

RBGL: R interface to boost graph library

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Summary. An interface from R to the Boost Graph Library (BGL, an alternative to STL programming for mathematical graph objects) is described. *This 2003 update employs the graph class of Bioconductor.*

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1 Working with the Bioconductor graph class

An example object representing file dependencies is included, as shown in Figure 1.

```
> library(RBGL)
> data(FileDep)
> print(FileDep)
```

```
A graph with directed edges
Number of Nodes = 15
Number of Edges = 19
```

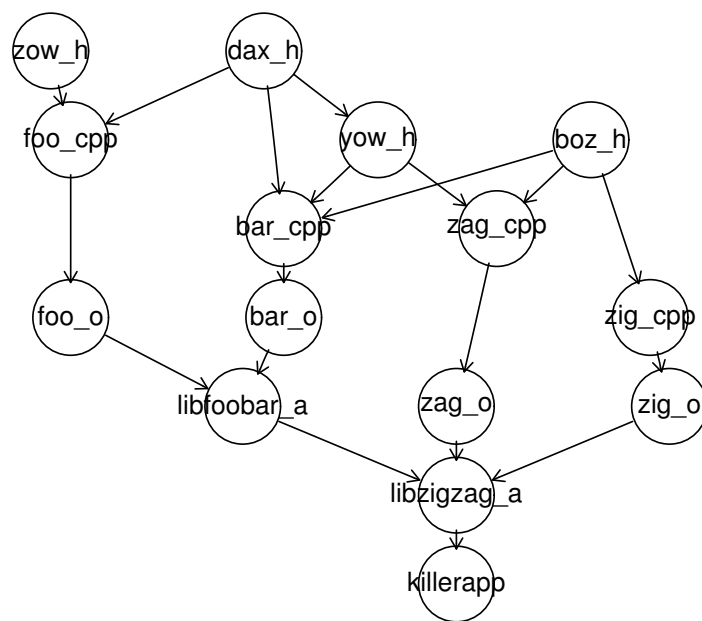


Figure 1: File dependency digraph example from Boost library.

2 Algorithms supported by RBGL

2.1 Topological sort

The `tsort` function will return the indices of vertices in topological sort order:

```
> ts <- tsort(FileDep)
```

Loading required package: Biobase

Welcome to Bioconductor

Vignettes contain introductory material. To view,
simply type: `openVignette()`
For details on reading vignettes, see
the `openVignette` help page.

```
> print(nodes(FileDep)[ts + 1])
```

```
[1] "zow_h"      "boz_h"      "zig_cpp"     "zig_o"      "dax_h"
[6] "yow_h"      "zag_cpp"     "zag_o"      "bar_cpp"     "bar_o"
[11] "foo_cpp"     "foo_o"      "libfoobar_a" "libzigzag_a" "killerapp"
```

Note that if the input graph is not a DAG, BGL `topological_sort` will check this and throw 'not a dag'. This is crudely captured in the interface (a message is written to the console and zeroes are returned).

```
#FD2 <- FileDep
# now introduce a cycle
#FD2@edgeL[["bar_cpp"]]$edges <- c(8,1)
#tsort(FD2)
```

2.2 Kruskal's minimum spanning tree

Function `mstree.kruskal` just returns a list of edges, weights and nodes determining the minimum spanning tree (MST) by Kruskal's algorithm.

```
> km <- fromGXL(file(system.file("GXL/kmstEx.gxl", package = "graph")))
> print(mstree.kruskal(km))
```

```
$edgeList
```

```
      [,1] [,2] [,3] [,4]
[1,]    1    4    5    2
[2,]    3    5    1    4
```

```
$weights
```

```
      [,1] [,2] [,3] [,4]
```

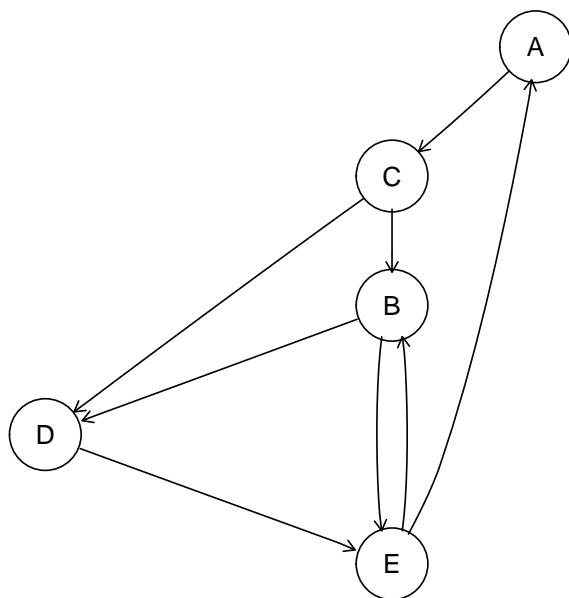


Figure 2: Kruskal MST example from Boost library.

```
[1,] 1 1 1 1
```

```
$nodes
```

```
[1] "A" "B" "C" "D" "E"
```

2.3 Depth first search

The `dfs` function returns a list of node indices by discovery and finish order.

```
> df <- fromGXL(file(system.file("XML/dfsex.gxl", package = "RBGL")))
> print(o <- dfs(df))
```

```
$discovered
```

```
[1] 1 2 5 4 3 6
```

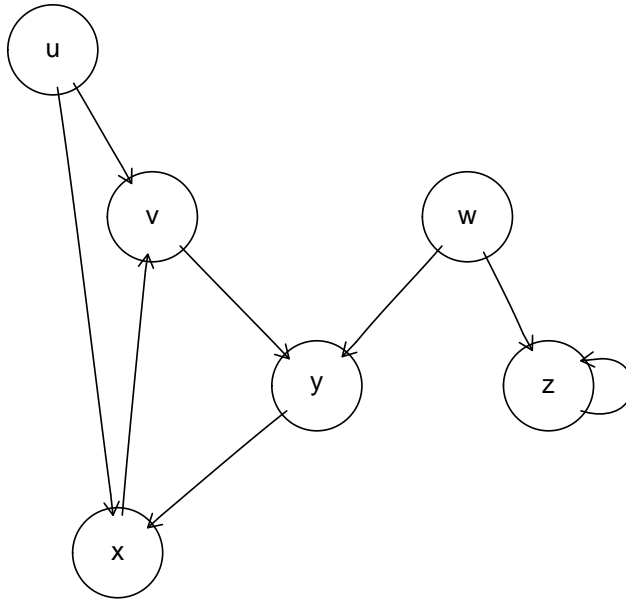


Figure 3: DFS example from Boost library.

```

$finish
[1] 4 5 2 1 6 3

```

Here is the list of nodes in DFS discovery order.

```

> print(nodes(df)[o$discovered])

[1] "u" "v" "y" "x" "w" "z"

```

2.4 Breadth first search

The `bfs` function returns a vector of node indices for a breadth-first search (BFS) starting at the node indexed by `init.node`.

```
> bf <- fromGXL(file(system.file("XML/bfsex.gxl", package = "RBGL")))
> bf@edgemode <- "undirected"
> print(o <- bfs(bf, nodes(bf)[2]))
```

```
[1] 1 2 3 4 5 6 7 8
```

The nodes in BFS order starting with the second node are

```
> print(nodes(bf)[o])
```

```
[1] "r" "s" "t" "u" "v" "w" "x" "y"
```

2.5 Dijkstra's shortest paths

```
> dd <- fromGXL(file(system.file("XML/dijkex.gxl", package = "RBGL")))
> print(dijkstra.sp(dd))
```

```
$distances
```

```
A B C D E
```

```
0 6 1 4 5
```

```
$penult
```

```
A B C D E
```

```
1 5 1 3 4
```

```
$start
```

```
A
```

```
1
```

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

```
$distances
```

RT1	RT2	RT3	RT4	RT5	RT6	RT7	RT8	RT9	RT10	RT11	RT12	N1	N2	N3	N4
7	7	6	7	6	0	8	8	11	7	10	11	10	10	7	8
N6	N7	N8	N9	N10	N11	N12	N13	N14	N15	H1					
8	12	10	11	13	14	10	14	14	17	21					

```
$penult
```

RT1	RT2	RT3	RT4	RT5	RT6	RT7	RT8	RT9	RT10	RT11	RT12	N1	N2	N3	N4
15	15	6	15	6	6	17	17	20	6	19	20	1	2	3	3
N6	N7	N8	N9	N10	N11	N12	N13	N14	N15	H1					

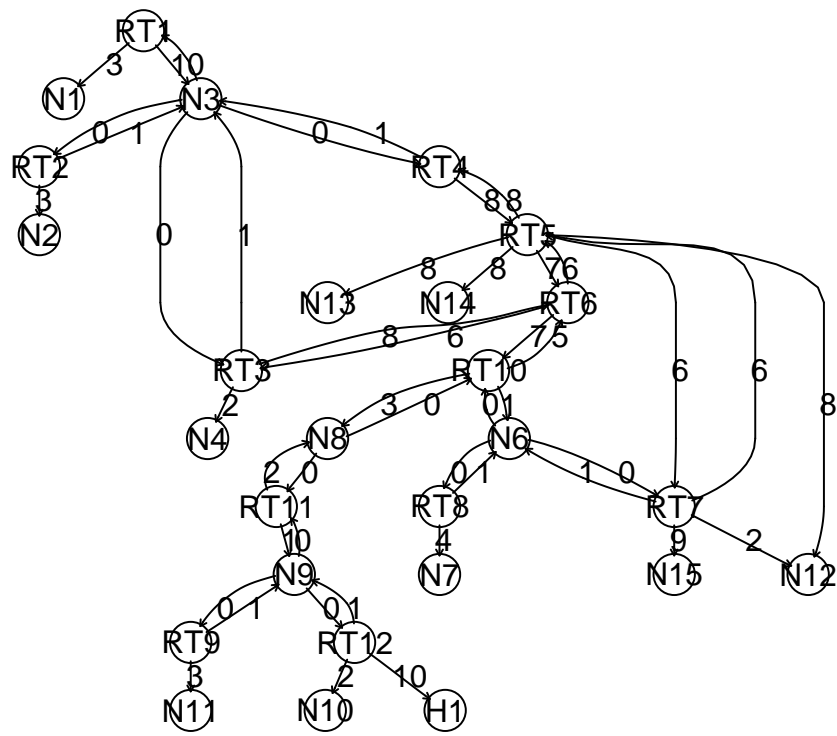


Figure 4: Network example from BGL.

```

10    8    10    11    12    9    7    5    5    7    12

$start
RT6
6

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

$"RT6:RT1"
$"RT6:RT1" $path
[1] "RT6" "RT3" "N3" "RT1"

$"RT6:RT1" $length
[1] 7

$"RT6:RT1" $pweights
RT6->RT3  RT3->N3  N3->RT1
      6      1      0

> dd <- fromGXL(file(system.file("XML/dijkex.gxl", package = "RBGL")))
> print(dijkstra.sp(dd))

$distances
A B C D E
0 6 1 4 5

$penult
A B C D E
1 5 1 3 4

$start
A
1

```

2.6 Connected components

```

> km <- fromGXL(file(system.file("GXL/kmstEx.gxl", package = "graph")))
> km@nodes <- c(km@nodes, "F", "G", "H")
> km@edgeL$F <- list(edges = numeric(0))
> km@edgeL$G <- list(edges = 8, weights = 1)
> km@edgeL$H <- list(edges = 7, weights = 1)
> km@edgemode <- "undirected"
> if (length(agrep("solaris", version[["platform"]])) == 0) print(connectedComp(ugrap

```



```

$"1"
[1] "A" "B" "C" "D" "E"

$"2"
[1] "F"

$"3"
[1] "G" "H"

```

2.7 Strongly connected components

```

> km <- fromGXL(file(system.file("GXL/kmstEx.gxl", package = "graph")))
> km@nodes <- c(km@nodes, "F", "G", "H")
> km@edgeL$F <- list(edges = numeric(0))
> km@edgeL$G <- list(edges = 8, weights = 1)
> km@edgeL$H <- list(edges = 7, weights = 1)
> km@edgemode <- "directed"
> print(strongComp(km))

```

```

$"1"
[1] "A" "B" "C" "D" "E"

$"2"
[1] "F"

$"3"
[1] "G" "H"

```

2.8 Edge connectivity and minimum disconnecting set

```

> coex <- fromGXL(file(system.file("XML/conn.gxl", package = "RBGL")))
> dcoex <- coex
> dcoex@edgemode <- "directed"
> udcoex <- ugraph(dcoex)

```

```

> if (length(agrep("solaris", version[["platform"]])) == 0) print(edgeConnectivity(co

```

```

$connectivity
[1] 2

```

```

$minDisconSet
$minDisconSet[[1]]

```

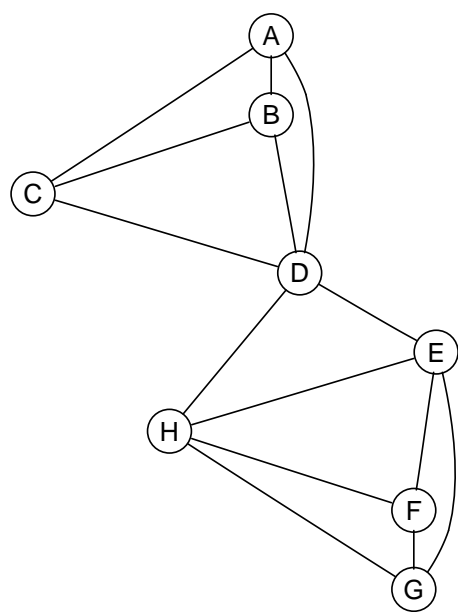


Figure 5: Edge connectivity example.

```
[1] "D" "E"
```

```
$minDisconSet[[2]]
```

```
[1] "D" "H"
```