cghMCR

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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

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Examples

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

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cghMCR-class   *Class "cghMCR" is a S4 class for the identification of minimum com-*
                    mon

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 segmenta-
    tion analysis using segment

DNAData: Object of class "data.frame" containing raw data derived used for the segmenta-
    tion 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)
```

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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)
```

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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"]])
```

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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

| plot.DNAcopy | *A function to plot the original data along with the segments identified* |

Description

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

Usage

```
plot.DNAcopy(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)
}
```

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