

Package ‘CNAnorm’

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Title A normalization method for Copy Number Aberration in cancer samples

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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.

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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
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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 $2 \cdot \sqrt{\text{mean}}$ from the mean are weighted down. The most stringent. Recommended for unbiased genome wide sequencing.

'gaussian': windows with coverage more or less than $2 \cdot \text{sd}$ 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

`segMean(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

| | |
|---------------------|--|
| <code>object</code> | An object of Class "CNAnorm" |
| <code>lambda</code> | Degree of smoothness. See reference for more details |
| <code>...</code> | Further arguments to pass to the function <code>smoothseg</code> |

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 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 | <i>A CNAnorm object with information about most abundant ploidy states, obtained from data LS041.</i> |
|----|---|

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 | <i>Class "CNAnorm"</i> |
|---------------|------------------------|

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 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

All arguments are explained in the relative functions

| | |
|-------------------|---|
| dataFrame | A data frame with columns Chr, Pos, Test, Norm and optional GC. See <code>dataFrame2object</code> |
| gc.do | Specify if GC correction need to be done. See <code>gcNorm</code> |
| gc.exclude | See <code>gcNorm</code> |
| gc.maxNumPoints | See <code>gcNorm</code> |
| smooth.do | Specify if smoothing need to be done. See <code>addSmooth</code> |
| smooth.lambda | See <code>addSmooth</code> |
| smooth.other | A list of other parameters to pass to the smoothing function. See <code>addSmooth</code> |
| peak.method | See <code>peakPloidy</code> |
| peak.exclude | See <code>peakPloidy</code> |
| peak.ploidyToTest | See <code>peakPloidy</code> |
| peak.sd | See <code>peakPloidy</code> |
| peak.dThresh | See <code>peakPloidy</code> |
| peak.n | See <code>peakPloidy</code> |
| peak.adjust | See <code>peakPloidy</code> |
| peak.force.smooth | See <code>peakPloidy</code> |
| peak.reg | See <code>peakPloidy</code> |
| peak.ds | See <code>peakPloidy</code> |

`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 | <i>Class "DerivData"</i> |
|-----------------|--------------------------|

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 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

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 abundant copy. Ratio of 1 means that the most abundant "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 purposes, if the number of points in <code>ratio(object)</code> is greater than <code>maxNumPoints</code> , only <code>maxNumPoints</code> 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"))
```

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 referring 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)
```

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 inized 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 ambiguous 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 recommended to use "force.smooth = TRUE" |
| sd | Parameter to filter outliers. Values greater than $i \text{ median} + sd * \text{standard deviation}$ will be ignored while detecting peaks and ploidy. |
| dThresh | Parameter to filter outliers. Values with a density lower than $\text{max}(\text{density}) * d\text{Thresh}$ 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 functions for peak detection, specific to each of the methods (density or mixture), see 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 $\text{maxPeakHeight}/\text{peakRatio}$ 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 $R^2 \geq \text{max}(R^2) * \text{spacingTolerance}$ 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

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 vector 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 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')
```

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)
```

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