Package 'CNTools'

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Title Convert segment data into a region by sample matrix to allow for other high level computational analyses.

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Depends R (>= 2.10), methods, tools, stats, genefilter

Description This package provides tools to convert the output of segmentation analysis using DNAcopy to a matrix structure with overlapping segments as rows and samples as columns so that other computational analyses can be applied to segmented data

Keyword copy number

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Contents

CNSeg-class	*Class "CNSeg" contains the output of DNACopy segmentation data that can be operated on by the associated methods*

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
```

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diffBy-methods	*A filter that filters out features that do not differ by a set threshold between a pair of samples*

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 iimplemented yet

object = "RS" method that handles RS objects

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

Description

getDist gets the data contained by an RS object ready to be passed to the generic functon 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

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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

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getCor-methods   *Method that extends the cor function of stats to handle reduced seg-
                             ment data*

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

---

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.

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

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 iimplemented yet

object = "RS" method that handles RS objects

RS-class   *Class "RS" contains the Reduced Segment data matrix derived from the output of segmentation*

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 intantiate an object of this class

Slots

rs: Object of class "ANY" eith 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 charactere 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 matix

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

Author(s)

Jianhua Zhang

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"]), 20))), ])
   rsByregion <- getRS(seg, by = "region", imput = TRUE, XY = FALSE, what = "median")
   rsByregion
```

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