Package ‘CGHbase’

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Contents

CGHbase-package 2
avedist 3
cghCall 3
cghRaw 6
cghRegions 7

cghSeg 9
chromosomes 11
copynumber 12
frequencyPlot 13
frequencyPlotCalls 14
make_cghRaw 15
plot.cghRaw 16
probloss 16
regions 17
summaryPlot 18
Wilting 19
WiltingCalled 20
WiltingNorm 20
WiltingRaw 21
WiltingRegions 21
WiltingSeg 22

Index **23**

`CGHbase-package` *CGHbase: Base functions and classes for arrayCGH data analysis.*

Description

CGHbase: Base functions and classes for arrayCGH data analysis.

Details

Main infrastructural classes: `cghRaw`, `cghSeg`, `cghCall`. Full help on methods and associated functions is available from withing class help pages.

Attached data sets: `Wilting`, `WiltingRaw`, `WiltingNorm`, `WiltingSeg`, `WiltingCalled`.

Author(s)

Sjoerd Vosse <sjoerdvos@yahoo.com>

avedist — *Retrieve regions information from cghRegions object.*

Description

This function accesses the regions information stored in the featureData of an object derived from the cghRegions-class.

Usage

```
avedist(object)
nclone(object)
```

Arguments

object	Object derived from class cghRegions

Value

avedist returns a vector containing the Average L1-distance of clone signatures to the medoid signature; nclone returns a vector containing the number of clones that is included in each region;

Author(s)

Sjoerd Vosse

See Also

cghRegions-class

cghCall — *Class to contain and describe called array comparative genomic hybridization data.*

Description

Container for aCGH data and experimental metadata. cghCall class is derived from eSet, and requires the following matrices of equal dimension as assayData members:

- copynumber
- segmented
- calls
- probloss
- probnorm
- probgain

Furthermore, columns named Chromosome, Start, and End are required as featureData members, containing feature position information.

Extends

Directly extends class eSet.

Creating Objects

new('cghCall', phenoData = [AnnotatedDataFrame], experimentData = [MIAME], annotation = [character], copynumber = [matrix], segmented = [matrix], calls = [matrix], probloss = [matrix], probnorm = [matrix], probgain = [matrix], featureData = [AnnotatedDataFrame], ...)

An object of class cghCall is generally obtained as output from CGHcall.

Slots

Inherited from eSet:

assayData: Contains matrices with equal dimensions, and with column number equal to nrow(phenoData). assayData must contain the following matrices

- copynumber
- segmented
- calls
- probloss
- probnorm
- probgain

with rows represening array probes and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData-class

phenoData: See eSet

featureData: An AnnotatedDataFrame with columns Chromosome, Start, and End containing array element position data.

experimentData: See eSet

annotation: See eSet

Methods

Class-specific methods.

copynumber(cghCall), copynumber(cghCall,matrix)<- Access and set elements named copynumber in the AssayData-class slot.

segmented(cghCall), segmented(cghCall,matrix)<- Access and set elements named segmented in the AssayData-class slot.

calls(cghCall), calls(cghCall,matrix)<- Access and set elements named calls in the AssayData-class slot.

probloss(cghCall), probloss(cghCall,matrix)<- Access and set elements named probloss in the AssayData-class slot.

probnorm(cghCall), probnorm(cghCall,matrix)<- Access and set elements named probnorm in the AssayData-class slot.

`probgain(cghCall)`, `probgain(cghCall,matrix)<-` Access and set elements named `probgain` in the `AssayData-class` slot.

`chromosomes`, `bpstart`, `bpend` Access the chromosomal positions stored in `featureData`

plot Create a plot containing log2ratios, segments and call probabilities ordered by chromosomal position. EXTRA OPTIONS PLUS DEFAULTS: dotres=10. Every dotres-th log2-ratio is plotted. dotres=1 plots all data. However, higher values save a lot of space and allow quicker browsing of the plots. ylimit=c(-5,5): limits of the y-axis. gaincol='green'; losscol='red';ampcol="darkgreen";dlcol="darkred": Colors used for gain, loss (bars) and amplifications, double loss (tick marks). build='GRCh37': build of humun genome used for determining positions of centromeres

plot.summary Create a plot summarizing the call probabilities of all samples

frequencyPlotCalls Create a frequency plot summarizing the calls of all samples

See `eSet` for derived methods.

Author(s)

Sjoerd Vosse

See Also

`eSet-class`, `cghRaw-class`, `cghSeg-class`

Examples

```
# create an instance of cghCall
new("cghCall")

# create an instance of cghCall through \code{\link{ExpandCGHcall}}
## Not run:
   data(Wilting)
   rawcgh <- make_cghSeg(Wilting)
   normalized <- normalize(rawcgh)
   segmented <- segmentData(normalized)
   perc.tumor <- rep(0.75, 3)
   listcalled <- CGHcall(segmented,cellularity=perc.tumor)
   called <- ExpandCGHcall(listcalled,segmented)

  # plot the first sample. Default only every 10th log2-ratio is plotted (dotres=10). Adjust using dotres= option be
   plot(called[,1])
   # plot the first chromosome of the first sample
   plot(called[chromosomes(called)==1,1])

   # get the copynumber values of the third and fourth sample
   log2ratios <- copynumber(called[,3:4])

   # get the names of the samples
   sampleNames(called)

   # get the names of the array elements
```

```
    featureNames(called)

## End(Not run)
```

---

cghRaw *Class to contain and describe raw or normalized array comparative genomic hybridization data.*

Description

Container for aCGH data and experimental metadata. cghRaw class is derived from eSet, and requires a matrix named copynumber as assayData member. Furthermore, columns named Chromosome, Start, and End are required as featureData members, containing feature position information.

Extends

Directly extends class eSet.

Creating Objects

new('cghRaw', phenoData = [AnnotatedDataFrame], experimentData = [MIAME], annotation = [character], copynumber = [matrix], featureData = [AnnotatedDataFrame], ...)

make_cghRaw is a function to convert a dataframe or textfile to an object of class cghRaw. The input should be either a dataframe or a tabseparated textfile (textfiles must contain a header). The first three columns should contain the name, chromosome and position in bp for each array target respectively. The chromosome and position column must contain numbers only. Following these is a column with log2 ratios for each of your samples. If the input type is a textfile, missing values should be represented as 'NA' or an empty field.

Slots

Inherited from eSet:

assayData: Contains matrices with equal dimensions, and with column number equal to nrow(phenoData). assayData must contain a matrix copynumber with rows represening array probes and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData-class

phenoData: See eSet

featureData: An AnnotatedDataFrame with columns Chromosome, Start, and End containing array element position data.

experimentData: See eSet

annotation: See eSet

Methods

Class-specific methods.

`copynumber(cghRaw)`, `copynumber(cghRaw,matrix)<-` Access and set elements named `copynumber` in the `AssayData-class` slot.

`chromosomes`, `bpstart`, `bpend` Access the chromosomal positions stored in `featureData`

plot Create a plot containing log2ratios ordered by chromosomal position

See `eSet` for derived methods. Annotation functionality is not yet supported.

Author(s)

Sjoerd Vosse

See Also

`eSet-class`, `cghSeg-class`, `cghCall-class`

Examples

```
# create an instance of cghRaw
new("cghRaw")

# create an instance of cghRaw from a dataframe
data(Wilting)
rawcgh <- make_cghRaw(Wilting)

# plot the first sample
plot(rawcgh[,1])
# first three chromosomes
plot(rawcgh[chromosomes(rawcgh)==1,1])

# get the copynumber values of the third and fourth sample
log2ratios <- copynumber(rawcgh[,3:4])

# get the names of the samples
sampleNames(rawcgh)

# get the names of the array elements
featureNames(rawcgh)
```

`cghRegions` *Class to contain and describe array comparative genomic hybridization regions data.*

Description

Container for aCGH regions data and experimental metadata. `cghRegions` class is derived from `eSet`, and requires a matrix named `regions` as assayData member. Furthermore, columns named `Chromosome`, `Start`, `End`, `Nclone`, and `Avedist` are required as featureData members, containing region and position information.

Extends

Directly extends class `eSet`.

Creating Objects

`new('cghRegions', phenoData = [AnnotatedDataFrame], experimentData = [MIAME], annotation = [character], regions = [matrix], featureData = [AnnotatedDataFrame], ...)`

An object of this class is generally obtained by running the function `CGHregions`.

Slots

Inherited from `eSet`:

`assayData`**:** Contains matrices with equal dimensions, and with column number equal to `nrow(phenoData)`. `assayData` must contain a matrix `regions` with rows represening regions and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in `assayData`. Class:`AssayData`

`phenoData`**:** See `eSet`

`featureData`**:** An `AnnotatedDataFrame` with columns `Chromosome`, `Start`, `End`, `Nclone`, and `Avedist` containing region and position information.

`experimentData`**:** See `eSet`

`annotation`**:** See `eSet`

Methods

Class-specific methods.

`regions(cghRegions)`**,** `regions(cghRegions,matrix)<-` Access and set elements named `regions` in the `AssayData-class` slot.

`chromosomes`**,** `bpstart`**,** `bpend`**,** `nclone`**,** `avedist` Access the region and position information stored in `featureData`

plot.cghRegions Create a plot displaying chromosomes on the Y-axis and base pair position on the X-axis. A new region is displayed by a slight jump with respect to the previous region. Each region is displayed as a bi-colored segment, the lower and upper part of which correspond to the proportions pl and pg of samples with a loss (red) or gain (green), respectively. The color coding is displayed as well: 1: pl (pg) < 10%; 2: 10% = pl (pg) < 30%; 3:30% = pl (pg) < 50%; 4: pl (pg) = 50%.

frequencyPlot Create a frequency plot

See `eSet` for derived methods. Annotation functionality is not yet supported.

Author(s)

Sjoerd Vosse

See Also

eSet, cghRaw-class, cghSeg-class, cghCall-class

Examples

```
# create an instance of cghRegions
new("cghRegions")

# load an instance of cghRegions
data(WiltingRegions)

# plot all region data
plot(WiltingRegions)
# make a frequency plot
frequencyPlot(WiltingRegions)

# extract the region values
values <- regions(WiltingRegions)

# get the names of the samples
sampleNames(WiltingRegions)
```

---

cghSeg — *Class to contain and describe segmented array comparative genomic hybridization data.*

Description

Container for aCGH data and experimental metadata. cghSeg class is derived from eSet, and requires a matrix named copynumber as well as a matrix named segmented as assayData members of equal dimensions. Furthermore, columns named Chromosome, Start, and End are required as featureData members, containing feature position information.

Extends

Directly extends class eSet.

Creating Objects

new('cghSeg', phenoData = [AnnotatedDataFrame], experimentData = [MIAME], annotation = [character], copynumber = [matrix], segmented = [matrix], featureData = [AnnotatedDataFrame], ...)

An object of class cghSeg is generally obtained as output from segmentData.

Slots

Inherited from eSet:

assayData: Contains matrices with equal dimensions, and with column number equal to nrow(phenoData). assayData must contain matrices copynumber and segmented with rows represening array probes and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData-class

phenoData: See eSet

featureData: An AnnotatedDataFrame with columns Chromosome, Start, and End containing array element position data.

experimentData: See eSet

annotation: See eSet

Methods

Class-specific methods.

copynumber(cghSeg), copynumber(cghSeg,matrix)<- Access and set elements named copynumber in the AssayData-class slot.

segmented(cghSeg), segmented(cghSeg,matrix)<- Access and set elements named segmented in the AssayData-class slot.

chromosomes, bpstart, bpend Access the chromosomal positions stored in featureData

plot Create a plot containing log2ratios and segments ordered by chromosomal position. TWO EXTRA OPTIONS PLUS DEFAULTS: dotres=10. Every dotres-th log2-ratio is plotted. dotres=1 plots all data. However, higher values save a lot of space and allow quicker browsing of the plots. ylimit=c(-2,5): limits of the y-axis

See eSet for derived methods.

Author(s)

Sjoerd Vosse

See Also

eSet-class, cghRaw-class, cghCall-class

Examples

```
# create an instance of cghSeg
new("cghSeg")

# create an instance of cghSeg through \code{segmentData}
## Not run:
   data(Wilting)
   rawcgh <- make_cghSeg(Wilting)
   normalized <- normalize(rawcgh)
   segmented <- segmentData(normalized)
```

```
  # plot the first sample. Default only every 10th log2-ratio is plotted (dotres=10). Adjust using dotres= option be
   plot(segmented[,1])
   # first three chromosomes
   plot(segmented[chromosomes(segmented)<=3,1])

   # get the copynumber values of the third and fourth sample
   log2ratios <- copynumber(segmented[,3:4])

   # get the names of the samples
   sampleNames(segmented)

   # get the names of the array elements
   featureNames(segmented)

## End(Not run)
```

---

chromosomes *Retrieve feature position data from cgh objects.*

Description

These generic functions access the position data stored in the featureData of an object derived from the cghRaw-class, cghSeg-class or cghCall-class.

Usage

```
chromosomes(object)
bpstart(object)
bpend(object)
```

Arguments

object	Object derived from class cghRaw, cghSeg, or cghCall

Value

chromosomes returns a vector of chromosome numbers; bpstart returns a vector of basepair start positions; bpend returns a vector of basepair end positions;

Author(s)

Sjoerd Vosse

See Also

cghRaw-class, cghSeg-class, cghCall-class

copynumber *Retrieve copynumber data from cgh objects.*

Description

These generic functions access the copynumber values of assay data stored in an object derived from the cghRaw-class, cghSeg-class or cghCall-class.

Usage

```
copynumber(object)
copynumber(object) <- value
segmented(object)
segmented(object) <- value
calls(object)
calls(object) <- value
```

Arguments

object	Object derived from class cghRaw, cghSeg, or cghCall
value	Matrix with rows representing features and columns samples.

Value

copynumber returns a matrix of copynumber values;

Author(s)

Sjoerd Vosse

See Also

cghRaw-class, cghSeg-class, cghCall-class

Examples

```
data(WiltingCalled)
log2ratios <- copynumber(WiltingCalled)
segments <- segmented(WiltingCalled)
calls <- calls(WiltingCalled)
```

`frequencyPlot` *Visualization of aCGH regions.*

Description

This function creates a frequency plot for aCGH regions.

Usage

```
frequencyPlot(x, y, ...)
```

Arguments

`x`	An object of class `cghRegions`.
`y`	This argument is not used and should be missing.
`...`	Arguments `plot`.

Details

We find plotted on the x-axis the array probes sorted by chromosomal position. The vertical bars represent the frequency of gains and losses across your samples. The black bars represent gains, the gray bars represent losses.

Value

This function creates a plot.

Author(s)

Mark van de Wiel and Sjoerd Vosse

References

Mark A. van de Wiel and Wessel N. van Wieringen (2007). CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. *Cancer Informatics, 2*, 55-63.

Examples

```
## Not run:
 data(WiltingRegions)
 frequencyPlot(WiltingRegions)

## End(Not run)
```

`frequencyPlotCalls` *Visualization of aCGH profiles.*

Description

This function creates a frequency plot for aCGH profiles.

Usage

```
frequencyPlotCalls(x,main='Frequency Plot', gaincol='blue', losscol='red', misscol=NA, build='GRCh37
```

Arguments

`x`	An object of class `cghCall`.
`main`	Title of plot
`gaincol`	Color to use for gains
`losscol`	Color to use for losses
`misscol`	Missings
`build`	Build of Humane Genome.Either `GRCh37`, `GRCh36`, `GRCh35` or `GRCh34`
`...`	Arguments `plot`.

Details

We find plotted on the x-axis the array probes sorted by chromosomal position. The vertical bars represent the frequency of gains or losses.

Value

This function creates a plot.

Author(s)

Sjoerd Vosse & Mark van de Wiel

References

Mark A. van de Wiel, Kyung In Kim, Sjoerd J. Vosse, Wessel N. van Wieringen, Saskia M. Wilting and Bauke Ylstra. CGHcall: calling aberrations for array CGH tumor profiles. *Bioinformatics, 23*, 892-894.

Examples

```
## Not run:
 data(Wilting)
 rawcgh <- make_cghSeg(Wilting)
 normalized <- normalize(rawcgh)
 segmented <- segmentData(normalized)
 called <- CGHcall(segmented,cellularity= rep(0.75, 3))
 frequencyPlotCalls(called)

## End(Not run)
```

---

make_cghRaw — *Convert a dataframe or textfile to an object of class cghRaw.*

Description

This function converts a dataframe of appropriote format to an object of class cghRaw.

Usage

```
make_cghRaw(input)
```

Arguments

input	Either a dataframe or character string containing a filename. See details for the format.

Details

The input should be either a dataframe or a tabseparated textfile (textfiles must contain a header). The first four columns should contain the name, chromosome and the start and end position in bp for each array target respectively. The chromosome and position column must contain numbers only. Following these is a column with log2 ratios for each of your samples. If the input type is a textfile, missing values should be represented as 'NA' or an empty field.

Value

This function returns an object of class cghRaw-class.

Author(s)

Sjoerd Vosse & Mark van de Wiel

Examples

```
data(Wilting)
## Convert to \code{\link{cghRaw}} object
cgh <- make_cghRaw(Wilting)
```

plot.cghRaw *Plot aCGH data.*

Description

Please see the class descriptions for more details on the plot functions.

Usage

```
  ## S3 method for class 'cghRaw'
plot(x, y, ...)
  ## S3 method for class 'cghSeg'
plot(x, y, ...)
  ## S3 method for class 'cghCall'
plot(x, y, ...)
  ## S3 method for class 'cghRegions'
plot(x, y, ...)
```

Arguments

x	An object of class cghRaw, cghSeg, cghCall, or cghSeg.
y	This argument is not used and should be missing.
...	Arguments plot.

Author(s)

Sjoerd Vosse

See Also

cghRaw-class, cghSeg-class, cghCall-class, cghRegions-class

probloss *Retrieve call probabilities from a cghCall object.*

Description

These generic functions access the call probabilities from assay data stored in a object derived from the cghCall-class.

Usage

```
probdloss(object)
probdloss(object) <- value
probloss(object)
probloss(object) <- value
probnorm(object)
probnorm(object) <- value
probgain(object)
probgain(object) <- value
probamp(object)
probamp(object) <- value
```

Arguments

`object`	Object derived from class `cghCall`
`value`	Matrix with rows representing features and columns samples.

Value

`probloss` returns matrix of call probabilities;

Author(s)

Sjoerd Vosse

See Also

`cghCall-class`

`regions` *Retrieve regions data from cghRegions object.*

Description

This function accesses the regions values of assay data stored in an object derived from the `cghRegions-class`.

Usage

```
regions(object)
regions(object) <- value
```

Arguments

`object`	Object derived from class `cghRegions`
`value`	Matrix with rows representing features and columns samples.

Value

`regions` returns a matrix of regions values;

Author(s)

Sjoerd Vosse

See Also

`cghRegions-class`

---

summaryPlot *Visualization of aCGH profiles.*

Description

This function creates a summary plot for aCGH profiles.

Usage

```
summaryPlot(x,main='Summary Plot', gaincol='blue', losscol='red', misscol=NA, build='GRCh37', ...)
```

Arguments

`x`	An object of class `cghCall`.
`main`	Title of plot
`gaincol`	Color to use for gains
`losscol`	Color to use for losses
`misscol`	Missings
`build`	Build of Humane Genome.Either `GRCh37`, `GRCh36`, `GRCh35` or `GRCh34`
`...`	Arguments `plot`.

Details

We find plotted on the x-axis the array probes sorted by chromosomal position. The vertical bars represent the average probability that the positions they cover are gained (green bars) or lost (red bars). The green bars represent gains, the red bars represent losses.

Value

This function creates a plot.

Author(s)

Sjoerd Vosse & Mark van de Wiel

References

Mark A. van de Wiel, Kyung In Kim, Sjoerd J. Vosse, Wessel N. van Wieringen, Saskia M. Wilting and Bauke Ylstra. CGHcall: calling aberrations for array CGH tumor profiles. *Bioinformatics, 23*, 892-894.

Examples

```
  ## Not run:
  data(Wilting)
   rawcgh <- make_cghSeg(Wilting)
   normalized <- normalize(rawcgh)
   segmented <- segmentData(normalized)
   called <- CGHcall(segmented,cellularity= rep(0.75, 3))
   summaryPlot(called)

## End(Not run)
```

`Wilting` *Cervical cancer arrayCGH data*

Description

A dataframe containing 4709 rows and 8 columns with arrayCGH data.

Usage

```
Wilting
```

Format

A dataframe containing the following 8 columns:

Name The unique identifiers of array elements.

Chromosome Chromosome number of each array element.

Position Chromosomal position in bp of each array element.

AdCA10 Raw log2 ratios for cervical cancer sample AdCA10.

SCC27 Raw log2 ratios for cervical cancer sample SCC27.

SCC32 Raw log2 ratios for cervical cancer sample SCC32.

SCC36 Raw log2 ratios for cervical cancer sample SCC36.

SCC39 Raw log2 ratios for cervical cancer sample SCC39.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology, 210*, 258-259.

WiltingCalled — *Cervical cancer arrayCGH data called with CGHcall*

Description

Cervical cancer arrayCGH data called with `CGHcall` with default settings, containing 3552 features for 5 samples.

Usage

```
WiltingCalled
```

Format

An object of class `cghCall`

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology, 210*, 258-259.

Mark A. van de Wiel, Kyung In Kim, Sjoerd J. Vosse, Wessel N. van Wieringen, Saskia M. Wilting and Bauke Ylstra. CGHcall: calling aberrations for array CGH tumor profiles. *Bioinformatics, 23*, 892-894.

WiltingNorm — *Normalized log2 ratios from cervical cancer arrayCGH data.*

Description

Normalized log2 ratios frm cervical cancer arrayCGH data, containing 3552 features for 5 samples. These data have been normalized using the `normalize` function with default settings.

Usage

```
WiltingCalled
```

Format

An object of class `cghRaw`.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology, 210*, 258-259.

WiltingRaw — *Raw log2 ratios from cervical cancer arrayCGH data.*

Description

Raw log2 ratios from cervical cancer arrayCGH data, containing 3552 features for 5 samples. These data have been preprocessed using `preprocess`.

Usage

```
WiltingCalled
```

Format

An object of class `cghRaw`.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology, 210*, 258-259.

WiltingRegions — *Regions of cervical cancer arrayCGH data as defined by CGHregions*

Description

Regions of cervical cancer arrayCGH data as defined by `CGHregions` with default settings, containing 90 regions over 5 samples.

Usage

```
WiltingRegions
```

Format

An object of class `cghRegions`

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology, 210*, 258-259.

Mark A. van de Wiel and Wessel N. van Wieringen (2007). CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. *Cancer Informatics, 2*, 55-63.

`WiltingSeg` *Segmented log2 ratios from cervical cancer arrayCGH data.*

Description

Segmented log2 ratios from cervical cancer arrayCGH data, containing 3552 features for 5 samples. These data have been segmented using `segmentData` with default settings.

Usage

```
WiltingCalled
```

Format

An object of class `cghSeg`.

Source

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Index

∗ **classes**
- cghCall, 3
- cghRaw, 6
- cghRegions, 7
- cghSeg, 9

∗ **datasets**
- Wilting, 19
- WiltingCalled, 20
- WiltingNorm, 20
- WiltingRaw, 21
- WiltingRegions, 21
- WiltingSeg, 22

∗ **manip**
- avedist, 3
- chromosomes, 11
- copynumber, 12
- probloss, 16
- regions, 17

∗ **misc**
- frequencyPlot, 13
- frequencyPlotCalls, 14
- make_cghRaw, 15
- summaryPlot, 18

∗ **package**
- CGHbase-package, 2

AnnotatedDataFrame, *4*, *6*, *8*, *10*
AssayData, *8*
avedist, 3
avedist,cghRegions-method *(*cghRegions*)*, 7

bpend *(*chromosomes*)*, 11
bpend,cghCall-method *(*cghCall*)*, 3
bpend,cghRaw-method *(*cghRaw*)*, 6
bpend,cghRegions-method *(*cghRegions*)*, 7
bpend,cghSeg-method *(*cghSeg*)*, 9
bpstart *(*chromosomes*)*, 11
bpstart,cghCall-method *(*cghCall*)*, 3
bpstart,cghRaw-method *(*cghRaw*)*, 6
bpstart,cghRegions-method *(*cghRegions*)*, 7
bpstart,cghSeg-method *(*cghSeg*)*, 9

calls *(*copynumber*)*, 12
calls,cghCall-method *(*cghCall*)*, 3
calls<- *(*copynumber*)*, 12
calls<-,cghCall,matrix-method *(*cghCall*)*, 3
CGHbase *(*CGHbase-package*)*, 2
CGHbase-package, 2
CGHcall, *4*, *20*
cghCall, *2*, 3, *14*, *16*, *18*, *20*
cghCall-class *(*cghCall*)*, 3
cghRaw, *2*, 6, *16*, *20*, *21*
cghRaw-class *(*cghRaw*)*, 6
CGHregions, *8*, *21*
cghRegions, 7, *13*, *21*
cghRegions-class *(*cghRegions*)*, 7
cghSeg, *2*, 9, *16*, *22*
cghSeg-class *(*cghSeg*)*, 9
chromosomes, 11
chromosomes,cghCall-method *(*cghCall*)*, 3
chromosomes,cghRaw-method *(*cghRaw*)*, 6
chromosomes,cghRegions-method *(*cghRegions*)*, 7
chromosomes,cghSeg-method *(*cghSeg*)*, 9
class:cghCall *(*cghCall*)*, 3
class:cghRaw *(*cghRaw*)*, 6
class:cghRegions *(*cghRegions*)*, 7
class:cghSeg *(*cghSeg*)*, 9
copynumber, 12
copynumber,cghCall-method *(*cghCall*)*, 3
copynumber,cghRaw-method *(*cghRaw*)*, 6
copynumber,cghSeg-method *(*cghSeg*)*, 9
copynumber<- *(*copynumber*)*, 12
copynumber<-,cghCall,matrix-method *(*cghCall*)*, 3
copynumber<-,cghRaw,matrix-method *(*cghRaw*)*, 6

copynumber<-,cghSeg,matrix-method (cghSeg), 9

eSet, *3–10*

frequencyPlot, 13
frequencyPlot,cghRegions,missing-method (cghRegions), 7
frequencyPlotCalls, 14
frequencyPlotCalls,cghCall,missing-method (cghCall), 3

initialize,cghCall-method (cghCall), 3
initialize,cghRaw-method (cghRaw), 6
initialize,cghRegions-method (cghRegions), 7
initialize,cghSeg-method (cghSeg), 9

make_cghRaw, 15

nclone (avedist), 3
nclone,cghRegions-method (cghRegions), 7
normalize, *20*

plot,cghCall,missing-method (cghCall), 3
plot,cghRaw,missing-method (cghRaw), 6
plot,cghSeg,missing-method (cghSeg), 9
plot.cghCall (plot.cghRaw), 16
plot.cghRaw, 16
plot.cghRegions (plot.cghRaw), 16
plot.cghRegions,cghRegions,missing-method (cghRegions), 7
plot.cghSeg (plot.cghRaw), 16
plot.summary,cghCall,missing-method (cghCall), 3
preprocess, *21*
probamp (probloss), 16
probamp,cghCall-method (cghCall), 3
probamp<- (probloss), 16
probamp<-,cghCall,matrix-method (cghCall), 3
probdloss (probloss), 16
probdloss,cghCall-method (cghCall), 3
probdloss<- (probloss), 16
probdloss<-,cghCall,matrix-method (cghCall), 3
probgain (probloss), 16
probgain,cghCall-method (cghCall), 3
probgain<- (probloss), 16
probgain<-,cghCall,matrix-method (cghCall), 3
probloss, 16
probloss,cghCall-method (cghCall), 3
probloss<- (probloss), 16
probloss<-,cghCall,matrix-method (cghCall), 3
probnorm (probloss), 16
probnorm,cghCall-method (cghCall), 3
probnorm<- (probloss), 16
probnorm<-,cghCall,matrix-method (cghCall), 3

regions, 17
regions,cghRegions-method (cghRegions), 7
regions<- (regions), 17
regions<-,cghRegions,matrix-method (cghRegions), 7

segmentData, *9*, *22*
segmented (copynumber), 12
segmented,cghCall-method (cghCall), 3
segmented,cghSeg-method (cghSeg), 9
segmented<- (copynumber), 12
segmented<-,cghCall,matrix-method (cghCall), 3
segmented<-,cghSeg,matrix-method (cghSeg), 9
summaryPlot, 18

Wilting, *2*, 19
WiltingCalled, *2*, 20
WiltingNorm, *2*, 20
WiltingRaw, *2*, 21
WiltingRegions, 21
WiltingSeg, *2*, 22