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
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)
```

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
graphcMAP

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

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(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

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

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("BCL2", "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)
**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**

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