pathRender

April 19, 2009

colorNodes	*attach node coloring information to a graphNEL instance*

Description

attach node coloring information to a graphNEL instance

Usage

```
colorNodes(g, nodeAss, pal, attgen)
```

Arguments

g	graphNEL instance
nodeAss	color map for nodes: vector with elements evaluating to colors and nodes as element names
pal	a palette (use colorRampPalette for color interpolation)
attgen	attribute generating function – pwayRendAttrs is prototype

Value

a graphNEL instance with additional rendering data

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
example(randomGraph)
nn = nodes(g1)
x = runif(length(nn))
names(x) = nn
h1 = colorNodes(g1, x, colorRampPalette(brewer.pal(9, "Blues"))(length(nn)),
 pwayRendAttrs)
h1
```

coloredGraph-class *Class "coloredGraph"*

Description

a graph to which color attributes have been attached

Objects from the Class

Objects can be created by calls of the form `new("coloredGraph", nodes, edgeL, edgemode)`. these are graphNEL instances with some additional graphData

Slots

`nodes`: Object of class `"vector"` ~~

`edgeL`: Object of class `"list"` ~~

`edgemode`: Object of class `"character"` ~~

`edgeData`: Object of class `"attrData"` ~~

`nodeData`: Object of class `"attrData"` ~~

`renderInfo`: Object of class `"renderInfo"` ~~

`graphData`: Object of class `"list"` ~~

Extends

Class `"graphNEL-class"`, directly. Class `"graph-class"`, by class "graphNEL", distance 2.

Methods

plot `signature(x = "coloredGraph")`: ...

Examples

```
showClass("coloredGraph")
example(randomGraph)
nn = nodes(g1)
x = runif(length(nn))
names(x) = nn
h1 = colorNodes(g1, x, colorRampPalette(brewer.pal(9, "Blues"))(length(nn)),
 pwayRendAttrs)
h1
plot(h1)
```

graphcMAP *obtain a graph object corresponding to a cMAP pathway*

Description

obtain a graph object corresponding to a cMAP pathway

Usage

```
graphcMAP(pname)
```

Arguments

`pname`	character token identifying a KEGG or cMAP pathway

Details

reuses code from pathRender but emits a `graphNEL-class` instance with some additional information for rendering

Value

an instance of pwayGraph, which extends graphNEL

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
G1 = graphcMAP("p53pathway")
G1
nodes(G1)
if (require(Rgraphviz)) plot(G1)
```

plotExGraph *plot a gene network, coloring nodes according to relative expression values*

Description

plot a gene network, coloring nodes according to relative expression values

Usage

```
plotExGraph(g, es, sampind=1, pal=colorRampPalette(brewer.pal(9, "Blues"))(lengt
```

Arguments

`g`	graph representing a gene network
`es`	an ExpressionSet instance
`sampind`	sample to be used to obtain relative expression values
`pal`	palette for coloring the nodes
`attgen`	attribute generating function

Details

plots a colored network on the current graphics display

Value

as returned by Rgraphviz plot method for graphNEL instances

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
library(graph)
data(pancrCaIni)
library(ALL)
data(ALL)
library(hgu95av2.db)
collap1 = reduceES( ALL, nodes(pancrCaIni), revmap(hgu95av2SYMBOL), "symbol", mean )
library(RColorBrewer)
plotExGraph( pancrCaIni, collap1, 1 )
```

`pwayGraph-class` *Class "pwayGraph" – extension to graphNEL for pathway rendering*

Description

extension to graphNEL for pathway rendering

Objects from the Class

Objects can be created by calls of the form `new("pwayGraph", nodes, edgeL, edgemode)`. There is a plot method that will work reasonably well if the plotting surface is big enough.

Slots

`pwaySource`: Object of class `"character"` KEGG or BIOCARTA

`nodes`: Object of class `"vector"` pathway constituents in the native vocabulary

`edgeL`: Object of class `"list"` constituent relations in the native vocabulary

`edgemode`: Object of class `"character"` directed, typically

`edgeData`: Object of class `"attrData"` relationship attributes

`nodeData`: Object of class `"attrData"` node attributes

`graphData`: Object of class `"list"` this holds the special rendering attributes for edges and nodes, for nodes it seems particularly important to have fixedsize = FALSE

Extends

Class graphNEL-class, directly. Class graph-class, by class "graphNEL", distance 2.

Methods

plot `signature(x = "pwayGraph")`: renders the pathway

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
showClass("pwayGraph")
G1 = graphcMAP("stresspathway")
G1@graphData$nAttrs$labels[1:10]
```

---

reduceES *collapse the assay values in an ExpressionSet to a set of specified genes, using a statistic when multiple probes map to a given gene*

Description

collapse the assay values in an ExpressionSet to a set of specified genes, using a statistic when multiple probes map to a given gene

Usage

```
reduceES(es, annovec, ann2featMap, pdvname="symbol", collapseFun=NULL)
```

Arguments

`es`	ExpressionSet instance
`annovec`	genes to retain
`ann2featMap`	either an AnnDbBimap from AnnotationDbi (typically constructed with revmap(), or a named vector mapping from symbols to probe set IDs
`pdvname`	featureData variable name to be used to hold the annotations of variables kept
`collapseFun`	statistical function for collapsing data across probes mapping to the same gene

Value

An ExpressionSet instance limited to genes in annovec, condensed if necessary using collapseFun to get one number per gene from multiple probes

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
library(ALL)
data(ALL)
library(hgu95av2.db)
rr = revmap(hgu95av2SYMBOL)
exprs(reduceES(ALL[,1:3], c("DDR1", "CPNE1"), rr, "sym", mean))
```

`rendercMAPPathway` *Render pathways from cMAP*

Description

Build graphs based on pathway or interaction data from cMAP database, render them using Rgraphviz.

Usage

```
rendercMAPPathway(pname, ino=0)
```

Arguments

`pname`	name of the pathway to render
`ino`	index of the interaction in the given pathway to render

Details

For a given pathway in cMAP database, we build a subgraph for each interaction in the pathway, join them together to form the graph for the complete pathway. The subgraphs for interactions and the graph for the pathway include info for rendering, such as labels/shapes/fillcolors for nodes, colors/styles/weights for edges. If user specifies an index of interaction, only the interaction is rendered. Otherwise, the complete pathway is rendered.

Value

None. A graphical output is presented.

Author(s)

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

Examples

```
   rendercMAPPathway("plateletapppathway")
   rendercMAPPathway("plateletapppathway", 5)
   rendercMAPPathway("hsa00601")
   rendercMAPPathway("hsa00601", 10)
```

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