quantsmooth

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R topics documented:

`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 abberation, 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"),
```

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 subsegment 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")
```

helperFunctions *arraysmooth Helper functions*

Description

quantsmooth Helper functions

Usage

```
getChangedIdx(changed,up)
```

Arguments

`changed`

`up`

Details

Should not be called directly

Value

A data.frame with 3 colums 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

getChangedRegions *getChangedRegions*

Description

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

Usage

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

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 - 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 + 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 colums 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` *getLambdaMin*

Description

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

Usage

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

Arguments

`intensities` numeric vector

`lambdas` numeric vector; see `quantsmooth`

`...` extra parameters for `quantsmooth.cv`; currently only `ridge.kappa`

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` *Draw a chromosome using the grid package*

Description

A chromosme is drawn including the cytobands

Usage

```
grid.chromosome(chrom, side = 1, units = c("cM", "bases", "ISCN"), chrom.width =
                bands = "major", legend = c("chrom", "band", "none"), cex.leg = 0.7
```

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, type of unit to use

`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` *Retrieve chromosomal length*

Description

Retrieve human chromosomal length from NCBI data

Usage

```
lengthChromosome(chrom, units = c("cM", "bases", "ISCN"))
```

Arguments

`chrom`	vector of chromosomal id, 1:22,X,Y
`units`	

Value

A vector numeric 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,"ISCN")
```

`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)
characterCHR(CHR)
```

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.

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)))
```

`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 = c("cM", "bases", "ISCN"), width = 0
            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` units along which to plot the chromosome

`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 *H*orizontally to the right of the starting point or *V*ertically 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` *Wrapper for plotSmoothed*

Description

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

Usage

```
plotChromosome(gendata, chrompos, chromosome, dataselection = NULL, ylim = 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` *plotSmoothed*

Description

Plot a smoothed line together with the original data values

Usage

```
plotSmoothed(intensities, position, ylim=NULL, ylab="intensity", xlab="positio
```

Arguments

`intensities` numeric vector or matrix, data are plotted by column

`position` numeric vector; the length should be the number of rows in intensities

`ylim` numeric vector of length 2, limits for plot. If `NULL` then the minimal and maximal value in `intensities` is used

`ylab` character, label for y-position

`xlab` character, label for x-position

`normalized.to` numeric, a line(s) is drawn at this horizontal position

`grid` numeric, a line(s) is drawn at this vertical position

`smooth.lambda` numeric, smoothing parameter see `quantsmooth`

`interval` numeric (0..1), plotting of extra smoothed lines around median. With `interval` = 0.5 the 0.25 and 0.75 quartiles are plotted, with `interval` = 0.9 the 0.05 and 0.95 quantiles are plotted,

`plotnew` logical, if TRUE a new plot is created, else the data are plotted into an existing plot

`cols` color vector, colors for columns in `intensities`

`cex.pts` size of the dots in the plot. Set to `0` to skip plotting the dots

`...` 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` *Determine cytoband position based on location of probe*

Description

Determine cytoband position based on location of probe

Usage

```
position2Cytoband(chrom, position, units = c("cM", "bases", "ISCN"), bands = c("
```

Arguments

`chrom`	chromosomal id, chromosome to plot 1:22,X,Y
`position`	numeric vector
`units`	character, type of positional unit
`bands`	chararcter, 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,
                  sexChromosomes = FALSE, units = c("bases", "cM", "ISCN"),...)
```

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, type of units for genomic data

`...` 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.

Value

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

Author(s)

Jan Oosting

quantsmooth.cv *quantsmooth.cv*

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 *quantsmooth*

Description

Quantile smoothing of array data

Usage

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

Arguments

`intensities`	numeric vector
`smooth.lambda`	numeric
`tau`	numeric [0..1], the quantile desired; see `rq.fit`
`ridge.kappa`	fudge parameter; see details
`smooth.na`	logical; handling of NA
`segment`	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.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 = leng
```

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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