Package 'cghMCR'

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Title Find chromosome regions showing common gains/losses

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Depends methods, DNAcopy, CNTools, limma

Imports BiocGenerics (>= 0.1.6), stats4

Description This package provides functions to identify genomic regions of interests based on segmented copy number data from multiple samples.

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Contents

cghMCR *The constructor for the cghMCR class*

Description

Instantiates a cghMCR object using the parameters passed.

Usage

```
cghMCR(segments, gapAllowed = 500, alteredLow = 0.03, alteredHigh =
0.97, spanLimit = 2e+07, recurrence = 75, thresholdType = c("quantile",
"value"))
```

Arguments

segments	segments is a data frame extracted from the "output" element of the object returned by segment of the package DNAcopy or getSegments
gapAllowed	gapAllowed is an integer specifying low threshold of base pair number to separate two adjacent segments, belower which the two segments will be joined as an altered span
alteredLow	alteredLow is a positive number between 0 and 1 specifying the lower reshold percential value. Only segments with values falling below this threshold are considered as altered span
alteredHigh	alteredHigh is a positive number between 0 and 1 specifying the upper reshold percential value. Only segments with values falling over this threshold are considered as altered span
recurrence	recurrence is an integer between 1 and 100 that specifies the rate of occurrence for a gain or loss that are observed across sample. Only gains/losses with ocurrence rate grater than the threshold values are declared as MCRs
spanLimit	spanLimit is an integer that defines the leangh of altered spans that can be considered as locus. It is not of any use at this time
thresholdType	thresholdType is a character string that can be either "quantile" or "value" indicating wether alteredLow or alteredHigh is quantial or actual value

Details

The function is just a constructor of the cghMCR class for the instantiation of a cghMCR object

Value

An object of the cghMCR class

Note

The function is a contribution of The Center for Applied Cancer Science of Dana-Farber Cancer Institute

Author(s)

Jianhua Zhang

References

References on S4 class

See Also

cghMCR

Examples

```
data("segData")
cghmcr <- cghMCR(segData, gapAllowed = 500,
       alteredLow = 0.20, alteredHigh = 0.80, recurrence = 50)
```

---

cghMCR-class *Class "cghMCR" is a S4 class for the identification of minimum common regions of gains or losses across samples*

Description

Objects of this class provides the functionalities to detecting chromosome regions that show gains or losses across differnet samples

Objects from the Class

Objects can be created by calls of the form `new("cghMCR", ...)`. A constructor cghMCR may be used to instantiate object of this class

Slots

`DNASeg`: Object of class `"data.frame"` containing segmentation data derived from segmentation analysis using segment

`DNAData`: Object of class `"data.frame"` containing raw data derived used for the segmentation analysisfrom segmentation analysis

`altered`: Object of class `"data.frame"` containing data for the altered regions

`gapAllowed`: Object of class `gapAllowed` is an integer specifying low threshold of base pair number to separate two adjacent segments, belower which the two segments will be joined as an altered span

`alteredLow`: Object of class `alteredLow` is a positive number between 0 and 1 specifying the lower reshold percential value. Only segments with values falling below this threshold are considered as altered span

`alteredHigh`: Object of class `alteredHigh` is a positive number between 0 and 1 specifying the upper reshold percential value. Only segments with values falling over this threshold are considered as altered span

`recurrence`: Object of class `recurrence` is an integer between 1 and 100 that specifies the rate of occurrence for a gain or loss that are observed across sample. Only gains or losses with ocurrence rate grater than the threshold values are declared as MCRs

`spanLimit`: Object of class `spanLimit` is an integer that defines the leangh of altered spans that can be considered as locus. It is not of any use at this time

`thresholdType`: A character string that can be either "quantile", "value" to indicate the type of the value for recurrence

Methods

MCR `signature(object = "cghMCR")`: identifies minimum common regions of gains/losses across samples

Note

The function is a contribution of The Center for Applied Cancer Science of Dana-Farber Cancer Institute

Author(s)

Jianhua Zhang

See Also

cghMCR

Examples

```
require("CNTools")
data("sampleData")
cghmcr <- cghMCR(sampleData[sampleData[, "ID"] %in%
       sample(unique(sampleData[, "ID"]), 20), ], gapAllowed = 500,
       alteredLow = 0.20, alteredHigh = 0.80, recurrence = 50)
```

---

colnames-methods *Methods for Function colnames/rownames in Package 'cghMCR'*

Description

Methods for function `colnames` or `rownames` in Package 'cghMCR' to extract row or column names from a SGOL object

Methods

x = "SGOL" Extract colnum/row names from SGOL object

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mergeMCRProbes *A function that appends probe ids to a data frame containing MCRs*

Description

This function takes a data frame generated by MCR and then append probe ids corresponding to each MCR as a column to the data frame.

Usage

```
mergeMCRProbes(mcr, rawData)
```

Arguments

mcr	mcr is a data frame generated by MCR that contains MCRs identified and other related data
rawData	rawData is a data frame with at least three columns. The first column should be probe ids, second the chromosome number the probes corresponding to, and the thrid the starting or ending chromosomal locations of the probes

Details

The mcr data frame passed must have the first column for chromosome numbers, the 7th column for the starting positions of the MCRs, and the 8th column for the ending positions of the MCRs.

Value

A data frame with MCRs and the corresponding probe ids and other data.

Note

The function is a contribution of The Center for Applied Cancer Science of Dana-Farber Cancer Institute

Author(s)

Jianhua Zhang

See Also

MCR

Examples

```
data("segData")
cghmcr <- cghMCR(segData, gapAllowed = 500, alteredLow = 0.20,
                 alteredHigh = 0.80, recurrence = 50)
mcrs <- MCR(cghmcr)
mcrs <- mergeMCRProbes(mcrs, segData[["data"]])
```

---

plot.DNAcopy *A function to plot the original data along with the segments identified using segment of DNAcopy.*

Description

This function takes a DNAcopy object generated by running getSegments and then plots the original data along with the segments identified.

Usage

```
## S3 method for class 'DNAcopy'
plot(x, ..., save = FALSE, layout)
```

Arguments

x	x is a DNAcopy object generated by getSegments
...	... may contain an optional boolean for save to indicate whether to show the plot on the screen (FALSE. Default) or return the name of the plot (TRUE) to allow the users to save the plot
save	save a boolean indicating wheather the plot will be draw on the screen only (FALSE) or the name of the png file of the plot be returned (TRUE)
layout	layout a numeric vector of two elements defining the values used for mfrow of the function par for the layout of figures on a plot

Details

This function only works with the DNAcopy returned by getSegments. It will work with the DNAcopy returned by segment of the DNAcopy package when the a column containing the probe ids is added as the first column of the "data" element of the object.

Value

This function returns invisible() or the name of the plot depending on whether save is set to FALSE of TRUE.

Note

The function is a contribution of The Center for Applied Cancer Science of Dana-Farber Cancer Institute

Author(s)

Jianhua Zhang

References

The DNAcopy package

See Also

getSegments

Examples

```
if(interactive()){
  require("cghMCR")
  data("segData")
  plot(segData)
}
```

SGOL-class *Class "SGOL" reprents segments of gain or loss across samples*

Description

Segments of gains or losses along chromosomes can be calculated based on segmentation data derived from the segment function of the DNAcopy package

Objects from the Class

Objects can be created by calls of the form `new("SGOL", ...)` or using a constructor SGOL.

Slots

`gol`: Object of class `"matrix"` holding the gain or loss data for chromosomal segments

`threshold`: Object of class `"vector"` of length 2 indicating the lower and upper thresholds below/over which data points will be included in the calculation of SGOL score using the method defined by method

`method`: Object of class `"function"` giving the method used to calculate SGOL scores. Common methods include sum, median, and mean

Methods

gol `signature(object = "SGOL")`: extracts SGOL scores

method `signature(object = "SGOL")`: gets the name of the function used to calculate the SGOL scores

plot `signature(x = "SGOL", y = "ANY",...)`: plots the data

threshold `signature(object = "SGOL")`: gets the thredhold used for the calculation

Author(s)

Jianhua Zhang

References

The SGOL score is a modified version of the GISTIC score published in PNAS 104: 20007-20012

Examples

```
showClass("SGOL")
require(CNTools)
```

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