CGHbase
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| 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)
chromosomes

**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

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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: WiltingData, WiltingRaw, WiltingNorm, WiltingSeg, WiltingCalled.

**Author(s)**

Sjoerd Vosse <sjoerdvos@yahoo.com>

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**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`
**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

---

**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 Log2 copynumber ratios.
- segmented Segmented log2 ratios.
- calls Called copynumber values.
- probloss Loss probabilities as returned by CGHcall.
- probnorm Normal probabilities as returned by CGHcall.
- probgain Gain probabilities as returned by CGHcall.
- probamp Optional amplification probabilities as returned by CGHcall when run with nclass=4.

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` Log2 copynumber ratios.
- `segmented` Segmented log2 ratios.
- `calls` Called copynumber values.
- `probloss` Loss probabilities as returned by `CGHcall`.
- `probnorm` Normal probabilities as returned by `CGHcall`.
- `probgain` Gain probabilities as returned by `CGHcall`.
- `probamp` Optional amplification probabilities as returned by `CGHcall` when run with `nclass=4`.

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.cghCall` Create a plot containing log2ratios, segments and call probabilities ordered by chromosomal position

- `summaryPlot` Create a plot summarizing the call probabilities of all samples

See `eSet` for derived methods.

**Author(s)**

Sjoerd Vosse
cghRaw

See Also
eSet-class, cghRaw-class, cghSeg-class

Examples

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

# load an instance of cghCall
data(WiltingCalled)

# plot the first sample
plot.cghCall(WiltingCalled[,1])

# plot the first chromosome of the first sample
plot.cghCall(WiltingCalled[chromosomes(WiltingCalled)==1,1])

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

# get the names of the samples
sampleNames(WiltingCalled)

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

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

everything('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.cghRaw` 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

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

# create an instance of cghRaw from a dataframe
data(WiltingData)
cghobj <- cghRaw(WiltingData)

# plot the first sample
plot.cghRaw(cghobj[,1])
# first three chromosomes
plot.cghRaw(cghobj[chromosomes(cghobj)==1,1])

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

# get the names of the samples
sampleNames(cghobj)

# get the names of the array elements
featureNames(cghobj)
```
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, cghSeg, cghCall

**Examples**

```r
# create an instance of cghRegions
ew("cghRegions")

# load an instance of cghRegions
data(WiltingRegions)

# plot all region data
plot.cghRegions(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**

```r
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 \( nrow(\text{phenoData}) \). 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.cghSeg** Create a plot containing log2ratios and segments ordered by chromosomal position

See eSet for derived methods.

Author(s)

Sjoerd Vosse

See Also

eSet-class, cghRaw-class, cghCall-class

Examples

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

# load an instance of cghSeg
data(WiltingSeg)

# plot the first sample
# plot.cghSeg(WiltingSeg[,1])
# first three chromosomes
# plot.cghSeg(WiltingSeg[chromosomes(WiltingSeg)==1,])

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

# get the names of the samples
sampleNames(WiltingSeg)
```
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 cgRegions.
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

Examples

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

## End(Not run)
plot.cghRaw  \hspace{1cm} \textit{Plot aCGH data.}

\section*{Description}

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

\section*{Usage}

\begin{verbatim}
plot.cghRaw(x, y, ...)
plot.cghSeg(x, y, ...)
plot.cghCall(x, y, ...)
plot.cghRegions(x, y, ...)
\end{verbatim}

\section*{Arguments}

\begin{itemize}
\item \texttt{x} \hspace{1cm} An object of class \texttt{cghRaw, cghSeg, cghCall}, or \texttt{cghSeg}.
\item \texttt{y} \hspace{1cm} This argument is not used and should be missing.
\item \texttt{...} \hspace{1cm} Arguments \texttt{plot}.
\end{itemize}

\section*{Author(s)}

Sjoerd Vosse

\section*{See Also}

\texttt{cghRaw-class, cghSeg-class, cghCall-class, cghRegions-class}

\section*{probloss  \hspace{1cm} Retrieve call probabilities from a cghCall object.}

\section*{Description}

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

\section*{Usage}

\begin{verbatim}
probloss(object)
probloss(object) <- value
probnorm(object)
probnorm(object) <- value
probgain(object)
probgain(object) <- value
probamp(object)
probamp(object) <- value
\end{verbatim}
regions

Arguments

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

Value

These functions return matrices of call probabilities.

Author(s)

Sjoerd Vosse

See Also

cghCall-class

cghRegions-class

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, y, ...)

Arguments

x
An object of class cghCall.

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 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. When 4 levels have been used for calling, amplifications are indicated with a blue tickmark at the top of the plot.

Value

This function creates a plot.

Author(s)

Sjoerd Vosse & Mark van de Wiel

References


Examples

```r
## Not run:
data(Wilting)
rawcgh <- make_cghSeg(Wilting)
normalized <- normalize(rawcgh)
segmented <- segmentData(normalized)
called <- CGHcall(segmented)
summaryPlot(called)

## End(Not run)
```
WiltingCalled

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


WiltingData

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.
WiltingRaw

Source

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

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
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


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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