

# Package ‘CGHbase’

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**Type** Package

**Title** CGHbase: Base functions and classes for arrayCGH data analysis.

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**Depends** R (>= 2.10), methods, Biobase (>= 2.5.5), marray

**Description** Contains functions and classes that are needed by arrayCGH packages.

**License** GPL

**Collate** allGeneric.R classes.R private.R tools.R methods-cghRaw.R  
methods-cghSeg.R methods-cghCall.R methods-cghRegions.R

**biocViews** Infrastructure, Microarray, CopyNumberVariation

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CGHbase-package	<i>CGHbase: Base functions and classes for arrayCGH data analysis.</i>
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## 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](mailto:sjoerdvos@yahoo.com)>

---

avedist	<i>Retrieve regions information from cghRegions object.</i>
---------	---

---

## 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 representing 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. `ylim=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 human 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= optio
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 representing 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 representing 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 representing 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
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**

<code>object</code>	Object derived from class <code>cghRaw</code> , <code>cghSeg</code> , or <code>cghCall</code>
<code>value</code>	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	<i>Visualization of aCGH regions.</i>
---------------	---------------------------------------

---

### Description

This function creates a frequency plot for aCGH regions.

### Usage

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

### Arguments

x	An object of class <a href="#">cghRegions</a> .
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 <code>cghCall</code> .
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 appropriate 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 \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](#)

---

probdloss

*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
probdloss(object)
probdloss(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	<i>Visualization of aCGH profiles.</i>
-------------	--

---

## 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 <code>cghCall</code> .
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 log<sub>2</sub> ratios for cervical cancer sample AdCA10.

**SCC27** Raw log<sub>2</sub> ratios for cervical cancer sample SCC27.

**SCC32** Raw log<sub>2</sub> ratios for cervical cancer sample SCC32.

**SCC36** Raw log<sub>2</sub> ratios for cervical cancer sample SCC36.

**SCC39** Raw log<sub>2</sub> 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 from 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.

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WiltingSeg

*Segmented log2 ratios from cervical cancer arrayCGH data.*

---

**Description**

Segmented log<sub>2</sub> 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**

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.

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