

# RBGL

April 20, 2011

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`astarSearch`                    *Compute astarSearch for a graph*

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## Description

Compute `astarSearch` for a graph

## Usage

```
astarSearch(g)
```

## Arguments

`g`                    an instance of the `graph` class

## Details

NOT IMPLEMENTED YET. TO BE FILLED IN

## Author(s)

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
astarSearch(coex)
```

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bandwidth	<i>Compute bandwidth for an undirected graph</i>
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**Description**

Compute bandwidth for an undirected graph

**Usage**

```
bandwidth(g)
```

**Arguments**

`g` an instance of the `graph` class with `edgemode` “undirected”

**Details**

The bandwidth of an undirected graph  $G=(V, E)$  is the maximum distance between two adjacent vertices. See documentation on bandwidth in Boost Graph Library for more details.

**Value**

`bandwidth` the bandwidth of the given graph

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
coex <- ugraph(coex)
bandwidth(coex)
```

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 betweenness centrality clustering

*Graph clustering based on edge betweenness centrality*


---

**Description**

Graph clustering based on edge betweenness centrality

**Usage**

```
betweenness centrality clustering(g, threshold = -1, normalize = T)
```

**Arguments**

<code>g</code>	an instance of the graph class with edgemode “undirected”
<code>threshold</code>	threshold to terminate clustering process
<code>normalize</code>	boolean, when TRUE, the edge betweenness centrality is scaled by $2 / ((n-1)(n-2))$ where $n$ is the number of vertices in $g$ ; when FALSE, the edge betweenness centrality is the absolute value

**Details**

To implement graph clustering based on edge betweenness centrality.

The algorithm is iterative, at each step it computes the edge betweenness centrality and removes the edge with maximum betweenness centrality when it is above the given `threshold`. When the maximum betweenness centrality falls below the threshold, the algorithm terminates.

See documentation on Clustering algorithms in Boost Graph Library for details.

**Value**

A list of

<code>no.of.edges</code>	number of remaining edges after removal
<code>edges</code>	remaining edges
<code>edge.betweenness centrality</code>	betweenness centrality of remaining edges

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[brandes.betweenness centrality](#)

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"))
coex <- fromGXL(con)
close(con)
coex <- ugraph(coex)
betweenness centrality clustering(coex, 0.5, TRUE)
```

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bellman.ford.sp      *Bellman-Ford shortest paths using boost C++*

---

**Description**

Algorithm for the single-source shortest paths problem for a graph with both positive and negative edge weights.

**Usage**

```
bellman.ford.sp(g, start=nodes(g)[1])
```

**Arguments**

<code>g</code>	instance of class graph
<code>start</code>	character: node name for start of path

**Details**

This function interfaces to the Boost graph library C++ routines for Bellman-Ford shortest paths. Choose the appropriate algorithm to calculate the shortest path carefully based on the properties of the given graph. See documentation on Bellman-Ford algorithm in Boost Graph Library for more details.

**Value**

A list with elements:

<code>all edges minimized</code>	true if all edges are minimized, false otherwise.
<code>distance</code>	The vector of distances from <code>start</code> to each node of <code>g</code> ; includes <code>Inf</code> when there is no path from <code>start</code> .
<code>penult</code>	A vector of indices (in <code>nodes(g)</code> ) of predecessors corresponding to each node on the path from that node back to <code>start</code> .

. For example, if the element one of this vector has value 10, that means that the predecessor of node 1 is node 10. The next predecessor is found by examining `penult[10]`.

<code>start</code>	The start node that was supplied in the call to <code>bellman.ford.sp</code> .
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**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[dag.sp](#), [dijkstra.sp](#), [johnson.all.pairs.sp](#), [sp.between](#)

**Examples**

```
con <- file(system.file("XML/conn2.gxl", package="RBGL"), open="r")
dd <- fromGXL(con)
close(con)
bellman.ford.sp(dd)
bellman.ford.sp(dd, nodes(dd) [2])
```

---

```
brandes.betweenness.centrality
```

*Compute betweenness centrality for an undirected graph*

---

**Description**

Compute betweenness centrality for an undirected graph

**Usage**

```
brandes.betweenness.centrality(g)
```

**Arguments**

`g` an instance of the graph class with edgemode “undirected”

**Details**

`Brandes.betweenness.centrality` computes the betweenness centrality of each vertex or each edge in the graph, using an algorithm by U. Brandes.

Betweenness centrality of a vertex  $v$  is calculated as follows:  $N_{st}(v)$  = no. of shortest paths from  $s$  to  $t$  that pass through  $v$ ,  $N_{st}$  = no. of shortest paths from  $s$  to  $t$ , betweenness centrality of  $v$  =  $\sum (N_{st}(v) / N_{st})$  for all vertices  $s \neq v \neq t$ .

Betweenness centrality of an edge is calculated similarly.

The relative betweenness centrality for a vertex is to scale the betweenness centrality of the given vertex by  $2 / (n^2 - 3n + 2)$  where  $n$  is the no. of vertices in the graph.

Central point dominance measures the maximum betweenness of any vertex in the graph.

See documentation on brandes betweenness centrality in Boost Graph Library for more details.

**Value**

A list of

```
betweenness.centralities.vertices  
    betweenness centrality of each vertex  
betweenness.centralities.edges  
    betweenness centrality of each edge  
relative.betweenness.centralities.vertices  
    relative betweenness centrality of each vertex  
dominance    maximum betweenness of any point in the graph
```

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[betweenness.centralities.clustering](#)

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")  
coex <- fromGXL(con)  
close(con)  
coex <- ugraph(coex)  
brandes.betweenness.centralities(coex)
```

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bfs

*Breadth and Depth-first search*

---

**Description**

These functions return information on graph traversal by breadth and depth first search using routines from the BOOST library.

**Usage**

```
bfs(object, node, checkConn=TRUE)  
dfs(object, node, checkConn=TRUE)
```

## Arguments

object	instance of class graph from Bioconductor graph class
node	node name where search starts; defaults to the node in first position in the node vector.
checkConn	logical for backwards compatibility; this parameter has no effect as of RBGL 1.7.9 and will be removed in future versions.

## Details

These two functions are interfaces to the BOOST graph library functions for breadth first and depth first search. Both methods handle unconnected graphs by applying the algorithms over the connected components.

Cormen et al note (p 542) that ‘results of depth-first search may depend upon the order in which the vertices are examined ... These different visitation orders tend not to cause problems in practice, as any DFS result can usually be used effectively, with essentially equivalent results’.

## Value

For `bfs` a vector of node indices in order of BFS visit.

For `dfs` a list of two vectors of nodes, with elements `discover` (order of DFS discovery), and `finish` (order of DFS completion).

## Author(s)

VJ Carey <stvjc@channing.harvard.edu>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
con1 <- file(system.file("XML/bfsex.gxl", package="RBGL"), open="r")
dd <- fromGXL(con1)
close(con1)

bfs(dd, "r")
bfs(dd, "s")

con2 <- file(system.file("XML/dfsex.gxl", package="RBGL"), open="r")
dd2 <- fromGXL(con2)
close(con2)

dfs(dd2, "u")
```

---

`biConnComp`*Compute biconnected components for a graph*

---

**Description**

Compute biconnected components for a graph

**Usage**

```
biConnComp(g)
articulationPoints(g)
```

**Arguments**

`g` an instance of the `graph` class

**Details**

A biconnected graph is a connected graph that remains connected when any one of its vertices, and all the edges incident on this vertex, is removed and the graph remains connected. A biconnected component of a graph is a subgraph which is biconnected. An integer label is assigned to each edge to indicate which biconnected component it's in.

A vertex in a graph is called an articulation point if removing it increases the number of connected components.

See the documentation for the Boost Graph Library for more details.

**Value**

For `biConnComp`: a vector whose length is no. of biconnected components, each entry is a list of nodes that are on the same biconnected components.

For `articulationPoints`: a vector of articulation points in the graph.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)

biConnComp(coex)
articulationPoints(coex)
```



---

boyerMyrvoldPlanarityTest  
*boyerMyrvoldPlanarityTest*

---

### **Description**

boyerMyrvoldPlanarityTest description

### **Usage**

boyerMyrvoldPlanarityTest (g)

### **Arguments**

g                    instance of class graphNEL from Bioconductor graph class

### **Author(s)**

Li Long <li.long@isb-sib.ch>

### **References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

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chrobakPayneStraightLineDrawing  
*chrobakPayneStraightLineDrawing*

---

### **Description**

chrobakPayneStraightLineDrawing description

### **Usage**

chrobakPayneStraightLineDrawing (g)

### **Arguments**

g                    instance of class graphNEL from Bioconductor graph class

### **Author(s)**

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
V <- LETTERS[1:7]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[1+1], g)
g <- addEdge(V[1+1], V[2+1], g)
g <- addEdge(V[1+2], V[3+1], g)
g <- addEdge(V[1+3], V[0+1], g)
g <- addEdge(V[1+3], V[4+1], g)
g <- addEdge(V[1+4], V[5+1], g)
g <- addEdge(V[1+5], V[6+1], g)
g <- addEdge(V[1+6], V[3+1], g)
g <- addEdge(V[1+0], V[4+1], g)
g <- addEdge(V[1+1], V[3+1], g)
g <- addEdge(V[1+3], V[5+1], g)
g <- addEdge(V[1+2], V[6+1], g)
g <- addEdge(V[1+1], V[4+1], g)
g <- addEdge(V[1+1], V[5+1], g)
g <- addEdge(V[1+1], V[6+1], g)

x3 <- chrobakPayneStraightLineDrawing(g)
x3
```

---

clusteringCoefAppr *Approximate clustering coefficient for an undirected graph*

---

## Description

Approximate clustering coefficient for an undirected graph

## Usage

```
clusteringCoefAppr(g, k=length(nodes(g)), Weighted=FALSE, vW=degree(g))
```

## Arguments

<code>g</code>	an instance of the graph class
<code>Weighted</code>	calculate weighted clustering coefficient or not
<code>vW</code>	vertex weights to use when calculating weighted clustering coefficient
<code>k</code>	parameter controls total expected runtime

**Details**

It is quite expensive to compute cluster coefficient and transitivity exactly for a large graph by computing the number of triangles in the graph. Instead, `clusteringCoefAppr` samples triples with appropriate probability, returns the ratio between the number of existing edges and the number of samples.

MORE ABOUT CHOICE OF K.

See reference for more details.

**Value**

Approximated clustering coefficient for graph `g`.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Approximating Clustering Coefficient and Transitivity, T. Schank, D. Wagner, Journal of Graph Algorithms and Applications, Vol. 9, No. 2 (2005).

**See Also**

`clusteringCoef`, `transitivity`, `graphGenerator`

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"))
g <- fromGXL(con)
close(con)

k = length(nodes(g))
cc <- clusteringCoefAppr(g, k)
ccw1 <- clusteringCoefAppr(g, k, Weighted=TRUE)
vW <- c(1, 1, 1, 1, 1, 1, 1, 1)
ccw2 <- clusteringCoefAppr(g, k, Weighted=TRUE, vW)
```

---

<code>clusteringCoef</code>	<i>Calculate clustering coefficient for an undirected graph</i>
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---

**Description**

Calculate clustering coefficient for an undirected graph

**Usage**

```
clusteringCoef(g, Weighted=FALSE, vW=degree(g))
```

**Arguments**

<code>g</code>	an instance of the <code>graph</code> class
<code>Weighted</code>	calculate weighted clustering coefficient or not
<code>vW</code>	vertex weights to use when calculating weighted clustering coefficient

**Details**

For an undirected graph  $G$ , let  $\delta(v)$  be the number of triangles with  $v$  as a node, let  $\tau(v)$  be the number of triples, i.e., paths of length 2 with  $v$  as the center node.

Let  $V'$  be the set of nodes with degree at least 2.

Define clustering coefficient for  $v$ ,  $c(v) = (\delta(v) / \tau(v))$ .

Define clustering coefficient for  $G$ ,  $C(G) = \text{sum}(c(v)) / |V'|$ , for all  $v$  in  $V'$ .

Define weighted clustering coefficient for  $G$ ,  $C_w(G) = \text{sum}(w(v) * c(v)) / \text{sum}(w(v))$ , for all  $v$  in  $V'$ .

**Value**

Clustering coefficient for graph  $G$ .

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Approximating Clustering Coefficient and Transitivity, T. Schank, D. Wagner, Journal of Graph Algorithms and Applications, Vol. 9, No. 2 (2005).

**See Also**

`clusteringCoefAppr`, `transitivity`, `graphGenerator`

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"))
g <- fromGXL(con)
close(con)
cc <- clusteringCoef(g)
ccw1 <- clusteringCoef(g, Weighted=TRUE)
vW <- c(1, 1, 1, 1, 1, 1, 1, 1)
ccw2 <- clusteringCoef(g, Weighted=TRUE, vW)
```

---

```
sequential.vertex.coloring
```

*Compute a vertex coloring for a graph*

---

## Description

Compute vertex coloring for a graph

## Usage

```
sequential.vertex.coloring(g)
```

## Arguments

`g` an instance of the `graph` class

## Details

A vertex coloring for a graph is to assign a color for each vertex so that no two adjacent vertices are of the same color. We designate the colors as sequential integers: 1, 2, ....

For ordered vertices,  $v_1, v_2, \dots, v_n$ , for  $k = 1, 2, \dots, n$ , this algorithm assigns  $v_k$  to the smallest possible color. It does NOT guarantee to use minimum number of colors.

See documentations on these algorithms in Boost Graph Library for more details.

## Value

```
no. of colors needed
      how many colors to use to color the graph
colors of nodes
      color label for each vertex
```

## Author(s)

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
sequential.vertex.coloring(coex)
```

---

connectedComp      *Identify Connected Components in an Undirected Graph*

---

### Description

The connected components in an undirected graph are identified. If the graph is directed then the weakly connected components are identified.

### Usage

```
connectedComp (g)
```

### Arguments

`g`                    graph with edgemode “undirected”

### Details

Uses a depth first search approach to identifying all the connected components of an undirected graph. If the input, `g`, is a directed graph it is first transformed to an undirected graph (using [ugraph](#)).

### Value

A list of length equal to the number of connected components in `g`. Each element of the list contains a vector of the node labels for the nodes that are connected.

### Author(s)

Vince Carey <stvjc@channing.harvard.edu>

### References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

### See Also

[connComp](#), [strongComp](#), [ugraph](#), [same.component](#)

### Examples

```
con <- file(system.file("GXL/kmstEx.gxl", package="graph"), open="r")
km <- fromGXL(con)
close(con)
km <- graph::addNode(c("F", "G", "H"), km)
km <- addEdge("G", "H", km, 1)
km <- addEdge("H", "G", km, 1)
ukm <- ugraph(km)
ukm
edges(ukm)
connectedComp(ukm)
```

---

 dag.sp

---

 DAG shortest paths using boost C++
 

---

### Description

Algorithm for the single-source shortest-paths problem on a weighted, directed acyclic graph (DAG)

### Usage

```
dag.sp(g, start=nodes(g)[1])
```

### Arguments

<code>g</code>	instance of class <code>graph</code>
<code>start</code>	source node for start of paths

### Details

These functions are interfaces to the Boost graph library C++ routines for single-source shortest-paths on a weighted directed acyclic graph. Choose appropriate shortest-path algorithms carefully based on the properties of the input graph. See documentation in Boost Graph Library for more details.

### Value

A list with elements:

<code>distance</code>	The vector of distances from <code>start</code> to each node of <code>g</code> ; includes <code>Inf</code> when there is no path from <code>start</code> .
<code>penult</code>	A vector of indices (in <code>nodes(g)</code> ) of predecessors corresponding to each node on the path from that node back to <code>start</code> . For example, if the element one of this vector has value 10, that means that the predecessor of node 1 is node 10. The next predecessor is found by examining <code>penult[10]</code> .
<code>start</code>	The start node that was supplied in the call to <code>dag.sp</code> .

### Author(s)

Li Long <li.long@isb-sib.ch>

### References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

### See Also

[bellman.ford.sp](#), [dijkstra.sp](#), [johnson.all.pairs.sp](#), [sp.between](#)

**Examples**

```
con <- file(system.file("XML/conn2.gxl", package="RBGL"), open="r")
dd <- fromGXL(con)
close(con)
dag.sp(dd)
dag.sp(dd, nodes(dd)[2])
```

---

dijkstra.sp

*Dijkstra's shortest paths using boost C++*


---

**Description**

dijkstra's shortest paths

**Usage**

```
dijkstra.sp(g, start=nodes(g)[1], eW=unlist(edgeWeights(g)))
```

**Arguments**

g	instance of class graph
start	character: node name for start of path
eW	numeric: edge weights.

**Details**

These functions are interfaces to the Boost graph library C++ routines for Dijkstra's shortest paths.

For some graph subclasses, computing the edge weights can be expensive. If you are calling `dijkstra.sp` in a loop, you can pass the edge weights explicitly to avoid the edge weight creation cost.

**Value**

A list with elements:

distance	The vector of distances from <code>start</code> to each node of <code>g</code> ; includes <code>Inf</code> when there is no path from <code>start</code> .
penult	A vector of indices (in <code>nodes(g)</code> ) of predecessors corresponding to each node on the path from that node back to <code>start</code>

. For example, if the element one of this vector has value 10, that means that the predecessor of node 1 is node 10. The next predecessor is found by examining `penult[10]`.

start	The start node that was supplied in the call to <code>dijkstra.sp</code> .
-------	--

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>



**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[bellman.ford.sp](#), [dag.sp](#), [johnson.all.pairs.sp](#), [sp.between](#)

**Examples**

```
con1 <- file(system.file("XML/dijkex.gxl",package="RBGL"), open="r")
dd <- fromGXL(con1)
close(con1)
dijkstra.sp(dd)
dijkstra.sp(dd,nodes(dd)[2])

con2 <- file(system.file("XML/ospf.gxl",package="RBGL"), open="r")
ospf <- fromGXL(con2)
close(con2)
dijkstra.sp(ospf,nodes(ospf)[6])
```

---

dominatorTree

---

*Compute dominator tree from a vertex in a directed graph*


---

**Description**

Compute dominator tree from a vertex in a directed graph

**Usage**

```
dominatorTree(g, start=nodes(g)[1])
lengauerTarjanDominatorTree(g, start=nodes(g)[1])
```

**Arguments**

`g` a directed graph, one instance of the `graph` class  
`start` a vertex in graph `g`

**Details**

As stated in documentation on Lengauer Tarjan dominator tree in Boost Graph Library:

A vertex `u` dominates a vertex `v`, if every path of directed graph from the entry to `v` must go through `u`.

This function builds the dominator tree for a directed graph.

**Value**

Output is a vector, giving each node its immediate dominator.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

**Examples**

```
con1 <- file(system.file("XML/dominator.gxl", package="RBGL"), open="r")
g1 <- fromGXL(con1)
close(con1)

dominatorTree(g1)
lengauerTarjanDominatorTree(g1)
```

---

edgeConnectivity     *computed edge connectivity and min disconnecting set for an undirected graph*

---

**Description**

computed edge connectivity and min disconnecting set for an undirected graph

**Usage**

```
edgeConnectivity(g)
```

**Arguments**

`g`                    an instance of the graph class with edgemode “undirected”

**Details**

Consider a graph  $G$  consisting of a single connected component. The edge connectivity of  $G$  is the minimum number of edges in  $G$  that can be cut to produce a graph with two (disconnected) components. The set of edges in this cut is called the minimum disconnecting set.

**Value**

A list:

`connectivity` the integer describing the number of edges that must be severed to obtain two components

`minDisconSet` a list (of length `connectivity`) of pairs of node names describing the edges that need to be cut to obtain two components

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[minCut](#), [edmonds.karp.max.flow](#), [push.relabel.max.flow](#)

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)

edgeConnectivity(coex)
```

---

edmondsMaxCardinalityMatching

*edmondsMaxCardinalityMatching*

---

**Description**

edmondsMaxCardinalityMatching description

**Usage**

```
edmondsMaxCardinalityMatching(g)
```

**Arguments**

`g` instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <[li.long@isb-sib.ch](mailto:li.long@isb-sib.ch)>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
V <- LETTERS[1:18]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[4+1], g);
g <- addEdge(V[1+1], V[5+1], g);
g <- addEdge(V[1+2], V[6+1], g);
g <- addEdge(V[1+3], V[7+1], g);
g <- addEdge(V[1+4], V[5+1], g);
g <- addEdge(V[1+6], V[7+1], g);
g <- addEdge(V[1+4], V[8+1], g);
g <- addEdge(V[1+5], V[9+1], g);
g <- addEdge(V[1+6], V[10+1], g);
g <- addEdge(V[1+7], V[11+1], g);
g <- addEdge(V[1+8], V[9+1], g);
g <- addEdge(V[1+10], V[11+1], g);
g <- addEdge(V[1+8], V[13+1], g);
g <- addEdge(V[1+9], V[14+1], g);
g <- addEdge(V[1+10], V[15+1], g);
g <- addEdge(V[1+11], V[16+1], g);
g <- addEdge(V[1+14], V[15+1], g);

x9 <- edmondsMaxCardinalityMatching(g)
x9

g <- addEdge(V[1+12], V[13+1], g);
g <- addEdge(V[1+16], V[17+1], g);

x10 <- edmondsMaxCardinalityMatching(g)
x10
```

---

edmondsOptimumBranching

*edmondsOptimumBranching*

---

**Description**

edmondsOptimumBranching description

**Usage**

edmondsOptimumBranching(g)

**Arguments**

g instance of class graphNEL from Bioconductor graph class

**Details**

This is an implementation of Edmonds' algorithm to find optimum branching in a directed graph. See references for details.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

See Edmonds' Algorithm on <http://edmonds-alg.sourceforge.net>.

**Examples**

```
V <- LETTERS[1:4]
g <- new("graphNEL", nodes=V, edgemode="directed")
g <- addEdge(V[1+0],V[1+1],g, 3)
g <- addEdge(V[1+0],V[2+1],g, 1.5)
g <- addEdge(V[1+0],V[3+1],g, 1.8)
g <- addEdge(V[1+1],V[2+1],g, 4.3)
g <- addEdge(V[1+2],V[3+1],g, 2.2)

x11 <- edmondsOptimumBranching(g)
x11
```

---

extractPath	<i>convert a dijkstra.sp predecessor structure into the path joining two nodes</i>
-------------	--

---

**Description**

determine a path between two nodes in a graph, using output of [dijkstra.sp](#).

**Usage**

```
extractPath(s, f, pens)
```

**Arguments**

s	index of starting node in nodes vector of the graph from which pens was derived
f	index of ending node in nodes vector
pens	predecessor index vector as returned in the preds component of <a href="#">dijkstra.sp</a> output

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[allShortestPaths](#)

**Examples**

```
data(FileDep)
dd <- dijkstra.sp(FileDep)
extractPath(1,9,dd$pen)
```

---

FileDep

*FileDep: a graphNEL object representing a file dependency dataset example in boost graph library*

---

**Description**

FileDep: a graphNEL object representing a file dependency dataset example in boost graph library

**Usage**

```
#data(FileDep)
```

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
# this is how the graph of data(FileDep) was obtained
library(graph)
fd <- file(system.file("XML/FileDep.gxl",package="RBGL"), open="r")
show(fromGXL(fd))
if (require(Rgraphviz))
{
  data(FileDep)
  plot(FileDep)
}
close(fd)
```

---

```
floyd.warshall.all.pairs.sp
```

*compute shortest paths for all pairs of nodes*

---

**Description**

compute shortest paths for all pairs of nodes

**Usage**

```
floyd.warshall.all.pairs.sp(g)
```

**Arguments**

`g` graph object with edge weights given

**Details**

Compute shortest paths between every pair of vertices for a dense graph. It works on both undirected and directed graph. The result is given as a distance matrix. The matrix is symmetric for an undirected graph, and asymmetric (very likely) for a directed graph. For a sparse graph, the `johnson.all.pairs.sp` functions should be used instead.

See documentation on these algorithms in Boost Graph Library for more details.

**Value**

A matrix of shortest path lengths between all pairs of nodes in the graph.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[johnson.all.pairs.sp](#)

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
floyd.warshall.all.pairs.sp(coex)
```

gprofile

*Compute profile for a graph*

---

**Description**

Compute profile for a graph

**Usage**

```
gprofile(g)
```

**Arguments**

`g` an instance of the `graph` class

**Details**

The profile of a given graph is the sum of bandwidths for all the vertices in the graph.

See documentation on this function in Boost Graph Library for more details.

**Value**

`profile` the profile of the graph

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
```

```
gprofile(coex)
```



---

graphGenerator      *Generate an undirected graph with adjustable clustering coefficient*

---

**Description**

Generate an undirected graph with adjustable clustering coefficient

**Usage**

```
graphGenerator(n, d, o)
```

**Arguments**

n	no. of nodes in the generated graph
d	parameter for preferential attachment
o	parameter for triple generation

**Details**

The graph generator works according to the preferential attachment rule. It also generates graphs with adjustable clustering coefficient. Parameter *d* specifies how many preferred edges a new node has. Parameter *o* limits how many triples to add to a new node.

See reference for details.

**Value**

no. of nodes	No. of nodes in the generated graph
no. of edges	No. of edges in the generated graph
edges	Edges in the generated graph

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Approximating Clustering Coefficient and Transitivity, T. Schank, D. Wagner, Journal of Graph Algorithms and Applications, Vol. 9, No. 2 (2005).

**See Also**

clusteringCoef, transitivity, clusteringCoefAppr

**Examples**

```
n <- 20
d <- 6
o <- 3
gg <- graphGenerator(n, d, o)
```

highlyConnSG

*Compute highly connected subgraphs for an undirected graph***Description**

Compute highly connected subgraphs for an undirected graph

**Usage**

```
highlyConnSG(g, sat=3, ldv=c(3,2,1))
```

**Arguments**

<code>g</code>	an instance of the <code>graph</code> class with <code>edgemode</code> “undirected”
<code>sat</code>	singleton adoption threshold, positive integer
<code>ldv</code>	heuristics to remove lower degree vertice, a decreasing sequence of positive integer

**Details**

A graph  $G$  with  $n$  vertices is highly connected if its connectivity  $k(G) > n/2$ . The HCS algorithm partitions a given graph into a set of highly connected subgraphs, by using minimum-cut algorithm recursively. To improve performance, the approach is refined by adopting singletons, removing low degree vertices and merging clusters.

On singleton adoption: after each round of partition, some highly connected subgraphs could be singletons (i.e., a subgraph contains only one node). To reduce the number of singletons, therefore reduce number of clusters, we try to get "normal" subgraphs to "adopt" them. If a singleton,  $s$ , has  $n$  neighbours in a highly connected subgraph  $c$ , and  $n > sat$ , we add  $s$  to  $c$ . To adapt to the modified subgraphs, this adoption process is repeated until no further such adoption.

On lower degree vertices: when the graph has low degree vertices, minimum-cut algorithm will just repeatedly separate these vertices from the rest. To reduce such expensive and non-informative computation, we "remove" these low degree vertices first before applying minimum-cut algorithm. Given `ldv = (d1, d2, ..., dp)`, ( $d[i] > d[i+1] > 0$ ), we repeat the following ( $i$  from 1 to  $p$ ): remove all the highly-connected-subgraph found so far; remove vertices with degrees  $< d_i$ ; find highly-connected-subgraphs; perform singleton adoptions.

The Boost implementation does not support self-loops, therefore we signal an error and suggest that users remove self-loops using the function `removeSelfLoops` function. This change does affect degree, but the original article makes no specific reference to self-loops.

**Value**

A list of clusters, each is given as vertices in the graph.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

A Clustering Algorithm based on Graph Connectivity by E. Hartuv, R. Shamir, 1999.

**See Also**

[edgeConnectivity](#), [minCut](#), [removeSelfLoops](#)

**Examples**

```
con <- file(system.file("XML/hcs.gxl", package="RBGL"))
coex <- fromGXL(con)
close(con)

highlyConnSG(coex)
```

---

incremental.components

*Compute connected components for an undirected graph*

---

**Description**

Compute connected components for an undirected graph

**Usage**

```
init.incremental.components(g)
incremental.components(g)
same.component(g, node1, node2)
```

**Arguments**

<code>g</code>	an instance of the <code>graph</code> class
<code>node1</code>	one vertex of the given graph
<code>node2</code>	another vertex of the given graph

**Details**

This family of functions work together to calculate the connected components of an undirected graph. The algorithm is based on the disjoint-sets. It works where the graph is growing by adding new edges. Call "init.incremental.components" to initialize the calculation on a new graph. Call "incremental.components" to re-calculate connected components after growing the graph. Call "same.component" to learn if two given vertices are in the same connected components. Currently, the codes can only handle ONE incremental graph at a time. When you start working on another graph by calling "init.incremental.components", the disjoint-sets info on the previous graph is lost. See documentation on Incremental Connected Components in Boost Graph Library for more details.

**Value**

Output from `init.incremental.components` is a list of component numbers for each vertex in the graph.

Output from `incremental.components` is a list of component numbers for each vertex in the graph.

Output from `same.component` is true if both nodes are in the same connected component, otherwise it's false.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[connComp](#), [connectedComp](#), [strongComp](#)

**Examples**

```
con <- file(system.file("XML/conn2.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)

init.incremental.components(coex)
incremental.components(coex)
v1 <- 1
v2 <- 5
same.component(coex, v1, v2)
```

---

isKuratowskiSubgraph  
*isKuratowskiSubgraph*

---

**Description**

isKuratowskiSubgraph description

**Usage**

```
isKuratowskiSubgraph(g)
```

**Arguments**

g                    instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```

V <- LETTERS[1:6]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[1+1], g)
g <- addEdge(V[1+0], V[2+1], g)
g <- addEdge(V[1+0], V[3+1], g)
g <- addEdge(V[1+0], V[4+1], g)
g <- addEdge(V[1+0], V[5+1], g)
g <- addEdge(V[1+1], V[2+1], g)
g <- addEdge(V[1+1], V[3+1], g)
g <- addEdge(V[1+1], V[4+1], g)
g <- addEdge(V[1+1], V[5+1], g)
g <- addEdge(V[1+2], V[3+1], g)
g <- addEdge(V[1+2], V[4+1], g)
g <- addEdge(V[1+2], V[5+1], g)
g <- addEdge(V[1+3], V[4+1], g)
g <- addEdge(V[1+3], V[5+1], g)
g <- addEdge(V[1+4], V[5+1], g)

x4 <- isKuratowskiSubgraph(g)
x4

```

---

isomorphism	<i>Compute isomorphism from vertices in one graph to those in another graph</i>
-------------	---

---

**Description**

Compute isomorphism from vertices in one graph to those in another graph

**Usage**

```
isomorphism(g1, g2)
```

**Arguments**

g1	one instance of the graph class
g2	one instance of the graph class

**Details**

As stated in documentation on isomorphism in Boost Graph Library: An isomorphism is a 1-to-1 mapping of the vertices in one graph to the vertices of another graph such that adjacency is preserved. Another words, given graphs  $G1 = (V1,E1)$  and  $G2 = (V2,E2)$  an isomorphism is a function  $f$  such that for all pairs of vertices  $a,b$  in  $V1$ , edge  $(a,b)$  is in  $E1$  if and only if edge  $(f(a),f(b))$  is in  $E2$ .

**Value**

Output is true if there exists an isomorphism between  $g1$  and  $g2$ , otherwise it's false.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
con1 <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
g1 <- fromGXL(con1)
close(con1)

con2 <- file(system.file("XML/conn2.gxl", package="RBGL"), open="r")
g2 <- fromGXL(con2)
close(con2)

isomorphism(g1, g2)
```

---

isStraightLineDrawing  
*isStraightLineDrawing*

---

**Description**

isStraightLineDrawing description

**Usage**

```
isStraightLineDrawing(g, drawing)
```

**Arguments**

g	instance of class graphNEL from Bioconductor graph class
drawing	coordinates of node positions

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```

V <- LETTERS[1:7]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[1+1], g)
g <- addEdge(V[1+1], V[2+1], g)
g <- addEdge(V[1+2], V[3+1], g)
g <- addEdge(V[1+3], V[0+1], g)
g <- addEdge(V[1+3], V[4+1], g)
g <- addEdge(V[1+4], V[5+1], g)
g <- addEdge(V[1+5], V[6+1], g)
g <- addEdge(V[1+6], V[3+1], g)
g <- addEdge(V[1+0], V[4+1], g)
g <- addEdge(V[1+1], V[3+1], g)
g <- addEdge(V[1+3], V[5+1], g)
g <- addEdge(V[1+2], V[6+1], g)
g <- addEdge(V[1+1], V[4+1], g)
g <- addEdge(V[1+1], V[5+1], g)
g <- addEdge(V[1+1], V[6+1], g)

x3 <- chrobakPayneStraightLineDrawing(g)

x8 <- isStraightLineDrawing(g, x3)
x8

```

---

is.triangulated      *Decide if a graph is triangulated*

---

**Description**

Decide if a graph is triangulated

**Usage**

```
is.triangulated(g)
```

**Arguments**

`g`                      an instance of the graph class

**Details**

An undirected graph  $G = (V, E)$  is triangulated (i.e. chordal) if all cycles  $[v_1, v_2, \dots, v_k]$  of length 4 or more have a chord, i.e., an edge  $[v_i, v_j]$  with  $j \neq i \pm 1 \pmod{k}$

An equivalent definition of chordal graphs is:

$G$  is chordal iff either  $G$  is an empty graph, or there is an  $v$  in  $V$  such that

1. the neighborhood of  $v$  (i.e.,  $v$  and its adjacent nodes) forms a clique, and
2. recursively,  $G-v$  is chordal

**Value**

The return value is `TRUE` if `g` is triangulated and `FALSE` otherwise. An error is thrown if the graph is not undirected; you might use `ugraph` to compute the underlying graph.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Combinatorial Optimization: algorithms and complexity (p. 403) by C. H. Papadimitriou, K. Steiglitz

**Examples**

```
con1 <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")
coex <- fromGXL(con1)
close(con1)

is.triangulated(coex)

con2 <- file(system.file("XML/hcs.gxl", package="RBGL"), open="r")
coex <- fromGXL(con2)
close(con2)

is.triangulated(coex)
```

---

johnson.all.pairs.sp

*compute shortest path distance matrix for all pairs of nodes*

---

**Description**

compute shortest path distance matrix for all pairs of nodes

**Usage**

```
johnson.all.pairs.sp(g)
```

**Arguments**

`g` graph object for which `edgeMatrix` and `edgeWeights` are defined

**Details**

Uses BGL algorithm.

**Value**

matrix of shortest path lengths, read from row node to col node



**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[bellman.ford.sp](#), [dag.sp](#), [dijkstra.sp](#), [sp.between](#)

**Examples**

```
con <- file(system.file("dot/joh.gxl", package="RBGL"), open="r")
z <- fromGXL(con)
close(con)

johnson.all.pairs.sp(z)
```

---

kCliques

*Find all the k-cliques in an undirected graph*

---

**Description**

Find all the k-cliques in an undirected graph

**Usage**

```
kCliques(g)
```

**Arguments**

`g` an instance of the graph class

**Details**

Notice that there are different definitions of k-clique in different context.

In computer science, a k-clique of a graph is a clique, i.e., a complete subgraph, of k nodes.

In Social Network Analysis, a k-clique in a graph is a subgraph where the distance between any two nodes is no greater than k.

Here we take the definition in Social Network Analysis.

Let  $D$  be a matrix,  $D[i][j]$  is the shortest path from node  $i$  to node  $j$ . Algorithm is outlined as following: (1) use Johnson's algorithm to fill  $D$ ; let  $N = \max(D[i][j])$  for all  $i, j$ ; (2) each edge is a 1-clique by itself; (3) for  $k = 2, \dots, N$ , try to expand each (k-1)-clique to k-clique: (3.1) consider a (k-1)-clique the current k-clique  $KC$ ; (3.2) repeat the following: if for all nodes  $j$  in  $KC$ ,  $D[v][j] \leq k$ , add node  $v$  to  $KC$ ; (3.3) eliminate duplicates; (4) the whole graph is  $N$ -clique.

**Value**

A list of length  $N$ ;  $k$ -th entry ( $k = 1, \dots, N$ ) is a list of all the  $k$ -cliques in graph  $g$ .

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Social Network Analysis: Methods and Applications. By S. Wasserman and K. Faust, pp. 258.

**Examples**

```
con <- file(system.file("XML/snacliqueex.gxl", package="RBGL"))
coex <- fromGXL(con)
close(con)

kCliques(coex)
```

---

kCores

*Find all the k-cores in a graph*


---

**Description**

Find all the  $k$ -cores in a graph

**Usage**

```
kCores(g, EdgeType=c("in", "out"))
```

**Arguments**

<code>g</code>	an instance of the <code>graph</code> class
<code>EdgeType</code>	what types of edges to be considered when <code>g</code> is directed

**Details**

A  $k$ -core in a graph is a subgraph where each node is adjacent to at least a minimum number,  $k$ , of the other nodes in the subgraph.

A  $k$ -core in a graph may not be connected.

The core number for each node is the highest  $k$ -core this node is in. A node in a  $k$ -core will be, by definition, in a  $(k-1)$ -core.

The implementation is based on the algorithm by V. Batagelj and M. Zaversnik, 2002.

The example `snacoreex.gxl` is in the paper by V. Batagelj and M. Zaversnik, 2002.

**Value**

A vector of the core numbers for all the nodes in `g`.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Social Network Analysis: Methods and Applications. By S. Wasserman and K. Faust, pp. 266. An O(m) Algorithm for Cores decomposition of networks, by V. Batagelj and M. Zaversnik, 2002.

**Examples**

```
con1 <- file(system.file("XML/snacorex.gxl", package="RBGL"))
kcoex <- fromGXL(con1)
close(con1)

kCores(kcoex)

con2 <- file(system.file("XML/conn2.gxl", package="RBGL"))
kcoex2 <- fromGXL(con2)
close(con2)

kCores(kcoex2)
kCores(kcoex2, "in")
kCores(kcoex2, "out")
```

---

lambdaSets

*Find all the lambda-sets in an undirected graph*


---

**Description**

Find all the lambda-sets in an undirected graph

**Usage**

```
lambdaSets(g)
```

**Arguments**

`g` an instance of the `graph` class

**Details**

From reference (1), p. 270: A set of nodes is a lambda-set if any pair of nodes in the lambda set has larger edge connectivity than any pair of nodes consisting of one node from within the lambda set and a second node from outside the lambda set.

As stated in reference (2), a lambda set is a maximal subset of nodes who have more edge-independent paths connecting them to each other than to outsiders.

A lambda set could be characterized by the minimum edge connectivity  $k$  among its members, and could be called `lambda-k` sets.

Let  $N$  be maximum edge connectivity of graph  $g$ , we output all the lambda-k set for all  $k = 1, \dots, N$ .

**Value**

Maximum edge connectivity,  $N$ , of the graph  $g$ , and A list of length  $N$ ;  $k$ -th entry ( $k = 1, \dots, N$ ) is a list of all the lambda- $k$  sets in graph  $g$ .

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

- (1) Social Network Analysis: Methods and Applications. By S. Wasserman and K. Faust, pp. 269.
- (2) LS sets, lambda sets and other cohesive subsets. By S. P. Borgatti, M. G. Everett, P. R. Shirey, Social Networks 12 (1990) p. 337-357

**Examples**

```
con <- file(system.file("XML/snlambdaex.gxl", package="RBGL"))
coex <- fromGXL(con)
close(con)

lambdaSets(coex)
```

---

layout

*Layout an undirected graph in 2D*

---

**Description**

Layout an undirected graph in 2D

**Usage**

```
circleLayout(g, radius=1)
kamadaKawaiSpringLayout(g, edge_or_side=1, es_length=1)
fruchtermanReingoldForceDirectedLayout(g, width=1, height=1)
randomGraphLayout(g, minX=0, maxX=1, minY=0, maxY=1)
```

**Arguments**

<code>g</code>	an instance of the graph class with edgemode “undirected”
<code>radius</code>	radius of a regular n-polygon
<code>edge_or_side</code>	boolean indicating the length is for an edge or for a side, default is for an edge
<code>es_length</code>	the length of an edge or a side for layout
<code>width</code>	the width of the display area, all x coordinates fall in $[-width/2, width/2]$
<code>height</code>	the height of the display area, all y coordinates fall in $[-height/2, height/2]$
<code>minX</code>	minimum x coordinate
<code>maxX</code>	maximum x coordinate
<code>minY</code>	minimum y coordinate
<code>maxY</code>	maximum y coordinate

## Details

If you want to simply draw a graph, you should consider using package *Rgraphviz*. The layout options in package *Rgraphviz*: `neato`, `circo` and `fdp`, correspond to `kamadaKawaiSpringLayout`, `circleLayout` and `fruchtermanReingoldForceDirectedLayout`, respectively.

Function `circleLayout` layouts the graph with the vertices at the points of a regular n-polygon. The distance from the center of the polygon to each point is determined by the `radius` parameter.

Function `kamadaKawaiSpringLayout` provides Kamada-Kawai spring layout for connected, undirected graphs. User provides either the unit length `e` of an edge in the layout or the length of a side `s` of the display area.

Function `randomGraphLayout` places the points of the graph at random locations.

Function `fruchtermanReingoldForceDirectedLayout` performs layout of unweighted, undirected graphs. It's a force-directed algorithm. The BGL implementation doesn't handle disconnected graphs very well, since it doesn't explicitly give each connected component a region proportional to its size.

See documentation on this function in Boost Graph Library for more details.

## Value

A (2 x n) matrix, where n is the number of nodes in the graph, each column gives the (x, y)-coordinates for the corresponding node.

## Author(s)

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## See Also

[layoutGraph](#)

## Examples

```
con <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)

coex <- ugraph(coex)

circleLayout(coex)

kamadaKawaiSpringLayout(coex)

randomGraphLayout(coex)

fruchtermanReingoldForceDirectedLayout(coex, 10, 10)
```

---

```
makeBiconnectedPlanar  
    makeBiconnectedPlanar
```

---

## Description

makeBiconnectedPlanar description

## Usage

```
makeBiconnectedPlanar(g)
```

## Arguments

g                    instance of class graphNEL from Bioconductor graph class

## Author(s)

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
V <- LETTERS[1:11]  
g <- new("graphNEL", nodes=V, edgemode="undirected")  
g <- addEdge(V[1+0], V[1+1], g)  
g <- addEdge(V[1+2], V[3+1], g)  
g <- addEdge(V[1+3], V[0+1], g)  
g <- addEdge(V[1+3], V[4+1], g)  
g <- addEdge(V[1+4], V[5+1], g)  
g <- addEdge(V[1+5], V[3+1], g)  
g <- addEdge(V[1+5], V[6+1], g)  
g <- addEdge(V[1+6], V[7+1], g)  
g <- addEdge(V[1+7], V[8+1], g)  
g <- addEdge(V[1+8], V[5+1], g)  
g <- addEdge(V[1+8], V[9+1], g)  
g <- addEdge(V[1+0], V[10+1], g)  
  
x6 <- makeBiconnectedPlanar(g)  
x6
```

---

makeConnected	<i>makeConnected</i>
---------------	----------------------

---

## Description

makeConnected description

## Usage

```
makeConnected(g)
```

## Arguments

`g` instance of class graphNEL from Bioconductor graph class

## Author(s)

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
V <- LETTERS[1:11]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[1+1], g)
g <- addEdge(V[1+2], V[3+1], g)
g <- addEdge(V[1+3], V[4+1], g)
g <- addEdge(V[1+5], V[6+1], g)
g <- addEdge(V[1+6], V[7+1], g)
g <- addEdge(V[1+8], V[9+1], g)
g <- addEdge(V[1+9], V[10+1], g)
g <- addEdge(V[1+10], V[8+1], g)
```

```
x5 <- makeConnected(g)
x5
```

---

makeMaximalPlanar *makeMaximalPlanar*

---

## Description

makeMaximalPlanar description

## Usage

```
makeMaximalPlanar(g)
```

## Arguments

`g` instance of class graphNEL from Bioconductor graph class

## Author(s)

Li Long <li.long@isb-sib.ch>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

## Examples

```
V <- LETTERS[1:10]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[1+1], g)
g <- addEdge(V[1+1], V[2+1], g)
g <- addEdge(V[1+2], V[3+1], g)
g <- addEdge(V[1+3], V[4+1], g)
g <- addEdge(V[1+4], V[5+1], g)
g <- addEdge(V[1+5], V[6+1], g)
g <- addEdge(V[1+6], V[7+1], g)
g <- addEdge(V[1+7], V[8+1], g)
g <- addEdge(V[1+8], V[9+1], g)

x7 <- makeMaximalPlanar(g)
x7
```



---

maxClique	<i>Find all the cliques in a graph</i>
-----------	--

---

**Description**

Find all the cliques in a graph

**Usage**

```
maxClique(g)
```

**Arguments**

`g` an instance of the graph class

**Details**

Notice the maximum clique problem is NP-complete, which means it cannot be solved by any known polynomial algorithm.

We implemented the algorithm by C. Bron and J. Kerbosch,

**Value**

maxClique list of all cliques in `g`

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Finding all cliques of an undirected graph, by C. Bron and J. Kerbosch, Communication of ACM, Sept 1973, Vol 16, No. 9.

**Examples**

```
con1 <- file(system.file("XML/conn.gxl",package="RBGL"), open="r")
coex <- fromGXL(con1)
close(con1)

maxClique(coex)

con2 <- file(system.file("XML/hcs.gxl",package="RBGL"), open="r")
coex <- fromGXL(con2)
close(con2)

maxClique(coex)
```

---

max.flow

*Compute max flow for a directed graph*


---

**Description**

Compute max flow for a directed graph

**Usage**

```
edmonds.karp.max.flow(g, source, sink)
push.relabel.max.flow(g, source, sink)
kolmogorov.max.flow(g, source, sink)
```

**Arguments**

<code>g</code>	an instance of the graph class with edgemode “directed”
<code>source</code>	node name (character) or node number (int) for the source of the flow
<code>sink</code>	node name (character) or node number (int) for the sink of the flow

**Details**

Given a directed graph  $G=(V, E)$  of a single connected component with a vertex `source` and a vertex `sink`. Each arc has a positive real valued capacity, currently it’s equivalent to the weight of the arc. The flow of the network is the net flow entering the vertex `sink`. The maximum flow problem is to determine the maximum possible value for the flow to the `sink` and the corresponding flow values for each arc.

See documentation on these algorithms in Boost Graph Library for more details.

**Value**

A list of

<code>maxflow</code>	the max flow from <code>source</code> to <code>sink</code>
<code>edges</code>	the nodes of the arcs with non-zero capacities
<code>flows</code>	the flow values of the arcs with non-zero capacities

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[minCut](#), [edgeConnectivity](#)

**Examples**

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
g <- fromGXL(con)
close(con)

ans1 <- edmonds.karp.max.flow(g, "B", "D")
ans2 <- edmonds.karp.max.flow(g, 3, 2)      # 3 and 2 equivalent to "C" and "B"

ans3 <- push.relabel.max.flow(g, 2, 4)     # 2 and 4 equivalent to "B" and "D"
ans4 <- push.relabel.max.flow(g, "C", "B")

# error in the following now
#ans5 <- kolmogorov.max.flow(g, "B", "D")
#ans6 <- kolmogorov.max.flow(g, 3, 2)
```

---

maximumCycleRatio *maximumCycleRatio*

---

**Description**

maximumCycleRatio description

**Usage**

```
maximumCycleRatio(g)
```

**Arguments**

g                    instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

minCut

*Compute min-cut for an undirected graph***Description**

Compute min-cut for an undirected graph

**Usage**

```
minCut(g)
```

**Arguments**

`g` an instance of the `graph` class with `edgemode` “undirected”

**Details**

Given an undirected graph  $G=(V, E)$  of a single connected component, a cut is a partition of the set of vertices into two non-empty subsets  $S$  and  $V-S$ , a cost is the number of edges that are incident on one vertex in  $S$  and one vertex in  $V-S$ . The min-cut problem is to find a cut  $(S, V-S)$  of minimum cost.

For simplicity, the returned subset  $S$  is the smaller of the two subsets.

**Value**

A list of

<code>mincut</code>	the number of edges to be severed to obtain the minimum cut
<code>S</code>	the smaller subset of vertices in the minimum cut
<code>V-S</code>	the other subset of vertices in the minimum cut

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[edgeConnectivity](#)

**Examples**

```
con <- file(system.file("XML/conn.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
```

```
minCut(coex)
```

---

`minimumCycleRatio` *minimumCycleRatio*

---

**Description**

minimumCycleRatio description

**Usage**

`minimumCycleRatio(g)`

**Arguments**

`g` instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

---

`mstree.kruskal` *Kruskal's minimum spanning tree in boost*

---

**Description**

compute the minimum spanning tree (MST) for a graph and return a representation in matrices

**Usage**

`mstree.kruskal(x)`

**Arguments**

`x` instance of class graph

**Details**

calls to kruskal minimum spanning tree algorithm of Boost graph library

**Value**

a list

edgeList      a matrix *m* of dimension 2 by number of edges in the MST, with *m*[*i*,*j*] the *j*th node in edge *i*

weights       a vector of edge weights corresponding to the columns of edgeList

nodes         the vector of nodes of the input graph *x*

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[prim.minST](#)

**Examples**

```
con1 <- file(system.file("XML/kmstEx.gxl",package="RBGL"), open="r")
km <- fromGXL(con1)
close(con1)

mstree.kruskal(km)
edgeData(km, "B", "D", "weight") <- 1.1
edgeData(km, "B", "E", "weight") <- .95
mstree.kruskal(km)

con2 <- file(system.file("XML/telenet.gxl",package="RBGL"), open="r")
km2 <- fromGXL(con2)
close(con2)

m <- mstree.kruskal(km2)
print(sum(m[[2]]))
```

---

mstree.prim

*Compute minimum spanning tree for an undirected graph*

---

**Description**

Compute minimum spanning tree for an undirected graph

**Usage**

```
mstree.prim(g)
prim.minST(g)
```

**Arguments**

`g` an instance of the graph class with edgemode “undirected”

**Details**

This is Prim’s algorithm for solving the minimum spanning tree problem for an undirected graph with weighted edges.

The function `prim.minST` is deprecated and renamed, use `mstree.prim` instead.

See documentations on this function in Boost Graph Library for more details.

**Value**

A list of

`edges` the edges that form the minimum spanning tree

`weights` the total weight of the minimum spanning tree

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[mstree.kruskal](#)

**Examples**

```
con <- file(system.file("XML/conn2.gxl", package="RBGL"))
coex <- fromGXL(con)
close(con)

mstree.prim(coex)
```

---

Ordering

*Compute vertex ordering for an undirected graph*

---

**Description**

Compute vertex ordering for an undirected graph

**Usage**

```
cuthill.mckee.ordering(g)
minDegreeOrdering(g, delta=0)
sloan.ordering(g, w1=1, w2=2)
```

**Arguments**

<code>g</code>	an instance of the <code>graph</code> class with <code>edgemode</code> “undirected”
<code>delta</code>	Multiple elimination control variable. If it is larger than or equal to zero then multiple elimination is enabled. The value of <code>delta</code> specifies the difference between the minimum degree and the degree of vertices that are to be eliminated.
<code>w1</code>	First heuristic weight for the Sloan algorithm.
<code>w2</code>	Second heuristic weight for the Sloan algorithm.

**Details**

The following details were obtained from the documentation of these algorithms in Boost Graph Library and readers are referred their for even more detail. The goal of the Cuthill-McKee (and reverse Cuthill-McKee) ordering algorithm is to reduce the bandwidth of a graph by reordering the indices assigned to each vertex.

The minimum degree ordering algorithm is a fill-in reduction matrix reordering algorithm.

The goal of the Sloan ordering algorithm is to reduce the profile and the wavefront of a graph by reordering the indices assigned to each vertex.

The goal of the King ordering algorithm is to reduce the bandwidth of a graph by reordering the indices assigned to each vertex.

**Value**

<code>cuthill.mckee.ordering</code>	returns a list with elements:
<code>reverse cuthill.mckee.ordering</code>	the vertices in the new ordering
<code>original bandwidth</code>	bandwidth before reordering vertices
<code>new bandwidth</code>	bandwidth after reordering of vertices
<code>minDegreeOrdering</code>	return a list with elements:
<code>inverse_permutation</code>	the new vertex ordering, given as the mapping from the new indices to the old indices
<code>permutation</code>	the new vertex ordering, given as the mapping from the old indices to the new indices
<code>sloan.ordering</code>	returns a list with elements:
<code>sloan.ordering</code>	the vertices in the new ordering
<code>bandwidth</code>	bandwidth of the graph after reordering
<code>profile</code>	profile of the graph after reordering
<code>maxWavefront</code>	maxWavefront of the graph after reordering
<code>aver.wavefront</code>	aver.wavefront of the graph after reordering
<code>rms.wavefront</code>	rms.wavefront of the graph after reordering



**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)

coex <- ugraph(coex)
cuthill.mckee.ordering(coex)
minDegreeOrdering(coex)
sloan.ordering(coex)
```

---

planarCanonicalOrdering  
*planarCanonicalOrdering*

---

**Description**

planarCanonicalOrdering description

**Usage**

```
planarCanonicalOrdering(g)
```

**Arguments**

g                    instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
V <- LETTERS[1:6]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0], V[1+1], g)
g <- addEdge(V[1+1], V[2+1], g)
g <- addEdge(V[1+2], V[3+1], g)
g <- addEdge(V[1+3], V[4+1], g)
g <- addEdge(V[1+4], V[5+1], g)
g <- addEdge(V[1+5], V[0+1], g)
g <- addEdge(V[1+0], V[2+1], g)
g <- addEdge(V[1+0], V[3+1], g)
g <- addEdge(V[1+0], V[4+1], g)
g <- addEdge(V[1+1], V[3+1], g)
g <- addEdge(V[1+1], V[4+1], g)
g <- addEdge(V[1+1], V[5+1], g)

x2 <- planarCanonicalOrdering(g)
x2
```

---

planarFaceTraversal

*planarFaceTraversal*

---

**Description**

planarFaceTraversal description

**Usage**

```
planarFaceTraversal(g)
```

**Arguments**

`g` instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```

V <- LETTERS[1:9]
g <- new("graphNEL", nodes=V, edgemode="undirected")
g <- addEdge(V[1+0],V[1+1],g)
g <- addEdge(V[1+1],V[1+2],g)
g <- addEdge(V[1+3],V[1+4],g)
g <- addEdge(V[1+4],V[1+5],g)
g <- addEdge(V[1+6],V[1+7],g)
g <- addEdge(V[1+7],V[1+8],g)
g <- addEdge(V[1+0],V[1+3],g)
g <- addEdge(V[1+3],V[1+6],g)
g <- addEdge(V[1+1],V[1+4],g)
g <- addEdge(V[1+4],V[1+7],g)
g <- addEdge(V[1+2],V[1+5],g)
g <- addEdge(V[1+5],V[1+8],g)

x1 <- planarFaceTraversal(g)
x1

```

---

RBGL.overview

*RBGL.overview*


---

**Description**

The RBGL package consists of a number of interfaces to the Boost C++ library for graph algorithms. This page follows, approximately, the chapter structure of the monograph on the Boost Graph Library by Siek et al., and gives hyperlinks to documentation on R functions currently available, along with the names of formal parameters to these functions.

**basicAlgs**

Functions	parameters
<a href="#">bandwidth</a>	<code>g</code>
<a href="#">bfs</a>	<code>object, node, checkConn</code>
<a href="#">dfs</a>	<code>object, node, checkConn</code>
<a href="#">edgeConnectivity</a>	<code>g</code>
<a href="#">gprofile</a>	<code>g</code>
<a href="#">isomorphism</a>	<code>g1, g2</code>
<a href="#">minCut</a>	<code>g</code>
<a href="#">transitive.closure</a>	<code>g</code>
<a href="#">tsort</a>	<code>x</code>

**ShortestPaths**

Functions

parameters

<code>bellman.ford.sp</code>	<code>g, start</code>
<code>dag.sp</code>	<code>g, start</code>
<code>dijkstra.sp</code>	<code>g, start</code>
<code>extractPath</code>	<code>s, f, pens</code>
<code>johnson.all.pairs.sp</code>	<code>g</code>
<code>sp.between</code>	<code>g, start, finish</code>
<code>sp.between.old</code>	<code>g, start, finish</code>
<code>sp.between.scalar</code>	<code>g, start, finish</code>

### MinimumSpanningTree

Functions	parameters
<code>mstree.kruskal</code>	<code>x</code>
<code>prim.minST</code>	<code>g</code>

### ConnectedComponents

Functions	parameters
<code>connectedComp</code>	<code>g</code>
<code>highlyConnSG</code>	<code>g, sat, ldv</code>
<code>incremental.components</code>	<code>g</code>
<code>init.incremental.components</code>	<code>g</code>
<code>same.component</code>	<code>g, node1, node2</code>
<code>strongComp</code>	<code>g</code>

### MaximumFlow

Functions	parameters
<code>edmonds.karp.max.flow</code>	<code>g, source, sink</code>
<code>push.relabel.max.flow</code>	<code>g, source, sink</code>

### SparseMatrixOrdering

Functions	parameters
<code>cuthill.mckee.ordering</code>	<code>g</code>
<code>minDegreeOrdering</code>	<code>g, delta</code>
<code>sloan.ordering</code>	<code>g, w1, w2</code>

**LayoutAlgorithms**

Functions	parameters
<code>circle.layout</code>	<code>g, radius</code>
<code>kamada.kawai.spring.layout</code>	<code>g, edge_or_side, es_length</code>

**GraphClustering**

Functions	parameters
<code>betweenness.centralty.clustering</code>	<code>g, threshold, normalize</code>

**Betweenness**

Functions	parameters
<code>brandes.betweenness.centralty</code>	<code>g</code>

**Wavefront**

Functions	parameters
<code>aver.wavefront</code>	<code>g</code>
<code>ith.wavefront</code>	<code>g, start</code>
<code>maxWavefront</code>	<code>g</code>
<code>rms.wavefront</code>	<code>g</code>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

---

`removeSelfLoops`      *remove self loops in a graph*

---

**Description**

remove self loops in a graph

**Usage**

```
removeSelfLoops(g)
```

**Arguments**

`g`                      one instance of the graph class

**Details**

If a given graph contains self-loop(s), `removeSelfLoops` removes them. This is for those functions that cannot handle graphs with self-loops.

**Value**

A new graph without self loops.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**Examples**

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"))
g1 <- fromGXL(con)
close(con)

g2 <- ugraph(g1)
removeSelfLoops(g2)
```

---

`separates`                      *A function to test whether a subset of nodes separates two other subsets of nodes.*

---

**Description**

The function tests to see whether a set of nodes, `S1`, separates all nodes in `a` from all nodes in `b`.

**Usage**

```
separates(a, b, S1, g)
```

**Arguments**

a	The names of the nodes in the from set.
b	The names of the nodes in the to set.
S1	The names of the nodes in the separation set.
g	An instance of the <code>graph</code> class. All nodes named in the other arguments must be nodes of this graph.

**Details**

The algorithm is quite simple. A subgraph is created by removing the nodes named in `S1` from `g`. Then all paths between elements of `a` to elements of `b` are tested for. If any path exists the function returns `FALSE`, otherwise it returns `TRUE`.

**Value**

Either `TRUE` or `FALSE` depending on whether `S1` separates `a` from `b` in `g1`.

**Author(s)**

R. Gentleman

**References**

S. Lauritzen, Graphical Models, OUP.

**See Also**

[johnson.all.pairs.sp](#)

**Examples**

```
con <- file(system.file("XML/kmstEx.gxl", package="RBGL"))
km <- fromGXL(con)
close(con)

separates("B", "A", "E", km)
separates("B", "A", "C", km)
```

---

sloanStartEndVertices

*sloanStartEndVertices*

---

**Description**

sloanStartEndVertices description

**Usage**

```
sloanStartEndVertices(g)
```

**Arguments**

`g` instance of class graphNEL from Bioconductor graph class

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

---

sp.between

*Dijkstra's shortest paths using boost C++*

---

**Description**

dijkstra's shortest paths

**Usage**

```
sp.between(g, start, finish, detail=TRUE)
```

**Arguments**

`g` instance of class graph  
`start` node name(s) for start of path(s)  
`finish` node name(s) for end of path(s)  
`detail` if TRUE, output additional info on the shortest path

**Details**

These functions are interfaces to the Boost graph library C++ routines for Dijkstra's shortest paths. Function `sp.between.scalar` is obsolete.

**Value**

When `start` and/or `finish` are vectors, we use the normal cycling rule in R to match both vectors and try to find the shortest path for each pair.

Function `sp.between` returns a list of info on the shortest paths. Each such shortest path is designated by its starting node and its ending node. Each element in the returned list contains:

`length` total length (using edge weights) of this shortest path

,

`path_detail` if requested, a vector of names of the nodes on the shortest path

,



length\_detail  
if requested, a list of edge weights of this shortest path

.

See [pathWeights](#) for caveats about undirected graph representation.

### Author(s)

VJ Carey <stvjc@channing.harvard.edu>, Li Long <li.long@isb-sib.ch>

### See Also

[bellman.ford.sp](#), [dag.sp](#), [dijkstra.sp](#), [johnson.all.pairs.sp](#)

### Examples

```
con <- file(system.file("XML/ospf.gxl", package="RBGL"), open="r")
ospf <- fromGXL(con)
close(con)

dijkstra.sp(ospf, nodes(ospf)[6])

sp.between(ospf, "RT6", "RT1")

sp.between(ospf, c("RT6", "RT2"), "RT1", detail=FALSE)

sp.between(ospf, c("RT6", "RT2"), c("RT1", "RT5"))

# see NAs for query on nonexistent path
sp.between(ospf, "N10", "N13")
```

---

strongComp

*Identify Strongly Connected Components*

---

### Description

The strongly connected components in a directed graph are identified and returned as a list.

### Usage

```
strongComp(g)
```

### Arguments

g graph with edgemode "directed".

### Details

Tarjan's algorithm is used to determine all strongly connected components of a *directed graph*.

**Value**

A list whose length is the number of strongly connected components in `g`. Each element of the list is a vector of the node labels for the nodes in that component.

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**See Also**

[connComp](#), [connectedComp](#), [same.component](#)

**Examples**

```
con <- file(system.file("XML/kmstEx.gxl", package="RBGL"), open="r")
km <- fromGXL(con)
close(con)

km<- graph::addNode(c("F", "G", "H"), km)
km<- addEdge("G", "H", km, 1)
km<- addEdge("H", "G", km, 1)
strongComp(km)
connectedComp(ugraph(km))
```

---

`transitive.closure` *Compute transitive closure of a directed graph*

---

**Description**

Compute transitive closure of a directed graph

**Usage**

```
transitive.closure(g)
```

**Arguments**

`g` an instance of the `graph` class

**Details**

This function calculates the transitive closure of a directed graph. See documentation on this function in Boost Graph Library for more details.

**Value**

An object of class graphNEL.

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"))
coex <- fromGXL(con)
close(con)

transitive.closure(coex)
```

---

transitivity

*Calculate transitivity for an undirected graph*

---

**Description**

Calculate transitivity for an undirected graph

**Usage**

```
transitivity(g)
```

**Arguments**

`g` an instance of the graph class

**Details**

For an undirected graph  $G$ , let  $\delta(v)$  be the number of triangles with  $v$  as a node, let  $\tau(v)$  be the number of triples, i.e., paths of length 2 with  $v$  as the center node.

Define transitivity  $T(G) = \text{sum}(\delta(v)) / \text{sum}(\tau(v))$ , for all  $v$  in  $V$ .

**Value**

Transitivity for graph  $g$ .

**Author(s)**

Li Long <li.long@isb-sib.ch>

## References

Approximating Clustering Coefficient and Transitivity, T. Schank, D. Wagner, Journal of Graph Algorithms and Applications, Vol. 9, No. 2 (2005).

## See Also

clusteringCoef, clusteringCoefAppr, graphGenerator

## Examples

```
con <- file(system.file("XML/conn.gxl", package="RBGL"))
g <- fromGXL(con)
close(con)

tc <- transitivity(g)
```

---

tsort

*topological sort of vertices of a digraph*

---

## Description

returns vector of zero-based indices of vertices of a DAG in topological sort order

## Usage

```
tsort(x) # now x assumed to be Bioconductor graph graphNEL
```

## Arguments

x                    instance of class graphNEL from Bioconductor graph class

## Details

calls to the `topological_sort` algorithm of BGL. will check in BGL whether the input is a DAG and return a vector of zeroes (of length `length(nodes(x))`) if it is not. Thus this function can be used to check for cycles in a digraph.

## Value

a numerical vector enumerating vertices in the topological sort sequence, 0-based

## Author(s)

VJ Carey <stvjc@channing.harvard.edu>

## References

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

**Examples**

```

data(FileDep)
tsind <- tsort(FileDep)
tsind
FD2 <- FileDep
# now introduce a cycle
FD2 <- addEdge("bar_o", "dax_h", FD2, 1)
tsort(FD2)

```

---

wavefront

---

*Compute the i-th/max/average/rms wavefront for a graph*


---

**Description**

Compute the i-th/max/average/rms wavefront for a graph

**Usage**

```

ith.wavefront(g, start)
maxWavefront(g)
aver.wavefront(g)
rms.wavefront(g)

```

**Arguments**

start	a vertex of the graph class
g	an instance of the graph class

**Details**

Assorted functions on wavefront of a graph.

**Value**

ith.wavefront	wavefront of the given vertex
maxWavefront	maximum wavefront of a graph
aver.wavefront	average wavefront of a graph
rms.wavefront	root mean square of all wavefronts

**Author(s)**

Li Long <li.long@isb-sib.ch>

**References**

Boost Graph Library ( [www.boost.org/libs/graph/doc/index.html](http://www.boost.org/libs/graph/doc/index.html) )

The Boost Graph Library: User Guide and Reference Manual; by Jeremy G. Siek, Lie-Quan Lee, and Andrew Lumsdaine; (Addison-Wesley, Pearson Education Inc., 2002), xxiv+321pp. ISBN 0-201-72914-8

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

```
con <- file(system.file("XML/dijkex.gxl", package="RBGL"), open="r")
coex <- fromGXL(con)
close(con)
```

```
ss <- 1
ith.wavefront(coex, ss)
maxWavefront(coex)
aver.wavefront(coex)
rms.wavefront(coex)
```

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