

# Package: CNTools (via r-universe)

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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

**License** LGPL

**ZipData** no

**biocViews** Microarray, CopyNumberVariation

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/CNTools>

**RemoteRef** HEAD

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CNSEg-class	<i>Class "CNSEg" contains the output of DNACopy segmentation data that can be operated on by the associated methods</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

```

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

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dist-methods	<i>A method that extends the generic function dist to handle reduced segments</i>
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**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

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

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### 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 segment data*

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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

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

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### 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	<i>Method that filters reduced segment matrix by the mean absolute deviation</i>
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**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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RS-class	<i>Class "RS" contains the Reduced Segment data matrix derived from the output of segmentation</i>
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**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

**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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