

CNTools

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CNSeg-class	<i>Class "CNSeg" contains the output of DNACopy segmentation data that can</i>
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Description

Segmentation results of copy number data can not be operated by other analysis tools such as classification. The class "CNSeg" provides methods to convert segmentation data into a (what is called Reduced segments (RS))matrix format so that other computations can be performed

Objects from the Class

Objects can be created by calls of the form `new ("CNSeg", ...)`. A constructor `CNSeg (segList)` can also be used to instantiate CNSeg object

Slots

segList: Object of class "data.frame" is the "output" element of the object return by the segment function of DNACopy

chromosome: Object of class "character" is the name of the column in segList that contains the chromosome name a given segment belong to

end: Object of class "character" is the name of the column in segList that contains the ending locatino of a given segment

start: Object of class "character" is the name of the column in segList that contains the starting location of a given segment

segMean: Object of class "character" is the name of the column in segList that contains the mean log ratio of a given segment

id: Object of class "character" is the name of the column in segList that contains the id of a given segment

Methods

getRS signature(object = "CNSeg"): get the Reduced Segment data matrix

segList signature(object = "CNSeg"): get the value for slot "segList" of a CNSeg object

segList<- signature(object = "CNSeg"): set the value for slot "segList" of a CNSeg object

show signature(object = "CNSeg"): print a CNSeg object

Author(s)

Jianhua Zhang

References

NA

See Also[RS](#)**Examples**

```

data("sampleData")
# take a subset of the data for speed
seg <- CNSeg(sampleData[which(is.element(sampleData[, "ID"],
  sample(unique(sampleData[, "ID"]), 10)), ])
rsBypair <- getRS(seg, by = "pair", imput = FALSE, XY = FALSE, what = "mean")
rsBypair

```

RS-class

Class "RS" contains the Reduced Segment data matrix derived from the

Description

The class contains the Reduced Segment data matrix derived from the output of the segment method of DNACopy and provides functions to manipulate the data or perform other computational operations

Objects from the Class

Objects can be created by calls of the form `new("RS", ...)`. A constructor `RS(rs, by, imput, XY)` can also be used to instantiate an object of this class

Slots

rs: Object of class "ANY" either a matrix if the RS is by region or gene or a list of matrix if the RS is by sample pairs

by: Object of class "character" a character string indicating how the RS matrix is obtained. Valid values include region, gene, or pair

Methods

cor signature(x = "RS"): Calculates the sample wise correlation coefficients using the Reduced Segment matrix

dist signature(x = "RS"): Calculates the distance between samples contained in the Reduced Segment matrix

genefilter signature(expr = "RS"): filters features by calling the genefilter function

madFilter signature(object = "RS"): filters features by mean absolute deviation

rs signature(object = "RS"): get method for the by slot of an RS object

rs<- signature(object = "RS"): assignment method for the rs slot
segBy signature(object = "RS"): get method for the by slot of an RS object
show signature(object = "RS"): show method for an RS object

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See Also

[CNSeg](#)

Examples

```
data("sampleData")
# take a subset of the data for speed
seg <- CNSeg(sampleData[which(is.element(sampleData[, "ID"], sample(unique(sampleData[, "ID"])))], "ID"), sample(unique(sampleData[, "ID"])))
rsByregion <- getRS(seg, by = "region", imput = TRUE, XY = FALSE, what = "median")
rsByregion
```

getCor-methods	<i>Method that extends the cor function of stats to handle reduced segments</i>
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Description

getCor gets data contained by an RS object ready and then calls the cor function for correlation calculations

Methods

x = "ANY" see function cor of stats
x = "RS" method that handles RS objects

diffBy-methods	<i>A filter that filters out features that do not differ by a set</i>
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Description

madFilter With a given threshold, the method checks each pair of samples to exclude features that do not differ by the threshold between two samples. This filter is only applicable to pairs of reduced segments

Methods

object = "ANY" not implemented yet
object = "RS" method that handles RS objects

dist-methods *A method that extends the generic function dist to handle reduced*

Description

getDist gets the data contained by an RS object ready to be passed to the generic function for distance calculations

Methods

x = "ANY" see dist of stats

x = "RS" takes an RS object and then call the dist function of stats for distance calculations

genefilter-methods *A method that filters feature based on reduced segment*

Description

Extends genefilter filtering functions to handle reduced segment data

Methods

expr = "RS" A character string to indicate that filtering is based on reduced segment data

getRS-methods *method that convert segment data into reduced segment matrix*

Description

getRS takes a CNSeg object containing the output of the segment function of DNACopy and format the data into a matrix based on overlapping chromosome region (by = region", gene (by = gene) or pair overlapping chromosome region (by = pair)

Methods

object = "CNSeg" a reduced segment can be generated in three ways; by chromosomal regions that overlap across sample (by = region), by genes (by = gene), or by pair of samples with chromosome regions aligned (by = pair). User may choose to imput cells (by region or gene only) where a value can not be assigned by setting imput = TRUE. The X and Y chromosomes can dropped by stting XY = FALSE.

madFilter-methods *Method that filters reduced segment matrix by the mean absolute*

Description

`madFilter` calculates the mean absolute deviation across samples for each rows and drops rows that are not above percentile defined by a user

Methods

object = "ANY" not implemented yet

object = "RS" method that handles RS objects

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