Package ‘CNAnorm’
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Title A normalization method for Copy Number Aberration in cancer samples
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Depends R (>= 2.10.1), methods
Description Performs ratio, GC content correction and normalization of data obtained using low coverage (one read every 100-10,000 bp) high throughput sequencing. It performs a "discrete" normalization looking for the ploidy of the genome. It will also provide tumour content if at least two ploidy states can be found.
License GPL-2
Imports DNAcopy
URL http://www.r-project.org.
LazyLoad yes
biocViews CopyNumberVariation, Sequencing, Coverage, Normalization, WholeGenome, DNASeq, GenomicVariation
NeedsCompilation yes

R topics documented:

  addDNACopy .................................................. 2
  addSmooth ................................................... 3
  chromosomesPosition ....................................... 4
  CN ............................................................ 5
  CNAnorm-class ............................................... 6
  CNAnormWorkflow ........................................... 7
Methods for Function `addDNACopy` in Package ‘CNAnorm’

Description

`addSmooth` segment ratio values in Package ‘CNAnorm’ using DNACopy

Usage

```r
## S4 method for signature 'CNAnorm'
addDNAcopy(object, independent.arms = FALSE, ideograms = NULL,
            DNAcopy.smooth = list(), DNAcopy.weight = character(), DNAcopy.segment = list())
```

Arguments

- `object`: An object of Class "CNAnorm"
- `independent.arms`: Boolean. If TRUE chromosomes arms will be treated as independent, ideograms must be provided
- `ideograms`: A data frame containing information about banding. See `?hg19_hs_ideogr` for more information
- `DNAcopy.smooth`: A list of parameters to be passed to function `smooth.CNA` in package DNAcopy
- `DNAcopy.weight`: A character value of one of these values, ‘poisson’, ‘gaussian’, ‘twoTailQuantile’, ‘oneTailQuantile’. It specifies a way to give weight to each window depending on how much coverage in the normal deviates from the median for that chromosome. Options are listed in decreasing order of stringency. See Details
- `DNAcopy.segment`: A list of parameters to be passed to function ‘segment’ in package DNAcopy. Parameters ‘weights’ and ‘verbose’ are not accepted
Details

'poisson': windows with coverage more or less than \(2\sqrt{\text{mean}}\) from the mean are weighted down. The most stringent. Recommended for unbiased genome wide sequencing.

'gaussian': windows with coverage more or less than \(2\sigma\) from the median are weighted down. Recommended for genome wide sequencing where coverage in the normal is far from poisson distribution.

'twoTailQuantile': windows with coverage outside 5-95th quantile are weighted down. Recommended when coverage is far from a normal distribution - such as capture experiments -

'oneTailQuantile': windows with coverage lower than 5th quantile are weighted down. Recommended when coverage is far from a normal distribution - such as capture experiments. Does not weight down windows with very high coverage.

Value

An object of class "CNAnorm"

Methods

\texttt{signature(object = "CNAnorm" )} Segment ratio values on an object of class "CNAnorm". Returns the same object with extra slots (\texttt{segMean, segID} )

Author(s)

Stefano Berri <s.berri@leeds.ac.uk> and Arief Gusnanto <a.gusnanto@leeds.ac.uk>

References

Venkatraman, E. S. and Olshen, A. B. (2007) \textit{A faster circular binary segmentation algorithm for the analysis of array CGH data}. Bioinformatics

See Also

\texttt{segMean, CNAnorm-class, DNAcopy, hg19_hs_ideogr}

Examples

data(LS041)
CN <- dataFrame2object(LS041)
CN <- addDNACopy(CN)

```r
addSmooth
```

Description

\texttt{addSmooth} segment and smooth perform ratio values in Package ‘CNAnorm’

Usage

```r
## S4 method for signature 'CNAnorm'
addSmooth(object, lambda = 7, ...)
```
Arguments

object: An object of Class "CNAnorm"
lambda: Degree of smoothness. See reference for more details
...

Value

An object of class "CNAnorm"

Methods

signature(object = "CNAnorm") Segment and smooth perform ratio values on an object of class "CNAnorm". Returns the same object with extra slot (ratio.s)

Author(s)

Stefano Berri <s.berri@leeds.ac.uk> and Arief Gusnanto <a.gusnanto@leeds.ac.uk>

References


See Also

t ratio.s, CNAnorm-class

Examples

data(LS041)
CN <- dataFrame2object(LS041)
CN.gcNorm <- gcNorm(CN, exclude = c("chrX", "chrY", "chrM"))
CN.smooth <- addSmooth(CN)

Description

chrs returns/set the name of chromosomes/contigs
arms returns the name of the chromosome and arm. A data frame containing ideogram information has to be provided. See ?hg19_hs_ideogr for an example
pos returns/set the position of starting window. Be careful! If you need to change data, it is better to change the input data and start over.

Usage

chrs(object)
## S4 method for signature 'CNAnorm'
pos(object, show = "start")
## S4 method for signature 'CNAnorm'
arms(object, banding_df)
Arguments

object An object of Class “CNAnorm”
show The position to show: ‘start’, ‘end’
banding_df A data frame with information about ideogram

Value

chrs and arms return a character vector, pos returns a numeric vector

Author(s)

Stefano Berri <s.berri@leeds.ac.uk>

See Also

gcNorm, CNAnorm-class, hg19_hs_ideogr

Examples

data(LS041)
data(hg19_hs_ideogr)
CN <- dataFrame2object(LS041)
dataFrameNames <- as.character(LS041$Chr)
objectNames <- chrs(CN)
armNames <- arms(CN, hg19_hs_ideogr)
# check the names are, indeed, the same
all(dataFrameNames == objectNames)
# make shorter names, drop the first three letters (‘chr’)
shortNames <- substr(chrs(CN),4,nchar(chrs(CN)))
chrs(CN) <- shortNames

# retrieve all new names
unique(chrs(CN))
unique(armNames)

CN A CNAnorm object with information about most abundant ploidy states, obtained from data LS041.

Description

This data is to provide an object to use in several examples without having to wait for computing it.
To see how it was generated, see documentation of function peakPloidy.

Usage

data(CN)

Format

A CNAnorm object
Class "CNAnorm"

**Description**

Class to Contain and Describe copy number aberration (CNA) data from low coverage (approx 0.01 - 0.5X) Next Generation Sequencing

**Objects from the Class**

Objects can be created by calls of the form `new("CNAnorm", InData)`.

**Slots**

- **InData**: Object of class "InData". Contains input data provided by the user. All slots have same length. Each element describe one window. See Class "InData"
- **DerivData**: Object of class "DerivData". Contains data derived from "InData". It can be Retrieved by the user, but methods should be used to populate "DerivData". All slots have same length as input data. See Class DerivData
- **Res**: Object of class "Res". Contains slots with obtained results. See Class "Res"
- **Params**: Object of class "Params". Contains crucial parameters passed to some of the methods for reusing in later steps or for documentation.

**Methods**

Summary of methods for class "CNAnorm". Type "methods ? methodName" for more details about methodName.

- **chrs** signature(object = "CNAnorm"): Retrieve Chromosomes/contig name
- **chrs<-** signature(object = "CNAnorm"): Set Chromosomes/contig name
- **guessPeaksAndPloidy** signature(object = "CNAnorm"): Estimate ploidy of the sample, tumor content and other results saved in Slot "Res"
- **length** signature(x = "CNAnorm"): Returns number of element/windows
- **[** signature(x = "CNAnorm"): Produce on object of class "CNAnorm" with a subser of windows
- **plotGenome** signature(object = "CNAnorm"): Plot annotated normalized genome copy number
- **plotPeaks** signature(object = "CNAnorm"): Plot peaks and estimated/validated ploidy
- **pos** signature(object = "CNAnorm"): Retrieve Chromosomes/contig position
- **pos<-** signature(object = "CNAnorm"): Set Chromosomes/contig position
- **ratio** signature(object = "CNAnorm"): Retrieve ratio (Test/Control). If gcNorm was called, ratio is GC normalized
- **ratio.n** signature(object = "CNAnorm"): Retrieve normalized ratio (not smoothed)
- **ratio.s** signature(object = "CNAnorm"): Retrieve smoothed ratio
- **ratio.n.s** signature(object = "CNAnorm"): Retrieve normalized smoothed ratio
- **segMean** signature(object = "CNAnorm"): Retrieve segmented ratio (as provided by DNA-copy)
- **segMean.n** signature(object = "CNAnorm"): Retrieve normalized segmented ratio
**CNAnormWorkflow**

**Author(s)**
Stefano Berri <s.berri@leeds.ac.uk> and Arief Gusnanto <a.gusnanto@leeds.ac.uk>

**References**
CNA-norm: Discrete Normalization of Copy Number Alteration data from clinical samples (in preparation)

**See Also**
*InData, DerivData* for documentation on the slots.

**Examples**
```r
data(LS041)
CNA <- new("CNAnorm", InData = new("InData", Chr = as.character(LS041$Chr), Pos = LS041$Pos,
Test = LS041$Test, Norm = LS041$Norm, GC = LS041$GC))
```

**Description**
This function is a wrapper to use for a fully automated CNAnorm workflow where interactivity is not required. It contains MOST possible parameters. Defaults are set to run a standard and conservative workflow.

**Usage**
```
CNAnormWorkflow(dataFrame, gc.do=FALSE, gc.exclude=character(0),
 gc.maxNumPoints=10000, smooth.do=TRUE, smooth.lambda=7,
 smooth.other=list(), peak.method="closest", peak.exclude=character(0),
 peak.ploidyToTest=12, peak.sd=5, peak.dThresh=0.01, peak.n=2048,
 peak.adjust=.9, peak.force.smooth=TRUE, peak.reg=FALSE, peak.ds=1.5,
 peak.zero.count=FALSE, peak.other=list(), DNAcopy.do=TRUE,
 DNAcopy.independent.arms=FALSE, DNAcopy.ideograms=NULL,
 DNAcopy.smooth=list(), DNAcopy.segment=list(), DNAcopy.weight=character(),
 dNorm.normBy=NULL)
```

**Arguments**
- `dataFrame`: A data frame with columns Chr, Pos, Test, Norm and optional GC. See `DataFrame2object`.
- `gc.do`: Specify if GC correction need to be done. See `gcNorm`.
- `gc.exclude`: See `gcNorm`.
- `gc.maxNumPoints`: See `gcNorm`.
- `smooth.do`: Specify if smoothing need to be done. See `addSmooth`.
- `smooth.lambda`: See `addSmooth`.

All arguments are explained in the relative functions.
smooth other  A list of other parameters to pass to the smoothing function. See addSmooth
peak method  See peakPloidy
peak exclude  See peakPloidy
peak ploidyToTest  See peakPloidy
peak sd  See peakPloidy
peak dThresh  See peakPloidy
peak n  See peakPloidy
peak adjust  See peakPloidy
peak force smooth  See peakPloidy
peak reg  See peakPloidy
peak ds  See peakPloidy
peak zero count  See peakPloidy
peak other  A list of other parameters to be passed to functions for peak detection. See peakPloidy
DNAcopy do  Specify if segmentation with DNAcopy need to be done. See addDNACopy
DNAcopy independent arms  See addDNACopy
DNAcopy ideograms  See addDNACopy
DNAcopy smooth  See addDNACopy
DNAcopy segment  See addDNACopy
DNAcopy weight  See addDNACopy
dNorm normBy  See discreteNorm

Value
An object of Class "CNAnorm"

Author(s)
Stefano Berri <s.berri@leeds.ac.uk>

See Also
dataFrame2object, gcNorm, addSmooth, peakPloidy, addDNACopy, discreteNorm

Examples
data(LS041)
CN <- CNAnormWorkflow(LS041)
**dataFrame2object**

Convert a data frame into an object of Class "CNAnorm"

**Description**

Convert a data frame with column: Chr, Pos, Test, Norm and optional GC into object of class "CNAnorm"

**Usage**

dataFrame2object(dataFrame)

**Arguments**

dataFrame A data frame with columns Chr, Pos, Test, Norm and optional GC

**Value**

An object of Class "CNAnorm"

**Author(s)**

Stefano Berri <s.berri@leeds.ac.uk>

**See Also**

CNAnorm-class, InData-class, data.frame

**Examples**

data(LS041)
CN <- dataFrame2object(LS041)

---

**DerivData-class**

Class "DerivData"

**Description**

A Class containing data derived from InData used for further computation and plotting.

**Objects from the Class**

Objects can be created by calls of the form new("DerivData"), however DerivData is typically populated using methods. If a slot has not been populated yet, it has zero length, otherwise slots have the same length as InData.
discreteNorm

Slots
ratio: Numeric vector with ratio Test/Normal. Optionally GC corrected.
ratio.s: Numeric vector with smoothed ratio.
ratio.n: Numeric vector with normalized ratio.
ratio.s.n: Numeric vector with normalized and smoothed ratio.
segID: Numeric vector with ID of segmented data (as provided by DNACopy). Each segment has a different ID.
segMean: Numeric vector with mean value of the segment (as provided by DNACopy.)
segMean.n: Numeric vector with normalized segMean.
ok4density: Logical vector. Specify which values have been used to calculate density.

Methods
length signature(x = "DerivData"): Returns number of windows.

Author(s)
Stefano Berri and Arief Gusnanto

References

See Also
CNAnorm, InData-class

Examples
data(LS041)
inObject <- new("InData", Chr = as.character(LS041$Chr),
             Pos = LS041$Pos, Test = LS041$Test, Norm = LS041$Norm,
             GC = LS041$GC)
CNA <- new("CNAnorm", InData = inObject)

discreteNorm

Methods for Function addSmooth in Package ‘CNAnorm’

Description
discreteNorm performs normalization of data using information on ploidy. Implicitly calls "validation" if no validation was performed

Usage
## S4 method for signature 'CNAnorm'
discreteNorm(object, normBy = object)
Arguments

object An object of Class "CNAnorm" to normalize
normBy An object of Class "CNAnorm" used to set normalization. It is possible, for instance, to normalize a sample at high resolution, using information obtained from the same sample at low resolution

Value

An object of class "CNAnorm"

Author(s)

Stefano Berri <s.berri@leeds.ac.uk> and Arief Gusnanto <a.gusnanto@leeds.ac.uk>

References


See Also

validation, peakPloidy

Examples

data(CN)
# see peakPloidy documentation to know how object CN is created
CN <- discreteNorm(CN)

Methods for Function exportTable in Package 'CNAnorm'

Description

exportTable write a table with normalised values of each window. A wrapper to "write.table"

Usage

## S4 method for signature 'CNAnorm'
exportTable(object, file = "CNAnorm_table.tab", show = 'ratio',
            sep = "\t", row.names = FALSE, ...)

Arguments

object an object of Class "CNAnorm"
file name of the file to save to
show what should be reported in the table: "ratio": the normalized ratio (a value of 1 means diploid). "ploidy": the same as ratio * 2. "center": report ratio centered on the most abundant copy. Ratio of 1 means that the most abundant "state" is centered to 1
gcNorm

sep        the field separator string.
row.names  either a logical value indicating whether the row number should be written or a character vector of row names to be written.
...        Extra arguments to be passed to "write.table"

Details

It produces a tab delimited text file with the following columns:
Chr: Chromosome/contig name.
Pos: Starting position of the window.
Ratio: Ratio Test/Normal for each window after GC correction.
Ratio.n: Ratio Test/Normal or ploidy for each window after normalisation.
Ratio.s.n: Smoothed and normalised ratio Test/Normal or ploidy for each window.
SegMean: Mean of the segment this window belongs to.
SegMean.n: Normalised mean ratio Test/Normal or ploidy of the segment this window belongs to.

Value

An object of class "CNAnorm"

Author(s)

Stefano Berri <s.berri@leeds.ac.uk>

See Also

write.table

Examples

data(CN)
CN <- validation(CN)
CN <- discreteNorm(CN)
exportTable(CN, file = "CNAnorm_table.tab", show = 'ploidy')

gcNorm

Methods for Function gcNorm in Package ‘CNAnorm’

Description

gcNorm perform GC content normalization on ratio Test/Normal in Package ‘CNAnorm’

Usage

## S4 method for signature 'CNAnorm'
gcNorm(object, exclude = character(0), maxNumPoints = 10000)
Arguments

object   An object of Class “CNAnorm”
exclude  A character vector with name of chromosomes/contigues not to use to calculate
GC content correction. All genome, however, will be corrected
maxNumPoints  Maximum number of data points to fit the loess correction. For computational
purposes, if the number of points in ratio(object) is greater than maxNumPoints,
only maxNumPoints randomly selected will be used

Value

An object of class "CNAnorm"

Methods

signature(object = "CNAnorm")  Perform GC content correction on an object of class "CNAnorm".
Returns the same object with corrected ratio

Author(s)

Stefano Berri <s.berri@leeds.ac.uk>

See Also

loess, CNAnorm-class, ratio

Examples

data(LS041)
CN <- dataFrame2object(LS041)
# correct for GC content, but ignoring data from sex chromosomes and
# mitochondria
CN.gcNorm <- gcNorm(CN, exclude = c("chrX", "chrY", "chrM"))

Description

This data object is used by some plotting methods and contains the default values. User can change
graphical parameters by changing this object

The object consists of several layers refering to different plots and different properties. Here an
indicative description
gPar$genome: parameters here refer to the plot produced by plotGenome
graphical parameters: see ?par
$colors: specify colors $cex: specify relative size - points, text...
$lwd: specify line width $lty: specify line type - solid, dashed $mar: specify margins

Usage

data(gPar)
Description

This is bundles data that can be provided to plotGenome in order to plot location of the centromere. In future release it might be used to produce an ideogram too

Usage

data(hg19_hs_ideogr)

Format

A data.frame

Description

A Class containing input data for CNA

Objects from the Class

Objects can be created by calls of the form new("InData", Chr, Pos, Test, Norm, ratio, GC).

Slots

Chr: Object of class "character". Name of the Chromosomes/Contigs of each window.
Pos: Object of class "numeric". Starting position of the each window.
Test: Object of class "numeric". Number of reads from Test in each window.
Norm: Object of class "numeric". Number of reads from Normal (Control) in each window.
ratio: Object of class "numeric". Ratio Test/Control in each window. Automatically computed if Test and Norm are provided, or user generated if Test and Norm are not know.
GC: Object of class "numeric". GC content of each window.

Methods

length signature(x = "InData"): Returns number of windows from input data.

Author(s)

Stefano Berri
References


See Also

CNAnorm

Examples

data(LS041)

inObject <- new("InData", Chr = as.character(LS041$Chr), Pos = LS041$Pos,
              Test = LS041$Test, Norm = LS041$Norm, GC = LS041$GC)

CNA <- new("CNAnorm", InData = inObject)

---

LS041

| Mapped reads in tumor and matched blood for patient LS041 |

Description

This data set provide reads in tumor and matched blood for patient LS041. Each row has information about non-overlapping window across the genome. In particular it reports: chromosome name, starting position of the window (1 based), number of mapped reads in the test (lung tumor), number of reads in the control (matched blood) and GC content of the window.

Usage

data(LS041)

Format

A dataframe

References

Description
A Class containing some Parameters used in the analysis. Not heavily used at the moment.

Objects from the Class
Objects can be created by calls of the form new("Params"), it is usually iniziated and populated with methods and functions of class CNAnorm.

Slots
method: variable of class "character". Record if the peakPloidy function was called using density or mixture.
density.n: The variable "n" used when calling peakPloidy. This variable is saved so that can be used later for drawing plots.
density.adjust: The variable "adjust" used when calling peakPloidy. This variable is saved so that can be used later for drawing plots
gc.excludeFromGCNorm: Vector of class "character". Name of the Chromosomes/Contigs not used for GC content correction.
gc.maxNumPoints: One element vector of class "numeric". Specify how many points to use for GC correction
gp.excludeFromDensity: Vector of class "character". Name of the Chromosomes/Contigs not used for peak guessing

Methods
length signature(x = "Params")

Author(s)
Stefano Berri

References

See Also
CNAnorm

Examples

data(LS041)
inObject <- new("InData", Chr = as.character(LS041$Chr), Pos = LS041$Pos, Test = LS041$Test, Norm = LS041$Norm, GC = LS041$GC)
CNA <- new("CNAnorm", InData = inObject)
peakPloidy

Methods for Function peakPloidy in Package ‘CNAnorm’

Description
peakPloidy Estimate most likely ploidy of genome looking at distribution of smoothed ratio.

Usage
## S4 method for signature 'CNAnorm'
peakPloidy(object, method = 'mixture', exclude = character(0),
            ploidyToTest = 12, sd = 5, dThresh = 0.01, n = 2048, adjust = .9, force.smooth = TRUE,
            reg = FALSE, ds = 1.5, zero.cont = FALSE, ...)

Arguments

object An object of Class "CNAnorm"
exclude A character vector with names of Chromosomes/Contigs not to use to estimate ploidy.
method A character element matching either "mixture", "density", "median", "mode" or "closest". "mixture" will fit a mixture model to find peaks; "density" will use the density function to find peaks; "median" "mode" and "closest" will only find one peak at the median, mode or peak closest to the median respectively. No tumour content or reliable estimated ploidy will be provided. These methods are ment to perform a more "standard" normalisation, without stretching the data. Suggested for germline CNV or a fully automated process that does not requires a normalisation on integer copy number or for highly heterogeneous sample where such normalisation would not be possible. Non ambigous partial matches can be used.
ploidyToTest Maximum ploidy allowed. Warnings! Computation time increases exponentially with this parameter if using "density".
adjust The "adjust" parameter passed to the density function.
n The "n" parameter passed to the density function.
force.smooth If the input object does not have smoothed ratio, it will smooth using "addSmooth". It is highly recomended to use "force.smooth = TRUE"
sd Parameter to filter outliers. Values greater than i median + sd * standard deviations will be ignored while detecting peaks and ploidy.
dThresh Parameter to filter outliers. Values with a density lower than max(density)*dThresh will be ignored while detecting peaks and ploidy.
reg Parameter for mixture model: If set TRUE, the starting point for EM algorithm will be optimized through several methods including regular grid on the ratio distribution. The default is FALSE, by which the starting values are taken from the quantiles of the distribution.
ds Parameter for mixture model: A constraint in EM algorithm of minimum distance between mean estimates, in terms of median standard deviation of the mixture components.
zero.cont Parameter for mixture model: An argument for the mixture model. If set TRUE, the EM algorithm considers exactly-zero ratios as a mixture component.
...
Extra parameters to be passed to funtions for peak detection, specific to each of the methods (deinsity or mixture), se below for details.
plotGenome

Value

An object of class "CNAnorm"

Note

Other optional parameters to be passed (...)

mixture method
density method

peakRatio Threshold used to call a peak. Peaks smaller than maxPeakHeight/peakRatio are not considered peaks.

spacingTolerance A parameter smaller than 1 which describes how strict the program should be on alternative solutions. Only solution with the best $R^2 \geq \max(R^2) \times \text{spacingTolerance}$ will be considered as valid.

interceptRatio Minimum value for the intercept of the linear model. Ideally, should be zero, but the default allows a little flexibility.

Author(s)

Stefano Berri <s.berri@leeds.ac.uk> and Arief Gusnanto <a.gusnanto@leeds.ac.uk>

References


See Also

CNAnorm-class, density

Examples

data(LS041)
CN <- dataFrame2object(LS041)
chr2skip <- c("chrY", "chrM")
CN <- gcNorm(CN, exclude = chr2skip)
CN <- addSmooth(CN, lambda = 3)
CN <- peakPloidy(CN, exclude = chr2skip)
# this object CN is what you obtain when you load
# data(CN)

plotGenome

Methods for Function plotGenome in Package ‘CNAnorm’

Description

plotGenome plot normalized ratio and optionally segmented and/or smoothed normalized ratio values in Package ‘CNAnorm’. It also shows annotation.
Usage

```r
usage <- "## S4 method for signature 'CNAnorm'
plotGenome(object, maxRatio = 8, minRatio = -1,
  superimpose = character(0), gPar = NULL, numHorLables = 10,
  colorful = FALSE, show.centromeres = TRUE, idiogram = NULL, fixVAxes = FALSE,
  supLineColor = character(0), supLineCex = character(0), dot.cex = .2, ...)
```

Arguments

- `object` An object of Class "CNAnorm"
- `maxRatio` The maximum ratio to be shown on the plot. Values or ratio greater than maxRatio will be displayed as green triangles
- `minRatio` The minimum ratio to be shown on the plot. Values or ratio smaller than minRatio will be displayed as green triangles
- `superimpose` A character vector with one or both of the following: "smooth", "DNACopy"
- `numHorLables` Number of maximum horizontal labels. The function will try to annotate numHorLables so that they are approximately equally spaced.
- `colorful` A switch to decide if the background dots representing the ratio of each window should be gray or colored according their value in relation to the peak closest to the median
- `show.centromeres` A switch to decide if location of centromere are displayed on the graph. The location of the centromere is stored in idiogram
- `idiogram` A data frame containing banding information. If NULL -default- human information will be loaded by data(hg19_hs_ideogr)
- `fixVAxes` A switch to decide if the vertical axes should be fixed to minRatio and maxRatio or fit the data within minRatio and maxRatio.
- `gPar` A S3 object with all graphical parameters. If NULL (default) data(gPar) is called
- `supLineColor` A three element character vector with colors to be used for first superimposed line, second superimposed line, normalized ratio dots. If none is provided, defaults are: c("black", "cyan", "grey60")
- `supLineCex` A two element vector with cex values to be used for width of first superimposed line and second superimposed line. If none is provided, defaults are: c(0.5, 0.5)
- `dot.cex` size of the dots in the plot
- `...` Further arguments to pass to the function `plot`

Value

An object of class "CNAnorm"

Author(s)

Stefano Berri <s.berri@leeds.ac.uk> and Arief Gusnanto <a.gusnanto@leeds.ac.uk>

See Also

plot, par, peakPloidy, gPar, hg19_hs_ideogr
Examples

data(CN)
# see peakPloidy documentation to know how object CN is created
CN <- addDNACopy(CN)
CN <- validation(CN)
CN <- discreteNorm(CN)
plotGenome(CN, superimpose = 'DNACopy')

plotPeaks

Methods for Function plotPeaks in Package 'CNAnorm'

Description

plotPeaks plot annotated distribution of ratio Test/Normal

Usage

## S4 method for signature 'CNAnorm'
plotPeaks(object, special1 = character(0), special2 = character(0),
  show = 'suggested', ...)

Arguments

object An object of Class "CNAnorm"
special1 The chromosome/contig whose distribution will be shown with a different color
special2 The chromosome/contig whose distribution will be shown with a different color
show A character vector with one or both of the following: "suggested", "validated".
      Specify what need to be plotted
...
      Further arguments to pass to the function plot

Author(s)

Stefano Berri <s.berri@leeds.ac.uk>

See Also

plot, validation, peakPloidy

Examples

data(CN)
# see peakPloidy documentation to know how object CN is created
plotPeaks(CN, special1 = 'chrX', special2 = 'chrY')
Methods for Function `ratio` in Package ‘CNAnorm’

Description

`ratio` returns the Test/Normal ratio from an object of class `CNAnorm`. `ratio` is corrected for GC content if `gcNorm` was called.

`ratio.n` returns the Test/Normal `normalized` ratio from an object of class `CNAnorm` after normalization. Its input is `ratio(object)`

`ratio.s` returns the Test/Normal `smoothed` ratio from an object of class `CNAnorm` Its input is `ratio(object)`

`ratio.s.n` returns the Test/Normal `smoothed and normalized` ratio from an object of class `CNAnorm`. Its input is `ratio.s(object)`

`segMean` returns the mean of the segments as produced by `DNACopy`

`segMean.n` returns the `normalized` mean of the segments

Usage

```r
ratio(object)  
ratio.n(object)  
ratio.s(object)  
ratio.s.n(object)  
segMean(object)  
segMean.n(object)
```

Arguments

- `object` An object of Class "`CNAnorm`"

Value

A numeric vector

Author(s)

Stefano Berri <s.berri@leeds.ac.uk>

See Also

`gcNorm`, `CNAnorm-class`, `DNAcopy`

Examples

```r
data(LS041)  
CN <- DataFrame2object(LS041)  
ratio.original <- ratio(CN)  
CN.gcNorm <- gcNorm(CN, exclude = c("chrX", "chrY", "chrM"))  
ratio.gc.corrected <- ratio(CN.gcNorm)
```
Methods for Function to retrieve suggested/validated ploidy and peaks in Package ‘CNAnorm’

Description

sugg.peaks returns the location of peaks before normalization as suggested by peakPloidy.
sugg.ploidy returns the ploidy of the peaks as suggested by peakPloidy.
valid.peaks returns the location of peaks before normalization as validated after calling method "validation"
valid.ploidy returns the validated ploidy of the peaks as validated after calling method "validation"

Usage

sugg.peaks(object)
sugg.ploidy(object)
valid.peaks(object)
valid.ploidy(object)

Arguments

object An object of Class “CNAnorm” after method "peakPloidy" was called

Value

A numeric vector

Author(s)

Stefano Berri <s.berri@leeds.ac.uk>

See Also

gcNorm, CNAnorm-class, DNAcopy

Examples

data(CN)
# see peakPloidy documentation to know how object CN is created
plot(sugg.ploidy(CN), sugg.peaks(CN))
Methods for Function `addSmooth` in Package ‘CNAnorm’

Description

Validation segment and smooth perform ratio values in Package ‘CNAnorm’

Usage

```r
## S4 method for signature 'CNAnorm'
validation(object, peaks = sugg.peaks(object),
           ploidy = sugg.ploidy(object))
```

Arguments

- `object` An object of Class “CNAnorm”
- `peaks` The user validated location (ratio Test/Normal) of the peaks before normalization.
- `ploidy` The user validated ploidy of the peaks before normalization.

Value

An object of class "CNAnorm"

Note

It is implicitly called by `discreteNorm` if no validation was manually performed.

Author(s)

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See Also

- `ratio.s`
- `CNAnorm-class`

Examples

```r
data(CN)
# see peakPloidy documentation to know how object CN is created
CN <- validation(CN)
```
Index

*Topic classes
  CNAnorm-class, 6
  DerivData-class, 9
  InData-class, 14
  Params-class, 16
*Topic convert, data.frame
dataFrame2object, 9
*Topic datasets, dataframe
  LS041, 15
*Topic datasets, object
  CN, 5
  gPar, 13
  hg19_hs_ideogr, 14
*Topic methods, accessor, get, set
  ratio, 21
  retrieve peaks and ploidy, 22
*Topic methods, accessor, get
  chromosomesPosition, 4
*Topic methods, export, dataframe, table
  exportTable, 11
*Topic methods, normalization
  gcNorm, 12
  peakPloidy, 17
*Topic methods, segmentation, smoothing
  addDNACopy, 2
  addSmooth, 3
*Topic workflow
  CNAnormWorkflow, 7
  chrs (chromosomesPosition), 4
  chrs< (chromosomesPosition), 4
  chrs<-, CNAnorm-method (CNAnorm-class), 6
  chrs<--methods (chromosomesPosition), 4
  CN, 5
  CNAnorm, 10, 15, 16
  CNAnorm (CNAnorm-class), 6
  CNAnorm-class, 6
  CNAnormWorkflow, 7
  data.frame, 9
dataFrame2object, 8, 9
density, 18
  DerivData, 7
  DerivData-class, 9
  discreteNorm, 8, 10
  discreteNorm, CNAnorm-method (discreteNorm), 10
  discreteNorm-methods (discreteNorm), 10
  exportTable, 11
  exportTable, CNAnorm-method (exportTable), 11
  exportTable-methods (exportTable), 11
  gcNorm, 5, 8, 12, 21, 22
  gcNorm, CNAnorm-method (gcNorm), 12
  gcNorm-methods (gcNorm), 12
  gPar, 13, 19
  hg19_hs_ideogr, 3, 5, 14, 19
  InData, 7
  InData-class, 14
  length, CNAnorm-method (CNAnorm-class), 6
  length, DerivData-method (DerivData-class), 9
  length, InData-method (InData-class), 14
  loess, 13
  LS041, 15
INDEX

par, 19
Params-class, 16
peakPloidy, 8, 11, 17, 19, 20
peakPloidy,CNAnorm-method (peakPloidy), 17
peakPloidy-methods (peakPloidy), 17
plot, 19, 20
plotGenome, 18
plotGenome,CNAnorm-method (plotGenome), 18
plotGenome-methods (plotGenome), 18
plotPeaks, 20
plotPeaks,CNAnorm-method (plotPeaks), 20
plotPeaks-methods (plotPeaks), 20
pos (chromosomesPosition), 4
pos,CNAnorm-method (chromosomesPosition), 4
pos-methods (chromosomesPosition), 4
pos<-(chromosomesPosition), 4
pos<--methods (chromosomesPosition), 4
ratio, 13, 21
ratio,CNAnorm-method (CNAnorm-class), 6
ratio-methods (ratio), 21
ratio.n (ratio), 21
ratio.n,CNAnorm-method (CNAnorm-class), 6
ratio.n-methods (ratio), 21
ratio.s, 4, 23
ratio.s,CNAnorm-method (CNAnorm-class), 6
ratio.s-methods (ratio), 21
ratio.s.n (ratio), 21
ratio.s.n,CNAnorm-method (CNAnorm-class), 6
ratio.s.n-methods (ratio), 21
retrieve peaks and ploidy, 22
segMean, 3
segMean (ratio), 21
segMean,CNAnorm-method (CNAnorm-class), 6
segMean-methods (ratio), 21
segMean.n (ratio), 21
segMean.n,CNAnorm-method (CNAnorm-class), 6
segMean.n-methods (ratio), 21
sugg.peaks (retrieve peaks and ploidy), 22
sugg.peaks,CNAnorm-method (CNAnorm-class), 6
sugg.ploidy-methods (retrieve peaks and ploidy), 22
sugg.ploidy (retrieve peaks and ploidy), 22
sugg.ploidy,CNAnorm-method (CNAnorm-class), 6
sugg.ploidy-methods (retrieve peaks and ploidy), 22
valid.peaks (retrieve peaks and ploidy), 22
valid.peaks,CNAnorm-method (CNAnorm-class), 6
valid.peaks-methods (retrieve peaks and ploidy), 22
valid.ploidy (retrieve peaks and ploidy), 22
valid.ploidy,CNAnorm-method (CNAnorm-class), 6
valid.ploidy-methods (retrieve peaks and ploidy), 22
validation, 11, 20, 23
validation,CNAnorm-method (validation), 23
validation-methods (validation), 23
write.table, 12