Package ‘CGHbase’

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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.


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
cghCall

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], ... 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

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= option.
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])

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 \( \text{nrow(phenodata)} \). 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)==1:3])

# 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

```r
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 = [char]

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**

```r
# 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**

```r
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**

```r
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**

```r
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


Examples

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

## End(Not run)
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 Human Genome. Either `GRCh37`, `GRCh36`, `GRCh35` or `GRCh34`.
- **...**: Arguments to `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


Examples

```r
## 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 \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.
## probloss

### Usage

```r
## 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

```r
probloss(object)
probloss(object) <- value
probloss(object)
probloss(object) <- value
probloss(object)
probloss(object) <- value
probloss(object)
probloss(object) <- value
probloss(object)
probloss(object) <- value
```

### Arguments

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

Value
probloss returns matrix of call probabilities;

Author(s)
Sjoerd Vosse

See Also
cghCall-class

description Retrieve regions data from cghRegions object.

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

Examples
```r
## 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.

Source

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
WiltingNorm

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.
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