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
eexample(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"~~
odeData: 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**

**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"))(length(es))
```
### 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`
reduceES

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

```r
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**

```r
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**

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