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.*

Contents

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
```

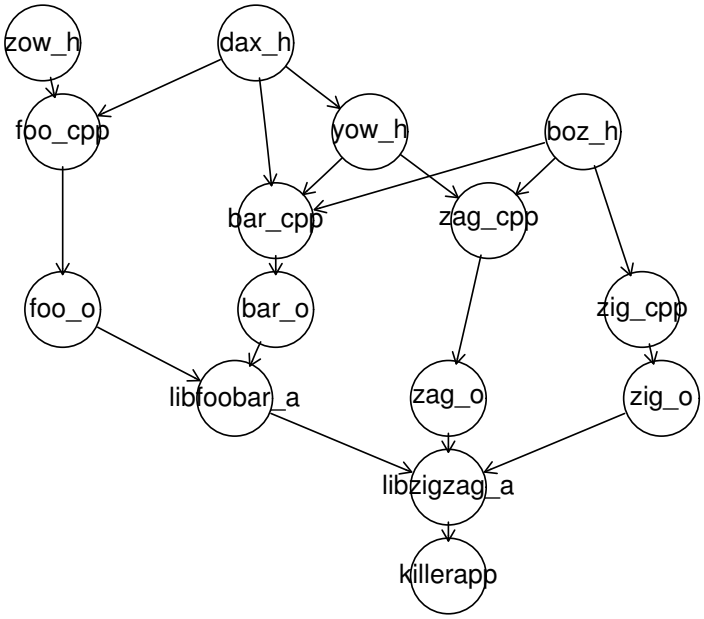

Figure 1: File dependency digraph example from Boost library.

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]
```

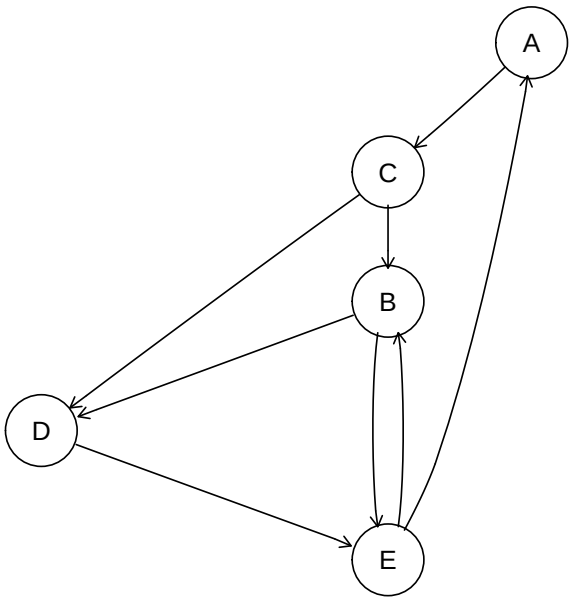

Figure 2: Kruskal MST example from Boost library.

```
[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
```

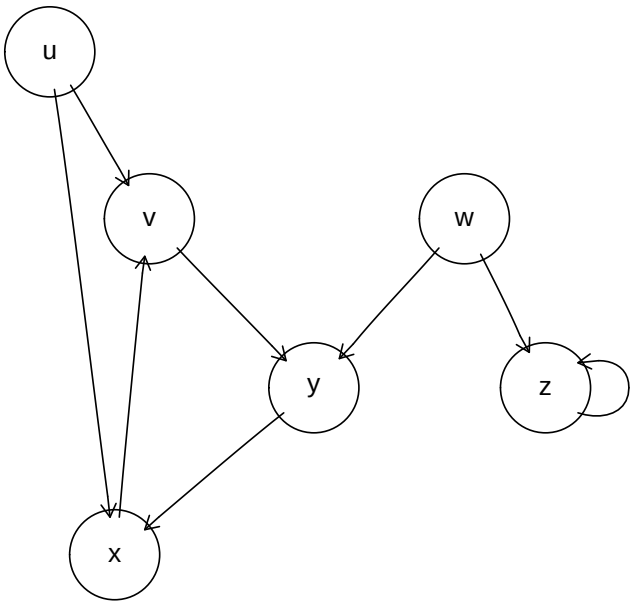

Figure 3: DFS example from Boost library.

```
$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
```

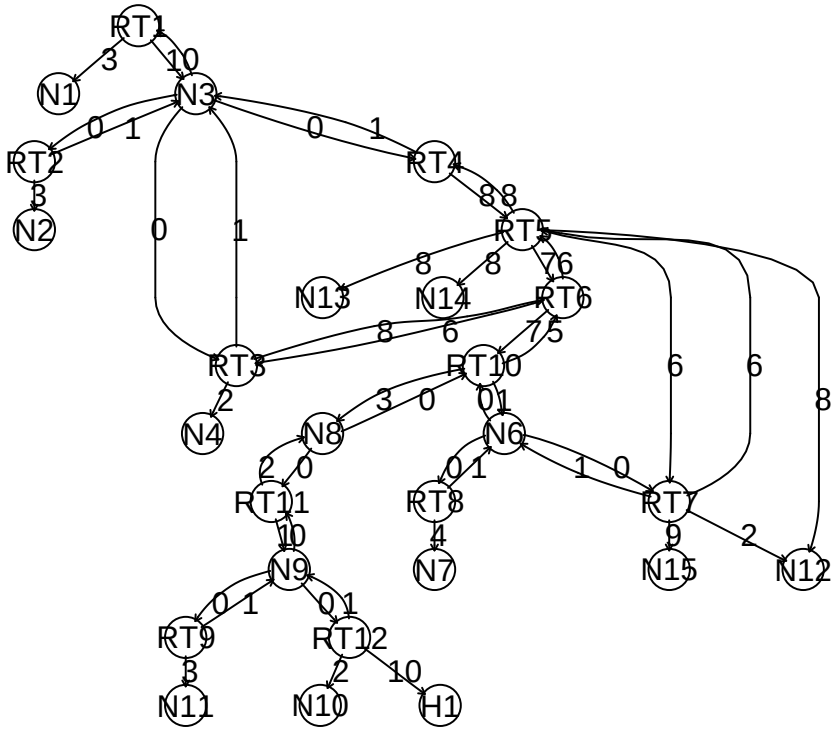

Figure 4: Network example from BGL.

```
  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] "not running on solaris, use windows or linux"
```

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

[1] "not running on solaris, use windows or linux"
```

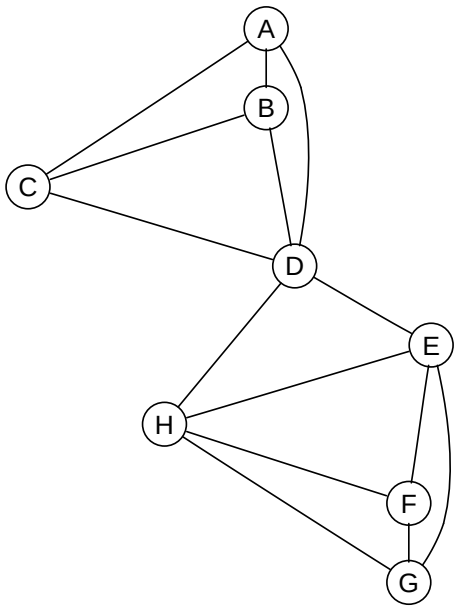

Figure 5: Edge connectivity example.