Package ‘pathRender’

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Title Render molecular pathways
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Depends graph, Rgraphviz, RColorBrewer, cMAP, AnnotationDbi, methods, stats4
Suggests ALL, hgu95av2.db
Description build graphs from pathway databases, render them by Rgraphviz.
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coloredGraph-class  Class "coloredGraph"

Description

a graph to which color attributes have been attached
colorNodes

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"
- `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)

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

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(nodes(g))), attgen=pwayRendAttrs)

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 )
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
- `edgeData`: Object of class "attrData" relationship attributes
- `nodeData`: Object of class "attrData" node attributes
- `renderInfo`: Object of class "renderInfo" render info
- `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**

```r
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("BCL2", "CPNE1"), rr, "sym", mean))
```

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**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)
```
rendercMAPPathway

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)

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Examples

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