

# graph

April 19, 2010

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acc-methods

*Methods for Accessibility Lists*

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## Description

This generic function takes an object that inherits from the `graph` class and a node in that graph and returns a vector containing information about all other nodes that are accessible from the given node. The methods are vectorized so that `index` can be a vector.

## Usage

```
## S4 method for signature 'graph,character':  
acc(object, index)  
## S4 method for signature 'clusterGraph,character':  
acc(object, index)
```

## Arguments

<code>object</code>	An instance of the appropriate graph class.
<code>index</code>	A character vector specifying the nodes for which accessibility information is wanted.

## Value

The methods should return a named list of integer vectors. The `names` of the list correspond to the names of the supplied nodes. For each element of the list the returned vector is named. The names of the vector elements correspond to the nodes that are accessible from the given node. The values in the vector indicate how many edges are between the given node and the node in the return vector.

## Methods

**object = graph** An object of class `graph`.

**object = clusterGraph** An instance of the `clusterGraph` class.

**index** A `character` vector of indices corresponding to nodes in the graph.

## Examples

```
set.seed(123)
gR3 <- randomGraph(LETTERS[1:10], M<-1:2, p=.5)
acc(gR3, "A")
acc(gR3, c("B", "D"))
```

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addEdge

*addEdge*

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## Description

A function to add an edge to a graph.

## Usage

```
addEdge(from, to, graph, weights)
```

## Arguments

<code>from</code>	The node the edge starts at
<code>to</code>	The node the edge goes to.
<code>graph</code>	The graph that the edge is being added to.
<code>weights</code>	A vector of weights, one for each edge.

## Details

Both `from` and `to` can be vectors. They need not be the same length (if not the standard rules for replicating the shorter one are used). Edges are added to the graph between the supplied nodes.

The `weights` are given for each edge.

The implementation is a bit too oriented towards the `graphNEL` class and will likely change in the next release to accomodate more general graph classes.

If the graph is undirected then the edge is bidirectional (and only needs to be added once). For directed graphs the edge is directional.

## Value

A new instance of a graph object with the same class as `graph` but with the indicated edges added.

## Author(s)

R. Gentleman

## See Also

[addNode](#), [removeEdge](#), [removeNode](#)

**Examples**

```
V <- LETTERS[1:4]
edL2 <- vector("list", length=4)
names(edL2) <- V
for(i in 1:4)
  edL2[[i]] <- list(edges=c(2,1,2,1)[i], weights=sqrt(i))
gR2 <- new("graphNEL", nodes=V, edgeL=edL2, edgemode="directed")

gX <- addEdge("A", "C", gR2, 1)

gR3 <- randomEGraph(letters[10:14], .4)
gY <- addEdge("n", "l", gR3, 1)
```

addNode

*addNode***Description**

Add one or more nodes to a graph.

**Usage**

```
addNode(node, object, edges)
```

**Arguments**

node	A character vector of node names.
object	A graph
edges	A named list of edges.

**Details**

The supplied nodes are added to the set of nodes of the `object`.

If `edges` are provided then their must be the same number as there are nodes and the must be in the same order. The elements of the `edges` list are vectors. They can be character vectors of node labels for nodes in `object` and if so then they are added with unit weights. If the vector is numeric then it must be named (with labels corresponding to nodes in the `object`) and the values are taken to be the edge weights.

When the `object` is a `distGraph` then the `edges` must be supplied and they must contain appropriate distances for all nodes both those in `object` and those supplied.

**Value**

A new graph of the same class as `object` with the supplied node added to the set of nodes.

**Author(s)**

R. Gentleman

**See Also**

[removeNode](#), [removeEdge](#), [addEdge](#)

**Examples**

```
V <- LETTERS[1:4]
edL1 <- vector("list", length=4)
names(edL1) <- V
for(i in 1:4)
  edL1[[i]] <- list(edges=c(2,1,4,3)[i], weights=sqrt(i))
gR <- new("graphNEL", nodes=V, edgeL=edL1)
gX <- addNode("X", gR)

set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p=.3)
g2 <- addNode("z", g1, edges=list(c("a", "h", "g")))
```

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 adj-methods

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*Methods for finding the adjacency list for selected nodes.*


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**Description**

This generic function takes an object that inherits from the `graph` class and a node in that graph and returns a vector containing information about all other nodes that are adjacent to the given node. This means that they are joined to the given node by an edge. The accessibility list, `acc` is the list of all nodes that can be reached from a specified node.

**Value**

The methods return vector of nodes that are adjacent to the specified node.

**Methods**

**object = graph** An object that inherits from class `graph`

**index** An index (could be multiple) which can be either the integer offset for the node(s) or their labels.

**See Also**

[acc-methods](#)

**Examples**

```
set.seed(123)
gR3 <- randomGraph(LETTERS[1:4], M<-1:2, p=.5)
adj(gR3, "A")
adj(gR3, c(2,3))
```

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apoptosisGraph      *KEGG apoptosis pathway graph*

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### Description

A graph representing the apoptosis pathway from KEGG, as well as a data.frame of attributes for use in plotting the graph with `Rgraphviz` and a list to compare the nodes with their respective LocusLink IDs.

### Usage

```
data (apopGraph)
```

### Details

The `apopGraph` data set contains three objects:

The first is `apopGraph`, which is an object of class `graphNEL` and represents the `hsa04210` graph from KEGG.

The second is `apopAttrs`, which is a data.frame with two columns, and a row for every node in `apopGraph`. The first column lists what color the node is represented with on the KEGG site. The second column lists the type of the node - either `genesym` or `text`. Most nodes are of type `genesym` as they represent genes, but some of the nodes in the KEGG graph were not genes and thus those nodes are of type `text`.

The third, `apopLocusLink` is a named list where the names correspond to the node names in `apopGraph`. The values of the list are the LocusLink IDs that correspond to that node in the KEGG graph.

### Source

<http://www.genome.ad.jp/kegg/pathway/hsa/hsa04210.html>

### Examples

```
data (apopGraph)
if (require("Rgraphviz") & interactive())
  plot (apopGraph)
```

---

`attrData-class`      *Class "attrData"*

---

### Description

A container class to manage generic attributes. Supports named attributes with default values with methods for vectorized access.

### Objects from the Class

Objects can be created by calls of the form `new("attrData", defaults)`. The `defaults` argument should be a named list containing the initial attribute names and default values.

**Slots**

**data:** Where custom attribute data is stored

**defaults:** A named list of known attribute names and default values.

**Methods**

```
attrDataItem<- signature(self = "attrData", x = "character", attr = "character"):
  ...
attrDataItem signature(self = "attrData", x = "character", attr = "missing"):
  ...
attrDataItem signature(self = "attrData", x = "character", attr = "character"):
  ...
attrDefaults<- signature(self = "attrData", attr = "character", value =
  "ANY"):...
attrDefaults<- signature(self = "attrData", attr = "missing", value = "list"):
  ...
attrDefaults signature(self = "attrData", attr = "missing"):...
attrDefaults signature(self = "attrData", attr = "character"):...
initialize signature(.Object = "attrData"):...
names return the names of the stored attributes
names<- set the names of the stored attributes
removeAttrDataItem signature(self="attrData", x="character", value="NULL"):
  Remove the data associated with the key specified by x.
```

**Author(s)**

Seth Falcon

**Examples**

```
defaultProps <- list(weight=1, color="blue", friends=c("Bob", "Alice"))
adat <- new("attrData", defaults=defaultProps)

## Get all defaults
attrDefaults(adat)

## Or get only a specific attribute
attrDefaults(adat, attr="color")

## Update default weight
attrDefaults(adat, attr="weight") <- 500

## Add new attribute
attrDefaults(adat, attr="length") <- 0

## Asking for the attributes of an element you haven't customized
## returns the defaults
attrDataItem(adat, x=c("n1", "n2"), attr="length")

## You can customize values
attrDataItem(adat, x=c("n1", "n2"), attr="length") <- 5
```

```
## What keys have been customized?
names(adat)
```

---

attrDataItem-methods

*Get and set attributes values for items in an attrData object*

---

### Description

The `attrDataItem` method provides get/set access to items stored in a `attrData-class` object.

### Usage

```
attrDataItem(self, x, attr)
attrDataItem(self, x, attr) <- value
```

### Arguments

<code>self</code>	A <code>attrData-class</code> instance
<code>x</code>	A character vector of item names
<code>attr</code>	A character vector of length 1 giving the attribute name to get/set. Note that the attribute name must have already been defined for the <code>attrData</code> object via <code>attrDefaults</code> . If missing, return a list of all attributes for the specified nodes.
<code>value</code>	An R object to set as the attribute value for the specified items. If the object has length one or does not have a length method defined, it will be assigned to all items in <code>x</code> . If the length of <code>value</code> is the same as <code>x</code> , the corresponding elements will be assigned. We will add an argument to indicate that the <code>value</code> is to be taken as-is for those cases where the lengths are the same coincidentally.

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attrDefaults-methods

*Get and set the default attributes of an attrData object*

---

### Description

The `attrDefaults` method provides access to a `attrData-class` object's default attribute list. The default attribute list of a `attrData-class` object defines what attributes can be customized for individual data elements by defining attribute names and default values.

### Usage

```
attrDefaults(self, attr)
attrDefaults(self, attr) <- value
```

**Arguments**

<code>self</code>	A <code>attrData-class</code> instance
<code>attr</code>	A character vector of length 1 giving the name of an attribute. Can be missing.
<code>value</code>	An R object that will be used as the default value of the specified attribute, or a named list of attribute name/default value pairs if <code>attr</code> is missing.

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<code>aveNumEdges</code>	<i>Calculate the average number of edges in a graph</i>
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**Description**

`aveNumEdges` divides the number of edges in the graph by the number of nodes to give the average number of edges.

**Usage**

```
aveNumEdges(objgraph)
```

**Arguments**

`objgraph` the graph object

**Value**

A double representing the average number of edges will be returned.

**Author(s)**

Elizabeth Whalen

**See Also**

[numEdges](#), [mostEdges](#), [numNoEdges](#)

**Examples**

```
set.seed(124)
g1 <- randomGraph(1:10, letters[7:12], p=.6)
aveNumEdges(g1)
```



---

`biocRepos`*A graph representing the Bioconductor package repository*

---

### Description

This graph is a rendition of the Bioconductor package repository and represents the dependency graph of that repository. An edge between two package denotes a dependency on the 'to' package by the 'from' package.

### Usage

```
data(biocRepos)
```

### Source

This graph was generated by the function `buildRepDepGraph`.

### See Also

`buildRepDepGraph`

### Examples

```
data(biocRepos)
## An example of usage will be here soon
```

---

`boundary`*Returns the Boundary between a Graph and a SubGraph*

---

### Description

The boundary of a subgraph is the set of nodes in the original graph that have edges to nodes in the subgraph. The function `boundary` computes the boundary and returns it as a list whose length is the same length as the number of nodes in the subgraph.

### Usage

```
boundary(subgraph, graph)
```

### Arguments

<code>graph</code>	the original graph from which the boundary will be created
<code>subgraph</code>	can either be the vector of the node labels or the subgraph itself.

### Details

The *boundary* of a *subgraph* is the set of nodes in the graph which have an edge that connects them to the specified subgraph but which are themselves not elements of the subgraph.

For convenience users can specify the subgraph as either a graph or a vector of node labels.

**Value**

This function returns a named list of length equal to the number of nodes in `subgraph`. The elements of the list correspond to the nodes in the `subgraph`. The elements are lists of the nodes in `graph` which share an edge with the respective node in `subgraph`.

**Author(s)**

Elizabeth Whalen and R. Gentleman

**See Also**

[subGraph](#), [graph-class](#)

**Examples**

```
set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p=.3)
##both should be "a"
boundary(c("g", "i"), g1)
```

---

buildRepDepGraph    *Functionality to manage repository dependency graphs*

---

**Description**

These functions can be used to represent and manipulate dependency graphs for a specified package repository.

**Usage**

```
buildRepDepGraph(repository, depLevel = c("Depends", "Suggests"))
pkgInstOrder(pkg, repGraph)
```

**Arguments**

<code>repository</code>	A URL to a CRAN style repository
<code>depLevel</code>	One of <code>Depends</code> or <code>Suggests</code> , detailing the level of dependencies to search. The <code>Suggests</code> value includes everything in <code>Depends</code> .
<code>pkg</code>	The package to get the installation order for
<code>repGraph</code>	A graph object representing a repository, as from <code>buildRepDepGraph</code>

**Value**

For `buildRepDepGraph`, a graph representing the dependency structure of the specified repository, where an edge from node A to node B represents a dependency on B by A.

For `pkgInstOrder`, a vector is returned, listing the appropriate order one would take to install all of the necessary packages to install the specified package. That is, it makes sure that at every step, any package being installed does not depend on one that has not yet been installed. This order can then be used with functions such as `install.packages`.

**Author(s)**

Jeff Gentry

**Examples**

```
if("FIXME"=="Jeff, we can't assume that we're always online - wh") {
  repos <- getOption("repositories")["BIOC"] ## Get BIOC repos
  buildRepDepGraph(repos)
}
```

---

`calcProb`*Calculate the hypergeometric probability of the subgraph's number of edges.*

---

**Description**

`calcProb` calculates the probability of having the number of edges found in the subgraph given that it was made from `origgraph`. The hypergeometric distribution is used to calculate the probability (using the pdf).

**Usage**

```
calcProb(subgraph, origgraph)
```

**Arguments**

<code>subgraph</code>	subgraph made from the original graph
<code>origgraph</code>	original graph object from which the subgraph was made

**Value**

The probability of the subgraph's number of edges is returned.

**Author(s)**

Elizabeth Whalen

**See Also**[calcSumProb](#)**Examples**

```
#none right now
```

---

calcSumProb	<i>Calculate the probability that a subgraph has an unusual number of edges.</i>
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---

### Description

For any graph a set of nodes can be used to obtain an induced subgraph (see [subGraph](#)). An interesting question is whether that subgraph has an unusually large number of edges. This function computes the probability that a *random* subgraph with the same number of nodes has more edges than the number observed in the presented subgraph. The appropriate probability distribution is the hypergeometric.

### Usage

```
calcSumProb(sg, g)
```

### Arguments

sg	subgraph made from the original graph
g	original graph object from which the subgraph was made

### Details

The computation is based on the following argument. In the original graph there are  $n$  nodes and hence  $N = n * (n - 1)/2$  edges in the complete graph. If we consider these  $N$  nodes to be of two types, corresponding to those that are either in our graph,  $g$ , or not in it. Then we think of the subgraph which has say  $m$  nodes and  $M = m * (m - 1)/2$  possible edges as representing  $M$  draws from an urn containing  $N$  balls of which some are white (those in  $g$ ) and some are black. We count the number of edges in the subgraph and use a Hypergeometric distribution to ask whether our subgraph is particularly dense.

### Value

The probability of having greater than or equal to the subgraph's number of edges is returned.

### Author(s)

Elizabeth Whalen

### See Also

[calcProb](#)

### Examples

```
set.seed(123)
V <- letters[14:22]
g1 <- randomEGraph(V, .2)

sg1 <- subGraph(letters[c(15,17,20,21,22)], g1)
calcSumProb(sg1, g1)
```

---

clearNode	<i>clearNode</i>
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## Description

This function removes all edges to or from the specified node in the graph.

## Usage

```
clearNode(node, object)
```

## Arguments

node	a node
object	a graph

## Details

All edges to and from `node` are removed. `node` can be a vector.

## Value

A new instance of the graph with all edges to and from the specified node(s) removed.

## Author(s)

R. Gentleman

## See Also

[removeNode](#), [removeEdge](#)

## Examples

```
V <- LETTERS[1:4]
edL3 <- vector("list", length=4)
for(i in 1:4)
  edL3[[i]] <- list(edges=(i%4)+1, weights=i)
names(edL3) <- V
gR3 <- new("graphNEL", nodes=V, edgeL=edL3, "directed")
g4 <- clearNode("A", gR3)
```

---

clusterGraph-class *Class "clusterGraph"*

---

### Description

A cluster graph is a special sort of graph for clustered data. Each cluster forms a completely connected subgraph. There are no edges between clusters.

### Objects from the Class

Objects can be created by calls of the form `new("clusterGraph", ...)`.

### Slots

**clusters:** Object of class "list" a list of the labels of the elements, one element of the list for each cluster.

### Extends

Class "graph", directly.

### Methods

**connComp** signature(object = "clusterGraph"): find the connected components; simply the clusters in this case.

**acc** signature(object = "clusterGraph"): find the accessible nodes from the supplied node.

**adj** signature(object = "clusterGraph"): find the adjacent nodes to the supplied node.

**nodes** signature(object = "clusterGraph"): return the nodes.

**nodes<-** signature(object="clusterGraph", value="character"): replace the node names with the new labels given in value.

**numNodes** signature(object = "clusterGraph"): return the number of nodes.

**edgeWeights** Return a list of edge weights in a list format similar to the edges method.

**edgeL** signature(graph = "clusterGraph"): A method for obtaining the edge list.

**coerce** signature(from = "clusterGraph", to = "matrix"): Convert the clusterGraph to an adjacency matrix. Currently, weights are ignored. The conversion assumes no self-loops.

### Author(s)

R. Gentleman

### See Also

[graph-class](#), [distGraph-class](#)

### Examples

```
cG1 <- new("clusterGraph", clusters=list(a=c(1,2,3), b=c(4,5,6)))
cG1
acc(cG1, c("1", "2"))
```

---

`clusteringCoefficient-methods`*Clustering coefficient of a graph*

---

### Description

This generic function takes an object that inherits from the `graph` class. The graph needs to have `edgemode=="undirected"`. If it has `edgemode=="directed"`, the function will return `NULL`.

### Usage

```
## S4 method for signature 'graph':
clusteringCoefficient(object, selfLoops=FALSE)
```

### Arguments

<code>object</code>	An instance of the appropriate graph class.
<code>selfLoops</code>	Logical. If true, the calculation takes self loops into account.

### Details

For a node with  $n$  adjacent nodes, if `selfLoops` is `FALSE`, the clustering coefficient is  $N/(n*(n-1))$ , where  $N$  is the number of edges between these nodes. The graph may not have self loops. If `selfLoops` is `TRUE`, the clustering coefficient is  $N/(n*n)$ , where  $N$  is the number of edges between these nodes, including self loops.

### Value

A named numeric vector with the clustering coefficients for each node. For nodes with 2 or more edges, the values are between 0 and 1. For nodes that have no edges, the function returns the value `NA`. For nodes that have exactly one edge, the function returns `NaN`.

### Author(s)

Wolfgang Huber <http://www.dkfz.de/mga/whuber>

### Examples

```
set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p=.3)
clusteringCoefficient(g1)
clusteringCoefficient(g1, selfLoops=TRUE)
```

---

combineNodes	<i>combineNodes</i>
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---

### Description

A function to combine, or collapse, a specified set of nodes in a graph.

### Usage

```
combineNodes(nodes, graph, newName, ...)
## S4 method for signature 'character,graphNEL,character':
combineNodes(nodes, graph, newName, collapseFunction=sum)
```

### Arguments

nodes	A set of nodes that are to be collapsed.
graph	The graph containing the nodes
newName	The name for the new, collapsed node.
collapseFunction	Function or character giving the name of a function used to collapse the edge weights after combining nodes. The default is to sum up the weights, but mean would be a useful alternative.
...	Additional arguments for the generic

### Details

The nodes specified are reduced to a single new node with label given by `newName`. The in and out edges of the set of nodes are all made into in and out edges for the new node.

### Value

An new instance of a graph of the same class as `graph` is returned. This new graph has the specified nodes reduced to a single node.

### Author(s)

R. Gentleman

### See Also

[inEdges](#), [addNode](#)

### Examples

```
V <- LETTERS[1:4]
edL1 <- vector("list", length=4)
names(edL1) <- V
for(i in 1:4)
  edL1[[i]] <- list(edges=c(2,1,4,3)[i], weights=sqrt(i))
gR <- new("graphNEL", nodes=V, edgeL=edL1, edgemode="directed")
gR <- addNode("M", gR)
gR <- addEdge("M", "A", gR, 1)
```



```

gR <- addEdge("B", "D", gR, 1)
gX <- combineNodes(c("B", "D"), gR, "X")

gR <- addNode("K", gR)
gR <- addEdge(c("K", "K"), c("D", "B"), gR, c(5, 3))
edgeWeights(combineNodes(c("B", "D"), gR, "X"))$K
edgeWeights(combineNodes(c("B", "D"), gR, "X", mean))$K

```

DFS

*Depth First Search***Description**

This function implements algorithm 4.2.1 of Gross and Yellen. The input is a `graph` and a node to start from. It returns a standard vertex labeling of `graph`. This is a vector with elements corresponding to the nodes of `graph` and with values that correspond to point in the depth first search the node is visited.

**Usage**

```
DFS(object, node, checkConn=TRUE)
```

**Arguments**

<code>object</code>	An instance of the <code>graph</code> class.
<code>node</code>	A character indicating the starting node.
<code>checkConn</code>	A logical indicating whether the connectivity of the graph should be checked.

**Details**

This function implements algorithm 4.2.1 of Gross and Yellen. Specific details are given there.

It requires that the graph be connected. By default, this is checked, but since the checking can be expensive it is optional.

A faster and mostly likely better implementation of depth first searching is given by `dfs` in the **RBGL** package.

**Value**

A vector with names given by the nodes of `graph` whose values are 0 to one less than the number of nodes. These indices indicate the point at which the node will be visited.

**Author(s)**

R. Gentleman

**References**

*Graph Theory and its Applications*, J. Gross and J. Yellen.

**See Also**

[boundary](#)

**Examples**

```
RNGkind("Mersenne-Twister")
set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p=.3)
RNGkind()
DFS(g1, "a")
```

---

distGraph-class      *Class "distGraph"*

---

**Description**

A class definition for graphs that are based on distances.

**Objects from the Class**

Objects can be created by calls of the form `new("distGraph", ...)`.

**Slots**

**Dist:** Object of class "dist" that forms the basis for the edge weights used in the distGraph.

**Extends**

Class "graph", directly.

**Methods**

**show** signature(object = "distGraph"): a print method

**Dist** signature(object = "distGraph"): return the dist object.

**adj** signature(object = "distGraph"): find the nodes adjacent to the supplied node.

**nodes** signature(object = "distGraph"): return the nodes in the graph.

**numNodes** signature(object = "distGraph"): return the number of nodes.

**threshold** signature(object = "distGraph", k, value): set all distances that are larger than the supplied threshold, k, to the supplied value. The default is value is zero (and so is appropriate for similarities, rather than distances).

**initialize** signature(object = "distGraph"): initialize a distGraph instance.

**edgeWeights** Return a list of edge weights in a list format similar to the edges method.

**edgeL** signature(graph = "distGraph"): A method for obtaining the edge list.

**Author(s)**

R. Gentleman

**References**

Shamir's paper and Butte et al

**See Also**

[graph-class](#), [clusterGraph-class](#)

**Examples**

```
set.seed(123)
x <- rnorm(26)
names(x) <- letters
library(stats)
d1 <- dist(x)
g1 <- new("distGraph", Dist=d1)
```

---

duplicatedEdges      *duplicatedEdges*

---

**Description**

A multigraph is a graph where edges between nodes can be represented several times. For some algorithms this causes problems. `duplicatedEdges` tests an instance of the `graphNEL` class to see if it has duplicated edges and returns `TRUE` if it does and `FALSE` otherwise.

**Usage**

```
duplicatedEdges(graph)
```

**Arguments**

`graph`            An instance of the class `graphNEL`

**Details**

It would be nice to handle other types of graphs.

**Value**

A logical, either `TRUE` if the graph has duplicated edges or `FALSE` if not.

**Author(s)**

R. Gentleman

**See Also**

[connComp](#), [ugraph](#)

**Examples**

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
```

---

 edgeDataDefaults-methods

*Get and set default attributes for the edges of a graph*


---

### Description

Set default values for attributes associated with the edges of a graph.

### Usage

```
edgeDataDefaults(self, attr)
edgeDataDefaults(self, attr) <- value
```

### Arguments

self	A <code>graph-class</code> instance
attr	A character vector of length one giving the name of the attribute
value	An R class to use as the default value for the specified attribute

---

 edgeData-methods

*Get and set attributes for the edges of a graph object*


---

### Description

Attributes of the edges of a graph can be accessed using `edgeData`. The attributes must be defined using `edgeDataDefaults`. You can omit the `from` or `to` argument to retrieve attribute values for all edges to (respectively, from) a given node.

### Usage

```
edgeData(self, from, to, attr)
edgeData(self, from, to, attr) <- value
```

### Arguments

self	A <code>graph-class</code> instance
from	A character vector of node names
to	A character vector of node names
attr	A character vector of length one specifying the name of a node attribute
value	An R object to store as the attribute value

edgeMatrix

*Compute an Edge Matrix or weight vector for a Graph***Description**

For our purposes an *edge matrix* is a matrix with two rows and as many columns as there are edges. The entries in the first row are the index of the node the edge is *from*, those in the second row indicate the node the edge is *to*.

If the graph is “undirected” then the `duplicates` option can be used to indicate whether reciprocal edges are wanted. The default is to leave them out. In this case the notions of *from* and *to* are not relevant.

**Usage**

```
edgeMatrix(object, duplicates=FALSE)
eWV(g, eM, sep = ifelse(edgemode(g) == "directed", "->",
                        "--"), useNNames=FALSE)
pathWeights(g, p, eM=NULL)
```

**Arguments**

<code>object</code>	An object that inherits from <code>graph</code> .
<code>g</code>	An object that inherits from <code>graph</code> .
<code>duplicates</code>	Whether or not duplicate edges should be produced for “undirected” graphs.
<code>eM</code>	An edge matrix
<code>sep</code>	a character string to concatenate node labels in the edge label
<code>useNNames</code>	a logical; if TRUE, node names are used in the edge label; if FALSE, node indices are used
<code>p</code>	a vector of node names constituting a path in graph <code>g</code>
<code>...</code>	arguments passed to <code>edgeMatrix</code> .

**Details**

Implementations for `graphNEL`, `clusterGraph` and `distGraph` are available.

**Value**

`edgeMatrix` returns a matrix with two rows, *from* and *to*, and as many columns as there are edges. Entries indicate the index in the node vector that corresponds to the appropriate end of the edge.

`eWV` uses the edge matrix to create an annotated vector of edge weights.

`pathWeights` returns an annotated vector of edge weights for a specified path in a graph.

**Note**

A path through an undirected graph may have several representations as a named vector of edges. Thus in the example, when the weights for path `b-a-i` are requested, the result is the pair of weights for edges `a-b` and `a-i`, as these are the edge labels computed for graph `g1`.

**Author(s)**

R. Gentleman

**See Also**[edges](#)**Examples**

```

set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p=.3)
edgeMatrix(g1)
g2 <- new("clusterGraph", clusters=list(a=c(1,2,3), b=c(4,5,6)))
em2 <- edgeMatrix(g2)
eWV(g1, edgeMatrix(g1))
eWV(g1, edgeMatrix(g1), useNNames=TRUE)
pathWeights(g1, c("b", "a", "i"))

```

edgeWeights

*Retrieve the edge weights of a graph***Description**

A generic function that returns the edge weights of a graph. If `index` is specified, only the weights for the edges from the specified nodes are returned. The user can control which edge attribute is interpreted as the weight, see the Details section.

**Usage**

```
edgeWeights(object, index, ..., attr = "weight", default = 1, type.checker = is.numeric)
```

**Arguments**

<code>object</code>	A graph, any object that inherits from the <code>graph</code> class.
<code>index</code>	If supplied, a character or numeric vector of node names or indices.
<code>...</code>	Unused.
<code>attr</code>	The name of the edge attribute to use as a weight. You can view the list of defined edge attributes and their default values using <code>edgeDataDefaults</code> . The default attribute name is "weight", see the Details section.
<code>default</code>	The value to use if <code>object</code> has no edge attribute named by the value of <code>attr</code> . The default is the value 1 (double).
<code>type.checker</code>	A function that will be used to check that the edge weights are of the correct type. This function should return TRUE if the input vector is of the right type and FALSE otherwise. The default is to check for numeric edge weights using <code>is.numeric</code> . If no type checking is desired, specify NULL.

## Details

If `index` is supplied, then edge weights from these nodes to all adjacent nodes are returned. If `index` is not supplied, then the edge weights for all nodes are returned. The value for nodes without any outgoing edges will be a zero-length vector of the appropriate mode.

The `edgeWeights` method is a convenience wrapper around `edgeData`, the general-purpose way to access edge attribute information for a `graph` instance. In general, edge attributes can be arbitrary R objects. However, for `edgeWeights` to make sense, the values must be vectors of length not more than one.

By default, `edgeWeights` looks for an edge attribute with name `"weight"` and, if found, uses these values to construct the edge weight list. You can make use of attributes stored under a different name by providing a value for the `attr` argument. For example, if `object` is a `graph` instance with an edge attribute named `"WTS"`, then the call `edgeWeights(object, attr="WTS")` will attempt to use those values.

The function specified by `type.checker` will be given a vector of edge weights; if the return value is not `TRUE`, then an error will be signaled indicating that the edge weights in the graph are not of the expected type. Type checking is skipped if `type.checker` is `NULL`.

If the `graph` instance does not have an edge attribute with name given by the value of the `attr` argument, `default` will be used as the weight for all edges. Note that if there is an attribute named by `attr`, then its default value will be used for edges not specifically customized. See `edgeData` and `edgeDataDefaults` for more information.

Because of their position after the `...`, no partial matching is performed for the arguments `attr`, `default`, and `type.checker`.

## Value

A named list of named edge weight vectors. The names on the list are the names of the nodes specified by `index`, or all nodes if `index` was not provided. The names on the weight vectors are node names to identify the edge to which the weight belongs.

## Author(s)

R. Gentleman and S. Falcon

## See Also

[nodes](#) [edges](#) [edgeData](#) [edgeDataDefaults](#) [is.numeric](#) [is.integer](#) [is.character](#)

## Examples

```
V <- LETTERS[1:4]
edL2 <- vector("list", length=4)
names(edL2) <- V
for(i in 1:4)
  edL2[[i]] <- list(edges=c(2,1,2,1)[i], weights=sqrt(i))
gR2 <- new("graphNEL", nodes=V, edgeL=edL2, edgemode="directed")
edgeWeights(gR2, "C")
edgeWeights(gR2)
edgeWeights(gR2, attr="foo", default=5)
edgeData(gR2, attr="weight")
edgeData(gR2, from="C", attr="weight")
```

---

fromGXL-methods      *Methods for GXL manipulations in package graph*

---

## Description

GXL <http://www.gupro.de/GXL> is "an XML sublanguage designed to be a standard exchange format for graphs". This document describes tools in the graph package for importing GXL data to R and for writing graph data out as GXL.

## Value

fromGXL	currently returns a graphNEL when possible. This function is based on <code>xmlEventParse</code> with handlers defined in the function <code>NELhandler</code> . The <code>dump()</code> element of this handler should emit information on all children of nodes and edges; the <code>asGraphNEL()</code> element will return a <code>graphNEL</code> object with weights if child <code>&lt;attr&gt;</code> with name attribute "weights" is present for each edge element.
toGXL	for an input of class "graphNEL", returns an object of class c("XMLInternalDOM", "XMLOutputStream"); see the example for how to convert this to a text stream encoding XML
dumpGXL	returns an R list with all the node, edge, and named attribute information specified in the GXL stream
validateGXL	returns silently (invisibly returns the parsed tree) for a DTD-compliant stream, or is otherwise very noisy

## Methods

**fromGXL** con = connection: returns a graphNEL based on a parsing of the GXL stream on the connection

**dumpGXL** con = connection: returns an R list based on a parsing of the GXL stream on the connection

**validateGXL** con = connection: checks the GXL stream against its DTD

**toGXL** object = graphNEL: creates an XMLInternalDOM representing the graph in GXL

## Note

At present, toGXL does not return a validating GXL stream because XML package does not properly handle the dtd and namespaces arguments to `xmlTree`. This is being repaired. To fix the stream, add `<!DOCTYPE gx1 SYSTEM "http://www.gupro.de/GXL/gx1-1.0.1.dtd">` as second record in the output.

Some structures in a graphNEL and some tags in GXL may not be handled at this time.

## Author(s)

Vince Carey <stvjc@channing.harvard.edu>



**Examples**

```

sf <- file(system.file("GXL/simpleExample.gxl", package="graph"))
show(fromGXL(sf))
print(dumpGXL(sf))
close(sf)
#validateGXL(sf)
# bad <- file(system.file("GXL/c2.gxl", package="graph"))
# here's how you can check if the GXL is well-formed, if
# you have a libxml2-based version of R XML package
#
# try( validateGXL(bad) )
#
gR <- new("graphNEL", nodes=letters[1:4], edgeL=list(
  a=list(edges=4), b=list(edges=3), c=list(edges=c(2,1)), d=list(edges=1)),
  edgemode="directed")
#
# following requires that you are using XML bound with recent libxml2
#
#an <- as.numeric
#if (an(libxmlVersion())$major)>=2 && an(libxmlVersion())$minor>=4
## since toGXL returns an XML object, we need to attach the XML
## package.
library("XML")
cat(saveXML(toGXL(gR)$value()))
wtd <- file(system.file("GXL/kmstEx.gxl", package="graph"))
wtdg <- fromGXL(wtd)
close(wtd)
print(edgeWeights(wtdg))

```

---

graph2SparseM

*Coercion methods between graphs and sparse matrices*


---

**Description**

These functions provide coercions between objects that inherit from the `graph` class to sparse matrices from the `SparseM` package.

**Usage**

```

graph2SparseM(g, useweights=FALSE)
sparseM2Graph(sM, nodeNames, edgemode=c("directed", "undirected"))

```

**Arguments**

<code>g</code>	An instance of the <code>graph</code> class.
<code>useweights</code>	A logical value indicating whether to use the edge weights in the graph as values in the sparse matrix.
<code>sM</code>	A sparse matrix.
<code>nodeNames</code>	A character vector of the node names.
<code>edgemode</code>	Specifies whether the graph to be created should have directed (default) or undirected edges. If undirected, the input matrix <code>sM</code> must be symmetric.

**Details**

A very simple coercion from one representation to another.

Currently it is presumed that the matrix is square. For other graph formats, such as bipartite graphs, some improvements will be needed; patches are welcome.

**Value**

`graph2SparseM` takes as input an instance of a subclass of the `graph` class and returns a sparse matrix.

`sparseM2Graph` takes a sparse matrix as input and returns an instance of the `graphNEL` class. By default, the `graphNEL` returned will have directed edges.

**Author(s)**

R. Gentleman

**See Also**

[graph-class](#), [graphNEL-class](#), and for other conversions, [aM2bpG](#) and [ftM2adjM](#)

**Examples**

```
set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p=.3)
s1 <- graph2SparseM(g1, useweights=TRUE)
g2 <- sparseM2Graph(s1, letters[1:10], edgemode="undirected")
## consistency check
stopifnot(all.equal(g1, g2))
```

---

graphAM-class

*Class "graphAM"*

---

**Description**

A graph class where node and edge information is represented as an adjacency matrix. The adjacency matrix is square and element `adjMat[i, j]` is one if there is an edge from node `i` to node `j` and zero otherwise.

**Details**

The non-zero matrix values can be used to initialize an edge attribute. If this is desired, use the `values` argument in the call to `new` and provide a list with a single named element. The name determines the attributes and the value provides the default value for that attribute.

**Objects from the Class**

Objects can be created by calls of the form `new("graphAM", adjMat, edgemode, values)`.

**Slots**

**adjMat:** An adjacency "matrix" describing the graph structure. The `colnames` of the matrix will be used as node names for the graph if present.

**edgeData:** Storage for edge attributes.

**nodeData:** Storage for node attributes.

**Extends**

Class "graph", directly.

**Methods**

**addEdge** signature(from = "character", to = "character", graph = "graphAM", weights = "missing"):...

**addNode** signature(object = "graphAM", nodes = "character"):...

**clearNode** signature(node = "character", object = "graphAM"):...

**coerce** signature(from = "graphAM", to = "graphNEL"):...

**coerce** signature(from = "graphAM", to = "matrix"): In converting to a matrix, if an edge attribute named "weight" is defined, the non-zero elements of the matrix will contain the corresponding attribute value. For more flexible matrix conversion, see `toMatrix`.

**coerce** signature(from = "matrix", to = "graphAM"): This coerce method exists for symmetry. In most cases, creating a new `graphAM` instance using `new` gives one more control over the resulting graph.

**edges** signature(object = "graphAM", which = "missing"):...

**edges** signature(object = "graphAM", which = "character"):...

**initialize** signature(.Object = "graphAM"):...

**inEdges** signature(node = "character", object = "graphNEL"): Return the incoming edges for the specified nodes. See `inEdges`.

**isAdjacent** signature(object = "graphAM", from = "character", to = "character"): ...

**nodes<-** signature(object = "graphAM", value = "character"):...

**nodes** signature(object = "graphAM"):...

**numEdges** signature(graph = "graphAM"):...

**numNodes** signature(object = "graphAM"):...

**removeEdge** signature(from = "character", to = "character", graph = "graphAM"): ...

**removeNode** signature(node = "character", object = "graphAM"):...

**Author(s)**

Seth Falcon

**See Also**

[graph-class](#), [graphNEL-class](#)

**Examples**

```

mat <- rbind(c(0, 0, 1, 1),
            c(0, 0, 1, 1),
            c(1, 1, 0, 1),
            c(1, 1, 1, 0))
rownames(mat) <- colnames(mat) <- letters[1:4]
g1 <- new("graphAM", adjMat=mat)
stopifnot(identical(mat, as(g1, "matrix")), validObject(g1))

## now with weights:
mat[1,3] <- mat[3,1] <- 10
gw <- new("graphAM", adjMat=mat, values=list(weight=1))

## consistency check:
stopifnot(identical(mat, as(gw, "matrix")),
          validObject(gw),
          identical(gw, as(as(gw, "graphNEL"), "graphAM")))

```

---

graph-class

Class "graph"

---

**Description**

A virtual class that all graph classes should extend.

**Details**

`degree` returns either a named vector (names correspond to the nodes in the graph) containing the degree for undirected graphs or a list with two components, `inDegree` and `outDegree` for directed graphs.

`connComp` returns a list of the connected components. Each element of this list contains the labels of all nodes in that component.

For a *directed graph* or *digraph* the *underlying graph* is the graph that results from removing all direction from the edges. This can be achieved using the function `ugraph`.

A *weakly connected* component of a *digraph* is one that is a connected component of the underlying graph. This is the default for `connComp`. A *digraph* is *strongly connected* if every two vertices are mutually reachable. A *strongly connected* component of a *digraph*, **D**, is a maximal *strongly connected* subdigraph of **D**. See the **RBGL** package for an implementation of Trajan's algorithm to find *strongly connected* components (`strongComp`).

In the **graph** implementation of `connComp` *weak connectivity* is used. If the argument to `connComp` is a directed graph then `ugraph` is called to create the underlying undirected graph and that is used to compute connected components. Users who want different behavior are encouraged to use **RBGL**.

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Slots**

**edgeData:** An `attrData` instance for edge attributes.

**nodeData:** An `attrData` instance for node attributes.

**graphData:** A list for graph-level attributes. Only mandatory list item is `edgemode` which indicates whether edges are "directed" or "undirected"

**renderInfo:** A list of graph rendering information.

**Methods**

**nodes** return a character vector containing the names of the nodes of the graph

**nodes<-** rename the nodes of the graph

**show** signature(object = "graph"): A print method for the graph.

**acc** signature(object = "graph"): find all nodes accessible from the specified node.

**complement** signature(x = "graph"): compute the complement of the supplied graph. The complement is defined with respect to the complete graph on the nodes in `x`. Currently this returns an object of class `graphNEL`.

**connComp** signature(object = "graph"): find the connected components of a graph.

**degree** signature(object = "graph", Nodes = "missing"): find the degree of a node (number of coincident edges).

**degree** signature(object = "graph", Nodes = "ANY"): as above.

**dfs** signature(object = "graph"): execute a depth first search on a graph starting with the specified node.

**edges** signature(object="graph", which="character"): return the edges indicated by `which`. `which` can be missing in which case all edges are returned or it can be a character vector with the node labels indicating the nodes whose edge lists are wanted.

**edgeDataDefaults** Get and set default attributes for the edges in the graph.

**edgeData** Get and set attributes for edges in the graph

**edgemode** signature(object="graph"): return the `edgemode` for the graph. Currently this can be either `directed` or `undirected`.

**edgemode<-** signature(object="graph", value="character"): set the `edgemode` for the graph. Currently this can be either `directed` or `undirected`.

**edgeWeights** Return a list of edge weights in a list format similar to the `edges` method.

**intersection** signature(x = "graph", y = "graph"): compute the intersection of the two supplied graphs. They must have identical nodes. Currently this returns an object of class `graphNEL`. With edge weights of 1 for any matching edge.

**isAdjacent** signature(from="character", to="character"): Determine if edges exists between nodes.

**isConnected** signature(object = "graph"): A boolean that details if a graph is fully connected or not.

**isDirected** Return `TRUE` if the graph object has directed edges and `FALSE` otherwise.

**join** signature(x = "graph", y = "graph"): returns the joining of two graphs. Nodes which are shared by both graphs will have their edges merged. Note that `edgeWeights` for the resulting graph are all set to 1. Users wishing to preserve weights in a join operation must perform `addEdge` operations on the resulting graph to restore weights.

**nodes<-** A generic function that allows different implementations of the `graph` class to reset the node labels

**nodeDataDefaults** Get/set default attributes for nodes in the graph.

**nodeData** Get/set attributes for nodes in the graph.

**numEdges** signature(object = "graph"): compute the number of edges in a graph.

**numNodes** signature(object = "graph"): compute the number of nodes in a graph.

**plot** Please see the help page for the `plot.graph` method in the `Rgraphviz` package

**union** signature(x = "graph", y = "graph"): compute the union of the two supplied graphs. They must have identical nodes. Currently this returns an object of class `graphNEL`.

**edgeNames** signature(object = "graph"): Returns a vector of the edge names for this graph, using the format `tail~head`, where `head` is the name of the tail node and `tail` is the name of the head node.

**updateGraph** signature(object = "graph"): Updates old instances of graph objects.

### Author(s)

R. Gentleman and E. Whalen.

### References

Graph Theory and its Applications, J. Gross and J. Yellen.

### See Also

[graphNEL-class](#), [graphAM-class](#), [distGraph-class](#).

### Examples

```
set.seed(123)
g1 <- randomGraph(letters[1:10], 1:4, p= 0.3)
numEdges(g1)
edgeNames(g1)
edges(g1)
edges(g1, c("a","d")) # those incident to 'a' or 'd'
```

---

graphExamples

*A List Of Example Graphs*

---

### Description

This data set contains a list of example `graphNEL` objects, which can then be used for plotting.

### Usage

```
data(graphExamples)
```

### Source

Various sources, primarily from [randomGraph](#) and [randomEGraph](#)

**Examples**

```
data(graphExamples)
a <- graphExamples[[1]]
a
```

---

graphNEL-class      *Class "graphNEL"*

---

**Description**

This is a class of graphs that are represented in terms of nodes and an edge list. This is a suitable representation for a graph with a large number of nodes and relatively few edges.

**Details**

The `graphNEL` class provides a very general structure for representing graphs. It will be reasonably efficient for lists with relatively more nodes than edges. Although this representation can support multi-edges, such support is not implemented and instances of `graphNEL` are assumed to be simple graphs with at most one edge between any pair of nodes.

The `edgeL` is a named `list` of the same length as the node vector. The names are the names of the nodes. Each element of `edgeL` is itself a list. Each element of this (sub)list is a vector (all must be the same length) and each element represents an edge to another node. The sublist named `edges` holds index values into the node vector. And each such entry represents an edge from the node which has the same name as the component of `edgeL` to the node with index provided. Another component that is often used is named `weights`. It represents edge weights. The user can specify any other edge attributes (such as types etc). They are responsible for any special handling that these might require.

For an `undirected` instance all edges are reciprocated (there is an edge from A to B and from B to A).

Note that the reason for using indices to represent the `to` end of a node is so that we can easily support permutation of the node labels as a way to generate randomizations of the graph.

**Objects from the Class**

Objects can be created by calls of the form `new("graphNEL", nodes, edgeL, edgemode)`.

**nodes** A character vector of node labels.

**edgeL** A named list either in the format returned by the `edges` method or a list of lists where each inner list has an element named `edges` and optionally an element named `weights`. If `weights` is present, it must be the same length as the `edges` element.

**edgemode** Either "directed" or "undirected".

**Slots**

**nodes:** Object of class "vector".

**edgeL:** Object of class "list". The `edgeL` must be the same length as `nodes`. The elements of this vector correspond to the same element in `nodes`. The elements are themselves lists. If the node has any edges then this list will have an element named `edges`. This will eventually change. Since edge weights are now stored in the edge attributes construct, we do not need the extra level of list.

**Extends**

Class "graph", directly.

**Methods**

**adj** signature(object = "graphNEL"): A method for finding nodes adjacent to the supplied node.

**edgeL** signature(graph = "graphNEL"): A method for obtaining the edge list.

**edgeWeights** signature(object = "graphNEL"): A method for obtaining the edge weights.

**edges** signature(object = "graphNEL"): A method for obtaining the edges.

**inEdges** signature(node = "character", object = "graphNEL"): Return the incoming edges for the specified nodes. See [inEdges](#).

**nodes** signature(object = "graphNEL"): A method for obtaining the nodes.

**numNodes** signature(object = "graphNEL"): A method for determining how many nodes are in the graph.

**subGraph** signature(snodes="character", graph = "graphNEL"): A method for obtaining the induced subgraph based on the set of supplied nodes and the supplied graph.

**plot** Please see the help page for `plot.graphNEL` in the `Rgraphviz` package

**graph2graphviz** signature(object = "graphNEL"): A method that will convert a `graphNEL` object into a matrix suitable for interaction with `Rgraphviz`. Not intended to be called directly. This function will insure that no NA's (or other undesired values) are in the graph, or created by coercion.

**nodes<-** signature(object="graphNEL", value="character"): A method for replacing the nodes in a graph object. It checks to be sure the values are the right length and unique.

**coerce** signature(from = "graphNEL", to = "graphAM"): Called via `as`, the method converts to an adjacency matrix representation. See [graphAM-class](#).

**Author(s)**

R. Gentleman

**See Also**

[graphAM-class](#), [distGraph-class](#), [clusterGraph-class](#)

**Examples**

```
set.seed(123)
V <- LETTERS[1:4]
edL <- vector("list", length=4)
names(edL) <- V
for(i in 1:4)
  edL[[i]] <- list(edges=5-i, weights=runif(1))
gR <- new("graphNEL", nodes=V, edgeL=edL)
edges(gR)
edgeWeights(gR)
```



---

graphRendering      *How to render a graph*

---

### Description

FIXME: Need content

---

integrinMediatedCellAdhesion  
*KEGG Integrin Mediated Cell Adhesion graph*

---

### Description

A graph representing the integrin-mediated cell adhesion pathway from KEGG, as well as a list of attributes for use in plotting the graph with Rgraphviz.

### Usage

```
data(integrinMediatedCellAdhesion)
```

### Details

The integrinMediatedCellAdhesion data set contains two objects:

The first is IMCAGraph, which is an object of class graph-NEL and represents the hsa04510 graph from KEGG.

The second is IMCAAttrs, which is a list of four elements. The first element, defAttrs corresponds to the attrs arguments of `agopen` and `plot.graph`. The second element is nodeAttrs which corresponds to the nodeAttrs argument in the same two functions from Rgraphviz. The third element, subGList corresponds to the subGList argument in those functions. Lastly, the fourth element, LocusLink provides a named list where the names are the nodes and the values are vectors of LocusLink ID values which correspond to those nodes.

The values from defAttrs, nodeAttrs and subGList in the IMCAAttrs list are part of an ongoing attempt by Bioconductor to provide the set of options to most accurately recreate the actual visual image of the pathway from the KEGG site using Rgraphviz. Users may try out their own combination of attributes and settings for their own needs, but these represent our own efforts at as closely recreating the image as possible.

### Source

<http://www.genome.ad.jp/kegg/pathway/hsa/hsa04510.html>

### Examples

```
data(integrinMediatedCellAdhesion)
if (require("Rgraphviz") & interactive())
  plot(IMCAGraph, attrs=IMCAAttrs$defAttrs,
       nodeAttrs=IMCAAttrs$nodeAttrs, subGList=IMCAAttrs$subGList)
```

---

`inEdges`*Generic Method inEdges*

---

**Description**

Returns a list of all incoming edges for the specified nodes.

**Usage**

```
inEdges(node, object)
```

**Arguments**

<code>node</code>	character vector of node names
<code>object</code>	a graph object

**Details**

If no `node` argument is specified, `inEdges` returns the incoming edges for all nodes in the graph.

For an undirected graph, `inEdges` returns all edges for the specified nodes.

**Value**

A list with length matching the length of `node`. If `node` was missing, a list containing an element for each node in the graph.

Each list element contains a character vector of node names giving the nodes that have outgoing edges to the node given by the name of the list element.

**Author(s)**

R. Gentleman

**See Also**

[removeNode](#), [clearNode](#)

**Examples**

```
V <- LETTERS[1:4]
edL3 <- vector("list", length=4)
for(i in 1:4)
  edL3[[i]] <- list(edges=(i%%4)+1, weights=i)
names(edL3) <- V
gR3 <- new("graphNEL", nodes=V, edgeL=edL3, "directed")
inEdges(c("A", "B"), gR3)
```

---

isAdjacent-methods *Determine if nodes share an edge in a graph*

---

### Description

For a given subclass of `graph-class`, returns `TRUE` if the graph contains an edge from node specified by `from` to the node specified by `to`.

The appropriate logical vector will be returned as long as `from` and `to` have the same length and contain nodes in the graph object specified by `object`.

### Usage

```
isAdjacent(object, from, to, ...)
```

### Arguments

<code>object</code>	An instance of a subclass of <code>graph-class</code> .
<code>from</code>	A character vector of nodes in the graph.
<code>to</code>	A character vector of nodes in the graph
<code>...</code>	May be used by methods called on subclasses of <code>graph</code>

---

isDirected-methods *Determine if a graph has directed or undirected edges*

---

### Description

The edges of a `graph-class` object are either directed or undirected. This function returns `TRUE` if the edges are directed and `FALSE` otherwise.

### Usage

```
isDirected(object)
```

### Arguments

<code>object</code>	A <code>graph-class</code> instance
---------------------	-------------------------------------

---

leaves *Find the leaves of a graph*

---

### Description

A leaf of an undirected graph is a node with degree equal to one. A leaf of a directed graph is defined with respect to in-degree or out-degree. The leaves of a directed graph with respect to in-degree (out-degree) are those nodes with in-degree (out-degree) equal to zero.

### Usage

```
leaves(object, degree.dir)
```

### Arguments

object	A graph object
degree.dir	One of "in" or "out". This argument is ignored when object is undirected and required otherwise. When degree.dir="in" (degree.dir="out"), nodes have no in coming (out going) edges will be returned.

### Value

A character vector giving the node labels of the leaves.

### Author(s)

Seth Falcon

### Examples

```
data(graphExamples)
graphExamples[[1]]
leaves(graphExamples[[1]])

data(apopGraph)
leaves(apopGraph, "in")
leaves(apopGraph, "out")
```

---

listEdges *List the Edges of a Graph*

---

### Description

A list where each element contains all edges between two nodes, regardless of orientation. The list has names which are node pairs, in lexicographic order, and elements all edges between those nodes.

### Usage

```
listEdges(object, dropNULL=TRUE)
```

**Arguments**

- `object` An instance of the `graphNEL-class` class.
- `dropNULL` Should those node pairs with no edges be dropped from the returned list.

**Details**

The function is currently only implemented for graphs of the `graphNEL-class`. The edges in the returned list are instances of the `simpleEdge-class`.

**Value**

A named list of `simpleEdge-class` objects.

**Author(s)**

R. Gentleman

**See Also**

`simpleEdge-class`, `edges`

**Examples**

```
set.seed(123)
V <- LETTERS[1:4]
edL <- vector("list", length=4)
names(edL) <- V
toE <- LETTERS[4:1]
for(i in 1:4)
  edL[[i]] <- list(edges=5-i, weights=runif(1))
gR <- new("graphNEL", nodes=V, edgeL=edL)
listEdges(gR)
```

---

MAPKsig

*A graph encoding parts of the MAPK signaling pathway*

---

**Description**

A graph encoding parts of the MAPK signaling pathway

**Usage**

```
data(MAPKsig)
```

**Format**

The format is: Formal class 'graphNEL' [package "graph"] with edgemode "directed".

**Source**

The KEGG pancreatic cancer pathway was visually inspected on 17 Sept 2007, and the subgraph associated with MAPK signaling was isolated. The HUGO names for each symbol in the KEGG visualization were obtained and checked for existence on hgu95av2. Some abbreviated terms for processes are also included as nodes.

**Examples**

```
data(MAPKsig)
if (require(Rgraphviz)) {
  nat = rep(FALSE, length(nodes(MAPKsig)))
  names(nat) = nodes(MAPKsig)
  plot(MAPKsig, nodeAttrs=list(fixedsize=nat))
}
```

---

Coercions between matrix and graph representations  
*Coercions between matrix and graph representations*

---

**Description**

A collection of functions and methods to convert various forms of matrices into graph objects.

**Usage**

```
aM2bpG(aM)
ftM2adjM(ft, W=NULL, V=NULL, edgemode="directed")
ftM2graphNEL(ft, W=NULL, V=NULL, edgemode="directed")
## S4 method for signature 'graphNEL,matrix':
coerce(from,to="matrix",strict=TRUE)
## S4 method for signature 'matrix,graphNEL':
coerce(from,to="graphNEL",strict=TRUE)
```

**Arguments**

<code>ft</code>	An nx2 matrix containing the <code>from/to</code> representation of graph edges.
<code>W</code>	An optional vector of edge weights.
<code>V</code>	An optional vector of node names.
<code>aM</code>	An affiliation matrix for a bipartite graph.
<code>edgemode</code>	Character. Specifies if the resulting graph is to be directed or undirected.
<code>from</code>	Object to coerce from, either of type <code>matrix</code> or <code>graphNEL</code>
<code>to</code>	Character giving class to coerce to. Either <code>"matrix"</code> or <code>"graphNEL"</code> .
<code>strict</code>	Strict object checking.

**Details**

In the functions `ftM2adjM` and `ftM2graphNEL`, a `from/to` matrix `ft` is converted into an adjacency matrix or a `graphNEL` object respectively. In `ft`, the first column represents the `from` nodes and the second column the `to` nodes.

To have unconnected nodes, use the `V` argument (see below). The `edgemode` parameter can be used to specify if the desired output is a directed or undirected graph.

The same edge must not occur twice in the `from/to` matrix. If `edgemode` is `undirected`, the edge  $(u, v)$  and  $(v, u)$  must only be specified once.

`W` is an optional vector of edge weights. The order of the edge weights in the vector should correspond to the order of the edges recorded in `ft`. If it is not specified, edge weights of 1 are assigned by default.

`V` is an optional vector of node names. All elements of `ft` must be contained in `V`, but not all names in `V` need to be contained in `ft`. If `V` is not specified, it is set to all nodes represented in `ft`. Specifying `V` is most useful for creating a graph that includes nodes with degree 0.

`aM` is an affiliation matrix as frequently used in social networks analysis. The rows of `aM` represent actors, and the columns represent events. An entry of "1" in the *i*th row and *j*th column represents affiliation of the *i*th actor with the *j*th event. Weighted entries may also be used. `aM2bpG` returns a `graphNEL` object with nodes consisting of the set of actors and events, and directed (possibly weighted) edges from the actors to their corresponding events. If plotted using `Rgraphviz` and the `dot` layout, the bipartite structure of the graph returned by `aM2bpG` should be evident.

An adjacency matrix can be coerced into a `graphNEL` using the `as` method. If the matrix is a symmetric matrix, then the resulting graph will be `undirected`, otherwise it will be `directed`.

**Value**

For `ftM2graphNEL` and `aM2bpG`, an object of class `graphNEL`. For `ftM2adjM`, a matrix (the adjacency matrix representation).

**Author(s)**

Denise Scholtens, Wolfgang Huber

**Examples**

```
## From-To matrix

From <- c("A", "A", "C", "C")
To   <- c("B", "C", "B", "D")
L   <- cbind(From, To)

W   <- 1:4
M1  <- ftM2adjM(L, W, edgemode="directed")
M2  <- ftM2adjM(L, W, edgemode="undirected")
stopifnot(all(M1+t(M1)==M2))

G1  <- ftM2graphNEL(L, W, edgemode="directed")
G2  <- ftM2graphNEL(L, W, edgemode="undirected")

## Adjacency matrix

From <- matrix(runif(100), nrow=10, ncol=10)
```

```
From <- (From+t(From)) > pi/4
rownames(From) <- colnames(From) <- LETTERS[1:10]

To <- as(From, "graphNEL")
Back <- as(To, "matrix")

stopifnot(all(From == Back))
```

---

mostEdges

*Find the node in a graph with the greatest number of edges*

---

### Description

mostEdges finds the node that has the most edges in the graph. This is the node with the highest degree.

### Usage

```
mostEdges(objGraph)
```

### Arguments

objGraph      the graph object

### Value

index          the index of the node with the most edges  
id             the node value with the most edges; may be affy id, locus link id, or genename depending on the node type  
maxLen        the number of edges for that node

### Author(s)

Elizabeth Whalen

### See Also

[numEdges](#), [aveNumEdges](#), [numNoEdges](#)

### Examples

```
set.seed(123)
g1 <- randomGraph(11:30, letters[20:26], p=.4)
mostEdges(g1)
```



---

multiGraph-class    *Class "multiGraph"*

---

### Description

A collection of classes to model multigraphs. These include the multiGraph class as well as classes to contain edge sets.

### Objects from the Class

Objects can be created from the multiGraph class, the edgeSet class is virtual, and particular variants should be used.

### Slots

These slots are for the multiGraph class.

**nodes** The names of the nodes.

**edgeL** A list of edge lists.

**nodeData** An instance of the attrData class.

**graphData** A list.

These slots are for the edgeSet class, or one of its subclasses.

**edgeData** An instance of the attrData class.

**edgemode** A character vector, one of directed, or undirected.

**edgeL** A list of the edges (graphNEL)

**adjMat** An adjacency matrix (graphAM)

### Methods

**show** Print a multigraph.

**isDirected** A vector indicating which of the edgeSets is directed.

**nodes** Retrieve the node names

**numNodes** Return the number of nodes

**edges** Return either all edges, or a subset of them, depending on the arguments supplied.

**numEdges** Return a vector with the number of edges, for each edge set.

---

 nodeDataDefaults-methods

*Get and set default attributes for the nodes of a graph*


---

### Description

You can associate arbitrary attributes with the nodes of a graph. Use `nodeDataDefaults` to specify the set of attributes that describe nodes. Each attribute must have a default value. You can set the attribute for a particular node or set of nodes using `nodeData`.

### Usage

```
nodeDataDefaults(self, attr)
nodeDataDefaults(self, attr) <- value
```

### Arguments

<code>self</code>	A <code>graph-class</code> instance
<code>attr</code>	A character vector of length one giving the name of an attribute
<code>value</code>	An R object to set as the default value for the given attribute

---

 nodeData-methods

*Get and set attributes for the nodes of a graph object*


---

### Description

Attributes of the nodes of a graph can be accessed using `nodeData`. The attributes must be defined using `nodeDataDefaults`. You can omit the `n` argument to retrieve attributes for all nodes in the graph. You can omit the `attr` argument to retrieve all attributes.

### Usage

```
nodeData(self, n, attr)
nodeData(self, n, attr) <- value
```

### Arguments

<code>self</code>	A <code>graph-class</code> instance
<code>n</code>	A character vector of node names
<code>attr</code>	A character vector of length one specifying the name of a node attribute
<code>value</code>	An R object to store as the attribute value

---

`numNoEdges`*Calculate the number of nodes that have an edge list of NULL*

---

**Description**

`numNoEdges` calculates the number of nodes that have an edge list of NULL (i.e. no edges).

**Usage**

```
numNoEdges(objGraph)
```

**Arguments**

`objGraph`      the graph object

**Value**

An integer representing the number of NULL edge lists in the graph.

**Author(s)**

Elizabeth Whalen

**See Also**

[numEdges](#), [aveNumEdges](#), [mostEdges](#)

**Examples**

```
set.seed(999)
g1 <- randomEGraph(letters, .01)
numNoEdges(g1)
```

---

`pancrCaIni`*A graph encoding parts of the pancreatic cancer initiation pathway*

---

**Description**

A graph encoding parts of the pancreatic cancer initiation pathway

**Usage**

```
data(pancrCaIni)
```

**Format**

The format is: Formal class 'graphNEL' [package "graph"] with edgemode "directed".

**Source**

The KEGG pancreatic cancer pathway was visually inspected on 17 Sept 2007 and a subgraph was isolated. The HUGO names for each symbol in the KEGG visualization were obtained and checked for existence on hgu95av2. Some abbreviated terms for processes are also included as nodes.

**Examples**

```
data(pancrCaIni)
if (require(Rgraphviz)) {
  nat = rep(FALSE, length(nodes(pancrCaIni)))
  names(nat) = nodes(pancrCaIni)
  plot(pancrCaIni, nodeAttrs=list(fixedsize=nat))
}
```

---

randomEGraph

*Random Edge Graph*


---

**Description**

A function to create random graphs according to a random edge model. The user supplies the set of nodes for the graph as  $V$  and either a probability,  $p$ , that is used for each edge or the number of edges,  $edges$  they want to have in the resulting graph.

**Usage**

```
randomEGraph(V, p, edges)
```

**Arguments**

$V$	The nodes for the graph.
$p$	The probability of an edge being selected.
$edges$	The number of edges wanted.

**Details**

The user must specify the set of nodes and either a probability for edge selection or the number of edges wanted, but not both. Let  $n_V$  denote the number of nodes. There are  $\text{choose}(n_V, 2)$  edges in the complete graph. If  $p$  is specified then a biased coin (probability of heads being  $p$ ) is tossed for each edge and if it is heads that edge is selected. If  $edges$  is specified then that many edges are sampled without replacement from the set of possible edges.

**Value**

An object of class `graphNEL-class` that contains the nodes and edges.

**Author(s)**

R. Gentleman

**See Also**

[randomGraph](#)

**Examples**

```
set.seed(123)
V <- letters[14:22]
g1 <- randomEGraph(V, .2)

g2 <- randomEGraph(V, edges=30)
```

---

randomGraph	<i>Random Graph</i>
-------------	---------------------

---

**Description**

This function generates a random graph according to a model that involves a latent variable. The construction is to randomly assign members of the set  $M$  to the nodes,  $V$ . An edge is assigned between two elements of  $V$  when they both have the same element of  $M$  assigned to them. An object of class `graphNEL` is returned.

**Usage**

```
randomGraph(V, M, p, weights=TRUE)
```

**Arguments**

<code>V</code>	The nodes of the graph.
<code>M</code>	A set of values used to generate the graph.
<code>p</code>	A value between 0 and 1 that indicates the probability of selecting an element of $M$ .
<code>weights</code>	A logical indicating whether to use the number of shared elements of $M$ as weights.

**Details**

The model is quite simple. To generate a graph,  $G$ , the user supplies the list of nodes,  $V$  and a set of values  $M$  which will be used to create the graph. For each node in  $V$  a logical vector with length equal to the length of  $M$  is generated. The probability of a `TRUE` at any position is determined by  $p$ . Once values from  $M$  have been assigned to each node in  $V$  the result is processed into a graph. This is done by creating an edge between any two elements of  $V$  that share an element of  $M$  (as chosen by the selection process).

The sizes of  $V$  and  $M$  and the values of  $p$  determine how dense the graph will be.

**Value**

An object of class `graphNEL-class` is returned.

**Author(s)**

R. Gentleman

**See Also**

[randomEGraph](#), [randomNodeGraph](#)

**Examples**

```

set.seed(123)
V <- letters[1:10]
M <- 1:4
g1 <- randomGraph(V, M, 0.2)
numEdges(g1) # 16, in this case
edgeNames(g1) # "<from> ~ <to>" since undirected

```

---

randomNodeGraph      *Generate Random Graph with Specified Degree Distribution*

---

**Description**

randomNodeGraph generates a random graph with the specified degree distribution. Self-loops are allowed. The resultant graph is directed (but can always be coerced to be undirected).

**Usage**

```
randomNodeGraph(nodeDegree)
```

**Arguments**

nodeDegree      A named integer vector specifying the node degrees.

**Details**

The input vector must be named, the names are taken to be the names of the nodes. The sum must be even (there is a theorem that says we require that to construct a graph). Self-loops are allowed, although patches to the code that make this a switchable parameter would be welcome.

**Value**

An instance of the graphNEL class. The graph is directed.

**Author(s)**

R. Gentleman

**References**

Random Graphs as Models of Networks, M. E. J. Newman.

**See Also**

[randomGraph](#), [randomEGraph](#)

**Examples**

```

set.seed(123)
c1 <- c(a = 1, b = 1, c = 2, d = 4)

(g1 <- randomNodeGraph(c1))
stopifnot(validObject(g1))

```

---

removeEdge	<i>removeEdge</i>
------------	-------------------

---

## Description

A function to remove the specified edges from a graph.

## Usage

```
removeEdge(from, to, graph)
```

## Arguments

from	from edge labels
to	to edge labels
graph	a graph object

## Details

A new graph instance is returned with the edges specified by corresponding elements of the `from` and `to` vectors removed. If `from` and `to` are not the same length, one of them should have length one. All edges to be removed must exist in `graph`.

## Value

A new instance of a graph with the same class as `graph` is returned with the specified edges removed.

## Author(s)

R. Gentleman

## See Also

[addNode](#), [addEdge](#), [removeNode](#)

## Examples

```
V <- LETTERS[1:4]
edL1 <- vector("list", length=4)
names(edL1) <- V
for(i in 1:4)
  edL1[[i]] <- list(edges=c(2,1,4,3)[i], weights=sqrt(i))
gR <- new("graphNEL", nodes=V, edgeL=edL1)

gX <- removeEdge("A", "B", gR)

set.seed(123)
g <- randomEGraph(V=letters[1:5], edges=5)
g2 <- removeEdge(from=c("a","b"), to=c("d","c"), g)
```

---

`removeNode`*removeNode*

---

### Description

A function to remove a node from a graph. All edges to and from the node are also removed.

### Usage

```
removeNode(node, object)
```

### Arguments

<code>node</code>	The label of the node to be removed.
<code>object</code>	The graph to remove the node from.

### Details

The specified node is removed from the graph as are all edges to and from that node. A new instance of the same class as `object` with the specified node(s) is returned.

Note, `node` can be a vector of labels, in which case all nodes are removed.

This is similar to [subGraph](#).

### Value

A new instance of a graph of the same class as `object` but with all specified nodes removed.

### Author(s)

R. Gentleman

### See Also

[removeEdge](#), [addEdge](#), [addNode](#), [subGraph](#)

### Examples

```
V <- LETTERS[1:4]
edL2 <- vector("list", length=4)
names(edL2) <- V
for(i in 1:4)
  edL2[[i]] <- list(edges=c(2,1,2,1)[i], weights=sqrt(i))
gR2 <- new("graphNEL", nodes=V, edgeL=edL2, edgemode="directed")
gX <- removeNode("C", gR2)
```



---

renderInfo-class    *Class "renderInfo"*


---

## Description

A container class to manage graph rendering attributes.

## Objects from the Class

Objects can be created by calls of the form `new("renderInfo")` or by using the initializer `.renderInfoPrototype`.

## Slots

**pars:** List of default rendering attributes with two items `nodes` and `edges`. When not set further down the parameter hierarchy, these defaults will be used for all nodes/edges in the graph.

**nodes:** Named list of attributes specific to nodes.

**edges:** Named list of attributes specific to edges.

**graph:** Named list of graph-wide attributes.

Each item of `nodes` and `edges` can take arbitrary vectors, the only restriction is that they have to be of either length 1 or length equal to the number of nodes or edges, respectively.

`pars` and `graph` can take arbitrary scalars, the latter for both edges and nodes.

## Methods

The following are functions rather than methods and build the API to control the graphical output of a graph when it is plotted using `renderGraph`. Please see [graphRendering](#) for more details.

**parRenderInfo, parRenderInfo<-** getter and setter for items of slot `pars`

**nodeRenderInfo, nodeRenderInfo<-** getter and setter for items of slot `nodes`

**edgeRenderInfo, edgeRenderInfo<-** getter and setter for items of slot `edges`

**graphRenderInfo, graphRenderInfo<-** getter and setter for items of slot `graph`

The getters all take two arguments: `g` is a graph object and `name` is a character giving the name of one of the item in the respective slot. When `name` is missing this will give you the whole list.

The setters are a bit more complex: `nodeRenderInfo<-` and `edgeRenderInfo<-` can take

**named list of named vectors** where the names have to match the node or edge names. Items in the vector that don't match a valid edge or node name will be silently ignored. For undirected edges the order of head nodes and tail nodes in edge names is ignored, i.e. `a~b` is equivalent to `codeb~a`

**named list of scalars** which will set all the attribute for all edges or nodes in the graph `parRenderInfo<-` will only take a list with items `nodes`, `edges` and `graph`. The content of these list items can be arbitrary named vectors. `parRenderInfo<-` takes an arbitrary list

Available rendering parameters for nodes are:

**col:** the color of the line drawn as node border. Defaults to `black`.

**lty:** the type of the line drawn as node border. Defaults to `solid`. Valid values are the same as for the R's base graphic parameter `lty`.

**lwd:** the width of the line drawn as node border. Defaults to 1. Note that the underlying low level plotting functions do not support vectorized `lwd` values. Instead, only the first item of the vector will be used.

**fill:** the color used to fill a node. Defaults to `transparent`.

**textCol:** the font color used for the node labels. Defaults to `black`.

**fontsize:** the font size for the node labels in points. Defaults to 14. Note that the `fontsize` will be automatically adjusted to make sure that all labels fit their respective nodes. You may want to increase the node size by supplying the appropriate layout parameters to `Graphviz` in order to allow for larger font sizes.

**cex:** Expansion factor to further control the `fontsize`. As default, this parameter is not set, in which case the `fontsize` will be clipped to the node size. This mainly exists to for consistency with the base graphic parameters and to override the clipping of `fontsize` to `nodesize`.

Available rendering parameters for edges are:

**col:** the color of the edge line. Defaults to `black`.

**lty:** the type of the edge line. Defaults to `solid`. Valid values are the same as for the R's base graphic parameter `lty`.

**lwd:** the width of the edge line. Defaults to 1.

**textCol:** the font color used for the edge labels. Defaults to `black`.

**fontsize:** the font size for the edge labels in points. Defaults to 14.

**cex:** Expansion factor to further control the `fontsize`. This mainly exists to be consistent with the base graphic parameters.

### Author(s)

Deepayan Sarkar, Florian Hahne

### Examples

```
g <- randomGraph(letters[1:4], 1:3, p=0.8)
nodeRenderInfo(g) <- list(fill=c("a"="red", "b"="green"))
edgeRenderInfo(g) <- list(lwd=3)
edgeRenderInfo(g) <- list(lty=3, col="red")
parRenderInfo(g) <- list(edges=list(lwd=2, lty="dashed"),
nodes=list(col="gray", fill="gray"))
nodeRenderInfo(g)
edgeRenderInfo(g, "lwd")
edgeRenderInfo(g, c("lwd", "col"))
parRenderInfo(g)
```

---

`reverseEdgeDirections`*Reverse the edges of a directed graph*

---

### Description

Return a new directed graph instance with each edge oriented in the opposite direction relative to the corresponding edge in the input graph.

### Usage

```
reverseEdgeDirections(g)
```

### Arguments

`g` A graph subclass that can be coerced to `graphAM`

### Details

WARNING: this doesn't handle edge attributes properly. It is a preliminary implementation and subject to change.

### Value

A `graphNEL` instance

### Author(s)

S. Falcon

### Examples

```
g <- new("graphNEL", nodes=c("a", "b", "c"),
        edgeL=list(a=c("b", "c"), b=character(0), c=character(0)),
        edgemode="directed")

stopifnot(isAdjacent(g, "a", "b"))
stopifnot(!isAdjacent(g, "b", "a"))

grev <- reverseEdgeDirections(g)
stopifnot(!isAdjacent(grev, "a", "b"))
stopifnot(isAdjacent(grev, "b", "a"))
```

---

graph.par

*Graphical parameters and other settings*


---

### Description

Functions providing an interface to persistent graphical parameters and other settings used in the package.

### Usage

```
graph.par(...)
graph.par.get(name)
```

### Arguments

... either character strings naming parameters whose values are to be retrieved, or named arguments giving values that are to be set.

name character string, giving a valid parameter name.

### Details

graph.par works sort of like [par](#), but the details are yet to be decided.

graph.par.get(name) is equivalent to graph.par(name)[[1]]

### Value

In query mode, when no parameters are being set, graph.par returns a list containing the current values of the requested parameters. When called with no arguments, it returns a list with all parameters. When a parameter is set, the return value is a list containing previous values of these parameters.

### Author(s)

Deepayan Sarkar, <deepayan.sarkar@r-project.org>

### See Also

[par](#)

---

simpleEdge-class

*Class "simpleEdge".*


---

### Description

A simple class for representing edges in graphs.

### Objects from the Class

Objects can be created by calls of the form `new("simpleEdge", ...)`.

**Slots**

`edgeType`: Object of class "character"; the type of the edge.

`weight`: Object of class "numeric"; the edge weight.

`directed`: Object of class "logical"; is the edge directed.

`bNode`: Object of class "character"; the beginning node.

`eNode`: Object of class "character"; the ending node.

**Methods**

No methods defined with class "simpleEdge" in the signature.

**Note**

All slots are length one vectors (this is not currently checked for). If the edge is not directed there is no real meaning to the concepts of beginning node or ending node and these should not be interpreted as such.

**Author(s)**

R. Gentleman

**Examples**

```
new("simpleEdge", bNode="A", eNode="D")
```

---

Standard labeling of edges with integers  
*Standard labeling of edges with integers*

---

**Description**

Functions to convert between from-to representation and standard labeling of the edges for undirected graphs with no self-loops.

**Usage**

```
ftM2int(ft)
int2ftM(i)
```

**Arguments**

<code>i</code>	Numeric vector.
<code>ft</code>	Numeric nx2 or 2xn matrix.

**Details**

A standard 1-based node labeling of a graph  $G=(V,E)$  is a one-to-one mapping between the integers from 1 to  $|V|$  and the nodes in  $V$ . A standard 1-based edge labeling of an undirected graph  $G=(V,E)$  with no self-loops is *the* one-to-one mapping between the integers from 1 to  $|V|$  choose 2 =  $|V|*(|V|-1)/2$  such that the edge labeled 1 is between nodes 2 and 1, the edge labeled 2 is between nodes 3 and 1, the edge labeled 3 is between nodes 3 and 2, and so on.

**Value**

For `ftM2int`, a numeric vector of length `n`. For `int2ftM`, a `length(i) × 2` matrix.

**Author(s)**

Wolfgang Huber

**Examples**

```
nNodes <- 200
nEdges <- choose(nNodes, 2)
i <- 1:nEdges
ft <- int2ftM(i)
ft[1:6,]
stopifnot(all(ft[,1]>ft[,2])) ## always from higher to lower
stopifnot(!any(duplicated(paste(ft[,1], ft[,2]))))
stopifnot(ft[nEdges, 1]==nNodes, ft[nEdges, 2]==nNodes-1)

j <- ftM2int(ft)
stopifnot(all(i==j))
```

---

subGraph

*Create a Subgraph*


---

**Description**

Given a set of nodes and a graph this function creates and returns subgraph with only the supplied nodes and any edges between them.

**Usage**

```
subGraph(snodes, graph)
```

**Arguments**

`snodes`            A character vector of node labels.  
`graph`             A graph object, it must inherit from the `graph` class.

**Details**

The returned subgraph is a copy of the graph. Implementations for `graphNEL`, `distGraph` and `clusterGraph`.

**Value**

A graph of the same class as the `graph` argument but with only the supplied nodes.

**Author(s)**

R. Gentleman

**See Also**[nodes,edges](#)**Examples**

```

set.seed(123)
x <- rnorm(26)
names(x) <- letters
library(stats)
d1 <- dist(x)
g1 <- new("distGraph", Dist=d1)
subGraph(letters[1:5], g1)

```

toDotR-methods

*Methods for Function toDotR, using R to generate a dot serialization***Description**

There are two basic methods of generating dot (<http://www.graphviz.org>) language serializations of R `graph-class` structures. First, using the `toDot` methods of the `Rgraphviz` package, the native `graphviz` agraph-associated methods can be employed to create the dot serialization. Second, with the methods described here, R functions can be used to perform the serialization directly from the graph data structure, without `Rgraphviz`.

**Methods**

- G = "graphNEL", outDotFile = "character", renderList = "list", optList = "list"** create dot language description of graph
- G = "graphNEL", outDotFile = "character", renderList = "missing", optList = "missing"** create dot language description of graph
- G = "graphNEL", outDotFile = "character", renderList = "missing", optList = "list"** create dot language description of graph
- G = "graphNEL", outDotFile = "missing", renderList = "missing", optList = "missing"** create dot language description of graph
- G = "graphNEL", outDotFile = "missing", renderList = "missing", optList = "list"** create dot language description of graph
- G = "graphNEL", outDotFile = "missing", renderList = "character", optList = "missing"** create dot language description of graph
- G = "graphNEL", outDotFile = "missing", renderList = "list", optList = "list"** create dot language description of graph
- G = "graphNEL", outDotFile = "missing", renderList = "list", optList = "missing"** create dot language description of graph
- G = "compoundGraph", outDotFile = "character", renderList = "list", optList = "missing"** create dot language description of graph
- G = "compoundGraph", outDotFile = "character", renderList = "list", optList = "list"** create dot language description of graph
- G = "compoundGraph", outDotFile = "missing", renderList = "list", optList = "missing"** create dot language description of graph

**See Also**[toDot-methods](#)**Examples**

```
example(randomGraph)
tmp <- tempfile()
toDotR(g1, tmp)
readLines(tmp)
unlink(tmp)
```

---

ugraph

*Underlying Graph*

---

**Description**

For a *directed* graph the underlying graph is the graph that is constructed where all edge orientation is ignored. This function carries out such a transformation on `graphNEL` instances.

**Usage**

```
ugraph(graph)
```

**Arguments**

`graph` a graph object.

**Details**

If `graph` is already *undirected* then it is simply returned.

If `graph` is a multi-graph (has multiple edges) an error is thrown as it is unclear how to compute the underlying graph in that context.

The method will work for any `graph` subclass for which an `edgeMatrix` method exists.

**Value**

An instance of `graphNEL` with the same nodes as the input but which is *undirected*.

**Author(s)**

R. Gentleman

**References**

Graph Theory and its Applications, J. Gross and J. Yellen.

**See Also**

[connComp edgeMatrix](#)



**Examples**

```
V <- letters[1:4]
edL2 <- vector("list", length=4)
names(edL2) <- V
for(i in 1:4)
  edL2[[i]] <- list(edges=c(2,1,2,1)[i], weights=sqrt(i))
gR2 <- new("graphNEL", nodes=V, edgeL=edL2, edgemode="directed")

ugraph(gR2)
```

---

validGraph	<i>Test whether graph object is valid</i>
------------	---

---

**Description**

validGraph is a validating function for a graph object.

**Usage**

```
validGraph(object, quietly=FALSE)
```

**Arguments**

object	a graph object to be tested
quietly	TRUE or FALSE indicating whether output should be printed.

**Value**

If the graph object is valid, TRUE is returned otherwise FALSE is returned. If object is not a valid graph and quietly is set to FALSE then descriptions of the problems are printed.

**Author(s)**

Elizabeth Whalen

**See Also**

[graph-class](#)

**Examples**

```
testGraph<-new("graphNEL")
testGraph@nodes<-c("node1", "node2", "node3")
validGraph(testGraph)
```

---

`write.tlp`*Write a graph object in a file in the Tulip format*

---

**Description**

Write a graph object in a file in the Tulip format.

**Usage**

```
write.tlp(graph, filename)
```

**Arguments**

<code>graph</code>	a graph object
<code>filename</code>	Name of the output file

**Details**

The Tulip format is used by the program Tulip.

**Author(s)**

Laurent Gautier <laurent@cbs.dtu.dk>

**References**

<http://www.tulip-software.org/>

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