

# GNG documentation

June 6, 2014

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GNG

*Constructor of GrowingNeuralGas object*

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## Description

Construct GNG object

## Usage

GNG

## Arguments

`beta` coefficient. Decrease the error variables of all node nodes by this fraction. Forgetting rate. Default 0.99

`alpha` Alpha coefficient. Decrease the error variables of the nodes neighboring to the newly inserted node by this fraction. Default 0.5

`uniformgrid.optimization` TRUE/FALSE. You cannot use utility option with this, so please pass FALSE here then.

`lazyheap.optimization` TRUE/FALSE. You cannot use utility option with this, so please pass FALSE here then.

`max.nodes` Maximum number of nodes (after reaching this size it will continue running, but won't add new nodes)

`eps_w` Default 0.05

`eps_n` Default 0.0006

`dataset.type` Dataset type. Possibilities `gng.dataset.bagging`, `gng.dataset.bagging.prob`, `gng.dataset.sequential`  
`experimental_utility_option`

EXPERIMENTAL Utility option `gng.experimental.utility.option.off` / `gng.experimental.utility.option.basi`  
`experimental_utility_k`

EXPERIMENTAL Utility option constant

`load_model_filename`

Set to path to file from which load serialized model

`experimental_vertex_extra_data`

if TRUE each example should have additional coordinate, that will be voted in graph. Each node (that you can get using `node` function) will have `extra_data` field that will be equal to mean of samples around given node. If used with probability dataset example layout is `<vertex position> <vertex_extra_data> <sampling_probability>`, for example `c(0.3, 0.6, 0.7, 100, 0.7)`

## Format

NULL

## Examples

```
# Default GNG instance, without optimizations and vertex dimensionality 3
```

```
gng <- GNG(dataset_type=gng.dataset.bagging.prob, max_nodes=max_nodes, dim=3)
```

```
# Construct GNG loaded from file with uniform grid
```

```
gng <- GNG(dataset_type=gng.dataset.bagging.prob, max_nodes=max_nodes, dim=3,
  uniformgrid_optimization=TRUE, lazyheap_optimization=FALSE,
  uniformgrid_boundingbox_sides=c(3,3,3), uniformgrid_boundingbox_origin=c(-0.5,-0.5,-0.5),
  load_model_filename="sphere_simple.bin")
```

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Growing-Neural-Gas	<i>Efficient C++ implementation of online clustering algorithm Growing Neural Gas.</i>
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## Description

This package contains fast C++ implementation of online clustering algorithm Growing Neural Gas. It produces topological graph, that you can easily convert to `igraph`, or you can dump your model to optimized binary file and load it later on.

## Details

Package:	Growing-Neural-Gas
Type:	Package
Version:	0.6
Date:	2014-06-03
License:	MIT License

For overview of usage please see exemplary code in `demo/` folder.

**Author(s)**

Stanislaw Jastrzebski

Maintainer: Stanislaw Jastrzebski <staszek<at>gmail<dot>com>

**References**

~~ Literature or other references for background information ~~

**Examples**

```
gng <- GNG(dataset_type=gng.dataset.bagging.prob, max_nodes=300, dim=3)
insert_examples(gng, preset=gng.preset.sphere, N=10000, prob=0.8)
run(gng)
insert_examples(gng, preset=gng.preset.box, N=10000, prob=0.8)
plot(gng, mode=gng.plot.2d.errors, vertex.color=gng.plot.color.cluster, layout=gng.plot.layout.igraph.v2d)
```

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centroids.gng

*centroids*

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**Description**

Using infomap.communities finds communities and for each community pick node with biggest betweenness score

**Usage**

```
centroids(gng)
```

**Format**

NULL

**Details**

Get centroids

**Examples**

```
# Print position of the first centroid
print(node(gng, centroids(gng)[1])$pos)
```

---

convert_igraph.gng	<i>convert_igraph</i>
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**Description**

Converts to igraph (O(n) method, writing intermediately to disk)

**Usage**

```
convert_igraph(gng)
```

**Format**

NULL

**Examples**

```
convert_igraph(gng)
```

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dump_model.gng	<i>dump_model</i>
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**Description**

Writes graph to a disk space efficient binary format. It can be used in GNG constructor to reconstruct graph from file.

**Usage**

```
dump_model(gng)
```

**Arguments**

filename	Dump destination
----------	------------------

**Format**

NULL

**Details**

Dump model to binary

**Examples**

```
dump_model(gng, graph.bin)
```

---

`error_statistics.gng`    *error\_statistics*

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**Description**

Gets vector with errors for every second of execution

**Usage**

```
error_statistics(gng)
```

**Format**

NULL

**Examples**

```
error_statistics(gng)
```

---

`insert_examples.gng`    *insert\_examples*

---

**Description**

Insert (inefficiently) examples to algorithm dataset. For efficient insertion use `gng$insert_examples`, and for setting memory pointer use `gng$set_memory_move_examples`

**Usage**

```
insert_examples(gng, M)
```

**Arguments**

<code>examples</code>	Matrix with examples of dimensionality N rows x C columns, where C columns = dim (passed as parameter to GNG object) + 1 or 0 (1 if <code>vertex_extra_data</code> is TRUE) + 1 or 0 (1 if <code>dataset_type=gng.dataset.bagging.prob</code> ).
<code>preset</code>	Use only if you are adding exemplary dataset. Possibilities: <code>gng.preset.sphere</code> , <code>gng.preset.box</code> . You can specify preset params: N=1000, center=c(0.5,0.5,0.5), prob=-1.

**Format**

NULL

**Note**

Complicated memory layout of the matrix is due to need for memory efficiency. In the future versions you can expect wrapper simplifying addition and also streaming from disk file

**Examples**

```
#Add preset examples with probability of being sampled (this assumed GNG was created with gng.dataset.bagging.prob
insert_examples(gng, preset=gng.preset.sphere)
```

```
#Insert efficiently examples
M <- matrix(0, ncol=3, nrow=10)
M[1,] = c(4,5,6)
gng$insert_examples(M)
```

```
#Set memory of the algorithm to point in memory. Note: you cannot remove this matrix while
in execution or you will experience memory error
gng$set_memory_move_examples(M)
```

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mean\_error.gng

*mean\_error*


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**Description**

Gets mean error of the graph (note: blocks the execution,  $O(n)$ )

**Usage**

```
mean_error(gng)
```

**Format**

NULL

**Examples**

```
mean_error(gng)
```

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`node.gng`*node*

---

**Description**

Retrieves node from resulting graph

**Usage**

```
node(gng, 10)
```

**Arguments**

<code>gng_id</code>	Id of the node to retrieve. This is the id returned by functions like predict, or centroids
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**Format**

NULL

**Details**

Get GNG node

**Examples**

```
print(node(gng, 10)$pos)
```

---

`pause.gng`*pause*

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**Description**

Pause algorithm

**Usage**

```
pause(gng)
```

**Format**

NULL

**Examples**

```
pause(gng)
```

plot.gng

*plot***Description**

Plot resulting graph using igraph plotting, or using rgl 3d engine.

**Usage**

```
plot(gng)
```

**Arguments**

mode	gng.plot.rgl3d (3d plot), gng.plot.2d (igraph plot) or gng.plot.2d.errors (igraph plot with mean error log plot)
layout	layout to be used when plotting. Possible values: gng.plot.layout.igraph.v2d (first two dimensions), gng.plot.layout.igraph.auto (auto layout from igraph) gng.plot.layout.igraph.fruchterman.fast (fast fruchterman reingold layout), or any function accepting igraph graph and returning layout
vertex.color	how to color vertexes. Possible values: gng.plot.color.cluster(vertex color is set to fastgreedy.community clustering), gng.plot.color.extra(rounds to integer extra dim if present), gng.plot.color.none(every node is white),

**Format**

NULL

**Details**

Plot GNG

**Note**

If you want to "power-use" plotting and plot for instance a subgraph, you might be interested in exporting igraph with `convert_igraph` function and plotting it using/reusing function from this package: `.visualizeIGraph2d`

**Examples**

```
# Plots igraph using first 2 coordinates and colors according to clusters
plot(gng, mode=gng.plot.2d.errors, layout=gng.plot.layout.v2d, vertex.color=gng.plot.color.cluster)

# Plot rgl (make sure you have installed rgl library)
plot(gng, mode=gng.plot.rgl, layout=gng.plot.layout.v2d, vertex.color=gng.plot.color.cluster)

# For more possibilities see gng.plot.* constants
```



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`run.gng`*run*

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**Description**

Run algorithm (in parallel)

**Usage**

`run(gng)`

**Format**

NULL

**Examples**

`run(gng)`

---

`terminate.gng`*pause*

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**Description**

Terminate algorithm

**Usage**

`terminate(gng)`

**Format**

NULL

**Examples**

`terminate(gng)`

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