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 troughput 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.

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Imports DNAcopy

Collate AllGenerics.R AllClasses.R dataFrame2object.R workflowWrapper.R initialize-methods.R summary-methods.R smoothseg.R bandsegment.R mixtureModel.R normalize.R length-methods.R CNAnorm-accessors.R CNAnorm-methods.R Data-methods.R makeDefaultGraphParamteres.R

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R topics documented:

`addDNACopy` *Methods for Function addDNACopy in Package 'CNAnorm'*

Description

`addSmooth` segment ratio values in Package 'CNAnorm' using DNACopy

Usage

```
## 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(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*sd 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

`signature(object = "CNAnorm")` Segment ratio values on an object of class `"CNAnorm"`. Returns the same object with extra slots (`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) *A faster circular binary segmentation algorithm for the analysis of array CGH data*. Bioinformatics

See Also

`segMean`, `CNAnorm-class`, `DNAcopy`, `hg19_hs_ideogr`

Examples

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

addSmooth *Methods for Function addSmooth in Package 'CNAnorm'*

Description

addSmooth segment and smooth perform ratio values in Package 'CNAnorm'

Usage

```
## 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
...	Further arguments to pass to the function smoothseg

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

Huang, J., Gusnanto, A., O'Sullivan, K., Staaf, J., Borg, A. and Pawitan, Y. (2007) *Robust smooth segmentation approach for array CGH data analysis*. Bioinformatics

See Also

ratio.s, CNAnorm-class

Examples

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

chromosomesPosition *Accessors methods for Function ratio in Package 'CNAnorm'*

Description

chrs returns/set the name of chromosomes/contigs

arms retruns 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 infromation 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

`CNAnorm-class` *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 DNAcopy)

segMean.n signature(object = "CNAnorm"): Retrieve normalized segmented ratio

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

```
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))
```

CNAnormWorkflow *Wrapper to "CNAnorm" workflow*

Description

This function is a wrapper to use for a fully automated CNAnorm workflow where interactivity is not required. It contains MOST possible paramenters. Defaults are set to 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

	All arguments are explained in the relative functions
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
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 funtions 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`.

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 vecotr 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 wich values have been used to calculate density.

Methods

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

Author(s)

Stefano Berri and Arief Gusnanto

References

Gusnanto, A., Wood, H.M., Pawitan, Y., Rabbitts, P. and Berri, S. (2011) *Correcting for cancer genome size and tumor cell content enables better estimation of copy number alterations from next generation sequence data.* Bioinformatics

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

Gusnanto, A., Wood, H.M., Pawitan, Y., Rabbitts, P. and Berri, S. (2011) *Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next generation sequence data.* Bioinformatics

See Also

validation, peakPloidy

Examples

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

---

exportTable *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 abbundant copy. Ratio of 1 means that the most abbundant "state" is centered to 1
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 pourposes, 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
# mitocondria
CN.gcNorm <- gcNorm(CN, exclude = c("chrX", "chrY", "chrM"))
```

---

gPar *An object with the default graphical parameters*

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: prameters 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)
```

Format

A S3 object

---

hg19_hs_ideogr *An object with the ideogram information for homo sapiens - hg19*

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

InData-class *Class "InData" ~~~*

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

Gusnanto, A., Wood, H.M., Pawitan, Y., Rabbitts, P. and Berri, S. (2011) *Correcting for cancer genome size and tumor cell content enables better estimation of copy number alterations from next generation sequence data.* Bioinformatics

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

Gusnanto, A., Wood, H.M., Pawitan, Y., Rabbitts, P. and Berri, S. (2011) *Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next generation sequence data.* Bioinformatics

Params-class *Class "Params"*

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

Gusnanto, A., Wood, H.M., Pawitan, Y., Rabbitts, P. and Berri, S. (2011) *Correcting for cancer genome size and tumor cell content enables better estimation of copy number alterations from next generation sequence data.* Bioinformatics

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 stratching 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 deivations 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.

Value

An object of class "CNAnorm"

Note

Other optional parameters to be passed (...)

mixture method

density method

peakRatioThreshold used to call a peak. Peaks smaller than maxPeakHight/peakRatio are not considered peaks.

spacingToleranceA parameter smaller than 1 which describes how strict the program should be on alternative solutions. Only solution with the best R^2 >= max(R^2)*spacingTolerance will be considered as valid.

interceptRatioMinimum 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

Gusnanto, A., Wood, H.M., Pawitan, Y., Rabbitts, P. and Berri, S. (2011) *Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next generation sequence data.* Bioinformatics

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

```
## 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 triangulars
minRatio	The minimum ratio to be shown on the plot. Values or ratio smaller than minRatio will be displayed as green triangulars
superimpose	A character verctor with one or both of the following: "smooth", "DNACopy"
numHorLables	. Number of maximum horizontal lables. 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 valeus 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 verctor 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')
```

`ratio` *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

```
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

```
data(LS041)
CN <- dataFrame2object(LS041)
ratio.original <- ratio(CN)
CN.gcNorm <- gcNorm(CN, exclude = c("chrX", "chrY", "chrM"))
ratio.gc.corrected <- ratio(CN.gcNorm)
```

---

retrieve peaks and ploidy

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))
```

---

validation *Methods for Function addSmooth in Package 'CNAnorm'*

Description

validation segment and smooth perform ratio values in Package 'CNAnorm'

Usage

```
## 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)

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

See Also

ratio.s, CNAnorm-class

Examples

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

Index