CGHbase
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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 within class help pages.

Attached data sets: WiltingData, WiltingRaw, WiltingNorm, WiltingSeg, WiltingCalled.

Author(s)

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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


### WiltingData

**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**

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

**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 \texttt{cghRegions}.

**Source**


### WiltingSeg

**Description**

Segmented log2 ratios from cervical cancer arrayCGH data.

**Usage**

WiltingCalled

**Format**

An object of class \texttt{cghSeg}.

**Source**

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

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

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

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

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`.

- **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
**See Also**

eSet-class, cghRaw-class, cghSeg-class

**Examples**

```r
# 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**

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

`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

# 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**

```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
\[\text{eSet, cghRaw, cghSeg, cghCall}\]

### Examples

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

### 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(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)==1,1])

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

# get the names of the samples
sampleNames(WiltingSeg)
```
# get the names of the array elements
featureNames(WiltingSeg)

## copynumber

Retrieves 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

```r
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

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

## End(Not run)
```
plot.cghRaw

Plot aCGH data.

Description

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

Usage

plot.cghRaw(x, y, ...)
plot.cghSeg(x, y, ...)
plot.cghCall(x, y, ...)
plot.cghRegions(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

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

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, 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)
```
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