

# Package ‘Lheuristic’

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**Title** Detection of scatterplots with L-shaped pattern

**Version** 1.3.0

**Description** The Lheuristic package identifies scatterplots that follow an L-shaped, negative distribution. It can be used to identify genes regulated by methylation by integration of an expression and a methylation array. The package uses two different methods to detect expression and methylation L-shaped scatterplots. The parameters can be changed to detect other scatterplot patterns.

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**Depends** R (>= 4.4.0)

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MultiAssayExperiment, ggplot2, ggpubr

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

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|          |                 |
|----------|-----------------|
| binScore | <i>binScore</i> |
|----------|-----------------|

---

Description

binScore can be used to score scatterplots by directly comparing the sample counts with a matrix of minimal or maximal percentages/counts to be found in each cell. It implements the three bands rule implicitly by setting threshold values.

Usage

binScore(aGrid, aReq)

Arguments

- aGrid           A matrix of counts as computed by ‘calcFreqs’ function.
- aReq           A matrix of minimum or maximum counts to be found in each cell if L-shape is TRUE.

Value

a score value for each scatterplot

**Examples**

```
# Generate some example data
aGrid <- matrix(c(20, 3, 0, 10, 2, 2, 20, 10, 20),
  nrow = 3, ncol = 3, byrow = TRUE
)
aReq <- matrix(c(15, 5, 0, 0, 5, 5, 10, 10, 15),
  nrow = 3, ncol = 3, byrow = TRUE
)

# Calculate the bin score
binScore(aGrid, aReq)
```

calcFreqs

*calcFreqs***Description**

calcFreqs Given a MultiAssayExperiment with methylation and expression data, the function overlays a grid on a YMet ~ Xmet scatterplot and returns a 3x3 matrix with point counts per grid cell based on the vertical and horizontal lines.

**Usage**

```
calcFreqs(
  mae,
  geneNum,
  x1,
  x2,
  y1 = NULL,
  y2 = NULL,
  percY1 = 1/3,
  percY2 = 2/3
)
```

**Arguments**

|                |                                                                                                                                                               |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mae            | MultiAssayExperiment object containing methylation and expression matrices.                                                                                   |
| geneNum        | row of expression/methylation matrix for which the frequencies will be computed.                                                                              |
| x1, x2         | Coordinates of vertical points in the X axis. Because it is expected to contain methylation values that vary between 0 and 1, default values are 1/3 and 2/3. |
| y1, y2         | Coordinates of vertical points on the Y-axis. If set to NULL, they will be automatically assigned as the percentiles of 'y' defined by 'percY1' and 'percY2'. |
| percY1, percY2 | Default values for 'y1' and 'y2' when set to 'NULL'                                                                                                           |

**Value**

a matrix with calculated frequencies

**Examples**

```
# Methylation data
methyldata <- matrix(runif(50), nrow = 10)
colnames(methyldata) <- paste0(
  "samp",
  1:ncol(methyldata)
)
rownames(methyldata) <- paste0(
  "gene",
  1:nrow(methyldata)
)
# Expression data
expresData <- matrix(rnorm(50), nrow = 10)
colnames(expresData) <- paste0(
  "samp",
  1:ncol(methyldata)
)
rownames(expresData) <- paste0(
  "gene",
  1:nrow(methyldata)
)
# ColData
colDat <- data.frame(
  sampleID = colnames(methyldata),
  name = letters[1:ncol(methyldata)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methyldata,
    expression = expresData
  ),
  colData = colDat
)

geneRow <- 1
x1 <- 1 / 3
x2 <- 2 / 3
y1 <- NULL
y2 <- NULL
percY1 <- 1 / 3
percY2 <- 2 / 3

calcFreqs(
  mae = mae, geneNum = geneRow,
  x1, x2, y1, y2, percY1, percY2
)
```

---

|              |                     |
|--------------|---------------------|
| checkPairing | <i>checkPairing</i> |
|--------------|---------------------|

---

**Description**

checkPairing function to check if two matrices have the same dimensions row and column names.

**Usage**

```
checkPairing(X, Y)
```

**Arguments**

|   |        |
|---|--------|
| X | matrix |
| Y | matrix |

**Value**

a logical value indicating if the two matrices have the same row and column names.

**Examples**

```
(X <- round(matrix(rnorm(30) * 10, ncol = 6), 1)) + 1:10
(Y <- round(X + matrix(rnorm(30) * 10, ncol = 6), 1)) - 10:1
(rownames(X) <- rownames(Y) <- letters[1:nrow(X)])
(m1 <- checkPairing(X, Y))
```

---

|                      |                                                                       |
|----------------------|-----------------------------------------------------------------------|
| correlationSelection | <i>correlationSelection: A vector correlation function calculator</i> |
|----------------------|-----------------------------------------------------------------------|

---

**Description**

correlationSelection Uses the function matCorrs; given two matrices X (m,n), Y (m,n) this function computes Pearson and Spearman correlation coefficients and their significance p-values for every pair of row vectors.

**Usage**

```
correlationSelection(
  mae,
  type = "Spearman",
  adj = TRUE,
  pValCutoff = 0.05,
  rCutoff = 0,
  sortByCorrs = FALSE
)
```

**Arguments**

|             |                                                                                                                                 |
|-------------|---------------------------------------------------------------------------------------------------------------------------------|
| mae         | a MultiAssayExperiment object containing the methylation                                                                        |
| type        | specifies the correlation to choose between Spearman and Pearson. Default is Spearman.                                          |
| adj         | logical variable indicating if the p-value returned should be adjusted or not. Default is TRUE, it returns an adjusted p-value. |
| pValCutoff  | the upper limit used for the p-value. Default is 0.05.                                                                          |
| rCutoff     | the upper limit used for the correlation coefficient. Default is 0, no cut off.                                                 |
| sortByCorrs | logical; if TRUE, results are ordered by ascending p-value. Default set to FALSE.                                               |

**Value**

dataframe with the correlations selected

**Examples**

```
# Methylation data
methyldata <- matrix(runif(50), nrow = 10)
colnames(methyldata) <- paste0("samp", 1:ncol(methyldata))
rownames(methyldata) <- paste0("gene", 1:nrow(methyldata))
# Expression data
expresdata <- matrix(rnorm(50), nrow = 10)
colnames(expresdata) <- paste0("samp", 1:ncol(methyldata))
rownames(expresdata) <- paste0("gene", 1:nrow(methyldata))
# ColData
colDat <- data.frame(
  sampleID = colnames(methyldata),
  name = letters[1:ncol(methyldata)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methyldata,
    expression = expresdata
  ),
  colData = colDat
)
correlationSelection(mae, pValCutoff = 0.25, rCutoff = 0.1,
  type = "Spearman", sortByCorrs = TRUE)
```

## Description

This function constructs a `MultiAssayExperiment` object using methylation and expression data, automatically ensuring consistency in sample names, feature names, and exposing dataset names. It internally uses `checkPairing` to validate that the provided datasets have matching row and column names.

## Usage

```
lhCreateMAE(  
  xDat,  
  yDat,  
  xName = "methylation",  
  yName = "expression",  
  colData = NULL  
)
```

## Arguments

|                      |                                                                                                    |
|----------------------|----------------------------------------------------------------------------------------------------|
| <code>xDat</code>    | A numeric matrix containing methylation data (features in rows, samples in columns).               |
| <code>yDat</code>    | A numeric matrix containing expression data (features in rows, samples in columns).                |
| <code>xName</code>   | A string specifying the name of the methylation dataset. Default: "methylation".                   |
| <code>yName</code>   | A string specifying the name of the expression dataset. Default: "expression".                     |
| <code>colData</code> | (Optional) A <code>DataFrame</code> containing sample-level metadata. Default: <code>NULL</code> . |

## Value

A `MultiAssayExperiment` object containing the provided datasets with sample metadata.

## Examples

```
library(MultiAssayExperiment)  
  
# Create synthetic methylation and expression data  
methyData <- matrix(runif(50), nrow = 10)  
colnames(methyData) <- paste0("samp", 1:ncol(methyData))  
rownames(methyData) <- paste0("gene", 1:nrow(methyData))  
  
expresData <- matrix(rnorm(50), nrow = 10)  
colnames(expresData) <- colnames(methyData)  
rownames(expresData) <- rownames(methyData)  
  
# Create sample metadata  
colDat <- data.frame(sampleID = colnames(methyData),  
  name = letters[1:ncol(methyData)])  
rownames(colDat) <- colDat$sampleID  
  
# Construct MultiAssayExperiment  
mae <- lhCreateMAE(methyData, expresData, colData = colDat)
```

```
# Display dataset names
names(experiments(mae))
```

---

matCorrs

*A row-wise correlation function calculator*


---

## Description

matCorrs Given a MultiAssayExperiment object, the function computes Pearson and Spearman correlation coefficients and their significance p-values for every pair of row vectors.

## Usage

```
matCorrs(mae)
```

## Arguments

mae A MultiAssayExperiment object containing the methylation and expression data.

## Value

matrix with a correlation value for each gene

## Examples

```
# Methylation data
methyldata <- matrix(runif(50), nrow = 10)
colnames(methyldata) <- paste0("samp", 1:ncol(methyldata))
rownames(methyldata) <- paste0("gene", 1:nrow(methyldata))
# Expression data
expresData <- matrix(rnorm(50), nrow = 10)
colnames(expresData) <- paste0("samp", 1:ncol(methyldata))
rownames(expresData) <- paste0("gene", 1:nrow(methyldata))
# ColData
colDat <- data.frame(
  sampleID = colnames(methyldata),
  name = letters[1:ncol(methyldata)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methyldata,
    expression = expresData
  ),
  colData = colDat
)
matCorrs(mae)
```

---

|              |                     |
|--------------|---------------------|
| messageTitle | <i>messageTitle</i> |
|--------------|---------------------|

---

**Description**

messageTitle A wrapper function for sending messages to console.

**Usage**

```
messageTitle(aMessage, underChar = "-")
```

**Arguments**

|           |                                               |
|-----------|-----------------------------------------------|
| aMessage  | text of the message.                          |
| underChar | character to use for underlining the message. |

**Value**

a message to console

**Examples**

```
messageTitle("Hello world", "$")
```

---

|          |                 |
|----------|-----------------|
| numScore | <i>numScore</i> |
|----------|-----------------|

---

**Description**

numScore A function to score scatterplot using a weight matrix. The scoring does not incorporate logical conditions such as 'if  $x_{ij} < C$  ...'

**Usage**

```
numScore(aGrid, LShaped, aWeightMifL, aWeightMifNonL)
```

**Arguments**

|                |                                                                                          |
|----------------|------------------------------------------------------------------------------------------|
| aGrid          | A matrix of counts computed by the 'calcFreqs' function.                                 |
| LShaped        | A boolean indicating whether the scatterplot can be classified as "L-shaped".            |
| aWeightMifL    | A matrix of weights applied to score counts if the scatterplot is classified as "L".     |
| aWeightMifNonL | A matrix of weights applied to score counts if the scatterplot is classified as "non-L". |

**Value**

a numeric score for each scatterplot

**Examples**

```
# Methylation data
methyldata <- matrix(runif(50), nrow = 10)
colnames(methyldata) <- paste0("samp", 1:ncol(methyldata))
rownames(methyldata) <- paste0("gene", 1:nrow(methyldata))
# Expression data
expresdata <- matrix(rnorm(50), nrow = 10)
colnames(expresdata) <- paste0("samp", 1:ncol(methyldata))
rownames(expresdata) <- paste0("gene", 1:nrow(methyldata))
# ColData
colDat <- data.frame(
  sampleID = colnames(methyldata),
  name = letters[1:ncol(methyldata)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methyldata,
    expression = expresdata
  ),
  colData = colDat
)

trueFreq <- calcFreqs(mae, x1 = 1 / 3, x2 = 2 / 3)
LShaped <- FALSE
weightsIfL <- matrix(c(2, -1, -99, 1, 0, -1, 1, 1, 2),
  nrow = 3, byrow = TRUE
)
weightsIfNonL <- matrix(c(0, -1, -99, 0, 0, -1, 0, 0, 0),
  nrow = 3, byrow = TRUE
)
numScore(
  trueFreq, LShaped,
  weightsIfL, weightsIfNonL
)
```

---

plotGeneByName

*plotGeneByName*


---

**Description**

plotGeneByName plots points on a scatterplot with a 3x3 grid superimposed. The name of a the gene is provided jointly with the MultiAssayExperiment object and used to select the row to be plotted.

**Usage**

```
plotGeneByName(
  geneName,
  mae,
  filename = NULL,
  text4Title = NULL,
  plotGrid = TRUE,
  figs = c(2, 2)
)
```

**Arguments**

|            |                                                                                                      |
|------------|------------------------------------------------------------------------------------------------------|
| geneName   | The name of the gene to be plotted.                                                                  |
| mae        | A MultiAssayExperiment object containing the methylation and expression data for the specified gene. |
| filename   | If provided, the name of the file to save the results as a PDF; defaults to NULL.                    |
| text4Title | A string used as the main title for the plot. Defaults to 'geneName' if set to NULL.                 |
| plotGrid   | A boolean parameter indicating whether to pass the grid option to the 'plotGeneSel' function.        |
| figs       | A two-component vector defining the 2-dimensional structure of the plots to be generated.            |

**Value**

a pdf with scatterplots of selected by gene name

**Examples**

```
# Plot gene by name based on example data
# Methylation data
methyldata <- matrix(runif(50), nrow = 10)
colnames(methyldata) <- paste0("samp", 1:ncol(methyldata))
rownames(methyldata) <- paste0("gene", 1:nrow(methyldata))
# Expression data
expresData <- matrix(rnorm(50), nrow = 10)
colnames(expresData) <- paste0("samp", 1:ncol(methyldata))
rownames(expresData) <- paste0("gene", 1:nrow(methyldata))
# ColData
colDat <- data.frame(
  sampleID = colnames(methyldata),
  name = letters[1:ncol(methyldata)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methyldata,
    expression = expresData
  )
)
```

```

    ),
    colData = colDat
)
plotGeneByName(gene = "gene7", mae = mae)

```

---

plotGeneSel

*plotGeneSel*


---

### Description

plotGeneSel plots points on a scatterplot with a 3x3 grid overimposed.

### Usage

```

plotGeneSel(
  mae,
  genePos,
  titleText,
  x1 = 1/3,
  x2 = 2/3,
  y1 = NULL,
  y2 = NULL,
  percY1 = 1/3,
  percY2 = 2/3,
  plotGrid = TRUE
)

```

### Arguments

|                |                                                                                                                                                                   |
|----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mae            | A MultiAssayExperiment object containing the methylation and expression data for the specified gene.                                                              |
| genePos        | The index of the gene to be plotted within the MultiAssayExperiment object.                                                                                       |
| titleText      | plot title.                                                                                                                                                       |
| x1, x2         | Coordinates of vertical points in the X axis. Because it is expected to contain methylation values that vary between 0 and 1. The default values are 1/3 and 2/3. |
| y1, y2         | Coordinates of vertical points in the Y axis. Leaving them as NULL assigns them the percentiles of yVec defined by 'percY1' and 'percY2'.                         |
| percY1, percY2 | Values used to act as default for 'y1' and 'y2' when these are set to 'NULL'.                                                                                     |
| plotGrid       | logical. Default to TRUE will plot gridlines over the scatterplot.                                                                                                |

### Value

a pdf with scatterplots for selected genes

## Examples

```
# Methylation data
methylData <- matrix(runif(50), nrow = 10)
colnames(methylData) <- paste0("samp", 1:ncol(methylData))
rownames(methylData) <- paste0("gene", 1:nrow(methylData))
# Expression data
expresData <- matrix(rnorm(50), nrow = 10)
colnames(expresData) <- paste0("samp", 1:ncol(methylData))
rownames(expresData) <- paste0("gene", 1:nrow(methylData))
# ColData
colDat <- data.frame(
  sampleID = colnames(methylData),
  name = letters[1:ncol(methylData)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methylData,
    expression = expresData
  ),
  colData = colDat
)

plotGeneSel(mae, genePos = 7, titleText = "L-shaped gene")
```

---

plotGenesMat

*plotGenesMat*


---

## Description

plotGenesMat wrapper function for plotting the scatterplots associated with two matrices.

## Usage

```
plotGenesMat(
  mae,
  geneNames = NULL,
  fileName = "Scatplot_Sel_Genes.pdf",
  text4Title = NULL,
  x1 = 1/3,
  x2 = 2/3,
  y1 = NULL,
  y2 = NULL,
  percY1 = 1/3,
  percY2 = 2/3,
  plotGrid = TRUE,
```

```

    logicSc = NULL,
    saveToPDF = FALSE,
    plotsPerPage = 9
  )

```

## Arguments

|                           |                                                                                                                                                                            |
|---------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>mae</code>          | A MultiAssayExperiment object containing the methylation and expression data.                                                                                              |
| <code>geneNames</code>    | A character vector of gene names to plot. If NULL, all genes are plotted.                                                                                                  |
| <code>fileName</code>     | The name of the file used to save the results as a PDF. If NULL, the plot is displayed on the screen.                                                                      |
| <code>text4Title</code>   | An optional title for the plot, incorporating the gene name and L-shape score. Defaults to NULL.                                                                           |
| <code>x1</code>           | The x-coordinate of vertical points on the X-axis. Expected to contain methylation values ranging between 0 and 1, with default values set to 1/3 and 2/3.                 |
| <code>x2</code>           | The x-coordinate of vertical points on the X-axis. Expected to contain methylation values ranging between 0 and 1, with default values set to 1/3 and 2/3.                 |
| <code>y1</code>           | The y-coordinate of vertical points on the Y-axis. If NULL, these are set to the percentiles of <code>yVec</code> defined by <code>percY1</code> and <code>percY2</code> . |
| <code>y2</code>           | The y-coordinate of vertical points on the Y-axis. If NULL, these are set to the percentiles of <code>yVec</code> defined by <code>percY1</code> and <code>percY2</code> . |
| <code>percY1</code>       | Values used as defaults for <code>y1</code> when it is set to NULL.                                                                                                        |
| <code>percY2</code>       | Values used as defaults for <code>y2</code> when it is set to NULL.                                                                                                        |
| <code>plotGrid</code>     | A logical value; defaults to TRUE, indicating whether to plot gridlines on the graph.                                                                                      |
| <code>logicSc</code>      | A numeric score representing the L-shape score. Defaults to NULL.                                                                                                          |
| <code>saveToPDF</code>    | Logical, if TRUE, saves the plots to a PDF file specified by <code>fileName</code> . If FALSE (default), plots are displayed interactively without saving.                 |
| <code>plotsPerPage</code> | A numeric value indicating the number of plots to be printed in each page. Default set to 9.                                                                               |

## Value

a pdf with scatterplots for all genes

## Examples

```

# Methylation data
methyldata <- matrix(runif(50), nrow = 10)
colnames(methyldata) <- paste0("samp", 1:ncol(methyldata))
rownames(methyldata) <- paste0("gene", 1:nrow(methyldata))
# Expression data
expresdata <- matrix(rnorm(50), nrow = 10)
colnames(expresdata) <- paste0("samp", 1:ncol(methyldata))
rownames(expresdata) <- paste0("gene", 1:nrow(methyldata))
# ColData

```

```

colDat <- data.frame(
  sampleID = colnames(methylData),
  name = letters[1:ncol(methylData)])

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methylData,
    expression = expresData
  ),
  colData = colDat
)
selectedGenes <- c("gene1", "gene5")
plotGenesMat(mae, geneNames = selectedGenes,
  saveToPDF = FALSE)

```

scoreGenesMat

*scoreGenesMat*

## Description

scoreGenesMat scores scatterplots using a binary and a numeric schemes row-wise.

## Usage

```

scoreGenesMat(
  mae,
  x1 = 1/3,
  x2 = 2/3,
  y1 = NULL,
  y2 = NULL,
  percY1 = 1/3,
  percY2 = 2/3,
  aReqPercentsMat,
  aWeightMifL = 0.5,
  aWeightMifNonL = 0.25
)

```

## Arguments

|                |                                                                                                                                                       |
|----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|
| mae            | MultiAssayExperiment object containing methylation and expression matrices.                                                                           |
| x1, x2         | Coordinates of vertical points on the X-axis. Expected to contain methylation values ranging between 0 and 1, with default values set to 1/3 and 2/3. |
| y1, y2         | Coordinates of vertical points on the Y-axis. If set to NULL, they default to the percentiles of yVec as defined by 'percY1' and 'percY2'.            |
| percY1, percY2 | Values used to act as default for 'y1' and 'y2' when these are set to 'NULL'.                                                                         |

**aReqPercentsMat** A matrix specifying the minimum and maximum percentage counts required in each cell.

**aWeightMifL** A matrix of weights applied to score counts when the scatterplot is classified as "L".

**aWeightMifNonL** A matrix of weights applied to score counts when the scatterplot is classified as "non-L".

### Value

A data frame with two columns: 'logicSc' (logical score indicating if the gene is 'active') and 'numericSc' (a numerical score).

### Examples

```
# Score genes based on example data

# Methylation data
methylData <- matrix(runif(50), nrow = 10)
colnames(methylData) <- paste0("samp", 1:ncol(methylData))
rownames(methylData) <- paste0("gene", 1:nrow(methylData))
# Expression data
expresData <- matrix(rnorm(50), nrow = 10)
colnames(expresData) <- paste0("samp", 1:ncol(methylData))
rownames(expresData) <- paste0("gene", 1:nrow(methylData))
# ColData
colDat <- data.frame(
  sampleID = colnames(methylData),
  name = letters[1:ncol(methylData)]
)

rownames(colDat) <- colDat$sampleID
mae <- MultiAssayExperiment::MultiAssayExperiment(
  experiments = list(
    methylation = methylData,
    expression = expresData
  ),
  colData = colDat
)
sampleSize <- ncol(MultiAssayExperiment::experiments(mae)[[1]])
reqPercentages <- matrix(c(3, 20, 5, 5, 40, 20, 4, 1, 2),
  nrow = 3, byrow = TRUE
)
(theWeightMifL <- matrix(c(2, -2, -sampleSize / 5, 1, 0, -2, 1, 1, 2),
  nrow = 3, byrow = TRUE
))
(theWeightMifNonL <- matrix(c(0, -2, -sampleSize / 5, 0, 0, -2, 0, 0, 0),
  nrow = 3, byrow = TRUE
))
scoreGenesMat(mae,
  x1 = 1 / 3, x2 = 2 / 3,
  y1 = NULL, y2 = NULL, percY1 = 1 / 3, percY2 = 2 / 3,
```

```
aReqPercentsMat = reqPercentages,  
aWeightMifL = theWeightMifL,  
aWeightMifNonL = theWeightMifNonL  
)
```

---

**TCGAexpression***Expression data matrix obtained from TCGA, TCGA-COAD dataset*

---

**Description**

A mxn matrix containing normalized gene expressions from TCGA

**Usage**

```
data(TCGAexpression)
```

**Format**

An object of class *matrix* (inherits from *array*) with 1000 rows and 30 columns.

**Value**

data matrix with gene expression data

**Source**

[TCGA.org](https://tcga.org)

---

**TCGAmethylation***Methylation data matrix obtained from TCGA, TCGA-COAD dataset*

---

**Description**

A mxn matrix containing normalized methylation values from TCGA

**Usage**

```
data(TCGAmethylation)
```

**Format**

An object of class *matrix* (inherits from *array*) with 1000 rows and 30 columns.

**Value**

data matrix with gene methylation data

**Source**

[TCGA.org](https://TCGA.org)

---

|          |                 |
|----------|-----------------|
| toReqMat | <i>toReqMat</i> |
|----------|-----------------|

---

**Description**

toReqMat can be used to turn a matrix of required percentages into a matrix of required counts to facilitate its scoring.

**Usage**

```
toReqMat(numPoints, aReqPercentMat)
```

**Arguments**

**numPoints**      Number of points in a scatterplot. Used to turn the required percentages into required counts.

**aReqPercentMat**   Matrix of required percentages.

**Value**

a counts matrix

**Examples**

```
reqPercentages <- matrix(
  c(
    3, 20, 5,
    5, 40, 20,
    4, 1, 2
  ),
  nrow = 3, byrow = TRUE
)
numberOfPoints <- 100
reqMat <- toReqMat(
  numPoints = numberOfPoints,
  aReqPercentMat = reqPercentages
)
```

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