

# Package ‘caOmicsV’

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**Type** Package

**Title** Visualization of multi-dimensional cancer genomics data

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**Description** caOmicsV package provides methods to visualize multi-dimensional 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 (>= 3.2), igraph (>= 0.7.1), bc3net (>= 1.0.2)

**biocViews** ImmunoOncology, Visualization, Network, RNASeq

**NeedsCompilation** no

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## R topics documented:

|                                    |    |
|------------------------------------|----|
| caOmicsV-package . . . . .         | 3  |
| bioMatrixLegend . . . . .          | 3  |
| biomatrixPlotDemoData . . . . .    | 4  |
| bioNetCircosPlot . . . . .         | 5  |
| bioNetLegend . . . . .             | 6  |
| bionetPlotDemoData . . . . .       | 7  |
| CA_OMICS_ENV . . . . .             | 8  |
| CA_OMICS_NAME . . . . .            | 9  |
| CA_OMICS_NA_STRING . . . . .       | 9  |
| CNVDemoData . . . . .              | 10 |
| convertToZScores . . . . .         | 12 |
| drawBioNetNodeBackground . . . . . | 12 |

|  |    |
|--|----|
| eraseBioNetNode . . . . .                  | 13 |
| getBezierCurve . . . . .                   | 14 |
| getBioMatrixDataRowTop . . . . .           | 14 |
| getBioMatrixParameters . . . . .           | 15 |
| getBioNetNodeLinkLine . . . . .            | 17 |
| getBioNetParameters . . . . .              | 18 |
| getBioNetPlotLocations . . . . .           | 19 |
| getBioNetSamplePlotPosition . . . . .      | 20 |
| getCaOmicsVColors . . . . .                | 20 |
| getCaOmicsVPlotTypes . . . . .             | 21 |
| getDefaultNaStrings . . . . .              | 21 |
| getHeatmapColorScales . . . . .            | 22 |
| getPlotDataSet . . . . .                   | 22 |
| getPlotOmicsData . . . . .                 | 24 |
| getPlotSampleData . . . . .                | 25 |
| getPlotSummaryData . . . . .               | 25 |
| getRelatedPlotData . . . . .               | 26 |
| initializeBioMatrixPlot . . . . .          | 27 |
| initializeBioNetCircos . . . . .           | 28 |
| labelBioNetNodeNames . . . . .             | 29 |
| linkBioNetNodes . . . . .                  | 30 |
| linkBioNetSamples . . . . .                | 30 |
| methylDemoData . . . . .                   | 31 |
| miRNA . . . . .                            | 33 |
| miRNADemoData . . . . .                    | 36 |
| plotBioMatrix . . . . .                    | 38 |
| plotBioMatrixBars . . . . .                | 39 |
| plotBioMatrixBinaryData . . . . .          | 40 |
| plotBioMatrixCategoryData . . . . .        | 41 |
| plotBioMatrixHeatmap . . . . .             | 42 |
| plotBioMatrixRowNames . . . . .            | 43 |
| plotBioMatrixSampleData . . . . .          | 44 |
| plotBioMatrixSampleNames . . . . .         | 45 |
| plotBioNetBars . . . . .                   | 45 |
| plotBioNetCircos . . . . .                 | 46 |
| plotBioNetHeatmap . . . . .                | 47 |
| plotBioNetLines . . . . .                  | 48 |
| plotBioNetPoints . . . . .                 | 49 |
| plotBioNetPolygons . . . . .               | 50 |
| plotHeatmapColorScale . . . . .            | 50 |
| resetBioNetNodePlotAreaBoundary . . . . .  | 51 |
| RNA2miRNA . . . . .                        | 52 |
| RNASeq . . . . .                           | 53 |
| RNASeqDemoData . . . . .                   | 55 |
| sampleDemoData . . . . .                   | 57 |
| setBioMatrixBaseCoordinates . . . . .      | 58 |
| setBioMatrixPlotArea . . . . .             | 59 |
| setBioMatrixPlotParameters . . . . .       | 59 |
| setBioNetCircosBasePlotPositions . . . . . | 60 |
| setBioNetNodeLayout . . . . .              | 61 |
| setBioNetPlotAreaBackground . . . . .      | 61 |
| setBioNetPlotParameters . . . . .          | 62 |

setCaOmicsVColors . . . . . 63  
 setDefaultNaStrings . . . . . 63  
 showBioMatrixPlotLayout . . . . . 64  
 showBioNetNodesLayout . . . . . 65  
 showSupportedBioNetCircosPlotType . . . . . 65  
 sortClinicalData . . . . . 66  
 sortOmicsDataByColumn . . . . . 67  
 sortOmicsDataByRow . . . . . 67

**Index 69**

caOmicsV-package      *caOmicsV bioMatrix and bioNetCircos Layout Plot*

**Description**

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

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

**Author(s)**

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

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=-3, heatmapMax=3, 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  | character vector, 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(biomatrixPlotDemoData)
plotBioMatrix(biomatrixPlotDemoData, summaryType="text")
bioMatrixLegend(heatmapNames=c("RNASeq", "miRNASeq"),
  categoryNames=c("Methyl H", "Methyl L"),
  binaryNames=c("CN LOSS", "CN Gain"),
  colorType="BlueWhiteRed")
```

---

biomatrixPlotDemoData *Demo Data for caOmicsV bioMatrix Plot*

---

### Description

Data for demo of caOmicsV bioMatrix Plot

### Usage

```
data("biomatrixPlotDemoData")
```

### 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" "sam-
ple_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(*, "dim-
names")=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")
```

---

|                  |                                   |
|------------------|-----------------------------------|
| 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 lines.

**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 numeric, 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 threshold. Set to NULL to use the smallest value in dataset. |

**Value**

None

**Author(s)**

Henry Zhang

**Examples**

```

data(bionetPlotDemoData)
expr <- bionetPlotDemoData$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()

binaryData <- bionetPlotDemoData$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=-3, heatmapMax=3,
             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, default -3 (z-score)   |
| heatmapMax | numeric, maximum value of heatmap color scale, default 3 (z-score)  |
| colorType  | character vector, 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(bionetPlotDemoData)
plotBioNetCircos(bionetPlotDemoData)
dataNames <- c("Tissue Type", "RNASeq", "miRNASeq", "Methylation", "CNV")
bioNetLegend(dataNames)
```

---

bionetPlotDemoData      *Demo Dataset for caOmicsV bioNetCircos Plot*

---

**Description**

Data for demo of caOmicsV bionetCircos Plot

**Usage**

```
data("bionetPlotDemoData")
```

**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" "sam-
ple_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 | <i>The Name of caOmicsV Environment</i> |
|---------------|---|

---

**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 | <i>The Default NA String Used by caOmicsV Package</i> |
|--------------------|---|

---

**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

*Demo Data Set for Copy Number Variation*


---

### Description

A data frame with copy number variation of 26 genes in 60 samples. Used for point plot demo on caOmicsV bioNetCircos layout, or binary data plot on caOmicsV bioMatrix layout after transformed to binary 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 BC02 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

**Value**

None

**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            character vector or R color specification for background color

**Value**

None

**Author(s)**

Henry Zhang

**Examples**

```
data(bionetPlotDemoData)
expr <- bionetPlotDemoData$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(bionetPlotDemoData)
expr <- bionetPlotDemoData$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)

showBioNetNodesLayout()
eraseBioNetNode()
```

---

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

---

### Description

Calculate x and y coordinates for a quadratic Bezier curve between two points with the equation:  $B(t) = (1-t)((1-t)P_0 + tP_1) + t((1-t)P_1 + tP_2)$  where  $P_0$  is the start point,  $P_2$  is the end point, and  $P_1$  is the control point.  $P_1$  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

Calculate 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()  
getBioMatrixPlotAreaHeight()  
getBioMatrixPlotAreaWidth()  
getBioMatrixRemarkWidth()  
getBioMatrixSummaryWidth()  
getBioMatrixRowPadding()  
getBioMatrixSampleHeight()  
getBioMatrixSampleIDHeight()  
getBioMatrixSampleNumber()  
getBioMatrixSampleWidth()
```

**Value**

`getBioMatrixBasePositions()` returns a numeric matrix of default 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.

`getBioMatrixPlotAreaHeight()` returns a non-negative numeric value in inch representing the 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.

`getBioMatrixSummaryWidth()` returns a non-negative numeric value in inch for width on the right side of data plot area to plot 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 sample 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 <- getBioMatrixPlotAreaHeight()
```



```

plotAreaWidth <- getBioMatrixPlotAreaWidth()
sumAreaWidth  <- getBioMatrixRemarkWidth()
rowPadding    <- getBioMatrixRowPadding()
sampleHeight  <- getBioMatrixSampleHeight()
sampleIDHeight <- getBioMatrixSampleIDHeight()
numOfSamples  <- getBioMatrixSampleNumber()
sampleWidth   <- getBioMatrixSampleWidth()

```

---

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

---

### Description

Calculate 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 a 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 a 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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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 locations 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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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. The bionetCircos layout must be initialized first.

### **Usage**

```
getBioNetSamplePlotPosition(totalSamples)
```

### **Arguments**

totalSamples    non-negative integer, total number 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()
```

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 dimension of 255 by 2.

**Author(s)**

Henry Zhang

**Examples**

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

---

getPlotDataSet      *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**

```
getPlotDataSet(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 list could 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 vector, sample names  |
| geneNames       | character vector, gene names  |
| secondGeneNames | character vector, 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)

plotData <- getPlotDataSet(sampleNames, geneNames, sampleDemoData,
  heatmapData=list(RNASeqDemoData, miRNADemoData),
  categoryData=list(methylDemoData),
  binaryData=list(CNVDemoData),
  summaryData=list(summaryData),
  secondGeneNames)

```

---

getPlotOmicsData      *Extract Subset from A Data Frame*

---

## Description

Extract a subset from the input 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 subset of plot data based on relational information, e.g., expression of miRNA or DNA copy number variations that are correlated 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, summaryWidth=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.          |
| summaryWidth     | non-negative numeric, width of data plot area in inch to plot summary info in text or bars.              |
| 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, summaryWidth=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 dimensional numeric matrix, node layout of the igraph returned by igraph layout method                             |

**Value**

None

**Author(s)**

Henry Zhang

**Examples**

```

data(bionetPlotDemoData)
expr <- bionetPlotDemoData$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-negative integer, index of node(s) on a bioNet layout                                      |
| labelColor    | character vector, colored 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(bionetPlotDemoData)
expr <- bionetPlotDemoData$heatmapData[[1]]
bioNet <- bc3net(expr)
initializeBioNetCircos(bioNet)

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

```

---

|                 |  |
|-----------------|--|
| linkBioNetNodes | <i>Draw A Customized Arrow between Two Nodes</i> |
|-----------------|--|

---

**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(bionetPlotDemoData)
expr <- bionetPlotDemoData$heatmapData[[1]]

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

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

---

|                   |   |
|-------------------|---|
| linkBioNetSamples | <i>Link Two samples Inside a Node with Quadratic Bezier Curve</i> |
|-------------------|---|

---

**Description**

Draw a quadratic 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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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 beta values of 26 genes in 60 samples. Used for bar plot on caOmicsV bioNet-Circos layout demo, and for category 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 AMIG03 ATP2A1 BC02 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 VDACC3

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

**Value**

None

**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

**Value**

None

**Examples**

```
data(miRNA)
```

---

miRNADemoData

*miRNASeq Demo Data Set*

---

**Description**

A data frame with miRNA read counts for 26 genes in 60 samples 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

**Value**

None

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

**Arguments**

|              |   |
|--------------|---|
| dataSet      | an object, returned from method of getPlotDataSet(), 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(biomatrixPlotDemoData)
plotBioMatrix(biomatrixPlotDemoData, summaryType="text",
  summarybyRow=TRUE, heatmapMax=3, heatmapMin=-3,
  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.

**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)), nrow=1)
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 numeric, 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-negative 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

Heatmap plot method for 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(biomatrixPlotDemoData)
exprData <- biomatrixPlotDemoData$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. Phenotype names, gene names, and remark notes are all plotted with this function. bioMatrix layout and graphic 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 phenotype 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**

|                           |  |
|---------------------------|--|
| <code>rowNumber</code>    | non-negative integer, number of the row where the data to be plotted |
| <code>areaName</code>     | character vector, either "phenotype" or "omicsdata"                  |
| <code>fillColor</code>    | character vector of color names or vector of R color specification   |
| <code>borderColor</code>  | character vector or a R colors specification for boarder color       |
| <code>topAdjust</code>    | non-negative numeric, height that will be reduced from top           |
| <code>bottomAdjust</code> | 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 phenotype 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 specification, color names for each sample, pre-generated to control sample colors.   |

**Value**

None

**Author(s)**

Henry Zhang

**Examples**

```

data(bionetPlotDemoData)
expr <- bionetPlotDemoData$heatmapData[[1]]
bioNet <- bc3net(expr)

initializeBioNetCircos(bioNet, totalSamples=60)
showBioNetNodesLayout()

methyl <- bionetPlotDemoData$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 igrph layout.

**Usage**

```

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

```

**Arguments**

|              |  |
|--------------|--|
| dataSet      | 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**

```
data(bionetPlotDemoData)
plotBioNetCircos(bionetPlotDemoData)
```

---

|                   |   |
|-------------------|---|
| plotBioNetHeatmap | <i>Heatmap Plot for Each Node on caOmicsV bioNetCircos Layout</i> |
|-------------------|---|

---

**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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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         | character for point type, same as the one in par()                          |

### Value

None

### Author(s)

Henry Zhang

### Examples

```
data(bionetPlotDemoData)
expr <- bionetPlotDemoData$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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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 bioNew-Circos 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 colour   |
| maxValue    | numeric, the biggest value associated with the highest colour   |
| 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**

```
# Internal use only
```

---

 RNA2miRNA

---

*Paired miRNA and Genes with Negative 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 AMIG03 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

**Value**

None

**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 BC02 C17orf68 CBLN4 CDKN3  
 CFP COL13A1 COL15A1 CSRN1 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

**Value**

None

**Examples**

```
data(RNASeq)
```

---

|                |                             |
|----------------|-----------------------------|
| RNASeqDemoData | <i>RNASeq Demo Data Set</i> |
|----------------|-----------------------------|

---

**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 BC02 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

**Value**

None

**Examples**

```
data(RNASeqDemoData)
```

---

sampleDemoData

*Sample Tissue Type Demo Data Set*

---

**Description**

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

### Value

None

### Examples

```
data(sampleDemoData)
```

---

```
setBioMatrixBaseCoordinates
```

*Set up 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 only.

### Usage

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

### 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 inch for each sample, default 0.4 |
| geneNameWidth | non-negative numeric, width of gene labeling area in inch, default 1           |

### Value

None

### Author(s)

Henry Zhang

### Examples

```
# Internal use only
```

---

setBioMatrixPlotArea    *Set up Plot Area for caOimcsV bioMatrix Layout*

---

### Description

Set up 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.

### Usage

```
setBioMatrixPlotArea()
```

### Value

None

### Author(s)

Henry Zhang

### Examples

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

---

setBioMatrixPlotParameters  
                                   *Set up Plot Parameters for caOmicsV bioMatrix Layout*

---

### Description

Put biomatrix plot parameters to CA\_OMICS\_ENV environment. All arguments should be validated outside in advance. This function is for internal use only.

### Usage

```
setBioMatrixPlotParameters(numOfGenes, numOfSamples, numOfPhenotypes,
                           sampleHeight, sampleWidth, columnPadding, rowPadding,
                           geneNameWidth, remarkWidth, summaryWidth, 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 |
| summaryWidth     | non-negative numeric, width of plot area in inch on right side of data plot area for summary info 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**

```
# Internal use only
```

---

```
setBioNetCircosBasePlotPositions
```

```
Set up 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 used 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**

```
# Internal use only
```

---

```
setBioNetNodeLayout    Set up 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(bionetPlotDemoData)
expr <- bionetPlotDemoData$heatmapData[[1]]
bioNet <- bc3net(expr)
setBioNetNodeLayout(bioNet, layout=layout.auto(bioNet))
```

---

```
setBioNetPlotAreaBackground
```

*Set up 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 used only.

**Usage**

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

**Arguments**

totalSamples    non-negative integer, total number of samples to be plotted  
sampleWidth    non-negative integer, 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**

```
# Internal used only.
```

---

setCaOmicsVColors      *Set up 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      *Set up 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,
                        secondGeneNames, 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 |
| secondGeneNames | character vector, second gene names shown at right side of omics data area   |
| sampleColors    | character vector for color name(s) of R color specification for samples      |
| geneColors      | character vector of color name or R color specification for genes            |
| phenoColors     | character vector of color name(s) or R color specification for phenotypes    |

**Value**

None

**Author(s)**

Henry Zhang

**Examples**

```
initializeBioMatrixPlot(numOfGenes=1, numOfSamples=50)
showBioMatrixPlotLayout(geneNames="Gene",
                        sampleNames=paste("Sample", 1:50),
                        phenotypes="Diagnosis", secondGeneNames="miRNA")
```



---

showBioNetNodesLayout *Display Nodes Layout of caOmicsV bioNetCircos Plot*

---

**Description**

Display 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(bionetPlotDemoData)
expr <- bionetPlotDemoData$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 | <i>Sort Clinical Data by a Column</i> |
|------------------|---------------------------------------|

---

**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)
```

# Index

## \* datasets

- biomatrixPlotDemoData, [4](#)
- bionetPlotDemoData, [7](#)
- CA\_OMICS\_ENV, [8](#)
- CA\_OMICS\_NA\_STRING, [9](#)
- CA\_OMICS\_NAME, [9](#)
- CNVDemoData, [10](#)
- methylDemoData, [31](#)
- miRNA, [33](#)
- miRNADemoData, [36](#)
- RNA2miRNA, [52](#)
- RNASeq, [53](#)
- RNASeqDemoData, [55](#)
- sampleDemoData, [57](#)

## \* methods

- bioMatrixLegend, [3](#)
- bioNetCircosPlot, [5](#)
- bioNetLegend, [6](#)
- convertToZScores, [12](#)
- drawBioNetNodeBackground, [12](#)
- eraseBioNetNode, [13](#)
- getBezierCurve, [14](#)
- getBioMatrixDataRowTop, [14](#)
- getBioMatrixParameters, [15](#)
- getBioNetNodeLinkLine, [17](#)
- getBioNetParameters, [18](#)
- getBioNetPlotLocations, [19](#)
- getBioNetSamplePlotPosition, [20](#)
- getCaOmicsVColors, [20](#)
- getCaOmicsVPlotTypes, [21](#)
- getDefaultNaStrings, [21](#)
- getHeatmapColorScales, [22](#)
- getPlotDataSet, [22](#)
- getPlotOmicsData, [24](#)
- getPlotSampleData, [25](#)
- getPlotSummaryData, [25](#)
- getRelatedPlotData, [26](#)
- initializeBioMatrixPlot, [27](#)
- initializeBioNetCircos, [28](#)
- labelBioNetNodeNames, [29](#)
- linkBioNetNodes, [30](#)
- linkBioNetSamples, [30](#)
- plotBioMatrix, [38](#)

- plotBioMatrixBars, [39](#)
- plotBioMatrixBinaryData, [40](#)
- plotBioMatrixCategoryData, [41](#)
- plotBioMatrixHeatmap, [42](#)
- plotBioMatrixRowNames, [43](#)
- plotBioMatrixSampleData, [44](#)
- plotBioMatrixSampleNames, [45](#)
- plotBioNetBars, [45](#)
- plotBioNetCircos, [46](#)
- plotBioNetHeatmap, [47](#)
- plotBioNetLines, [48](#)
- plotBioNetPoints, [49](#)
- plotBioNetPolygons, [50](#)
- plotHeatmapColorScale, [50](#)
- resetBioNetNodePlotAreaBoundary, [51](#)
- setBioMatrixBaseCoordinates, [58](#)
- setBioMatrixPlotArea, [59](#)
- setBioMatrixPlotParameters, [59](#)
- setBioNetCircosBasePlotPositions, [60](#)
- setBioNetNodeLayout, [61](#)
- setBioNetPlotAreaBackground, [61](#)
- setBioNetPlotParameters, [62](#)
- setCaOmicsVColors, [63](#)
- setDefaultNaStrings, [63](#)
- showBioMatrixPlotLayout, [64](#)
- showBioNetNodesLayout, [65](#)
- showSupportedBioNetCircosPlotType, [65](#)
- sortClinicalData, [66](#)
- sortOmicsDataByColumn, [67](#)
- sortOmicsDataByRow, [67](#)

## \* package

- caOmicsV-package, [3](#)

  

- (getBioMatrixParameters), [15](#)
- getBioMatrixBasePositions
  - (getBioMatrixParameters), [15](#)
- getBioMatrixColumnPadding
  - (getBioMatrixParameters), [15](#)
- getBioMatrixDataAreaWidth
  - (getBioMatrixParameters), [15](#)

- getBioMatrixGeneLabelWidth  
(getBioMatrixParameters), 15
- getBioMatrixGeneNumber  
(getBioMatrixParameters), 15
- getBioMatrixLegendHeight  
(getBioMatrixParameters), 15
- getBioMatrixPhenotypeNumber  
(getBioMatrixParameters), 15
- getBioMatrixPlotAreaHeight  
(getBioMatrixParameters), 15
- getBioMatrixPlotAreaWidth  
(getBioMatrixParameters), 15
- getBioMatrixRemarkWidth  
(getBioMatrixParameters), 15
- getBioMatrixRowPadding  
(getBioMatrixParameters), 15
- getBioMatrixSampleHeight  
(getBioMatrixParameters), 15
- getBioMatrixSampleIDHeight  
(getBioMatrixParameters), 15
- getBioMatrixSampleNumber  
(getBioMatrixParameters), 15
- getBioMatrixSampleWidth  
(getBioMatrixParameters), 15
- getBioMatrixSummaryWidth  
(getBioMatrixParameters), 15
- getBioNetGraph (getBioNetParameters),  
18
- getBioNetNodePaddingScale  
(getBioNetParameters), 18
- getBioNetNodeParameters  
(getBioNetParameters), 18
- getBioNetNodePlotAreaBoundary  
(getBioNetParameters), 18
- getBioNetNodeRadius  
(getBioNetParameters), 18
- getBioNetPlotAreaWidth  
(getBioNetParameters), 18
- getBioNetPlotSampleWidth  
(getBioNetParameters), 18
- getBioNetPlotTotalSample  
(getBioNetParameters), 18
  
- bioMatrixLegend, 3
- biomatrixPlotDemoData, 4
- bioNetCircosPlot, 5
- bioNetLegend, 6
- bionetPlotDemoData, 7
  
- CA\_OMICS\_ENV, 8
- CA\_OMICS\_NA\_STRING, 9
- CA\_OMICS\_NAME, 9
- caOmicsV (caOmicsV-package), 3
  
- caOmicsV-package, 3
- CNVDemoData, 10
- convertToZScores, 12
  
- drawBioNetNodeBackground, 12
  
- eraseBioNetNode, 13
  
- getBezierCurve, 14
- getBioMatrixDataRowTop, 14
- getBioMatrixParameters, 15
- getBioNetBasePositions  
(getBioNetParameters), 18
- getBioNetNodeLinkLine, 17
- getBioNetParameters, 18
- getBioNetPlotLocations, 19
- getBioNetSamplePlotPosition, 20
- getCaOmicsVColors, 20
- getCaOmicsVPlotTypes, 21
- getDefaultNaStrings, 21
- getHeatmapColorScales, 22
- getPlotDataSet, 22
- getPlotOmicsData, 24
- getPlotSampleData, 25
- getPlotSummaryData, 25
- getRelatedPlotData, 26
  
- initializeBioMatrixPlot, 27
- initializeBioNetCircos, 28
  
- labelBioNetNodeNames, 29
- linkBioNetNodes, 30
- linkBioNetSamples, 30
  
- methylDemoData, 31
- miRNA, 33
- miRNADemoData, 36
  
- plotBioMatrix, 38
- plotBioMatrixBars, 39
- plotBioMatrixBinaryData, 40
- plotBioMatrixCategoryData, 41
- plotBioMatrixHeatmap, 42
- plotBioMatrixRowNames, 43
- plotBioMatrixSampleData, 44
- plotBioMatrixSampleNames, 45
- plotBioNetBars, 45
- plotBioNetCircos, 46
- plotBioNetHeatmap, 47
- plotBioNetLines, 48
- plotBioNetPoints, 49
- plotBioNetPolygons, 50
- plotHeatmapColorScale, 50

resetBioNetNodePlotAreaBoundary, [51](#)  
RNA2miRNA, [52](#)  
RNASeq, [53](#)  
RNASeqDemoData, [55](#)  
  
sampleDemoData, [57](#)  
setBioMatrixBaseCoordinates, [58](#)  
setBioMatrixPlotArea, [59](#)  
setBioMatrixPlotParameters, [59](#)  
setBioNetCircosBasePlotPositions, [60](#)  
setBioNetNodeLayout, [61](#)  
setBioNetPlotAreaBackground, [61](#)  
setBioNetPlotParameters, [62](#)  
setCaOmicsVColors, [63](#)  
setDefaultNaStrings, [63](#)  
showBioMatrixPlotLayout, [64](#)  
showBioNetNodesLayout, [65](#)  
showSupportedBioNetCircosPlotType, [65](#)  
sortClinicalData, [66](#)  
sortOmicsDataByColumn, [67](#)  
sortOmicsDataByRow, [67](#)