Package 'caOmicsV'

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Type Package

Title Visualization of multi-dimentional cancer genomics data

Version 0.99.0

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Author Henry Zhang

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Description caOmicsV package provides methods to visualize multi-dimentional cancer genomics data including of patient information, gene expressions, DNA methylations, DNA copy number variations, and SNP/mutations in matrix layout or network layout.

License GPL (>=2.0)

Depends R (>= 3.1.1), igraph (>= 0.7.1), bc3net (>= 1.0.2)

biocViews Visualization, Network

R topics documented:

caOmicsV-package *caOmicsV bioMatrix and bioNetCircos Layout Plot*

Description

This package provides methods to display genomics data with two layouts:

bioMatrix layout: sample info and multiple genomics data are displayed as matrix with rows for features(phenotypes and genes, and columns for each sample. Omics data will be plotted with different layers when necessary.

bioNetCircos layout: sample info and multiple genomics data are displayed on an biological network with node for features (e.g., genes) and on each node, sample info and genomics data are plotted with circular layout.

Details

Package:	caOmicsV
Type:	Package
Version:	0.99.0
Date:	2015-03-06
License:	GPL >= 2.0

Author(s)

Henry Zhang Maintainer: Henry Zhang <hzhang@mail.nih.gov>

Examples

```
library(caOmicsV)
```

bioMatrixLegend *Plot Legend on caOmicsV bioMatrix Layout*

Description

Draw legend including of heatmap color scale and data categories. Graphic device must be initialized first.

Usage

```
bioMatrixLegend(heatmapNames=NULL, categoryNames=NULL, binaryNames=NULL,
    heatmapMin=NULL, heatmapMax=NULL, colorType="BlueWhiteRed")
```

Arguments

heatmapNames	character vector of length 2, name(s) of dataset for heatmap, e.g., "RNASeq" and/or "miRNASeq"
categoryNames	character vector of length 2 or more, names of categories, e.g., "Methylation High", "Methylation Low", ...
binaryNames	character vector of length 2 , names of binary data, e.g., "DNA Amplification" and "DNA Deletion".
heatmapMin	numeric, minimum values of heatmap plot data, default -3 (z-scores)
heatmapMax	numeric, maximum values of heatmap plot data, default 3 (z-scores)
colorType	characte veector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed" , or "YellowToRed"

Details

This function will plot legend on the bottom of matrix layout if any argument is defined. The order of legend items (from left to right) is heatmap color scale followed by colored boxes for category data legend then colored points for binary data legend.

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.biomatrix.eset)
plotBioMatrix(caOmicsV.biomatrix.eset, summaryType="text")
bioMatrixLegend(heatmapNames=c("RNASeq", "miRNASeq"),
    categoryNames=c("Methyl H", "Methyl ZL"),
    binaryNames=c("CN LOSS", "CN Gain"),
    heatmapMin=-3, heatmapMax=3, colorType="BlueWhiteRed")
```

---

bioNetCircosPlot *caOmicsV bioNetCircos Layout Plot*

Description

Plot one track of caOmics data on each node of a biological network. Supported plot types include polygon, bar, points, heatmap, and line plots.

Usage

```
bioNetCircosPlot(dataValues=NULL, plotType="polygon", outer, inner,
    plotColors=NULL, maxValue=NULL, minValue=NULL)
```

Arguments

dataValues	an numeric matrix with columns for samples and rows for genes
plotType	character vector for plot type, supporting polygon, points, and lines.
outer	non-negative numeric, outer location of a data track
inner	non-negative numeroc, inner location of a data track
plotColors	character vector specifying Colors for plot items
maxValue	numeric, the biggest value of plot data or user defined top threshold. Set to NULL to use the biggest value in dataset.
minValue	numeric, the smallest value of plot data or user defined bottom threshol. Set to NULL to use the smallest value in dataset.

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()

binaryData <- caOmicsV.bionet.eset$binaryData[[1]]
sampleColors <- c(rep("blue", ncol(binaryData)))
plotType <- "points"
inner <- 2
outer <- 3
bioNetCircosPlot(binaryData, plotType, outer, inner, sampleColors)
```

---

bioNetLegend *Draw Legend for caOmicsV bioNet Plot*

Description

The bioNet legend includes a heatmap color scale and names for each track, such as "1. Tissue: T(red), N(blue)", "2. Methylation", "3. miRNA hsa-mir-424", "4. Gene Expression", ... A graphic device and igraph object must be initialized first

Usage

```
bioNetLegend(dataNames, textCoor=NULL, heatmapCoor=NULL,
    scaleWidth, scaleHeight, heatmapMin=NULL, heatmapMax=NULL,
    colorType="BlueWhiteRed", direction="h")
```

Arguments

dataNames	character vector, names of data on each circular track
textCoor	numeric vector of length 2, x and y coordinates for legend text.
heatmapCoor	numeric vector of length 2, x and y coordinates for heatmap colour scale
scaleWidth	non-negative numeric, length (width) of heatmap color scale
scaleHeight	non-negative numeric, height of heatmap color scale
heatmapMin	numeric, minimum value of heatmap color scale
heatmapMax	numeric, maximum value of heatmap color scale
colorType	characte veector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed" , or "YellowToRed"
direction	character, direction of heatmap color scale, either 'h' for horizontal or 'v' for vertical.

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
plotBioNetCircos(caOmicsV.bionet.eset)
dataNames <- c("Tissue Type", "RNASeq", "miRNASeq", "Methylation", "CNV")
bioNetLegend(dataNames, heatmapMin=-3, heatmapMax=3)
```

---

caOmicsV.biomatrix.eset

Demo Dataset for caOmicsV bioMatrix Plot

Description

eset for demo of caOmicsV bioMatrix Plot

Usage

```
data("caOmicsV.biomatrix.eset")
```

Format

The format is: List of 8

$ sampleNames : chr [1:60] "BC.A216.Normal" "BD.A2L6.Normal"

"BD.A3EP.Normal" "DD.A113.Normal" ...

$ geneNames : chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...

$ secondGeneNames: chr [1:26] "hsa-mir-10b" "hsa-mir-139"

"hsa-mir-10b" "hsa-mir-10b" ...
$ sampleInfo : chr [1:2, 1:60] "TCGA.BC.A216.Normal"
"Solid Tissue Normal" "TCGA.BD.A2L6.Normal" "Solid Tissue Normal" ...
..- attr(*, "dimnames")=List of 2
.. ..$: chr [1:2] "sampleID" "sample_type"
.. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"
"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...
$ heatmapData :List of 2
..$: num [1:26, 1:60] 1.157 -0.623 0.667 0.976 0.868 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"
"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...
..$: num [1:26, 1:60] -1.5 1.08 -1.5 -1.5 -1.5 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"
"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...
$ categoryData :List of 1
..$: num [1:26, 1:60] 1 0 1 1 1 0 0 0 1 0 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"
"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...
$ binaryData :List of 2
..$: num [1:26, 1:60] 0 0 0 0 0 0 0 0 0 0 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"
"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...
..$: num [1:26, 1:60] 0 0 0 0 0 0 0 0 0 0 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"
"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...
$ summaryInfo :List of 1
..$: chr [1:26, 1:2] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...
.. .. ..$: chr [1:2] "GeneSymbol" "logFC"

Value

None

Examples

```
data("caOmicsV.biomatrix.eset")
```

`caOmicsV.bionet.eset` *Demo Dataset for caOmicsV bioNetCircos Plot*

Description

eset for demo of caOmicsV bionetCircos Plot

Usage

```
data("caOmicsV.bionet.eset")
```

Format

The format is: List of 8

$ sampleNames : chr [1:60] "BC.A216.Normal" "BD.A2L6.Normal"

"BD.A3EP.Normal" "DD.A113.Normal" ...

$ geneNames : chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...

$ secondGeneNames: NULL

$ sampleInfo : chr [1:2, 1:60] "TCGA.BC.A216.Normal"

"Solid Tissue Normal" "TCGA.BD.A2L6.Normal" "Solid Tissue Normal" ...

..- attr(*, "dimnames")=List of 2

.. ..$: chr [1:2] "sampleID" "sample_type"

.. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"

"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...

$ heatmapData :List of 2

..$: num [1:26, 1:60] 1.157 -0.623 0.667 0.976 0.868 ...

.. ..- attr(*, "dimnames")=List of 2

.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...

.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"

"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...

..$: num [1:26, 1:60] -1.5 1.08 -1.5 -1.5 -1.5 ...

.. ..- attr(*, "dimnames")=List of 2

.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...

.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"

"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...

$ categoryData :List of 1

..$: num [1:26, 1:60] 0.825 0.364 0.545 0.798 0.606 ...

.. ..- attr(*, "dimnames")=List of 2

.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...

.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal"

"TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...

$ binaryData :List of 1

..$: num [1:26, 1:60] 0.0266 0.0069 0.0193 0.0117 0.0081 0.0242

0.0069 0.0079 0.0348 0.01 ...

.. ..- attr(*, "dimnames")=List of 2

.. .. ..$: chr [1:26] "ECM1" "SLC26A6" "ADAMTS13" "FCN3" ...

.. .. ..$: chr [1:60] "TCGA.BC.A216.Normal" "TCGA.BD.A2L6.Normal" "TCGA.BD.A3EP.Normal" "TCGA.DD.A113.Normal" ...

$ summaryInfo : NULL

Value

None

Examples

```
data("caOmicsV.bionet.eset")
```

CA_OMICS_ENV *caOmicsV Environment*

Description

The caOmicsV Environment holds and protects all parameters and objects used for caOmicsV plot.

Usage

```
CA_OMICS_ENV
```

Format

The format is: <environment: 0x26b3e00>

Value

None

Examples

```
is.environment(CA_OMICS_ENV)
```

CA_OMICS_NAME *The Name of caOmicsV Environment*

Description

"CA_OMICS_ENV" is used for caOmicsV environment name.

Usage

```
CA_OMICS_NAME
```

Format

The format is: chr "CA_OMICS_ENV"

Value

None

Examples

```
caOmicsVEnvironment <- get(CA_OMICS_NAME, envir=globalenv())
```

CA_OMICS_NA_STRING *The Default NA String Used by caOmicsV Package*

Description

The default NA string used by caOmicV package is NULL

Usage

```
CA_OMICS_NA_STRING
```

Format

The format is: NULL

Value

None

Examples

```
CA_OMICS_NA_STRING
```

CNVDemoData *Copy Number Variation Demo Data Set*

Description

A data frame with copy number variation of 26 genes in 60 samples. Used for point plot demo on caOmicsV bioNetCircos layout, or bianry data plot on caOmicsV bioMatrix layout after transformed to bionary data.

Usage

```
data("CNVDemoData")
```

Format

A data frame with 26 observations on the following 61 variables.

`Gene_Symbol` a factor with levels ACTN1 ADAMTS13 AMIGO3 ATP2A1 BCO2 CDKN3 CFP CNBP COL15A1 CSRNP1 CXCL12 DBH DDX55 ECM1 ELOVL1 ESM1 FAM81A FCN3 KCNQ1 LEPREL1 LIFR LILRA6 LILRB5 LOC222699 LOC283050 LRRC16A LYVE1 MAEL MAN1B1 MRPS25 MT1F NIPA2 NPHP4 NR5A2 OLFML3 PLVAP PROX1 PTH1R RBL2 RCAN1 RND3 SEMA3F SLC26A6 TOMM40L TSEN34 VDAC3

`TCGA.BC.A216.Normal` a numeric vector

`TCGA.BD.A2L6.Normal` a numeric vector

`TCGA.BD.A3EP.Normal` a numeric vector

`TCGA.DD.A113.Normal` a numeric vector

`TCGA.DD.A114.Normal` a numeric vector

`TCGA.DD.A118.Normal` a numeric vector

`TCGA.DD.A119.Normal` a numeric vector

`TCGA.DD.A11A.Normal` a numeric vector

`TCGA.DD.A11B.Normal` a numeric vector

`TCGA.DD.A11C.Normal` a numeric vector

`TCGA.DD.A11D.Normal` a numeric vector

`TCGA.DD.A1EB.Normal` a numeric vector

`TCGA.DD.A1EC.Normal` a numeric vector

`TCGA.DD.A1EG.Normal` a numeric vector

`TCGA.DD.A1EH.Normal` a numeric vector

`TCGA.DD.A1EI.Normal` a numeric vector

`TCGA.DD.A1EJ.Normal` a numeric vector

`TCGA.DD.A1EL.Normal` a numeric vector

`TCGA.DD.A39V.Normal` a numeric vector

`TCGA.DD.A39W.Normal` a numeric vector

`TCGA.DD.A39X.Normal` a numeric vector

`TCGA.DD.A39Z.Normal` a numeric vector

`TCGA.DD.A3A1.Normal` a numeric vector

`TCGA.DD.A3A2.Normal` a numeric vector
`TCGA.DD.A3A3.Normal` a numeric vector
`TCGA.EP.A12J.Normal` a numeric vector
`TCGA.EP.A26S.Normal` a numeric vector
`TCGA.ES.A2HT.Normal` a numeric vector
`TCGA.FV.A23B.Normal` a numeric vector
`TCGA.FV.A2QR.Normal` a numeric vector
`TCGA.BC.A216.Tumor` a numeric vector
`TCGA.BD.A2L6.Tumor` a numeric vector
`TCGA.BD.A3EP.Tumor` a numeric vector
`TCGA.DD.A113.Tumor` a numeric vector
`TCGA.DD.A114.Tumor` a numeric vector
`TCGA.DD.A118.Tumor` a numeric vector
`TCGA.DD.A119.Tumor` a numeric vector
`TCGA.DD.A11A.Tumor` a numeric vector
`TCGA.DD.A11B.Tumor` a numeric vector
`TCGA.DD.A11C.Tumor` a numeric vector
`TCGA.DD.A11D.Tumor` a numeric vector
`TCGA.DD.A1EB.Tumor` a numeric vector
`TCGA.DD.A1EC.Tumor` a numeric vector
`TCGA.DD.A1EG.Tumor` a numeric vector
`TCGA.DD.A1EH.Tumor` a numeric vector
`TCGA.DD.A1EI.Tumor` a numeric vector
`TCGA.DD.A1EJ.Tumor` a numeric vector
`TCGA.DD.A1EL.Tumor` a numeric vector
`TCGA.DD.A39V.Tumor` a numeric vector
`TCGA.DD.A39W.Tumor` a numeric vector
`TCGA.DD.A39X.Tumor` a numeric vector
`TCGA.DD.A39Z.Tumor` a numeric vector
`TCGA.DD.A3A1.Tumor` a numeric vector
`TCGA.DD.A3A2.Tumor` a numeric vector
`TCGA.DD.A3A3.Tumor` a numeric vector
`TCGA.EP.A12J.Tumor` a numeric vector
`TCGA.EP.A26S.Tumor` a numeric vector
`TCGA.ES.A2HT.Tumor` a numeric vector
`TCGA.FV.A23B.Tumor` a numeric vector
`TCGA.FV.A2QR.Tumor` a numeric vector

Examples

```
data(CNVDemoData)
```

convertToZScores *Calculate z-scores for A Data Matrix*

Description

Calculate z-scores for data values in a data frame. The row ID must be in the first column followed by data values.

Usage

```
convertToZScores(exprData)
```

Arguments

exprData	A data frame with first column as row IDs and others are numeric values.

Value

A data frame with z scores for each row. The first column is still row IDs.

Author(s)

Henry Zhang

Examples

```
data(RNASeqDemoData)
exprZ <- convertToZScores(RNASeqDemoData)
```

---

drawBioNetNodeBackground *Draw Background for A Data Track On Nodes of caOmicsV bioNet Layout*

Description

Paint (with any color other than white) background for a circular track on each node on caOmicsV bioNetCircos layout. Graphic device and igraph object must exist.

Usage

```
drawBioNetNodeBackground(trackLocations, bgColor=gray(0.9, alpha=0.5))
```

Arguments

trackLocations	a list returned by getBioNetPlotLocations() function.
bgColor	charactor vector or R color specification for background color

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)

bioNetGraph <- getBioNetGraph()
outer <- 1.5
inner <- 1.0

nodeCenter <- as.numeric(bioNetGraph$layout[1,])
plotLocations <- getBioNetPlotLocations(nodeCenter, outer, inner)

showBioNetNodesLayout()
eraseBioNetNode()
drawBioNetNodeBackground(plotLocations)
```

---

eraseBioNetNode *Erase Background of All Nodes on caOmicsV bioNetCircos Layout*

Description

Erase all nodes on a caOmicsV bioNetCircos layout except of the edges. Graphic device and igraph object must be initialized first.

Usage

```
eraseBioNetNode()
```

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)

showBioNetNodesLayout()
eraseBioNetNode()
```

getBezierCurve *Calculate x and y Coordinates for A Quandratic Bezier Curve*

Description

Calculate x and y coordinates for a quandratic Bezier curve between two points with the equation: B(t) = (1-t) ((1-t)P0 + tP1) + t((1-t)P1 + tP2) where P0 is the start point, P2 is the end point, and P1 is the control point. P1 will be adjusted based on the distance of two points.

Usage

```
getBezierCurve(lineStart, lineEnd, totalPoints)
```

Arguments

lineStart	numeric vector, the coordinate of a point where Bezier line starts
lineEnd	numeric vector, the coordinate of a point where Bezier line ends
totalPoints	non-negative numeric, total number of points that form a Bezier line

Value

posX	x coordinates of points that form Bezier line
posY	y coordinates of points that form Bezier line

Author(s)

Henry Zhang

Examples

```
lineStart   <- c(0, 1)
lineEnd     <- c(1, 0)
totalPoints <- 2000
the_line <- getBezierCurve(lineStart, lineEnd, totalPoints)
```

getBioMatrixDataRowTop *Get y Coordinate for Top of A Row on bioMatrix Layout*

Description

Caluclate the y coordinate of a row top on bioMatrix layout. The bioMatrix layout must be initialized first

Usage

```
getBioMatrixDataRowTop(rowNumber, areaName=c("omicsData", "phenotype"))
```

Arguments

rowNumber	non-negative integer, number of the row
areaName	character vector, either "phenotype" or "omicsdata"

Value

non-negative numeric, the y coordinate of the row top.

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot()
yTop <- getBioMatrixDataRowTop(2, areaName="omicsData")
```

---

getBioMatrixParameters

Methods to Get caOmicsV BioMatrix Plot Parameters

Description

Get methods to retrieve parameters for caOmicsV bioMatrix layout plot stored in caOmicsV environment. bioMatrix layout must be initialized first.

Usage

```
getBioMatrixBasePositions()
getBioMatrixColumnPadding()
getBioMatrixDataAreaWidth()
getBioMatrixGeneLabelWidth()
getBioMatrixGeneNumber()
getBioMatrixLegendHeight()
getBioMatrixPhenotypeNumber()
getBioMatrixPlotAreaHeigth()
getBioMatrixPlotAreaWidth()
getBioMatrixRemarkWidth()
getBioMatrixRowPadding()
getBioMatrixSampleHeight()
getBioMatrixSampleIDHeight()
getBioMatrixSampleNumber()
getBioMatrixSampleWidth()
```

Value

getBioMatrixBasePositions() returns a numeric matrix of defult x and y coordinates of rectangles for each samples at a row.

getBioMatrixColumnPadding() returns a non-negative numeric value in inch for padding between two samples, default 0.025.

getBioMatrixDataAreaWidth() returns a non-negative numeric value in inch for width of data plot area, total samples times the sum of sample width and columnPadding.

getBioMatrixDataRowTop() returns y coordinate for the top of a sample row.

getBioMatrixGeneLabelWidth() returns a non-negative numeric value in inch for length of left labels (gene names).

getBioMatrixGeneNumber() returns total number of genes to be plotted.

getBioMatrixLegendHeight() returns a non-negative numeric value in inch for the height of legend area.

getBioMatrixPhenotypeNumber() returns total number of phenotypes.

getBioMatrixPlotAreaHeigth() returns a non-negative numeric value in inch height of all plot areas (sample name area, data plot area, and legend area).

getBioMatrixPlotAreaWidth() returns a non-negative numeric value in inch for width of all plot areas (left labels (gene names), data plot area, and right labels).

getBioMatrixRemarkWidth() returns a non-negative numeric value in inch for width on the right side of data plot, usually for second gene labels or summary data plot.

getBioMatrixRowPadding() returns a non-negative numeric value in inch for height of padding between two rows.

getBioMatrixSampleHeight() returns a non-negative numeric value in inch for height of a sample row.

getBioMatrixSampleIDHeight() returns a non-negative numeric value in inch for height of smaple labels (on the top of phenotype plot area).

getBioMatrixSampleNumber() returns the total number of samples in plot datasets.

getBioMatrixSampleWidth() returns a non-negative numeric value in inch for width of a rectangle (sample).

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot()

positions      <- getBioMatrixBasePositions()
colPadding     <- getBioMatrixColumnPadding()
dataAreaWidth  <- getBioMatrixDataAreaWidth()
geneNameWidth  <- getBioMatrixGeneLabelWidth()
numOfGenes     <- getBioMatrixGeneNumber()
legendHeight   <- getBioMatrixLegendHeight()
numOfFeatures  <- getBioMatrixPhenotypeNumber()
dataAreaHeight <- getBioMatrixPlotAreaHeigth()
plotAreaWidth  <- getBioMatrixPlotAreaWidth()
sumAreaWidth   <- getBioMatrixRemarkWidth()
rowPadding     <- getBioMatrixRowPadding()
sampleHeight   <- getBioMatrixSampleHeight()
sampleIDHeight <- getBioMatrixSampleIDHeight()
numOfSamples   <- getBioMatrixSampleNumber()
sampleWidth    <- getBioMatrixSampleWidth()
```

`getBioNetNodeLinkLine` *Get X and Y Coordinates for An Anrrow between Two Nodes*

Description

Caluculate x and y coordinates for an customized arrow head and tail with defined length to connect two nodes.

Usage

```
getBioNetNodeLinkLine(lineX, lineY, arrowSize=1, lineLength)
```

Arguments

`lineX`	numeric vector, x coordinates of the link line
`lineY`	numeric vector, y coordinates of the link line
`arrowSize`	non-negative numeric, scaling factor for arrow size, default 1
`lineLength`	non negative integer, the length of link line

Details

An arrow is drawn as an polygon. By default, the arrow is in inside of a circle (radius 1) without tail and it points to radian 0. The tail, if any, will be added to the left.

Value

A two dimensional numeric matrix for x and y coordinates of the arrow.

Author(s)

Henry Zhang

Examples

```
from <- c(1, 1)
to   <- c(2, 2)
lineX <- seq(from[1], to[1], 1000)
lineY <- seq(from[2], to[2], 1000)

lineLength <- sqrt((from[1]-to[1])^2 + (from[2]-to[2])^2)
positions <- getBioNetNodeLinkLine(lineX, lineY, arrowSize=1, lineLength)
```

getBioNetParameters *Methods to Get caOmicsV BioNetCircos Plot Parameters*

Description

Methods for retrieving plot parameters of caOmicsV bioNetCircos layout stored in caOmicsV environment. The bioNetCircos layout must be initialized first.

Usage

```
getBioNetBasePositions()
getBioNetGraph()
getBioNetNodePaddingScale()
getBioNetNodeParameters()
getBioNetNodePlotAreaBoundary()
getBioNetNodeRadius()
getBioNetPlotAreaWidth()
getBioNetPlotSampleWidth()
getBioNetPlotTotalSample()
```

Value

getBioNetBasePositions() returns numeric matrix containing x and y coordinates of points on a circular line with radius of 1 and degrees of text rotation on each point.

getBioNetGraph() returns an igraph object which representing the biological network built with user's inputs.

getBioNetNodePaddingScale() returns a numeric value for padding between two nodes.

getBioNetNodeParameters() returns a list containing totalSamples, sampleWidth, nodeRadius, nodePadding, plotAreaWidth, inner, and outer boundary of plot area.

getBioNetNodePlotAreaBoundary() returns a numeric vector for outer and inner boundary of a node on caOmicsV bioNetCircos layout.

getBioNetNodeRadius() returns the numeric value for radius of a node on caOmicsV bioNetCircos layout.

getBioNetPlotAreaWidth() returns the width of bioNetCircos layout plot area.

getBioNetPlotSampleWidth() returns total points a sample will need on a circular track.

getBioNetPlotTotalSample() returns the total number of samples to be plotted on each node.

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
eSet <- caOmicsV.bionet.eset
expr <- eSet$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)
```

```
positions   <- getBioNetBasePositions()
bioGraph    <- getBioNetGraph()
paddScale   <- getBioNetNodePaddingScale()
nodeParams  <- getBioNetNodeParameters()
plotBound   <- getBioNetNodePlotAreaBoundary()
nodeRadius  <- getBioNetNodeRadius()
areaWidth   <- getBioNetPlotAreaWidth()
sampleWidth <- getBioNetPlotSampleWidth()
numOfSample <- getBioNetPlotTotalSample()
```

`getBioNetPlotLocations` *Get bioNetCircos Plot Locations*

Description

Get plot loactions for a node on caOmicsC bioNetCircos layout

Usage

```
getBioNetPlotLocations(nodeCenter, outer, inner)
```

Arguments

`nodeCenter`	numeric, x and y coordinates of the node center
`outer`	non-negative numeric, outer limit of plot track relative to node center
`inner`	non-negative numeric, inner limit of plot track relative to ode center

Value

`nodeCenter`	numeric, x and y coordinates of the node center
`outPositions`	two dimensional numeric matrix for x and y coordinates of outer boundary for plot
`inPositions`	two dimensional numeric matrix for x and y coordinates of inner boundary for plot
`positionIndex`	matrix with index of x and y coordinates of base plot position for each sample

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet)

bioNetGraph <- getBioNetGraph()
outer <- 1.5
```

```
inner <- 1.0

nodeCenter <- as.numeric(bioNetGraph$layout[1,])
plotLocations <- getBioNetPlotLocations(nodeCenter, outer, inner)
```

`getBioNetSamplePlotPosition` *Calculate x and y Coordinates for Each Sample on Default Node*

Description

Calculate x and y coordinates for each sample on default node. The output will be a three column matrix representing the left, center, and right position for each sample on circumference of default node. The center positions are for points plot and others are for polygon plot. bionetCircos layout must be initialized first.

Usage

```
getBioNetSamplePlotPosition(totalSamples)
```

Arguments

`totalSamples`	non-negative integer, total numbe of samples to be plotted

Value

matrix with index of x and y coordinates for each sample

Author(s)

Henry Zhang

Examples

```
totalSamples <- 100
samplePositions <- getBioNetSamplePlotPosition(totalSamples)
```

`getCaOmicsVColors` *Get Default Colors Used by caOmicsV Plot*

Description

Display default colors used by caOmicsV package

Usage

```
getCaOmicsVColors()
```

Value

A character vector of length 8 for R colors including of "red", "blue", "black", "green", "cyan", "brown", "magenta", and "gold".

Author(s)

Henry Zhang

Examples

```
defaultColors <- getCaOmicsVColors()
```

---

getCaOmicsVPlotTypes *Get Plot Types Supported by caOmicsV Package*

Description

Retrieve the plot types supported by current version of caOmicsV package

Usage

```
getCaOmicsVPlotTypes()
```

Value

Character vector including "polygon", "bar", "points", "heatmap", "line", "category", "binary"

Author(s)

Henry Zhang

Examples

```
plotType <- getCaOmicsVPlotTypes()
```

---

getDefaultNaStrings *Default NA String*

Description

Get the default NS strings used by caOmicsV package

Usage

```
getDefaultNaStrings()
```

Value

Returns na strings used by caOmicsV package. Default is "NULL".

Author(s)

Henry Zhang

Examples

```
naStr <- getDefaultNaStrings()
```

getESet *Prepare Data Set for caOmicsV Plot*

Description

This function will validate each dataset then convert them to matrix and wrap all of them in one list object.

Usage

```
getESet(sampleNames, geneNames, sampleData, heatmapData=list(),
    categoryData=list(), binaryData=list(), summaryData=list(),
    secondGeneNames=NULL)
```

Arguments

sampleNames	character vector, sample names, must be same or exist in every data set.
geneNames	character vector, gene names, must be same or exist in every data set.
sampleData	data frame with rows for samples and columns for features.
heatmapData	list of data frame(s) for heatmap plot. The first column of each data frame is row names and others are numeric values. The list could be empty, or having one or more data frame in a list object. Heatmap data should be log2 values or z-scores.
categoryData	list of data frame(s). The first column of each data frame is row names and others are numeric values. The list could be empty, or having one or more data frame in a list object
binaryData	list of data frame(s). The first column of each data frame is row names and others are binary values. The listcould be none, or one or more data frame in a list object
summaryData	list of data frames with summary information for samples (columns) or for genes (rows). The first column is for ID following by one or more columns of summary data.
secondGeneNames	character vector, gene names that will be plot on right side of biomatrix plot layout

Value

sampleNames	character verctor, sample names
geneNames	character verctor, gene names
secondGeneNames	character verctor, for example, miRNA names
sampleInfo	a data frame, sample information such as Tumor/Normal, age, diagnosis
heatmapData	list of data matrix(s), e.g., RNASeq read counts at gene level
categoryData	list of data matrix(s), such as SNP in a gene, homozygous, or heterozygous, or wildtype
binaryData	list of data matrix(s), e.g., mutation status of the gene
summaryInfo	list of data matrix(s), such as percentage of highly expressed miRNA in all samples

Author(s)

Henry Zhang

Examples

```
data(sampleDemoData)
data(RNA2miRNA)
data(RNASeqDemoData)
data(miRNADemoData)
data(methylDemoData)
data(CNVDemoData)

sampleNames <- as.character(sampleDemoData[,1])
geneNames <- as.character(RNA2miRNA[,1])
secondGeneNames <- as.character(RNA2miRNA[,2])

normals <- grep("Normal", colnames(RNASeqDemoData))
tumors  <- grep("Tumor", colnames(RNASeqDemoData))
tumorExpr <- RNASeqDemoData[, tumors]
normalExpr <- RNASeqDemoData[, normals]
meanLog2Fold <- log2(rowMeans(tumorExpr/normalExpr))
summaryData <- data.frame(geneNames, meanLog2Fold)

eSet <- getESet(sampleNames, geneNames, sampleDemoData,
                heatmapData=list(RNASeqDemoData, miRNADemoData),
                categoryData=list(methylDemoData),
                binaryData=list(CNVDemoData),
                summaryData=list(summaryData),
                secondGeneNames)
```

---

getHeatmapColorScales *Get caOmicsV Heatmap Color Scales*

Description

Generate a color map for heatmap color scales

Usage

```
getHeatmapColorScales(colorType)
```

Arguments

colorType	character vector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed", "YellowToRed", and "Black".

Value

An RGB color matrix with demension of 255 by 2.

Author(s)

Henry Zhang

Examples

```
colorMap <- getHeatmapColorScales("BlueWhiteRed")
```

---

getPlotOmicsData *Extract Subset from A Data Frame*

Description

Extract a subset from the imput data for a set of samples and genes

Usage

```
getPlotOmicsData(omicsData, sampleNames, geneNames)
```

Arguments

omicsData	a data frame with all samples and all genes
sampleNames	character vector, names of samples to be extracted from dataset.
geneNames	Character vector, names of genes to be extracted from dataset.

Value

A data frame with subset of input data

Author(s)

Henry Zhang

Examples

```
data(RNASeq)
data(RNASeqDemoData)
geneNames  <- as.character(RNASeqDemoData[,1])
sampleNames <- colnames(RNASeqDemoData)[-1]
plotData <- getPlotOmicsData(RNASeq, sampleNames, geneNames)
```

---

getPlotSampleData *Extract Subset of Sample Information*

Description

Extract required rows and columns from a sample dataset

Usage

```
getPlotSampleData(sampleData, sampleNames)
```

Arguments

sampleData	Data frame with rows for samples and columns for features. Column 1 must be sample names.
sampleNames	character vector, names of samples to select.

Value

A data frame with subset of sample data and with the row order same as sampleNames.

Author(s)

Henry Zhang

Examples

```
data(sampleDemoData)
sampleNames <- as.character(sampleDemoData[10:40,1])
sampleInfo <- getPlotSampleData(sampleDemoData, sampleNames)
```

---

getPlotSummaryData *Extract Summary Subset for Plotting*

Description

Extract required rows and columns from a summary data set.

Usage

```
getPlotSummaryData(summaryData, sampleNames=NULL, geneNames=NULL)
```

Arguments

summaryData	a data frame with summary data for each gene (rows are for genes and columns are summary values) or for each sample (rows are summary values and columns are sample names)
sampleNames	character vector, names of samples/columns to be extracted. Set to NULL when summary data is for genes.
geneNames	character vector, names of genes to be extracted. Set to NULL when summary data is for samples

Value

A data frame with subset of input data and with the same orders as geneNames and sampleNames.

Author(s)

Henry Zhang

Examples

```
data(RNASeqDemoData)
exprValue <- as.matrix(RNASeqDemoData[, 2:ncol(RNASeqDemoData)])

summaryData <- data.frame(as.character(RNASeqDemoData[,1]),
    rowMeans(exprValue), log2(rowMeans(exprValue)))
geneSymbols <- c("ECM1", "SLC26A6", "ADAMTS13", "FCN3", "CFP")
sumByGene <- getPlotSummaryData(summaryData, geneNames=geneSymbols)

summaryData <- rbind(colMeans(exprValue),  log2(colMeans(exprValue)))
summaryData <- data.frame(c("sampleMean", "log2mean"), summaryData)
colnames(summaryData) <- colnames(exprValue)
sampleID <- colnames(exprValue)[c(2:21, 32:41)]
sumBySample <- getPlotSummaryData(summaryData, sampleID)
```

---

getRelatedPlotData *Extract subset from A Data Frame Based on Relational Information*

Description

Extract a subset of plot data based on relational information, e.g., expression of miRNA or DNA copy number variationa that are corelated to differentially expressed genes

Usage

```
getRelatedPlotData(omicsData, linkData, geneNames)
```

Arguments

omicsData	a data frame, the dataset from which subset is extracted
linkData	a data frame, usually gene names and their related items. The first column must be the items to which the second item is linked to.
geneNames	character vector, subset of gene names for subset.

Value

A data frame with subset of the first input data.

Author(s)

Henry Zhang

Examples

```
data(miRNA)
data(RNA2miRNA)
geneNames <- as.character(RNA2miRNA[,1])
miRNAexpr <- getRelatedPlotData(miRNA, RNA2miRNA, geneNames)
```

`initializeBioMatrixPlot` *Set Up Parameters for caOmicsV bioMatrix Plot Layout*

Description

Initialize parameters for caOmicsV bioMatrix layout to set up plot area size and item sizes.

Usage

```
initializeBioMatrixPlot(numOfGenes=100, numOfSamples=100,
    numOfPhenotypes=1, sampleHeight=0.4, sampleWidth=0.1,
    columnPadding=0.025, rowPadding=0.1, geneNameWidth=1,
    remarkWidth=1, sampleNameHeight=1, legendHeight=1)
```

Arguments

`numOfGenes`	non-negative numeric, total number of genes to be plotted
`numOfSamples`	non-negative numeric, total number of samples to be plotted
`numOfPhenotypes`	non-negative numeric, total number of phenotypes to be plotted
`sampleHeight`	non-negative numeric, height of rectangle area in inch for a sample plot
`sampleWidth`	non-negative numeric, width of rectangle area in inch for a sample plot
`columnPadding`	non-negative numeric, width of padding in inch between two rectangles (samples)
`rowPadding`	non-negative numeric, height of padding in inch between two rows (genes)
`geneNameWidth`	non-negative numeric, width of plot area in inch for gene name plot
`remarkWidth`	non-negative numeric, width of plot area in inch for second set of gene names and summary data.
`sampleNameHeight`	non-negative numeric, height of plot area in inch for sample names (sample name are plotted vertically).
`legendHeight`	non-negative numeric, height of plot area in inch for legend.

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=100, numOfSamples=100,
    numOfPhenotypes=1, sampleHeight=0.4, sampleWidth=0.1,
    columnPadding=0.025, rowPadding=0.1, geneNameWidth=1,
    remarkWidth=1, sampleNameHeight=1, legendHeight=1)
```

initializeBioNetCircos *Initialize caOmicsV bioNetCircos Layout Plot*

Description

Set up parameters for layout of caOmicsV bioNetCircos plot including total number of samples, default width of a sample on a circos track , node radius, padding width between two nodes, plot area of each node, default x and y coordinates of points on a circle with radius of 1, and node layout.

Usage

```
initializeBioNetCircos(bioNet, totalSamples=100, sampleWidth=100, nodeRadius=1,
    nodePadding=1, plotAreaWidth=1, layout=layout.fruchterman.reingold(bioNet))
```

Arguments

bioNet	an igraph object
totalSamples	non-negative numeric, total number of samples to be plotted
sampleWidth	non-negative numeric, total number of points to represent a sample on a circular track.
nodeRadius	non-negative numeric, radius of a node on biological network.
nodePadding	non-negative numeric, padding width between two node on biological network.
plotAreaWidth	non-negative numeric, outside boundary of plot area of a node, relative to node radius, default 1 (same as nodeRadius)
layout	two dimentioanl numeric matrix, node layout of the igraph returned by igraph layout method

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=100, sampleWidth=100, nodeRadius=1,
    nodePadding=1, plotAreaWidth=1, layout=layout.fruchterman.reingold(bioNet))
```

`labelBioNetNodeNames` *Label Names for Each Node on Network Graph*

Description

Plot name for one or more nodes on an igraph network. igraph object and graphic device must be initialized first.

Usage

```
labelBioNetNodeNames(nodeList=NULL, labelColor="black",
    labelLocation=c("bottom", "left", "top", "right"),
    labelOffset=0.5)
```

Arguments

`nodeList`	non-negatice integer, index of node(s) on a bioNet layout
`labelColor`	character vector, colord for text (labels)
`labelLocation`	character vector, location relative to node center, either "bottom", "left", "top", or "right"
`labelOffset`	non-negative numeric, distance from node outside boundary

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)

showBioNetNodesLayout()
labelBioNetNodeNames(nodeList=c(1, 4, 7), labelColor="black",
    labelLocation="bottom")
```

linkBioNetNodes *Draw A Customized Arrow between Two Nodes*

Description

Plot a customized arrow between two nodes to replace the edge. bioNetCorcos layout must be initialized first.

Usage

```
linkBioNetNodes(fromNode, toNode, lineColor = "black", arrowSize = 1)
```

Arguments

fromNode	non negative integer, the start node to be linked
toNode	non negative integer, the end node to be linked
lineColor	character vector, color of the arrow
arrowSize	non-negative numeric, scaling factor for arrow size, default 1

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]

bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)
showBioNetNodesLayout()

linkBioNetNodes(fromNode=2, toNode=5, lineColor="red", arrowSize=1)
```

linkBioNetSamples *Link Two samples Inside a Node with Quandratic Bezier Curve*

Description

Draw a quandratic Bezier curve line between two samples inside of a node. bioNetCorcos layout must be initialized first.

Usage

```
linkBioNetSamples(nodeIndex, fromSample, toSample, outer, plotColors)
```

Arguments

nodeIndex	non-negative integer, the node on which link line is drawn
fromSample	non-negative integer, the first sample to be linked
toSample	non-negative integer, the second sample to be linked
outer	non-negative numeric, the start and end of link line relative to node center
plotColors	character vector, color for the link line (ribbon)

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]

bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)
showBioNetNodesLayout()

linkBioNetSamples(nodeIndex=2, fromSample=10, toSample=20, outer=0.9,
    plotColors="red")
```

---

methylDemoData *Methylation Demo Data Set*

Description

A data frame with bea values of 26 genes in 60 samples. Used for bar plot on caOmicsV bioNet-Circos layout demo, and for categoray plot on caOmicsV bioNet layout demo after transforming to category data.

Usage

```
data("methylDemoData")
```

Format

A data frame with 26 observations on the following 61 variables.

Gene_Symbol a factor with levels ACTN1 ADAMTS13 AMIGO3 ATP2A1 BCO2 CDKN3 CFP CNBP COL15A1 CSRNP1 CXCL12 DBH DDX55 ECM1 ELOVL1 ESM1 FAM81A FCN3 KCNQ1 LEPREL1 LIFR LILRA6 LILRB5 LOC222699 LOC283050 LRRC16A LYVE1 MAEL MAN1B1 MRPS25 MT1F NIPA2 NPHP4 NR5A2 OLFML3 PLVAP PROX1 PTH1R RBL2 RCAN1 RND3 SEMA3F SLC26A6 TOMM40L TSEN34 VDAC3

TCGA.BC.A216.Normal a numeric vector

TCGA.BD.A2L6.Normal a numeric vector

TCGA.BD.A3EP.Normal a numeric vector
TCGA.DD.A113.Normal a numeric vector
TCGA.DD.A114.Normal a numeric vector
TCGA.DD.A118.Normal a numeric vector
TCGA.DD.A119.Normal a numeric vector
TCGA.DD.A11A.Normal a numeric vector
TCGA.DD.A11B.Normal a numeric vector
TCGA.DD.A11C.Normal a numeric vector
TCGA.DD.A11D.Normal a numeric vector
TCGA.DD.A1EB.Normal a numeric vector
TCGA.DD.A1EC.Normal a numeric vector
TCGA.DD.A1EG.Normal a numeric vector
TCGA.DD.A1EH.Normal a numeric vector
TCGA.DD.A1EI.Normal a numeric vector
TCGA.DD.A1EJ.Normal a numeric vector
TCGA.DD.A1EL.Normal a numeric vector
TCGA.DD.A39V.Normal a numeric vector
TCGA.DD.A39W.Normal a numeric vector
TCGA.DD.A39X.Normal a numeric vector
TCGA.DD.A39Z.Normal a numeric vector
TCGA.DD.A3A1.Normal a numeric vector
TCGA.DD.A3A2.Normal a numeric vector
TCGA.DD.A3A3.Normal a numeric vector
TCGA.EP.A12J.Normal a numeric vector
TCGA.EP.A26S.Normal a numeric vector
TCGA.ES.A2HT.Normal a numeric vector
TCGA.FV.A23B.Normal a numeric vector
TCGA.FV.A2QR.Normal a numeric vector
TCGA.BC.A216.Tumor a numeric vector
TCGA.BD.A2L6.Tumor a numeric vector
TCGA.BD.A3EP.Tumor a numeric vector
TCGA.DD.A113.Tumor a numeric vector
TCGA.DD.A114.Tumor a numeric vector
TCGA.DD.A118.Tumor a numeric vector
TCGA.DD.A119.Tumor a numeric vector
TCGA.DD.A11A.Tumor a numeric vector
TCGA.DD.A11B.Tumor a numeric vector
TCGA.DD.A11C.Tumor a numeric vector
TCGA.DD.A11D.Tumor a numeric vector
TCGA.DD.A1EB.Tumor a numeric vector

TCGA.DD.A1EC.Tumor a numeric vector

TCGA.DD.A1EG.Tumor a numeric vector

TCGA.DD.A1EH.Tumor a numeric vector

TCGA.DD.A1EI.Tumor a numeric vector

TCGA.DD.A1EJ.Tumor a numeric vector

TCGA.DD.A1EL.Tumor a numeric vector

TCGA.DD.A39V.Tumor a numeric vector

TCGA.DD.A39W.Tumor a numeric vector

TCGA.DD.A39X.Tumor a numeric vector

TCGA.DD.A39Z.Tumor a numeric vector

TCGA.DD.A3A1.Tumor a numeric vector

TCGA.DD.A3A2.Tumor a numeric vector

TCGA.DD.A3A3.Tumor a numeric vector

TCGA.EP.A12J.Tumor a numeric vector

TCGA.EP.A26S.Tumor a numeric vector

TCGA.ES.A2HT.Tumor a numeric vector

TCGA.FV.A23B.Tumor a numeric vector

TCGA.FV.A2QR.Tumor a numeric vector

Examples

```
data(methylDemoData)
```

---

miRNA *Selected miRNA Read Counts*

Description

A data frame with read counts of 14 miRNA in 86 samples.

Usage

```
data("miRNA")
```

Format

A data frame with 14 observations on the following 86 variables.

miRNA_ID a factor with levels hsa.mir.101.1 hsa.mir.101.2 hsa.mir.10b hsa.mir.1180 hsa.mir.125b.2 hsa.mir.139 hsa.mir.142 hsa.mir.151 hsa.mir.183 hsa.mir.22 hsa.mir.25 hsa.mir.424 hsa.mir.450b hsa.mir.93

TCGA.2Y.A9H1.Tumor a numeric vector

TCGA.BC.4073.Tumor a numeric vector

TCGA.BC.A10W.Tumor a numeric vector

TCGA.BC.A112.Tumor a numeric vector

TCGA.BC.A216.Tumor a numeric vector

TCGA.BC.A216.Normal a numeric vector

TCGA.BD.A2L6.Tumor a numeric vector

TCGA.BD.A2L6.Normal a numeric vector

TCGA.BD.A3EP.Tumor a numeric vector

TCGA.BD.A3EP.Normal a numeric vector

TCGA.BW.A5NP.Tumor a numeric vector

TCGA.CC.A1HT.Tumor a numeric vector

TCGA.CC.A7IG.Tumor a numeric vector

TCGA.CC.A9FS.Tumor a numeric vector

TCGA.DD.A113.Tumor a numeric vector

TCGA.DD.A113.Normal a numeric vector

TCGA.DD.A114.Tumor a numeric vector

TCGA.DD.A114.Normal a numeric vector

TCGA.DD.A118.Tumor a numeric vector

TCGA.DD.A118.Normal a numeric vector

TCGA.DD.A119.Tumor a numeric vector

TCGA.DD.A119.Normal a numeric vector

TCGA.DD.A11A.Tumor a numeric vector

TCGA.DD.A11A.Normal a numeric vector

TCGA.DD.A11B.Tumor a numeric vector

TCGA.DD.A11B.Normal a numeric vector

TCGA.DD.A11C.Tumor a numeric vector

TCGA.DD.A11C.Normal a numeric vector

TCGA.DD.A11D.Tumor a numeric vector

TCGA.DD.A11D.Normal a numeric vector

TCGA.DD.A1EB.Tumor a numeric vector

TCGA.DD.A1EB.Normal a numeric vector

TCGA.DD.A1EC.Tumor a numeric vector

TCGA.DD.A1EC.Normal a numeric vector

TCGA.DD.A1EE.Normal a numeric vector

TCGA.DD.A1EG.Tumor a numeric vector

TCGA.DD.A1EG.Normal a numeric vector

TCGA.DD.A1EH.Tumor a numeric vector

TCGA.DD.A1EH.Normal a numeric vector

TCGA.DD.A1EI.Tumor a numeric vector

TCGA.DD.A1EI.Normal a numeric vector

TCGA.DD.A1EJ.Tumor a numeric vector

TCGA.DD.A1EJ.Normal a numeric vector

TCGA.DD.A1EL.Tumor a numeric vector

TCGA.DD.A1EL.Normal a numeric vector
TCGA.DD.A39V.Tumor a numeric vector
TCGA.DD.A39V.Normal a numeric vector
TCGA.DD.A39W.Tumor a numeric vector
TCGA.DD.A39W.Normal a numeric vector
TCGA.DD.A39X.Tumor a numeric vector
TCGA.DD.A39X.Normal a numeric vector
TCGA.DD.A39Z.Tumor a numeric vector
TCGA.DD.A39Z.Normal a numeric vector
TCGA.DD.A3A1.Tumor a numeric vector
TCGA.DD.A3A1.Normal a numeric vector
TCGA.DD.A3A2.Tumor a numeric vector
TCGA.DD.A3A2.Normal a numeric vector
TCGA.DD.A3A3.Tumor a numeric vector
TCGA.DD.A3A3.Normal a numeric vector
TCGA.DD.A3A6.Normal a numeric vector
TCGA.DD.A4NG.Tumor a numeric vector
TCGA.DD.A4NV.Tumor a numeric vector
TCGA.ED.A4XI.Tumor a numeric vector
TCGA.ED.A82E.Tumor a numeric vector
TCGA.EP.A12J.Tumor a numeric vector
TCGA.EP.A12J.Normal a numeric vector
TCGA.EP.A26S.Tumor a numeric vector
TCGA.EP.A26S.Normal a numeric vector
TCGA.ES.A2HS.Tumor a numeric vector
TCGA.ES.A2HT.Tumor a numeric vector
TCGA.ES.A2HT.Normal a numeric vector
TCGA.FV.A23B.Tumor a numeric vector
TCGA.FV.A23B.Normal a numeric vector
TCGA.FV.A2QR.Tumor a numeric vector
TCGA.FV.A2QR.Normal a numeric vector
TCGA.FV.A4ZQ.Tumor a numeric vector
TCGA.G3.A3CH.Tumor a numeric vector
TCGA.G3.A6UC.Tumor a numeric vector
TCGA.G3.AAV3.Tumor a numeric vector
TCGA.K7.A5RF.Tumor a numeric vector
TCGA.LG.A9QD.Tumor a numeric vector
TCGA.O8.A75V.Tumor a numeric vector
TCGA.RC.A7SH.Tumor a numeric vector
TCGA.UB.AA0U.Tumor a numeric vector
TCGA.ZP.A9CZ.Tumor a numeric vector

Examples

```
data(miRNA)
```

`miRNADemoData` *miRNASeq Demo Data Set*

Description

A data frame with miRNA read counts for 26 genes in 60 samples. Used for heatmap plot demo on both caOmicsV bioNetCircos layout and bioMatrix layout after transformed to log2 values.

Usage

```
data("miRNADemoData")
```

Format

A data frame with 26 observations on the following 61 variables.

`miRNA_ID` a character vector

`TCGA.BC.A216.Normal` a numeric vector

`TCGA.BD.A2L6.Normal` a numeric vector

`TCGA.BD.A3EP.Normal` a numeric vector

`TCGA.DD.A113.Normal` a numeric vector

`TCGA.DD.A114.Normal` a numeric vector

`TCGA.DD.A118.Normal` a numeric vector

`TCGA.DD.A119.Normal` a numeric vector

`TCGA.DD.A11A.Normal` a numeric vector

`TCGA.DD.A11B.Normal` a numeric vector

`TCGA.DD.A11C.Normal` a numeric vector

`TCGA.DD.A11D.Normal` a numeric vector

`TCGA.DD.A1EB.Normal` a numeric vector

`TCGA.DD.A1EC.Normal` a numeric vector

`TCGA.DD.A1EG.Normal` a numeric vector

`TCGA.DD.A1EH.Normal` a numeric vector

`TCGA.DD.A1EI.Normal` a numeric vector

`TCGA.DD.A1EJ.Normal` a numeric vector

`TCGA.DD.A1EL.Normal` a numeric vector

`TCGA.DD.A39V.Normal` a numeric vector

`TCGA.DD.A39W.Normal` a numeric vector

`TCGA.DD.A39X.Normal` a numeric vector

`TCGA.DD.A39Z.Normal` a numeric vector

`TCGA.DD.A3A1.Normal` a numeric vector

`TCGA.DD.A3A2.Normal` a numeric vector

`TCGA.DD.A3A3.Normal` a numeric vector

`TCGA.EP.A12J.Normal` a numeric vector

TCGA.EP.A26S.Normal a numeric vector

TCGA.ES.A2HT.Normal a numeric vector

TCGA.FV.A23B.Normal a numeric vector

TCGA.FV.A2QR.Normal a numeric vector

TCGA.BC.A216.Tumor a numeric vector

TCGA.BD.A2L6.Tumor a numeric vector

TCGA.BD.A3EP.Tumor a numeric vector

TCGA.DD.A113.Tumor a numeric vector

TCGA.DD.A114.Tumor a numeric vector

TCGA.DD.A118.Tumor a numeric vector

TCGA.DD.A119.Tumor a numeric vector

TCGA.DD.A11A.Tumor a numeric vector

TCGA.DD.A11B.Tumor a numeric vector

TCGA.DD.A11C.Tumor a numeric vector

TCGA.DD.A11D.Tumor a numeric vector

TCGA.DD.A1EB.Tumor a numeric vector

TCGA.DD.A1EC.Tumor a numeric vector

TCGA.DD.A1EG.Tumor a numeric vector

TCGA.DD.A1EH.Tumor a numeric vector

TCGA.DD.A1EI.Tumor a numeric vector

TCGA.DD.A1EJ.Tumor a numeric vector

TCGA.DD.A1EL.Tumor a numeric vector

TCGA.DD.A39V.Tumor a numeric vector

TCGA.DD.A39W.Tumor a numeric vector

TCGA.DD.A39X.Tumor a numeric vector

TCGA.DD.A39Z.Tumor a numeric vector

TCGA.DD.A3A1.Tumor a numeric vector

TCGA.DD.A3A2.Tumor a numeric vector

TCGA.DD.A3A3.Tumor a numeric vector

TCGA.EP.A12J.Tumor a numeric vector

TCGA.EP.A26S.Tumor a numeric vector

TCGA.ES.A2HT.Tumor a numeric vector

TCGA.FV.A23B.Tumor a numeric vector

TCGA.FV.A2QR.Tumor a numeric vector

Examples

```
data(miRNADemoData)
```

plotBioMatrix *Default Plot Method for caOmicsV bioMatrix Layout Plot*

Description

A sample way to plot sample information and genomic data with default settings.

Usage

```
plotBioMatrix(eSet, summaryType=c("text", "bar"), summarybyRow=TRUE,
    heatmapMax=NULL, heatmapMin=NULL, heatmapColor="BlueWhiteRed")
```

Arguments

eSet	an object, returned from method of getESet(), with all plot data
summaryType	character vector, either "text" or "bar", for plot type of summary data
summarybyRow	logic, if the summary data is for each row or for each column
heatmapMax	numeric, maximum value for heatmap plot, set to NULL to use the maximum value in input data.
heatmapMin	numeric, minimum value for heatmap plot, set to NULL to use the minimum value in input data.
heatmapColor	character vector,one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed" , or "YellowToRed"

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.biomatrix.eset)
plotBioMatrix(caOmicsV.biomatrix.eset, summaryType="text", summarybyRow=TRUE,
    heatmapMax=NULL, heatmapMin=NULL, heatmapColor="BlueWhiteRed")
```

plotBioMatrixBars *Bar Plot on caOmicsV bioMatrix Layout*

Description

Bar plot method for caOmicsV bioMatrix layout with non-negative numeric matrix or vector with values in range of 0 ~ 1. bioMatrix layout and graphic device must be initialized first. must be initialized first.

Usage

```
plotBioMatrixBars(barData, barColor="red", areaName="omicsData", byRow=TRUE,
    skipPlotRow=0, skipPlotColumns=0)
```

Arguments

barData	non-negative numeric matrix or vector with values in range of 0 ~ 1
barColor	character vector for color name or R color specification
areaName	character vector, name of plot area, currentlt use "omicsData" only
byRow	logic, whether plot bars for each row or not
skipPlotRow	non-negative integer, how many row(s) to be skipped from first row
skipPlotColumns	non-negative integer, how many row(s) to be skipped from first column

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout("Gene", paste("Sample", 1:50),  "Diagnosis")

barData <- matrix(c(rep(0.25, 15), rep(0.75, 20), rep(0.5, 15)), byrow=TRUE)
plotBioMatrixBars(barData, barColor="red")
```

---

plotBioMatrixBinaryData

Binary Data Plot on caOmicsV bioMatrix Layout

Description

Plot binary data as points in the inside of each rectangle(sample). This function plot all rows on omics data area and only the positive samples will be shown with colored points. For one row plot, pass data as vector and supply correct skipPlotRow parameter to define where to plot. bioMatrix layout and graphic device must be initialized first.

Usage

```
plotBioMatrixBinaryData(binaryData, areaName="omicsData", scatterType=19,
    scatterSize=1, totalSubRow=1, subRowIndex=1, sampleColor="black",
    skipPlotRow=0)
```

Arguments

binaryData	vector or matrix with values of 0 and 1 only
areaName	character vector, either "omicsData" or "phenotype"
scatterType	non-negative integer, same as pch, default 19
scatterSize	non-negative numric, same as cex
totalSubRow	non-negative integer, how many sub-rows in a sample area
subRowIndex	non-negative integer, which subrow will be plotted
sampleColor	character vector for color name(s) or R color specification
skipPlotRow	non-negative integer, total rows on plot area that should be skipped, default 0

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout("Gene", paste("Sample", 1:50),  "Diagnosis")

binaryData <- matrix(c(rep(1, 15), rep(0, 20), rep(1, 15)), nrow=1)
plotBioMatrixBinaryData(binaryData, scatterType=16)
```

---

plotBioMatrixCategoryData

Plot Category Data on caOmicsV bioMatrix Layout

Description

Draw rectangle outline for one or more row(s) of samples to represent categorical values. This function highlights all samples on each row. bioMatrix layout and graphic device must be initialized first.

Usage

```
plotBioMatrixCategoryData(categoryData, areaName=c("omicsData", "phenotype"),
    sampleColors=palette(), lineWidth=1, skipPlotRow=0)
```

Arguments

categoryData	vector or matrix of categorical values, such as 'High', 'low', and 'No'
areaName	character vector, either "omicsdata" or "phenotype"
sampleColors	character vector for color names or vector of R color specification
lineWidth	non-negatice integer, graphic parameter for lwd (line width), default 1
skipPlotRow	non-negative integer, total rows on plot area that should be skipped when only one row to plot, default 0.

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout("Gene", paste("Sample", 1:50),  "Diagnosis")

categoryData <- matrix(c(rep(1, 15), rep(0, 20), rep(1, 15)), nrow=1)
plotBioMatrixCategoryData(categoryData, areaName="omicsData")
```

---

plotBioMatrixHeatmap *Heatmap Plot on caOmicsV bioMatrix Layout*

Description

Headmap plot method for caOmicsV bioMatrix layout. This function will plot all rows of the input data. bioMatrix layout and graphic device must be initialized first.

Usage

```
plotBioMatrixHeatmap(exprData, topAdjust=0, bottomAdjust=0, maxValue=NULL,
    minValue=NULL, heatmapColor="BlueWhiteRed", skipPlotRow=0)
```

Arguments

exprData	numeric matrix (log2 values) with row names
topAdjust	non-negative numeric, height of top y coordinate should be reduced to show different layers, default 0
bottomAdjust	non-negative numeric, height of bottom y coordinate should be reduced for a small rectangle, default 0
maxValue	numeric, value for highest color in heatmap, set to NULL to use the maximum value in expression dataset
minValue	numeric, value for lowest color in heatmap, set to NULL to use the minimum value in expression dataset
heatmapColor	character vector,one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed" , or "YellowToRed"
skipPlotRow	non-negative integer, total rows on plot area that should be skipped, default 0

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout("Gene", paste("Sample", 1:50),  "Diagnosis")

data(caOmicsV.biomatrix.eset)
exprData <- caOmicsV.biomatrix.eset$heatmapData[[1]]
exprData <- matrix(exprData[1, 1:50], nrow=1)
plotBioMatrixHeatmap(exprData, maxValue=3, minValue=-3)
```

---

plotBioMatrixRowNames *Plot Row Names on caOmicsV bioMatrix Layout*

Description

Plot row names on the left or right side of biomatrix plot area. Penotype names, gene names, and remark notes are all plotted with this function. bioMatrix layout an dgraphic device must be initialized first.

Usage

```
plotBioMatrixRowNames(geneNames, areaName, colors, side="left",
    skipPlotRows=0, skipPlotColumns=0)
```

Arguments

geneNames	character vector, row names to be plotted
areaName	character vector, either "omicsData" or "phenotype"
colors	character vector of color names or R color specification
side	character vector, either "left" or "right"
skipPlotRows	non-negative integer, total rows on plot area that should be skipped from the first row, default 0
skipPlotColumns	non-negative integer, columns (sampleWidth) will be skipped when plotting items on remark area

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=20, numOfSamples=50)

geneNames  <- paste0("gene_", 1:20)
miRNANames <- paste0("miRNA_", 1:20)

showBioMatrixPlotLayout(geneNames, paste("Sample", 1:50),  "Diagnosis")
plotBioMatrixRowNames(miRNANames, areaName="omicsData", colors="blue",
    side="right")
```

`plotBioMatrixSampleData` *Plot Sample Data on caOmicsV bioMatrix Layout*

Description

Plot colored polygons on phenotyp area of caOmicsV bioMatrix layout to show sample information such as diagnosis, tissue type, ... bioMatrix layout and graphic device must be initialized first.

Usage

```
plotBioMatrixSampleData(rowNumber, areaName, fillColor=NA, borderColor=NA,
    topAdjust=0, bottomAdjust=0)
```

Arguments

`rowNumber`	non-negative integer, number of the row where the data to be ploted
`areaName`	chracter vector, either "phenotype" or "omicsdata"
`fillColor`	chracter vector of color names or vector of R color specification
`borderColor`	chracter vector or a R colors specification for boarder color
`topAdjust`	non-negative numeric, height that will be reduced from top
`bottomAdjust`	non-negative numeric, height that will be reduced from bottom

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout("Gene", paste("Sample", 1:50),  "Diagnosis")

sampleColor <- c(rep("blue", 25), rep("red", 25))
plotBioMatrixSampleData(rowNumber=1, sampleColor, areaName="phenotype")
```

plotBioMatrixSampleNames *Label Sample Names on the Top of caOmicsV bioMatrix Layout*

Description

Text plot on the top of phenotyp area to show sample names. bioMatrix layout and graphic device must be initialized first.

Usage

```
plotBioMatrixSampleNames(sampleNames, sampleColors)
```

Arguments

sampleNames	character vector, sample names to be plotted
sampleColors	character vector or R color name(s) for text color(s)

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
setBioMatrixPlotArea()

sampleNames <- paste("Sample", 1:50)
sampleColors <- c(rep("red", 30), rep("blue", 30))

plotBioMatrixSampleData(1, areaName = "phenotype",
            fillColor = sampleColors)
plotBioMatrixSampleNames(sampleNames, sampleColors)
```

plotBioNetBars *Bar Plot on caOmicsV bioNetCircos Layout*

Description

Bar plot method for caOmicsV bioNetCircos layout. This will plot one track of bars for every node. bioNetCircos layout and graphic device must be initialized first.

Usage

```
plotBioNetBars(dataValues, outer, inner, plotColors)
```

Arguments

dataValues	numeric matrix with range of 0 ~ 1 for bar height. total rows of the matrix must be same as the number of nodes and row names must be same as the vertex names in bioNetGraph
outer	non-negative numeric, the outside boundary of plot area from node center
inner	non-negative numeric, the inside boundary of plot area from node center
plotColors	character vector or vector of R color specificaiton, color names for each sample, pre-generated to control sample colors

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()

methyl <- caOmicsV.bionet.eset$categoryData[[1]]
sampleColors <- c(rep("red", 20), rep("blue", 20), rep("cyan", 20))
plotBioNetBars(methyl, outer=1.6, inner=1.5, plotColors=sampleColors)
```

---

plotBioNetCircos *Default Plot Method for caOmicsV bioNetCircos Layout*

Description

A sample way to plot sample information and genomic data with default settings. This method is mainly for demo purpose. In most cases, users need make changes based on this display, specifically, the igraph layout.

Usage

```
plotBioNetCircos(eSet, graph=NULL, heatmapMax=NULL, heatmapMin=NULL,
    heatmapColor="BlueWhiteRed")
```

Arguments

eSet	an object returned from method of getESet() that contains all data for plot
graph	an igraph object generated with one plot dataset, e.g, gene expression value
heatmapColor	character vector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed", "YellowToRed", and "Black".

heatmapMax	numeric, maximum value for heatmap plot, set to NULL to use the biggest value in input data set.
heatmapMin	numeric, minimum value for heatmap plot, set to NULL to use the smallest value in input data set.

Value

None

Author(s)

Henry Zhang

Examples

```
library(caOmicsV)
data(caOmicsV.bionet.eset)
plotBioNetCircos(caOmicsV.bionet.eset)
```

---

plotBioNetHeatmap *Heatmap Plot for Each Node on caOmicsV bioNetCircos Layout*

Description

Headmap plot on caOmicsv bioNetCircos layout. This method plots one track of heatmap for every node. bioNetCircos layout and graphic device must be initialized first.

Usage

```
plotBioNetHeatmap(dataValues, maxValue=NULL, minValue=NULL, outer, inner,
    plotColors)
```

Arguments

dataValues	numeric matrix of log2 values for heatmap plot. Total rows of the matrix must be same as the number of nodes and rownames must be same as the vertex names in bioNetGraph
maxValue	numeric, the biggest value of plot data
minValue	numeric, the smallest value of plot data
outer	non-negative numeric, the outside boundary of plot area from node center
inner	non-negative numeric, the inside boundary of plot area close to node center
plotColors	character vector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed", "YellowToRed", "BlackOnly".

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()
plotBioNetHeatmap(expr, outer=3, inner=2, plotColors="BlueWhiteRed")
```

---

plotBioNetLines *Line Plot on caOmicsV bioNetCircos Layout*

Description

Line plot on caOmicsv bioNetCircos layout. This method plots one track of line for every node. bionetCircos layout and graphic device must be initialized first.

Usage

```
plotBioNetLines(dataValues, outer, inner, maxValue=NULL, minValue=NULL,
    plotColors=rep("black", ncol(dataValues)))
```

Arguments

dataValues	numeric matrix of plot data
outer	non-negative numeric, the outside boundary of plot area from node center
inner	non-negative numeric, the inside boundary of plot area from node center
maxValue	numeric, the biggest value of plot data
minValue	numeric, the smallest value of plot data
plotColors	character vector or vector of R specification, colours for each sample

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()
plotBioNetLines(expr, outer=13, inner=2)
```

plotBioNetPoints *Point Plot on caOmicsV bioNetCircos Layout*

Description

Point plot on caOmicsv bioNetCircos layout. This method plots one track of points for every node. bioNetCircos layout and graphic device must be initialized first.

Usage

```
plotBioNetPoints(dataValues, maxValue=NULL, minValue=NULL, outer, inner,
    plotColors=rep("black", ncol(dataValues)), sizeByValue=FALSE, pch=".")
```

Arguments

dataValues	numeric matrix of plot data
maxValue	numeric, the biggest value of plot data
minValue	numeric, the smallest value of plot data
outer	non-negative numeric, the outer boundary of plot area from node center
inner	non-negative numeric, the inner boundary of plot area from node center
plotColors	character vector or vector of R color specification, colors for each sample
sizeByValue	logic, if true, the data value will be used for point size
pch	charcter for point type, same as the one in par()

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()
plotBioNetPoints(expr, outer=3, inner=2)
```

plotBioNetPolygons *Polygon Plot on caOmicsV bioNetCircos Layout*

Description

Plot category data as polygons on node(s) of caOmicsV bioNetCircos layout. bioNetCircos layout and graphic device must be initialized first. Polygon colours are converted from category value with build in colour series. Use getcaOmicsVColors() and setcaOmicsVColors(colorList) to see or reset customized colours.

Usage

```
plotBioNetPolygons(dataValues, outer, inner)
```

Arguments

dataValues	matrix of character or numeric for category data
outer	non-negative numeric, the outer boundary of plot area from node center
inner	non-negative numeric, the innner boundary of plot area from node center

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()
dataValues <- matrix(rep(c(1:3), each=20), nrow=1)
plotBioNetPolygons(dataValues, outer=3, inner=2)
```

plotHeatmapColorScale *Plot Heatmap Color Scale for both caOmicsV bioMatrix and bioNetCircos Layout*

Description

Draw heatmap color scale for legends of bioMatrix plot and bioNetCircos plot. Graphic device must be initialized.

Usage

```
plotHeatmapColorScale(coorX, coorY, colorType="BlueWhiteRed", scaleWidth,
    scaleHeight, minValue, maxValue, direction="h")
```

Arguments

coorX	numeric, x coordinates for the top left location of color scale
coorY	numeric, y coordinates for the top left location of color scale
scaleWidth	non-negative numeric, width of color scale
scaleHeight	non-negative numeric, height of color scale
colorType	character vector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed", "GreenBlackRed", "YellowToRed", and "BlackOnly"
minValue	numeric, the smallest value associated with the lowest coluor
maxValue	numeric, the biggest value associated with the highest coluor
direction	One character, either "h" for horizontal or "v" for vertical

Value

None

Author(s)

Henry Zhang

Examples

```
plot.new()
plot.window(xlim=c(1,5), ylim=c(1,5))
axis(1)
axis(2)
plotHeatmapColorScale(coorX=2, coorY=4, colorType="BlueWhiteRed",
    scaleWidth=2, scaleHeight=0.5, minValue=-3, maxValue=3)
```

---

resetBioNetNodePlotAreaBoundary

Update Node Plot Area Boundary on caOmicsV bioNetCircos Layout

---

Description

Record the plotted area boundary for all nodes on the igraph. These boundary may be needed for drawn customized arrows and label node names. bioNetCircos layout must be initialized first. This function is for internal use only.

Usage

```
resetBioNetNodePlotAreaBoundary(inner=getBioNetNodeRadius(), outer)
```

Arguments

inner	non-negative numeric, the inner boundary of area that has been plotted
outer	non-negative numeric, the outer boundary of area that has been plotted

Value

None

Author(s)

Henry Zhang

Examples

```
resetBioNetNodePlotAreaBoundary(outer=1.5)
```

RNA2miRNA *Paired miRNA and Genes with Nagetive Correlation Coefficients*

Description

A data frame contains 26 genes and their most negative correlated miRNA. Used for demo of generation a new data frame with gene names and related miRNA read counts.

Usage

```
data("RNA2miRNA")
```

Format

A data frame with 26 observations on the following 2 variables.

GeneSymbol a factor with levels ADAMTS13 AMIGO3 BCO2 CDKN3 CFP COL15A1 CSRNP1 CXCL12 DBH ECM1 ESM1 FCN3 LEPREL1 LIFR LILRB5 LOC222699 LYVE1 MT1F OLFML3 PLVAP PTH1R RCAN1 RND3 SEMA3F SLC26A6 TOMM40L

miRNA_ID a factor with levels hsa.mir.101.1 hsa.mir.101.2 hsa.mir.10b hsa.mir.139 hsa.mir.424 hsa.mir.450b

Examples

```
data(RNA2miRNA)
```

RNASeq *An Sample of RNASeq Data Set*

Description

A data frame with RNASeq reads of 47 genes in 76 samples.

Usage

```
data("RNASeq")
```

Format

A data frame with 47 observations on the following 77 variables.

`GeneSymbol` a factor with levels `A1BG` `ADAMTS13` `AMIGO3` `ARMCX6` `BCO2` `C17orf68` `CBLN4` `CDKN3` `CFP` `COL13A1` `COL15A1` `CSRNP1` `CXCL12` `DBH` `DNA2` `ECM1` `ESM1` `FAM20A` `FCN3` `GJB2` `HOXD9` `KIF12` `LEPREL1` `LIFR` `LILRB5` `LOC222699` `LOC441455` `LYVE1` `MOBKL1A` `MT1F` `NPM3` `OLFML3` `PCDHB7` `PLVAP` `PRICKLE4` `PTH1R` `RCAN1` `RND3` `RNF125` `SEMA3F` `SIRT5` `SLC26A6` `SPACA5` `TKTL1` `TOMM40L` `UBE2J2` `ZNF273`

`TCGA.DD.A3A3.Normal` a numeric vector

`TCGA.DD.A1EI.Normal` a numeric vector

`TCGA.BC.A216.Normal` a numeric vector

`TCGA.DD.A11A.Normal` a numeric vector

`TCGA.EP.A26S.Normal` a numeric vector

`TCGA.DD.A118.Normal` a numeric vector

`TCGA.DD.A3A1.Normal` a numeric vector

`TCGA.BD.A3EP.Normal` a numeric vector

`TCGA.EP.A12J.Normal` a numeric vector

`TCGA.DD.A11B.Normal` a numeric vector

`TCGA.BD.A2L6.Normal` a numeric vector

`TCGA.DD.A3A2.Normal` a numeric vector

`TCGA.FV.A2QR.Normal` a numeric vector

`TCGA.DD.A1EJ.Normal` a numeric vector

`TCGA.DD.A11D.Normal` a numeric vector

`TCGA.DD.A39X.Normal` a numeric vector

`TCGA.DD.A39V.Normal` a numeric vector

`TCGA.FV.A23B.Normal` a numeric vector

`TCGA.DD.A1EH.Normal` a numeric vector

`TCGA.DD.A1EG.Normal` a numeric vector

`TCGA.DD.A11C.Normal` a numeric vector

`TCGA.DD.A113.Normal` a numeric vector

`TCGA.DD.A1EC.Normal` a numeric vector

`TCGA.ES.A2HT.Normal` a numeric vector

TCGA.DD.A119.Normal a numeric vector
TCGA.DD.A1EL.Normal a numeric vector
TCGA.DD.A1EB.Normal a numeric vector
TCGA.DD.A39W.Normal a numeric vector
TCGA.DD.A39Z.Normal a numeric vector
TCGA.DD.A114.Normal a numeric vector
TCGA.DD.A1EH.Tumor a numeric vector
TCGA.ED.A4XI.Tumor a numeric vector
TCGA.DD.A4NB.Tumor a numeric vector
TCGA.DD.A118.Tumor a numeric vector
TCGA.BD.A3EP.Tumor a numeric vector
TCGA.DD.A1ED.Tumor a numeric vector
TCGA.DD.A39X.Tumor a numeric vector
TCGA.DD.A39Z.Tumor a numeric vector
TCGA.BC.A216.Tumor a numeric vector
TCGA.DD.A11A.Tumor a numeric vector
TCGA.DD.A113.Tumor a numeric vector
TCGA.BC.A10Z.Tumor a numeric vector
TCGA.DD.A119.Tumor a numeric vector
TCGA.DD.A3A3.Tumor a numeric vector
TCGA.ED.A82E.Tumor a numeric vector
TCGA.FV.A2QR.Tumor a numeric vector
TCGA.DD.A1EL.Tumor a numeric vector
TCGA.FV.A23B.Tumor a numeric vector
TCGA.CC.5258.Tumor a numeric vector
TCGA.EP.A12J.Tumor a numeric vector
TCGA.DD.A3A1.Tumor a numeric vector
TCGA.DD.A11D.Tumor a numeric vector
TCGA.ED.A5KG.Tumor a numeric vector
TCGA.DD.A114.Tumor a numeric vector
TCGA.DD.A39W.Tumor a numeric vector
TCGA.DD.A1EC.Tumor a numeric vector
TCGA.EP.A26S.Tumor a numeric vector
TCGA.RC.A7S9.Tumor a numeric vector
TCGA.BD.A2L6.Tumor a numeric vector
TCGA.UB.A7MD.Tumor a numeric vector
TCGA.DD.A11B.Tumor a numeric vector
TCGA.ED.A7XP.Tumor a numeric vector
TCGA.DD.A1EI.Tumor a numeric vector
TCGA.UB.A7MA.Tumor a numeric vector

TCGA.DD.A73A.Tumor a numeric vector

TCGA.DD.A3A2.Tumor a numeric vector

TCGA.DD.A1EB.Tumor a numeric vector

TCGA.HP.A5MZ.Tumor a numeric vector

TCGA.DD.A1EJ.Tumor a numeric vector

TCGA.DD.A1EG.Tumor a numeric vector

TCGA.RC.A7SB.Tumor a numeric vector

TCGA.RC.A6M4.Tumor a numeric vector

TCGA.ES.A2HT.Tumor a numeric vector

TCGA.DD.A11C.Tumor a numeric vector

TCGA.DD.A39V.Tumor a numeric vector

TCGA.MI.A75C.Tumor a numeric vector

Examples

```
data(RNASeq)
```

RNASeqDemoData *RNASeq Demo Data Set*

Description

A data frame with RNASeq read counts of 26 genes in 60 samples. Used for heatmap plot on caOimcsV bioNetCircos layout and bioMatirx layout after transformed to log2 values

Usage

```
data("RNASeqDemoData")
```

Format

A data frame with 26 observations on the following 61 variables.

GeneSymbol a factor with levels A1BG ADAMTS13 AMIGO3 ARMCX6 BCO2 C17orf68 CBLN4 CDKN3 CFP COL13A1 COL15A1 CSRNP1 CXCL12 DBH DNA2 ECM1 ESM1 FAM20A FCN3 GJB2 HOXD9 KIF12 LEPREL1 LIFR LILRB5 LOC222699 LOC441455 LYVE1 MOBKL1A MT1F NPM3 OLFML3 PCDHB7 PLVAP PRICKLE4 PTH1R RCAN1 RND3 RNF125 SEMA3F SIRT5 SLC26A6 SPACA5 TKTL1 TOMM40L UBE2J2 ZNF273

TCGA.BC.A216.Normal a numeric vector

TCGA.BD.A2L6.Normal a numeric vector

TCGA.BD.A3EP.Normal a numeric vector

TCGA.DD.A113.Normal a numeric vector

TCGA.DD.A114.Normal a numeric vector

TCGA.DD.A118.Normal a numeric vector

TCGA.DD.A119.Normal a numeric vector

TCGA.DD.A11A.Normal a numeric vector

TCGA.DD.A11B.Normal a numeric vector
TCGA.DD.A11C.Normal a numeric vector
TCGA.DD.A11D.Normal a numeric vector
TCGA.DD.A1EB.Normal a numeric vector
TCGA.DD.A1EC.Normal a numeric vector
TCGA.DD.A1EG.Normal a numeric vector
TCGA.DD.A1EH.Normal a numeric vector
TCGA.DD.A1EI.Normal a numeric vector
TCGA.DD.A1EJ.Normal a numeric vector
TCGA.DD.A1EL.Normal a numeric vector
TCGA.DD.A39V.Normal a numeric vector
TCGA.DD.A39W.Normal a numeric vector
TCGA.DD.A39X.Normal a numeric vector
TCGA.DD.A39Z.Normal a numeric vector
TCGA.DD.A3A1.Normal a numeric vector
TCGA.DD.A3A2.Normal a numeric vector
TCGA.DD.A3A3.Normal a numeric vector
TCGA.EP.A12J.Normal a numeric vector
TCGA.EP.A26S.Normal a numeric vector
TCGA.ES.A2HT.Normal a numeric vector
TCGA.FV.A23B.Normal a numeric vector
TCGA.FV.A2QR.Normal a numeric vector
TCGA.BC.A216.Tumor a numeric vector
TCGA.BD.A2L6.Tumor a numeric vector
TCGA.BD.A3EP.Tumor a numeric vector
TCGA.DD.A113.Tumor a numeric vector
TCGA.DD.A114.Tumor a numeric vector
TCGA.DD.A118.Tumor a numeric vector
TCGA.DD.A119.Tumor a numeric vector
TCGA.DD.A11A.Tumor a numeric vector
TCGA.DD.A11B.Tumor a numeric vector
TCGA.DD.A11C.Tumor a numeric vector
TCGA.DD.A11D.Tumor a numeric vector
TCGA.DD.A1EB.Tumor a numeric vector
TCGA.DD.A1EC.Tumor a numeric vector
TCGA.DD.A1EG.Tumor a numeric vector
TCGA.DD.A1EH.Tumor a numeric vector
TCGA.DD.A1EI.Tumor a numeric vector
TCGA.DD.A1EJ.Tumor a numeric vector
TCGA.DD.A1EL.Tumor a numeric vector

TCGA.DD.A39V.Tumor a numeric vector

TCGA.DD.A39W.Tumor a numeric vector

TCGA.DD.A39X.Tumor a numeric vector

TCGA.DD.A39Z.Tumor a numeric vector

TCGA.DD.A3A1.Tumor a numeric vector

TCGA.DD.A3A2.Tumor a numeric vector

TCGA.DD.A3A3.Tumor a numeric vector

TCGA.EP.A12J.Tumor a numeric vector

TCGA.EP.A26S.Tumor a numeric vector

TCGA.ES.A2HT.Tumor a numeric vector

TCGA.FV.A23B.Tumor a numeric vector

TCGA.FV.A2QR.Tumor a numeric vector

Examples

```
data(RNASeqDemoData)
```

---

sampleDemoData *Sample Tissue Type Demo Data Set*

Description

A data frame with sample names and tissue type for 60 samples. Used to plot tissue type on both caOmicsV bioMatrix layout and bioNetCircos layout.

Usage

```
data("sampleDemoData")
```

Format

A data frame with 60 observations on the following 2 variables.

sample_names a factor with levels TCGA.BC.A216.Normal TCGA.BC.A216.Tumor TCGA.BD.A2L6.Normal TCGA.BD.A2L6.Tumor TCGA.BD.A3EP.Normal TCGA.BD.A3EP.Tumor TCGA.DD.A113.Normal TCGA.DD.A113.Tumor TCGA.DD.A114.Normal TCGA.DD.A114.Tumor TCGA.DD.A118.Normal TCGA.DD.A118.Tumor TCGA.DD.A119.Normal TCGA.DD.A119.Tumor TCGA.DD.A11A.Normal TCGA.DD.A11A.Tumor TCGA.DD.A11B.Normal TCGA.DD.A11B.Tumor TCGA.DD.A11C.Normal TCGA.DD.A11C.Tumor TCGA.DD.A11D.Normal TCGA.DD.A11D.Tumor TCGA.DD.A1EB.Normal TCGA.DD.A1EB.Tumor TCGA.DD.A1EC.Normal TCGA.DD.A1EC.Tumor TCGA.DD.A1EG.Normal TCGA.DD.A1EG.Tumor TCGA.DD.A1EH.Normal TCGA.DD.A1EH.Tumor TCGA.DD.A1EI.Normal TCGA.DD.A1EI.Tumor TCGA.DD.A1EJ.Normal TCGA.DD.A1EJ.Tumor TCGA.DD.A1EL.Normal TCGA.DD.A1EL.Tumor TCGA.DD.A39V.Normal TCGA.DD.A39V.Tumor TCGA.DD.A39W.Normal TCGA.DD.A39W.Tumor TCGA.DD.A39X.Normal TCGA.DD.A39X.Tumor TCGA.DD.A39Z.Normal TCGA.DD.A39Z.Tumor TCGA.DD.A3A1.Normal TCGA.DD.A3A1.Tumor TCGA.DD.A3A2.Normal TCGA.DD.A3A2.Tumor TCGA.DD.A3A3.Normal TCGA.DD.A3A3.Tumor TCGA.EP.A12J.Normal TCGA.EP.A12J.Tumor TCGA.EP.A26S.Normal TCGA.EP.A26S.Tumor TCGA.ES.A2HT.Normal TCGA.ES.A2HT.Tumor TCGA.FV.A23B.Normal TCGA.FV.A23B.Tumor TCGA.FV.A2QR.Normal TCGA.FV.A2QR.Tumor

tissue_type a factor with levels Normal Tumor

Examples

```
data(sampleDemoData)
```

`setBioMatrixBaseCoordinates` *Setup Base Coordinates for caOmicsV bioMatrix Layout*

Description

Initialize x and y coordinates for each plot area on bioMatrix layout. This function is for internal use.

Usage

```
setBioMatrixBaseCoordinates(numOfSamples, sampleWidth, columnPadding,
    sampleHeight, geneNameWidth, remarkWidth)
```

Arguments

`numOfSamples`	non-negative integer, number of samples to be plotted
`sampleWidth`	non-negative numeric, width of rectangle in inch for each sample, default 0.1
`columnPadding`	non-negative numeric, padding width in inch between two samples, default 0.025
`sampleHeight`	non-negative numeric, height of rectangle in inchfor each sample, default 0.4
`geneNameWidth`	non-negative numeric, width of gene labeling area in inch, default 1
`remarkWidth`	non-negative numeric, width of remark area in inch, default 1

Value

None

Author(s)

Henry Zhang

Examples

```
setBioMatrixBaseCoordinates(numOfSamples=100, sampleWidth=0.2,
    columnPadding=0.05, sampleHeight=0.4, geneNameWidth=1, remarkWidth=2)
```

setBioMatrixPlotArea *Setup Plot Area for caOimcsV bioMatrix Layout*

Description

Setup plot area including of sample name area (sampleHeight), phenotype area, gene label area (geneNameWidth), and remark area (remarkWidth, and other descriptions). bioMatrix layout muse be initialized first. This function is for internal use only.

Usage

```
setBioMatrixPlotArea()
```

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
setBioMatrixPlotArea()
```

setBioMatrixPlotParameters *Setup Plot Parameters for caOmicsV bioMatrix Layout*

Description

Put biomatrix plot parameters to CA_OMICS_ENV environment. This function is for internal use only and all arguments are validated outside in advance.

Usage

```
setBioMatrixPlotParameters(numOfGenes, numOfSamples, numOfPhenotypes,
    sampleHeight, sampleWidth, columnPadding, rowPadding, geneNameWidth,
    remarkWidth, sampleNameHeight, legendHeight)
```

Arguments

numOfGenes	non-negative integer, total number of genes to be plotted
numOfSamples	non-negative integer, total number of samples to be plotted
numOfPhenotypes	non-negative integer, total number of phenotypes to be plotted
sampleHeight	non-negative numeric, height of polygon (sample) in inch on each row
sampleWidth	non-negative numeric, width of polygon (sample) in inch on each row

columnPadding	non-negative numeric, padding width in inch between two polygons (samples)
rowPadding	non-negative numeric, padding height in inch between two rows
geneNameWidth	non-negative numeric, width of left text plot area in inch for gene names
remarkWidth	non-negative numeric, width of plot area in inch for right side text plot (second set of gene names) and/or summary data plot
sampleNameHeight	non-negative numeric, height of plot area in inch for sample names
legendHeight	non-negative numeric, height of legend area

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
setBioMatrixPlotParameters(numOfGenes=30, numOfSamples=50, numOfPhenotypes=1,
    sampleHeight=0.4, sampleWidth=0.2, columnPadding=0.05, rowPadding=0.5,
    geneNameWidth=1, remarkWidth=2, sampleNameHeight=2, legendHeight=2)
```

---

setBioNetCircosBasePlotPositions

Setup Default Plot Positions for a Node on caOmicsV bioNetCircor Layout

---

Description

This function calculates default x and y coordinates for points on a circular line. Degrees a character string should be rotated on each point are also calculated. THis function is for internal call only.

Usage

```
setBioNetCircosBasePlotPositions(totalSamples=100, sampleWidth=100)
```

Arguments

totalSamples	non-negative numeric, total number of samples to be plotted
sampleWidth	non-negative numeric, width (how many points) of a sample on the circular line

Value

None

Author(s)

Henry Zhang

Examples

```
setBioNetCircosBasePlotPositions(totalSamples=100, sampleWidth=100)
```

---

setBioNetNodeLayout *Setup Layout for the igraph Object*

Description

Set up node layout on a biological network. The layout is taken from an igraph layout and scaled to allocate circos plot area for each node.

Usage

```
setBioNetNodeLayout(bioNet, layout=layout.auto(bioNet))
```

Arguments

bioNet	an igraph object for which layout will be set
layout	layout object from layout method of igraph package

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)
setBioNetNodeLayout(bioNet, layout=layout.auto(bioNet))
```

---

setBioNetPlotAreaBackground *Setup Plot Area Background for Nodes of caOmicsV bioNetCircos Layout*

Description

Change the plot area background of igraph nodes. Use white color to erase background and grey to show the plot area boundary.

Usage

```
setBioNetPlotAreaBackground(bgColor=grey(0.75, alpha=0.5))
```

Arguments

bgColor	character vector of a colour name or a R colour specification

Value

None

Author(s)

Henry Zhang

Examples

```
setBioNetPlotAreaBackground(grey(0.75, alpha=0.5))
```

---

setBioNetPlotParameters

Initialize Plot Parameters for caOmicsV bioNetCircos Plot

Description

Set up plot parameters for bioNetCircos layout including of totalSamples, sampleWidth, nodeRadius, nodePadding, plotAreaWidth, outer and inner boundaries of plotArea, as well as default plot colors. This function is for internal use only.

Usage

```
setBioNetPlotParameters(totalSamples, sampleWidth, nodeRadius, nodePadding,
    plotAreaWidth)
```

Arguments

totalSamples	non-negative integer, total number of samples to be plotted
sampleWidth	non-negative integer, width (number of points) of a sample on the circular line
nodeRadius	non-negative numeric, radius of the node
nodePadding	non-negative numeric, padding width in inch between two nodes
plotAreaWidth	non-negative numeric, total width of plot area.

Value

None.

Author(s)

Henry zhang

Examples

```
setBioNetPlotParameters(totalSamples=50, sampleWidth=100,
    nodeRadius=2, nodePadding=0.1, plotAreaWidth=5)
```

setCaOmicsVColors *Setup Default Plot Colors for caOmicsV Plot*

Description

Set or change default colors used for caOmicsV Plot.

Usage

```
setCaOmicsVColors(colorList=NULL)
```

Arguments

colorList	character vector, list of colour names or R colour specification

Value

None

Author(s)

Henry Zhang

Examples

```
setCaOmicsVColors(colorList=c("red", "blue", "black", "green", "cyan",
    "purple", "magenta", "grey"))
```

setDefaultNaStrings *Setup Default NA Strings for caOmicsV Package*

Description

Set or change default NA strings used by caOmicsV Package.

Usage

```
setDefaultNaStrings(nullStrings)
```

Arguments

nullStrings	character vector of null strings

Value

None

Author(s)

Henry Zhang

Examples

```
setDefaultNaStrings("null")
```

---

showBioMatrixPlotLayout

Display caOmicsV bioMatrix Layout

Description

Display caOmicsV bioMatrix layout with default information for each plot area for purpose of optimizing the layout. A bioMatrix layout must be initialized first.

Usage

```
showBioMatrixPlotLayout(geneNames, sampleNames, phenotypes, sampleColors=NULL,
    geneColors=NULL, phenoColors=NULL)
```

Arguments

geneNames	character vector, gene names shown at left side of omics data plot area
sampleNames	character vector, sample names shown on the top of phenotype plot area
phenotypes	character vector, phenotype names listed on left side of phenotype plot area
sampleColors	character vector for colour name(s) of R colour specification for samples
geneColors	character vector of colour name or R colour specification for genes
phenoColors	character vector of colour name(s) or R colour specification for phenotypes

Value

None

Author(s)

Henry Zhang

Examples

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout("Gene", paste("Sample", 1:50),  "Diagnosis")
```

showBioNetNodesLayout *Display Nodes Layout of caOmicsV bioNetCircos Plot*

Description

Display caOmicsV bioNetCircos layout with empty nodes and edges in order to optimize bioNetCircos layout. An igraph object must be initialized first.

Usage

```
showBioNetNodesLayout(bgColor=grey(0.75, alpha=0.5))
```

Arguments

bgColor	character vector for a color name or a R color specification

Value

None

Author(s)

Henry Zhang

Examples

```
data(caOmicsV.bionet.eset)
expr <- caOmicsV.bionet.eset$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout(bgColor=grey(0.75, alpha=0.5))
```

showSupportedBioNetCircosPlotType *Display the Plot Types Supported by caOmicsV bioNetCircos Plot*

Description

Display plot types supported by current version of caOmicsV bioNetCircos plot. A bioNetCircos layout must be initialized first.

Usage

```
showSupportedBioNetCircosPlotType()
```

Value

None

Author(s)

Henry Zhang

Examples

```
showSupportedBioNetCircosPlotType()
```

---

sortClinicalData *Sort Clinical Data by a Column*

Description

Sort sample information by a column defined by byItem (a column header). This function is for sorting sample information only.

Usage

```
sortClinicalData(clinicalData, byItem)
```

Arguments

clinicalData	A data frame with rows for samples and columns for features. Sample names must be in the first column.
byItem	character vector of a feature (column header) by which the data will be sorted.

Value

sampleData	copy of the first argument with new row order.

Author(s)

Henry Zhang

Examples

```
data(sampleDemoData)
sampleInfo <- sortClinicalData(sampleDemoData, colnames(sampleDemoData)[1])
```

sortOmicsDataByColumn *Sort Omics Data by Column Header*

Description

Sort omics data by column header (sample names) based on the order of the second argument. The sample names in the first argument must have same items as the second argument except of order. After sorting, the sample names in omics data and the second argument will be in same order.

Usage

```
sortOmicsDataByColumn(omicsData, sampleNames)
```

Arguments

omicsData	A data frame that holds genomic data such as gene expression, SNV, RNASeq ... The column headers must be the sample names that are same as the sample names in clinical data.
sampleNames	character vector, sample names in a given order (such as diagnosis). No redundant entries allowed.

Value

omicsData	copy of the first argument with columns in new order.

Author(s)

Henry Zhang

Examples

```
data(RNASeqDemoData)
sampleNames <- colnames(RNASeqDemoData)[-1]
sampleNames <- sampleNames[length(sampleNames):1]
expr <- sortOmicsDataByColumn(RNASeqDemoData, sampleNames)
```

sortOmicsDataByRow *Sort Omics Data by Row*

Description

Sort omics data by row (genes) in order to get omics data in a specific order, e.g., ordered by p values or by fold changes in expression data. After sorting, the order of row names in omics data will be same as the second argument.

Usage

```
sortOmicsDataByRow(omicsData, geneNames)
```

Arguments

omicsData	a data frame that holds genomic data such as gene expression, SNV, RNASeq. The first column must be gene names that are same as the second argument except of order.
geneNames	character vector, gene names in a given order (such as by p values). Redundant gene names are allowed.

Value

omicsData	copy of the first argument with new row order.

Author(s)

Henry Zhang

Examples

```
data(RNASeqDemoData)
geneNames <- as.character(RNASeqDemoData[,1])
geneNames <- geneNames[order(RNASeqDemoData[,2])]
expr <- sortOmicsDataByRow(RNASeqDemoData, geneNames)
```

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