

Package ‘quantsmooth’

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Type Package

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Depends R(>= 2.10.0), quantreg, grid

Description Implements quantile smoothing as introduced in: Quantile smoothing of array CGH data; Eilers PH, de Menezes RX; Bioinformatics. 2005 Apr 1;21(7):1146-53.

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| | |
|-------------|--|
| chrom.bands | <i>Dataset of human chromosomes and their banding patterns</i> |
|-------------|--|

Description

Dataset used to produce human chromosomal ideograms for plotting purposes.

Usage

```
data(chrom.bands)
```

Format

A data frame with 4068 observations on the following 12 variables.

```
chr a character vector
arm a character vector
band a character vector
ISCN.top a numeric vector
ISCN.bot a numeric vector
bases.top a numeric vector
bases.bot a numeric vector
stain a character vector
cM.top a numeric vector
cM.bot a numeric vector
n.markers a numeric vector
p.markers a numeric vector
```

Details

The original file gives only the physical map positions. The genetic map positions are interpolated from the Rutgers linkage map (Kong et al 2004).

Source

ftp://ftp.ncbi.nlm.nih.gov/genomes/H_sapiens/maps/mapview/BUILD.35.1/ideogram.gz.

References

Kong X, Murphy K, Raj T, He C, White PS, Matisse TC. 2004. A Combined Linkage-Physical Map of the Human Genome. *American Journal of Human Genetics*, 75(6):1143-8.

Chromosome14

Example data from several quantitative genomic methods

Description

A collection of arrays that contains data of chromosome 14 of 3 colorectal tumors. The first tumor shows 1 region of loss, the second tumor shows no aberration, while the third tumor shows loss of 1 copy of the chromosome.

affy.cn Copy number values of 358 probes from Affymetrix 10K genechip. Data was obtained from DChip

affy.pos corresponding probe positions

bac.cn Copy number values of 112 probes from a 1 mb spaced BAC array-CGH

bac.pos corresponding probe positions

ill.cn Copy number values of 207 probes from Illumina GoldenGate Linkage IV data

ill.pos corresponding probe positions

Usage

```
data(chr14)
```

Format

Matrices of copy number values and vectors of chromosomal probe positions

Author(s)

Jan Oosting

drawSimpleChrom *Draw chromosome-like icons*

Description

This function paints chromosomal icons on an existing plot

Usage

```
drawSimpleChrom(x, y, len = 3, width = 1, fill, col, orientation = c("h", "v"), centromere.size = 0.6)
```

Arguments

| | |
|-----------------|---|
| x | start x-position |
| y | start y-position |
| len | total length of the chromosome |
| width | width of the chromosome |
| fill | character, {"a","p","q","q[1-3]","p[1-3]"}. Events to a chromosome can be depicted by coloring "a"ll of the chromosome, the complete p or q-arm, or a sub-segment of the arms |
| col | color(s) of fill |
| orientation | either "h"orizontal or "v"ertical |
| centromere.size | The size of the centromere as fraction of the width |

Value

This function is executed for its side effects

Author(s)

Jan Oosting

Examples

```
plot(c(0,4),c(0,3),type="n",xaxt="n",yaxt="n",xlab="",ylab="")
drawSimpleChrom(2,3,fill=c("p","q3"),col=c("red","blue"),orientation="v")
```

getChangedRegions *getChangedRegions*

Description

retrieve regions of interest in a vector of intensities using quantile smoothing

Usage

```
getChangedRegions(intensities, positions, normalized.to=1, interval, threshold, minlength=2, ...)
```

Arguments

| | |
|---------------|--|
| intensities | numeric vector |
| positions | numeric vector of the same length as intensities. If this argument is not given the results contain the indexes of the intensities vector, else the values in positions are used. Both vectors are sorted in the order of positions. |
| normalized.to | numeric, reference value. Changes are compared to this value |
| interval | numeric [0,1], bandwidth around reference. If the smoothed line at the higher quantile drops below the normalized.to value, a deleted region is recognized, and vice versa. |
| threshold | numeric, if the median smoothed value drops below normalized.to - threshold, or above normalized.to + threshold a changed region is called |
| minlength | integer, not used currently |
| ... | extra arguments for quantsmooth function |

Details

This function uses `quantsmooth` to detect regions in the genome that are abnormal. If `interval` is set then a smoothed line is calculated for $\tau = 0.5 - \text{interval}/2$, and a region is determined as upregulated if this line is above the reference. Down regulation is determined when the smoothed line for $\tau = 0.5 + \text{interval}/2$ is below the reference value. If `threshold` is set then a smoothed line is calculated for $\tau = 0.5$ and up- or down regulation are determined when this line is outside the range `[normalized.t - threshold:normalized.to + threshold]`

Value

A data.frame with 3 cols is returned. Each row contains a region with columns `up`, `start` and `end`. `start` and `end` indicate positions in the vector of the first and last position that were up- or downregulated

Author(s)

Jan Oosting

Examples

```
data(chr14)
getChangedRegions(ill.cn[,1],ill.pos,normalized.to=2,interval=0.5)
```

| | |
|--------------|---------------------|
| getLambdaMin | <i>getLambdaMin</i> |
|--------------|---------------------|

Description

Test a set of smoothing parameters to find best fit to data

Usage

```
getLambdaMin(intensities, lambdas, ...)
```

Arguments

| | |
|--------------------------|--|
| <code>intensities</code> | numeric vector |
| <code>lambdas</code> | numeric vector; see quantsmooth |
| <code>...</code> | extra parameters for <code>quantsmooth.cv</code> ; currently only <code>ridge.kappa</code> |

Details

Cross validation is performed using a set of lambda values in order to find the lambda value that shows the best fit to the data.

Value

This function returns the lambda value that has the lowest cross validation value on this dataset

Author(s)

Jan Oosting

See Also

[quantsmooth.cv](#)

Examples

```
data(chr14)
lambdas<-2^seq(from=-2, to=5, by=0.25)
getLambdaMin(bac.cn[,1], lambdas)
```

| | |
|-----------------|---|
| grid.chromosome | <i>Draw a chromosome using the grid package</i> |
|-----------------|---|

Description

A chromosome is drawn including the cytobands

Usage

```
grid.chromosome(chrom, side = 1, units = "hg19", chrom.width = 0.5, length.out,
                bands = "major", legend = c("chrom", "band", "none"), cex.leg = 0.7, bleach = 0, ...)
```

Arguments

| | |
|-------------|---|
| chrom | numeric or character, id of chromosome to plot |
| side | numeric [1:4], side of rectangle to draw, 4 sides, side 2 and 4 are vertical |
| units | character or data.frame, type of units for genomic data, or a dataframe with UCSC cytoband data, see lengthChromosome |
| chrom.width | numeric [0,1], The width relative to the width (sides 2 and 4) or height(sides 1 and 3) of the viewport |
| length.out | numeric, size of native units of viewport |
| bands | character, draw either major or minor bands |
| legend | character, type of legend |
| cex.leg | numeric, relative size of legend text |
| bleach | numeric [0,1], proportion by which to bleach the chromosome |
| ... | arguments for viewport(), especially x,y, width, and height |

Details

The chromosome is drawn within a rectangle defined by x, y, width, and height, which is pushed as a viewport. The legend is drawn within the same rectangle in the space left over by chrom.width.

Value

This function is executed for its side effects

Author(s)

David L Duffy ,Jan Oosting

References

lodplot package

See Also[paintCytobands](#)**Examples**

```
grid.newpage()  
grid.chromosome(1,units="bases",height=0.15)
```

| | |
|------------------|------------------------------------|
| lengthChromosome | <i>Retrieve chromosomal length</i> |
|------------------|------------------------------------|

Description

Retrieve human chromosomal length from NCBI data

Usage

```
lengthChromosome(chrom, units = "hg19")
```

Arguments

| | |
|-------|---------------------------------------|
| chrom | vector of chromosomal id, 1:22,X,Y |
| units | character, or data.frame, see details |

Details

The cytoband data was originally obtained from the lodplot package by David Duffy, which contained basepair data from genome version hg17, but also the linkage related positions in cM. These datasets have units "bases" and "cM" respectively. Cytoband data for genome versions "hg18", "hg19", "hg38" and "mm10" has been included, and can be referenced by these strings. It is also possible to use cytoband data as obtained from the UCSC site, by downloading the cytoBand.txt.gz or cytoBandIdeo.txt.gz annotation file for a species (see example below). Note however that this information is not available for most species.

Value

A numeric vector in the requested units

Author(s)

Jan Oosting

Examples

```
# Show length of chromosome 1 in several types of units
lengthChromosome(1,"cM")
lengthChromosome(1,"bases")
lengthChromosome(1,"hg38")
# mm9 cytoband data
temp <- tempfile(fileext = ".txt.gz")
download.file("http://hgdownload.soe.ucsc.edu/goldenPath/mm9/database/cytoBand.txt.gz",temp)
mm9cytobands <- read.table(temp,sep="\t")
lengthChromosome(1,mm9cytobands)
# remove temp file
unlink(temp)
```

numericCHR

Conversion of chromosome IDs between numeric and character

Description

The function converts chromosomal ids to their numeric form, and the sex chromosomes to values between 98 and 100. This simplifies sorting on chromosome ID

Usage

```
numericCHR(CHR, prefix="chr")
characterCHR(CHR, prefix="")
```

Arguments

| | |
|--------|---|
| CHR | character/numeric vector for both functions the mode of the input is not forced. For numericCHR strings "X","Y" and "XY" are converted to 98,99 and 100 respectively. |
| prefix | character, string is excluded from (numericCHR) or prepended to (characterCHR) all items of the output |

Value

numericCHR returns a numeric vector of same length as CHR characterCHR returns a character vector of same length as CHR

Author(s)

Jan Oosting

Examples

```
chroms<-c("3","2","8","X","7","Y","5","1","9","10","11","12","4","6")
sort(chroms)
sort(numericCHR(chroms))
characterCHR(sort(numericCHR(chroms)),prefix="chr")
```

paintCytobands *Paint a chromosomal idiogram*

Description

Paints a human chromosomal idiogram in an existing plot Adapted from the paint.chromosome function in the lodplot package by David L Duffy

Usage

```
paintCytobands(chrom, pos = c(0, 0), units = "hg19", width = 0.4,
               length.out, bands = "major", orientation = c("h","v"), legend = TRUE,
               cex.leg = 0.7, bleach = 0, ...)
```

Arguments

| | |
|-------------|---|
| chrom | chromosomal id, chromosome to plot 1:22,X,Y |
| pos | numeric vector of length 2, position in the plot to start the plot |
| units | character or data.frame, type of units for genomic data, or a dataframe with UCSC cytoband data, see lengthChromosome |
| width | numeric, width of the chromosome, the chromosome is plotted between pos[2] and pos[2]-width |
| length.out | numeric, if given, the chromosome will have this length in the plot |
| bands | if not equal to "major", then also the minor bands will be plotted |
| orientation | chromosome is plotted either <i>Horizontally</i> to the right of the starting point or <i>Vertically</i> down from the starting point |
| legend | logical, if TRUE then the bandnames are plotted next to the chromosome |
| cex.leg | numeric, relative size of legend text |
| bleach | numeric [0,1], proportion by which to bleach the chromosome |
| ... | extra parameters for plot |

Value

This function is executed for its side effects

Author(s)

David L Duffy , Jan Oosting

References

lodplot package

Examples

```
plot(c(0,lengthChromosome(14,"bases")),c(-2,2),type="n",xaxt="n",yaxt="n",xlab="",ylab="")
paintCytobands(14,units="bases")
```

| | |
|----------------|---------------------------------|
| plotChromosome | <i>Wrapper for plotSmoothed</i> |
|----------------|---------------------------------|

Description

This function is a wrapper for plotSmoothed, to make data subsetting easier

Usage

```
plotChromosome(gendata, chrompos, chromosome, dataselection = NULL, ylim = NULL, normalized.to = NULL, ...)
```

Arguments

| | |
|---------------|--|
| gendata | numeric matrix or data.frame |
| chrompos | chrompos object with same numer of rows as gendata |
| chromosome | numeric, chromosme to show |
| dataselection | optional, subset of samples/columns in gendata |
| ylim | limits for plot |
| normalized.to | y-value(s) for line |
| grid | x-value(s) for line |
| smooth.lambda | smoothing parameter, see quantsmooth |
| interval | position of extra lines besides median, see plotSmoothed |
| ... | extra arguments for plotSmoothed |

Value

The function is used for its side effects

Author(s)

Jan Oosting

See Also

[plotSmoothed](#), [quantsmooth](#)

| | |
|--------------|---------------------|
| plotSmoothed | <i>plotSmoothed</i> |
|--------------|---------------------|

Description

Plot a smoothed line together with the original data values

Usage

```
plotSmoothed(intensities, position, ylim=NULL, ylab="intensity", xlab="position", normalized.to=NULL)
```

Arguments

| | |
|----------------------------|---|
| <code>intensities</code> | numeric vector or matrix, data are plotted by column |
| <code>position</code> | numeric vector; the length should be the number of rows in <code>intensities</code> |
| <code>ylim</code> | numeric vector of length 2, limits for plot. If <code>NULL</code> then the minimal and maximal value in <code>intensities</code> is used |
| <code>ylab</code> | character, label for y-position |
| <code>xlab</code> | character, label for x-position |
| <code>normalized.to</code> | numeric, a line(s) is drawn at this horizontal position |
| <code>grid</code> | numeric, a line(s) is drawn at this vertical position |
| <code>smooth.lambda</code> | numeric, smoothing parameter see <code>quantsmooth</code> |
| <code>interval</code> | numeric (0..1), plotting of extra smoothed lines around median. With <code>interval = 0.5</code> the 0.25 and 0.75 quartiles are plotted, with <code>interval = 0.9</code> the 0.05 and 0.95 quartiles are plotted, |
| <code>plotnew</code> | logical, if <code>TRUE</code> a new plot is created, else the data are plotted into an existing plot |
| <code>cols</code> | color vector, colors for columns in <code>intensities</code> |
| <code>cex.pts</code> | size of the dots in the plot. Set to <code>0</code> to skip plotting the dots |
| <code>...</code> | extra parameters for plot |

Details

This function plots the raw data values as dots and the median smoothed values as a continuous line. If `interval` is supplied these are plotted as lines in different line types. More than 1 interval can be given.

Value

This function is used for its side effects

Author(s)

Jan Oosting

See Also[quantsmooth](#)**Examples**

```
data(chr14)
plotSmoothed(bac.cn,bac.pos,ylim=c(1,2.5),normalized.to=2,smooth.lambda=2.5)
```

| | |
|-------------------|---|
| position2Cytoband | <i>Determine cytoband position based on location of probe</i> |
|-------------------|---|

Description

Determine cytoband position based on location of probe

Usage

```
position2Cytoband(chrom, position, units = "hg19", bands = c("major", "minor"))
```

Arguments

| | |
|----------|---|
| chrom | chromosomal id, chromosome to plot 1:22,X,Y |
| position | numeric vector |
| units | character, type of positional unit |
| bands | character, type of cytoband |

Value

Character vector with cytobands, if an illegal position was used, the value "-" is returned. All positions within a single function call should be for a single chromosome

Author(s)

Jan Oosting

See Also[lengthChromosome](#)**Examples**

```
position2Cytoband(1,c(50e6,125e6,200e6),units="bases")
position2Cytoband(1,c(50,125,200),units="cM",bands="minor")
```

```
prepareGenomePlot      Set up a full genome plot
```

Description

This function starts up a plot consisting of all chromosomes of a genomen, including axes with chromosome names.

Usage

```
prepareGenomePlot(chrompos, cols = "grey50", paintCytobands = FALSE, bleach = 0, topspace = 1, organism,
                  sexChromosomes = FALSE, units = "hg19",...)
```

Arguments

| | |
|----------------|---|
| chrompos | chrompos object, data.frame with CHR column identifying the chromosome of probes, and a MapInfo column identifying the position on the chromosome |
| cols | color(s) for the chromosome lines |
| paintCytobands | logical, use paintCytoband to plot ideograms for all chromosomes |
| bleach | numeric [0,1], proportion by which to bleach the ideograms |
| topspace | numerical, extra space on top of plot, i.e. for legends |
| organism | character, if given a 2 column plot is created with the chromosomes for the given species. Currently "hsa", "mmu", and "rno" are supported |
| sexChromosomes | logical, if TRUE then also the sex chromosomes X and Y are plotted |
| units | character or data.frame, type of units for genomic data, or a dataframe with UCSC cytoband data, see lengthChromosome |
| ... | extra arguments for plot function |

Details

If organism is not supplied then a single column is plotted of the available chromosomes in chrompos\$CHR. The arguments paintCytobands, bleach, and sexChromosomes are not used in that case. If organism is supplied and chrompos is NULL then a result is generated with the starting Y and X position of each chromosome

Value

A matrix with 2 columns that contain the Y and X positions for the probes on the plot

Author(s)

Jan Oosting

| | |
|-------------|--------------------|
| quantsmooth | <i>quantsmooth</i> |
|-------------|--------------------|

Description

Quantile smoothing of array data

Usage

```
quantsmooth(intensities, smooth.lambda=2, tau=0.5, ridge.kappa=0, smooth.na=TRUE, segment)
```

Arguments

| | |
|----------------------------|--|
| <code>intensities</code> | numeric vector |
| <code>smooth.lambda</code> | numeric |
| <code>tau</code> | numeric [0..1], the quantile desired; see rq.fit |
| <code>ridge.kappa</code> | fudge parameter; see details |
| <code>smooth.na</code> | logical; handling of NA |
| <code>segment</code> | integer, length of overlapping segments |

Value

This function returns a vector of the same length as `intensities`, or a matrix if the length of `tau` is greater than 1.

Author(s)

Jan Oosting

Examples

```
data(chr14)
plot(quantsmooth(bac.cn[,1], smooth.lambda=2.8), type="l")
```

| | |
|----------------|-----------------------|
| quantsmooth.cv | <i>quantsmooth.cv</i> |
|----------------|-----------------------|

Description

Cross validation of smoothing parameters

Usage

```
quantsmooth.cv(intensities, smooth.lambda=2, ridge.kappa=0)
```

Arguments

intensities numeric vector
smooth.lambda numeric; see [quantsmooth](#)
ridge.kappa fudge parameter; see [quantsmooth](#)

Details

Cross validation is performed by calculating the fit from the even indices on the odd indices and vice versa.

Value

This function returns the sum of squared differences or NA if the fitting function gave an error

Author(s)

Jan Oosting

See Also

[getLambdaMin](#)

Examples

```
data(chr14)
# A low value is indicative of a better fit to the data
quantsmooth.cv(bac.cn[,1],1)
quantsmooth.cv(bac.cn[,1],2.8)
```

quantsmooth.seg *quantsmooth.seg*

Description

segmented Quantile smoothing of array data

Usage

```
quantsmooth.seg(y, x = 1:length(y), lambda = 2, tau = 0.5, kappa = 0, nb = length(x))
```

Arguments

y numeric vector
x numeric vector of same length as y. Position of values
lambda numeric
tau numeric [0..1], the quantile desired; see [rq.fit](#)
kappa fudge parameter; see details
nb integer, basis

Value

This function returns a vector of the same length as y

Author(s)

Jan Oosting

Examples

```
data(chr14)
plot(quantsmooth.seg(bac.cn[,1],lambda=2.8,nb=50),type="l")
```

scaleto

Scales data within a range to a new range

Description

This function scales data to a new range while enforcing the boundaries. This can be helpful in preventing overlap between chromosomal plots that display multiple chromosomes in the same plot

Usage

```
scaleto(x, fromlimits = c(0, 50), tolimits = c(0.5, -0.5), adjust = TRUE)
```

Arguments

| | |
|------------|---|
| x | numeric |
| fromlimits | numeric vector with length 2, original range of data |
| tolimits | numeric vector with length 2, target range of data |
| adjust | logical, if TRUE then the target values are clipped to the target range |

Value

numeric of same size as x

Author(s)

Jan Oosting

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