Package ‘cghMCR’

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Description This package provides functions to identify genomic regions of interests based on segmented copy number data from multiple samples.
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The constructor for the cghMCR class

**Description**

Instantiates a cghMCR object using the parameters passed.

**Usage**

```r
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, below which the two segments will be joined as an altered span
- `alteredLow`: alteredLow is a positive number between 0 and 1 specifying the lower threshold 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 threshold 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 occurrence rate grater than the threshold values are declared as MCRs
- `spanLimit`: spanLimit is an integer that defines the length 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 whether `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
cghMCR-class

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)

Description
Objects of this class provides the functionalities to detecting chromosome regions that show gains or losses across different 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
DNAD ata: Object of class "data.frame" containing raw data derived used for the segmentation analysis from 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, below 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 threshold 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 threshold 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 occurrence rate greater than the threshold values are declared as MCRs.

spanLimit: Object of class spanLimit is an integer that defines the length 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)

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.
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 third 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

```r
## 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 whether the plot will be drawn 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
SGOL-class

See Also

getSegments

Examples

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

SGOL-class

Class "SGOL" represents 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 threshold 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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