot the histogram, if None, new ones are created.
- **show** (*bool, optional (default: True)*) – Show the Figure right away if True, else keep it warm for later use.

`nngt.plot.`**`node_attributes_distribution`**(*network*, *attributes*, *nodes=None*, *num_bins='auto'*, *logx=False*, *logy=False*, *norm=False*, *title=None*, *colors=None*, *show=True*, ***kwargs*)

Return node *attributes* for a set of *nodes*.

Parameters

- **network** (`Graph`) – The graph where the *nodes* belong.

- **attributes** (*str or list*) – Attributes which should be returned, among: * “betweenness” * “clustering” * “in-degree”, “out-degree”, “total-degree” * “subgraph_centrality” * “b2” (requires NEST) * “firing_rate” (requires NEST)
- **nodes** (*list, optional (default: all nodes)*) – Nodes for which the attributes should be returned.
- **num_bins** (*int or list, optional (default: ‘auto’)*) – Number of bins to plot the distributions. If only one int is provided, it is used for all attributes, otherwize a list containing one int per attribute in *attributes* is required. Defaults to unsupervised Bayesian blocks method.
- **logx** (*bool or list, optional (default: False)*) – Use log-spaced bins.
- **logy** (*bool or list, optional (default: False)*) – use logscale for the node count.

`nngt.plot.`**`compare_population_attributes`**(*network*, *attributes*, *nodes=None*, *reference_nodes=None*, *num_bins='auto'*, *reference_color='gray'*, *title=None*, *logx=False*, *logy=False*, *show=True*, ***kwargs*)

Compare node *attributes* between two sets of nodes. Since number of nodes can vary, normalized distributions are used.

Parameters

- **network** (`Graph`) – The graph where the *nodes* belong.
- **attributes** (*str or list*) – Attributes which should be returned, among: * “betweenness” * “clustering” * “in-degree”, “out-degree”, “total-degree” * “subgraph_centrality” * “b2” (requires NEST) * “firing_rate” (requires NEST)
- **nodes** (*list, optional (default: all nodes)*) – Nodes for which the attributes should be returned.
- **reference_nodes** (*list, optional (default: all nodes)*) – Reference nodes for which the attributes should be returned in order to compare with *nodes*.
- **num_bins** (*int or list, optional (default: ‘auto’)*) – Number of bins to plot the distributions. If only one int is provided, it is used for all attributes, otherwize a list containing one int per attribute in *attributes* is required. Defaults to unsupervised Bayesian blocks method.
- **logx** (*bool or list, optional (default: False)*) – Use log-spaced bins.
- **logy** (*bool or list, optional (default: False)*) – use logscale for the node count.

`nngt.plot.`**`correlation_to_attribute`**(*network*, *reference_attribute*, *other_attributes*, *nodes=None*, *title=None*, *show=True*)

For each node plot the value of *reference_attributes* against each of the *other_attributes* to check for correlations.

Parameters

- **network** (`Graph`) – The graph where the *nodes* belong.
- **reference_attribute** (*str or array-like*) – Attribute which should serve as reference, among:
  - “betweenness”
  - “clustering”
  - “in-degree”, “out-degree”, “total-degree”
  - “subgraph_centrality”
  - “b2” (requires NEST)
  - “firing_rate” (requires NEST)

  - a custom array of values, in which case one entry per node in *nodes* is required.
- **other_attributes** (*str or list*) – Attributes that will be compared to the reference.
- **nodes** (*list, optional (default: all nodes)*) – Nodes for which the attributes should be returned.

Tutorial

This page provides a step-by-step walkthrough of the basic features of NNGT.

To run this tutorial, it is recommended to use either IPython or Jupyter, since they will provide automatic autocompletion of the various functions, as well as easy access to the docstring help.

First, import the NNGT package:

```
>>> import nngt
```

Then, you will be able to use the help from IPython by typing, for instance:

```
>>> nngt.Graph?
```

In Jupyter, the docstring can be viewed using Shift+Tab.

Content:

The `Graph` object

Basic functions

Let's create an empty `Graph`:

```
>>> g = nngt.Graph()
```

We can then add some nodes to it

```
>>> g.new_node(10)  # create nodes 0, 1, ... to 9
>>> g.node_nb()     # returns 10
```

And create edges between these nodes:

```
>>> g.new_edge(1, 4)   # create on connection going from 11 to 56
>>> g.edge_nb()        # returns 1
>>> g.new_edges([(0, 3), (5, 9), (9, 3)])
>>> g.edge_nb()        # returns 4
```

Node and edge attributes

Adding a node with specific attributes:

```
g2 = nngt.Graph()
g2.new_node(attributes={'size': 2., 'color': 'blue'},
            value_types={'size': 'double', 'color': 'string'})
print(g2.node_attributes)
```

Adding several:

```
g2.new_node(3, attributes={'size': [4., 5., 1.], 'color': ['r', 'g', 'b']},
            value_types={'size': 'double', 'color': 'string'})
print(g2.node_attributes)
```

Attributes can also be created afterwards:

```
import numpy as np
g3 = nngt.Graph(nodes=100)
g3.new_node_attribute('size', 'double',
                      values=np.random.uniform(0, 20, 100))
g3.node_attributes
```

All the previous techniques can also be used with `new_edge()` or `new_edges()`, and `new_edge_attribute()`. Note that attributes can also be set selectively:

```
edges = g3.new_edges(np.random.randint(0, 100, (50, 2)))
g3.new_edge_attribute('rank', 'int', val=0)
g3.set_edge_attribute('rank', val=2, edges=edges[:3, :])
g3.edge_attributes
```

Generating and analyzing more complex networks

NNGT provides a whole set of methods to connect nodes in specific fashions inside a graph. These methods are present in the `nngt.generation` module, and the network properties can then be plotted and analyzed via the tools present in the `nngt.plot` and `nngt.analysis` modules.

```
from nngt import generation as ng
from nngt import analysis as na
from nngt import plot as nplt
```

NNGT implements some fast generation tools to create several of the standard networks, such as Erdős-Rényi

```
g = ng.erdos_renyi(nodes=1000, avg_deg=100)
nplt.degree_distribution(g, ('in', 'total'))
print(na.clustering(g))
```

More heterogeneous networks, with scale-free degree distribution (but no correlations like in Barabasi-Albert networks and user-defined exponents) are also implemented:

```
g = ng.random_scale_free(1.8, 3.2, nodes=1000, avg_deg=100)
nplt.degree_distribution(g, ('in', 'out'), num_bins=30, logx=True,
                         logy=True, show=True)
print("Clustering: {}".format(na.clustering(g)))
```

Making complex populations

The `NeuralGroup` allows the creation of nodes that belong together. You can then make a population from these groups and connect them with specific connectivities using the `connect_neural_groups()` function.

```
num_nodes = 1000


'''
Make the population
'''

# two groups of neurons
g1 = nngt.NeuralGroup(500)  # neurons 0 to 499
g2 = nngt.NeuralGroup(500)  # neurons 500 to 999

# make population (without NEST models)
pop = nngt.NeuralPop.from_groups(
    (g1, g2), ("left", "right"), with_models=False)

# create network from this population
net = nngt.Network(population=pop)


'''
Connect the groups
'''

# inter-groups (Erdos-Renyi)
prop_er1 = {"density": 0.005}
ng.connect_neural_groups(net, "left", "right", "erdos_renyi", prop_er1)

# intra-groups (Newman-Watts)
prop_nw = {
    "coord_nb": 20,
    "proba_shortcut": 0.1
}

ng.connect_neural_groups(net, "left", "left", "newman_watts", prop_nw)
ng.connect_neural_groups(net, "right", "right", "newman_watts", prop_nw)
```

Real neuronal culture and NEST interaction: the `Network`

Besides connectivity, the main interest of the :class:~nngt.NeuralGroup‘ is that you can pass it the biological properties that the neurons belonging to this group will share.

Since we are using NEST, these properties are:

- the model’s name
- its non-default properties
- the synapses that the neurons have and their properties
- the type of the neurons (`1` for excitatory or `-1` for inhibitory)

```
''' Create groups with different parameters '''
# adaptive spiking neurons
base_params = {
    'E_L': -60., 'V_th': -55., 'b': 10., 'tau_w': 100.,
    'V_reset': -65., 't_ref': 1., 'g_L': 10., 'C_m': 250.
}
# oscillators
params1, params2 = base_params.copy(), base_params.copy()
params1.update({'E_L': -65., 'b': 30., 'I_e': 350., 'tau_w': 400.})
# bursters
params2.update({'b': 20., 'V_reset': -50., 'tau_w': 500.})

oscill = nngt.NeuralGroup(
    nodes=400, model='aeif_psc_alpha', neuron_param=params1,
    syn_model='tsodyks2_synapse', syn_param={'U': 0.5})
burst = nngt.NeuralGroup(
    nodes=200, model='aeif_psc_alpha', neuron_param=params2,
    syn_model='tsodyks2_synapse')
adapt = nngt.NeuralGroup(
    nodes=200, model='aeif_psc_alpha', neuron_param=base_params,
    syn_model='tsodyks2_synapse')

'''
Create the population that will represent the neuronal
network from these groups
'''
pop = nngt.NeuralPop.from_groups(
    [oscill, burst, adapt],
    names=['oscillators', 'bursters', 'adaptive'])

'''
Create the network from this population,
using a Gaussian in-degree
'''
net = ng.gaussian_degree(
    100., 15., population=pop, weights=1500.)
```

Once this network is created, it can simply be sent to nest through the command: `gids = net.to_nest()`, and the NEST gids are returned.

In order to access the gids from each group, you can do:

```
oscill_gids = net.nest_gid[oscill.ids]
```

Using the graph library of the NNGT object

As mentionned in the installation and introduction, NNGT uses existing graph library objects to store the graph. The library was designed so that most of the functions of the underlying graph library can be used directly on the *Graph* object.

Warning: One notable exception to this behaviour relates to the creation and deletion of nodes or edges, for which you have to use the functions provided by NNGT. As a general rule, any operation that might alter the graph structure should be done thourgh NNGT and never directly using the underlying library.

Apart from this, you can use any analysis or drawing tool from the graph library.

Example using graph-tool

```
>>> import graph_tool as gt
>>> import matplotlib.pyplot as plt
>>> print(gt.centrality.closeness(g, harmonic=True))
>>> gt.draw.graph_draw(g)
>>> nngt.plot.draw_network(g)
>>> plt.show()
```

Example using igraph

```
>>> import igraph as ig
>>> import matplotlib.pyplot as plt
>>> print(g.closeness(mode='out'))
>>> ig.plot(g)
>>> nngt.plot.draw_network(g)
>>> plt.show()
```

Example using networkx

```
>>> import networkx as nx
>>> import matplotlib.pyplot as plt
>>> print(nx.closeness_centrality(g))
>>> nx.draw(g)
>>> nngt.plot.draw_network(g)
>>> plt.show()
```

Note: People testing these 3 codes will notice that all closeness results are different (though I made sure the functions of each libraries worked on the same outgoing edges)! This example is given voluntarily to remind you, when using these libraries, to check that they indeed compute what you think they do. And even when they compute it, check how they do it!

NNGT configuration status

```
>>> nngt.get_config()
```

CHAPTER 3

Indices and tables

- genindex
- modindex
- search

Python Module Index

Index