

Package ‘karyoploteR’

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Type Package

Title Plot customizable linear genomes displaying arbitrary data

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Author Bernat Gel <bgel@igtp.cat>

Maintainer Bernat Gel <bgel@igtp.cat>

Description karyoploteR creates karyotype plots of arbitrary genomes and offers a complete set of functions to plot arbitrary data on them. It mimicks many R base graphics functions coupling them with a coordinate change function automatically mapping the chromosome and data coordinates into the plot coordinates. In addition to the provided data plotting functions, it is easy to add new ones.

License Artistic-2.0

Depends R (>= 3.4), regioneR, GenomicRanges, methods

Imports regioneR, GenomicRanges, IRanges, Rsamtools, stats, graphics, memoise, rtracklayer, GenomeInfoDb, S4Vectors, biovizBase, digest, bezier, GenomicFeatures, bamsignals, AnnotationDbi, grDevices

Suggests BiocStyle, knitr, testthat, magrittr, BSgenome.Hsapiens.UCSC.hg19, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, org.Hs.eg.db, org.Mm.eg.db, pasillaBamSubset

URL <https://github.com/bernatgel/karyoploteR>

BugReports <https://github.com/bernatgel/karyoploteR/issues>

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addGeneNames	<i>addGeneNames</i>
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Description

Adds the gene names (defaults to symbols) to a GenesData object to be used by kpPlotGenes

Usage

```
addGeneNames(genes.data, orgDb="auto", keys=NULL, keytype="ENTREZID", names="SYMBOL")
```

Arguments

genes.data	(GenesData object) A valid genes.dat object like the ones obtained by makeGenesDataFromTxDb
orgDb	The orgDb object to use to extract the gene symbols. If "auto" the function will try to determine automatically the correct organism. See available objects at https://bioconductor.org/packages/release/BiocViews.html#___OrgDb (defaults to "auto")
keys	(character vector) The keys to be used in the internal select statement to get the names. If NULL, the first column of <code>mcols(GenesData\$genes)</code> will be used. (defaults to NULL)
keytype	(character) The keytype used in the internal select statement. (defaults to "ENTREZID", that is, <code>gene_id</code>)
names	The column to extract from orgDb to use as gene names. (defaults to "SYMBOL")

Details

This function takes a valid data object and uses an OrgDb object to find the gene names (symbols by default) and add them. Names are added as a column named names to the genes element of GenesData and they replace anything that was present there before. If no OrgDb object is given, the function will try to identify the correct organism using the data in GenesData\$metadata and select the OrgDb object if available. If it cannot identify the organism or there's no valid OrgDb for that organism it will fail with an error. Internally, the function uses a call to `AnnotationDbi::select` on the OrgDb. It is possible to specify the keys and keytypes as well as the column we want to use as names (defaults to SYMBOL for gene symbols).

Value

The original GenesData object with one additional column named "names" in `GenesData$genes$names`.

See Also

[kpPlotGenes](#), [makeGenesDataFromTxDb](#)

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)

zoom <- toGRanges("chr17:29e6-30e6")
kp <- plotKaryotype(genome="hg19", zoom=zoom)
genes.data <- makeGenesDataFromTxDb(TxDb.Hsapiens.UCSC.hg19.knownGene,
                                   karyoplot=kp, plot.transcripts=FALSE,
                                   plot.transcripts.structure=FALSE)
genes.data <- addGeneNames(genes.data)
kpPlotGenes(kp, data=genes.data, r1=0.5, plot.transcripts=FALSE,
            gene.name.position = "left")
```

autotrack

autotrack

Description

Computes r_0 and r_1 given track definition

Usage

```
autotrack(current.track, total.tracks, margin=0.05, r0=0, r1=1)
```

Arguments

<code>current.track</code>	(numeric) The track or tracks the current plot will occupy, starting from 1. If more than one value is provided, the plot will expand from $\min(\text{current.track})$ to $\max(\text{current.track})$.
<code>total.tracks</code>	(numeric) The total number of tracks
<code>margin</code>	(numeric) The margin is specified as the part of a track, by default 0.05, 5 percent of the track height.
<code>r0</code>	(numeric) the original r_0
<code>r1</code>	(numeric) the original r_1

Details

Small utility function to help compute r_0 and r_1 given the total number of tracks and the track(s) the current plot will occupy. It also takes into account a margin between tracks and original r_0 and r_1 , so we can say something like, "Out of 5 tracks between 0 and 0.5, this plot will be at track 2", and it will return $r_0=0.1$ and $r_1=0.2$

Value

A list of two numerics: r_0 and r_1

Examples

```
#first track out of 4
autotrack(1, 4)

#the same, but without margin
autotrack(1, 4, 0)

#first and second tracks out of 4
autotrack(c(1,2), 4)

#The first track out of 4, fitting the four track between 0 and 0.5
autotrack(1, 4, r0=0, r1=0.5)
```

colByChr

colByChr

Description

Given a set of data elements, return a color for each one based on their chromosome

Usage

```
colByChr(data, colors="2grays", all.chrs=NULL, default.col="black")
```

Arguments

data	Either a vector of characters or a GRanges object
colors	The name of a color set ("2grays", "blackgreen", "rainbow"...) or a vector of colors. If the vector is named, names are expected to be the chromosome names. (defaults to "2grays")
all.chrs	A vector with all possible chromosomes. If NULL, the list will be extracted from data (using seqlevels if available). (defaults to NULL)
default.col	The default color to return when something is unavailable

Details

Returns a color for each data element based on its chromosome. The returned colors might come from one of the predefined color sets or passed in as a parameter.

If colors is the name of one of the available color sets, it the color set is used. If it's a named character vector with the chromosome as names, they will be assigned by name and any missing chromosome will be default.col. If it's a non-named character vector, will be used in order and recycled if necessary.

Data might be either a GRanges object or a vector of chromosomes.

Value

A vector of colors

Note

```
Available color.sets: "2grays"=c("#888888", "#444444"), "2blues"=c("#6caeff", "#2b5d9b") "black-
green"=c("black", "green"), "greengray"=c("#c6ffb7", "#888888"), "brewer.set1"=c("#E41A1C",
"#377EB8", "#4DAF4A", "#984EA3", "#FF7F00", "#FFFF33", "#A65628", "#F781BF", "#999999")
"brewer.set2"=c("#66C2A5", "#FC8D62", "#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F", "#E5C494",
"#B3B3B3") "brewer.set3"=c("#8DD3C7", "#FFFFB3", "#BEBADA", "#FB8072", "#80B1D3",
"#FDB462", "#B3DE69", "#FCCDE5", "#D9D9D9", "#BC80BD", "#CCEBC5", "#FFED6F") "brewer.pastel1"=c("#FB
"#B3CDE3", "#CCEBC5", "#DECBE4", "#FED9A6", "#FFFFCC", "#E5D8BD", "#FDDAEC",
"#F2F2F2"), "brewer.pastel2"=c("#B3E2CD", "#FDCDAC", "#CBD5E8", "#F4CAE4", "#E6F5C9",
"#FFF2AE", "#F1E2CC", "#CCCCCC"), "rainbow"=rainbow(n=length(all.chrs))
```

See Also

[kpPoints](#)

Examples

```
chrs <- c("chr1", "chr2", "chr2", "chr1", "chr5")
points <- toGRanges(paste0("chr", c(1:22, "X", "Y")), rep(10e6, 24), rep(10e6, 24))

colByChr(chrs)
colByChr(points)

kp <- plotKaryotype(plot.type=4, labels.plotter=NULL, ideogram.plotter=NULL)
kpAddChromosomeNames(kp, srt=45)
kpAddChromosomeSeparators(kp)

total.tracks <- 6

kpPoints(kp, points, col=colByChr(points), y=0.5, cex=1, r0=autotrack(1,total.tracks)$r0, r1=autotrack(1,total.tracks)$r1)
colors <- NULL
kpPoints(kp, points, y=0.5, col=colByChr(points, colors=colors), cex=1, r0=autotrack(2,total.tracks)$r0, r1=autotrack(2,total.tracks)$r1)
colors <- c("red", "blue")
kpPoints(kp, points, y=0.5, col=colByChr(points, colors=colors), cex=1, r0=autotrack(3,total.tracks)$r0, r1=autotrack(3,total.tracks)$r1)
colors <- c(chr1="red", chr7="blue")
kpPoints(kp, points, y=0.5, col=colByChr(points, colors=colors), cex=1, r0=autotrack(4,total.tracks)$r0, r1=autotrack(4,total.tracks)$r1)
kpPoints(kp, points, y=0.5, col=colByChr(points, colors=colors, default.col="green"), cex=1, r0=autotrack(5,total.tracks)$r0, r1=autotrack(5,total.tracks)$r1)
colors <- c("red", "yellow", 3, "orchid", "blue")
kpPoints(kp, points, y=0.5, col=colByChr(points, colors=colors), cex=1, r0=autotrack(6,total.tracks)$r0, r1=autotrack(6,total.tracks)$r1)

#Color sets
pp <- getDefaultPlotParams(plot.type=4)
pp$leftmargin <- 0.2
kp <- plotKaryotype(plot.type=4, labels.plotter=NULL, ideogram.plotter=NULL, plot.params=pp)
kpAddChromosomeNames(kp, srt=45)
kpAddChromosomeSeparators(kp)

color.sets <- c( "2grays", "2blues", "blackgreen", "greengray", "brewer.set1",
"brewer.set2", "brewer.set3", "brewer.pastel1", "brewer.pastel2", "rainbow" )
total.tracks <- length(color.sets)
for(i in seq_len(length(color.sets))) {
  kpPoints(kp, points, y=0.5, col=colByChr(points, colors=color.sets[i]), cex=1, r0=autotrack(i,total.tracks)$r0, r1=autotrack(i,total.tracks)$r1)
  kpAddLabels(kp, labels=color.sets[i], cex=0.7, r0=autotrack(i,total.tracks)$r0, r1=autotrack(i,total.tracks)$r1)
}
```

colByRegion	<i>colByRegion</i>
-------------	--------------------

Description

Given a set of data elements, return a color for each one based on whether they overlap a given set of regions. This might be useful, for example, to set a different color for data points overlapping a certain region of interest.

Usage

```
colByRegion(data, regions, colors=NULL, default.col="black")
```

Arguments

data	Either a vector of characters or a GRanges object
regions	(GRanges or equivalent) A set of regions where the color will be modified. Internally it will be converted into a Genomic Ranges object by toGRanges (from regioneR package) and so it can be either a GRanges, a data.frame, a character or any other value type accepted by that function. If colors is NULL (the default) and regions has additional columns in addition to chr, start and end, if any has a name in c("color", "colors", "col", "cols") it will be used. Otherwise the first additional column will be used.
colors	(color) The colors to be used for each region. The content will be recycled if needed. If NULL, the colors are assumed to be available in the regions object. (defaults to NULL)
default.col	The default color to return for data elements not overlapping the regions. (defaults to "black")

Details

Given a set of data elements, return a color for each one based on whether they overlap a given set of regions. The colors might be different for each region and can be specified either in the regions object itself or in a separate colors parameter. If specified in colors, the values will be recycled as needed.

Value

A vector of colors

See Also

[kpPoints](#), [colByChr](#), [toGRanges](#)

Examples

```
data <- toGRanges("chr1", c(1e6*1:245), c(1e6*1:245)+10)
data$y <- rnorm(n = length(data), mean = 0.5, sd = 0.15)

regions <- toGRanges(c("chr1:10e6-20e6", "chr1:100e6-150e6"))
```

```

regions$col <- c("red", "blue")

kp <- plotKaryotype(chromosomes="chr1")
kpPoints(kp, data=data, r0=0, r1=0.2)
kpPoints(kp, data=data, r0=0.2, r1=0.4, col=colByRegion(data, regions = regions) )
kpText(kp, data=data, r0=0.4, r1=0.6, col=colByRegion(data, regions = regions), label="A", cex=0.5 )
kpBars(kp, data=data, y0=0, y1=data$y, r0=0.6, r1=0.8, border=colByRegion(data, regions = regions))
#It might not work wor objects where R expects a single color such as lines. Segments should be used instead
kpLines(kp, data=data, r0=0.8, r1=1, col=colByRegion(data, regions = regions) )

kp <- plotKaryotype(chromosomes="chr1")
kpPoints(kp, data=data, r0=0, r1=0.25)
kpPoints(kp, data=data, r0=0.25, r1=0.5, col=colByRegion(data, regions = regions, colors="green") )
kpText(kp, data=data, r0=0.5, r1=0.75, col=colByRegion(data, regions = regions, color=c("gray", "gold")), label="A", cex=0.5 )
kpBars(kp, data=data, y0=0, y1=data$y, r0=0.75, r1=1, border=colByRegion(data, regions = regions))

```

darker

darker

Description

Given a color, return a darker one

Usage

```
darker(col, amount=150)
```

Arguments

col	(color) The original color. Might be specified as a color name or a "#RRGGBB(AA)" hex color definition.
amount	(integer, [0-255]) The fixed amount to subtract to each RGB channel (Defaults to 150).

Details

Very simple utility function to create darker colors. Given a color, it transforms it to rgb space, adds a set amount to all channels and transforms it back to a color.

Value

A darker color

See Also

[lighter](#)

Examples

```
darker("red")
darker("#333333")
darker(c("red", 3, "#FF00FF"))
```

filterParams

filterParams

Description

Given a list, select just only the valid.elements from each member. Also works with vectors instead of lists

Usage

```
filterParams(p, valid.elements, orig.length)
```

Arguments

p a list or a single vector
valid.elements a boolean vector with the elements to keep
orig.length the length of the elements on which to apply the filtering

Details

This function is used in filtering the graphical parameters when plotting only a part of the genome. For each element of the list, if it has the exact specified length, filters it using the 'valid.elements' parameter.

Value

p with some members filtered

Examples

```
a <- 1:10
b <- 3:5
c <- 2

filterParams(list(a,b,c), c(rep(TRUE,5), rep(FALSE,5)), 10)
filterParams(a, c(rep(TRUE,5), rep(FALSE,5)), 10)
```

`getChromosomeNamesBoundingBox`
getChromosomeNamesBoundingBox

Description

Return the regions where the chromosome names should be placed

Usage

```
getChromosomeNamesBoundingBox(karyoplot)
```

Arguments

`karyoplot` a `karyoplot` object returned by a call to `plotKaryotype`

Details

Given a `KaryoPlot` object, return the regions where the chromosome labels should be placed. The positions will depend on the plot type used.

Value

Returns a list with four elements (`x0`, `x1`, `y0` and `y1`), each of them a named vector of integers with one coordinate for every chromosome in the plot.

Note

In general, this function is automatically called by `karyoploteR` and the user never needs to call it.

See Also

[plotKaryotype](#), [kpAddChromosomeNames](#)

Examples

```
kp <- plotKaryotype()
bb <- getChromosomeNamesBoundingBox(kp)
```

getCytobandColors *getCytobandColors*

Description

Returns a named character vector with the colors of associated with the cytoband names

Usage

```
getCytobandColors(color.table=NULL, color.schema=c("circos", "biovizbase", "only.centromeres"))
```

Arguments

`color.table` (named character vector) if present, it's returned as-is. Useful to specify your own color.tables.

`color.schema` (character) The name of the color schema to use: `circos`, `biovizBase`, `only.centromeres` (everything in gray, except for centromeres in red). (defaults to `circos`)

Details

The function returns a named character vector with the colors of associated with the cytoband names. Two color schemas are available: `circos` (which copies the colors used by `Circos`) and `biovizbase` (that gets the cytoband colors from the `biovizBase` Bioconductor package). If a `color.table` is given, it is returned untouched.

Value

a named character vector with the colors associated to each cytoband name

See Also

[plotKaryotype](#), [kpAddCytobands](#)

Examples

```
getCytobandColors()
getCytobandColors(color.schema="biovizbase")
```

getCytobands *getCytobands*

Description

Get the cytobands of the specified genome.

Usage

```
getCytobands(genome="hg19", use.cache=TRUE)
```

Arguments

genome	(character or other) specifies a genome using the UCSC genome name. Defaults to "hg19". If it's not a character, genome is ignored and an empty GRanges is returned.
use.cache	(boolean) whether to use or not the cytoband information included in the package. use.cache=FALSE will force a download from the UCSC.

Details

It returns a GRanges object with the cytobands of the specified genome. The cytobands for some organisms and genome versions have been pre-downloaded from UCSC and included in the karyoploteR package. For any other genome, getCytobands will use rtracklayer to try to fetch the cytoBandIdeo table from UCSC. If for some reason it is not possible to retrieve the cytobands, it will return an empty GRanges object. Setting the parameter use.cache to FALSE, the data included in the package will be ignored and the cytobands will be downloaded from UCSC.

The genomes (and versions) with pre-downloaded cytobands are: hg19, hg38, mm9, mm10, rn5, rn6, danRer10, dm6, ce6 and sacCer3.

Value

It returns a [GenomicRanges](#) object with the cytobands of the specified genome. If no cytobands are available for any reason, an empty GRanges is returned.

Note

This function is memoised (cached) using the [memoise](#) package. To empty the cache, use [forget](#)(getCytobands)

See Also

[plotKaryotype](#)

Examples

```
#get the cytobands for hg19 (using the data included in the package)
cyto <- getCytobands("hg19")

#do not use the included data and force the download from UCSC
cyto <- getCytobands("hg19", use.cache=FALSE)

#get the cytobands for Drosophila Melanogaster
cyto <- getCytobands("dm6")

#get the cytobands for Chimpanzee (not included in the package)
cyto <- getCytobands("panTro4")
```

```
getDataPanelBoundingBox  
      getDataPanelBoundingBox
```

Description

Return the bounding box of a data panel in plot coordinates

Usage

```
getDataPanelBoundingBox(karyoplot, data.panel)
```

Arguments

<code>karyoplot</code>	a karyoplot object returned by a call to <code>plotKaryotype</code>
<code>data.panel</code>	a valid data panel name (i.e. 1, 2, "ideogram", "all")

Details

Given a KaryoPlot object and a data.panel name, return the region where the data panel is placed. The returned values are in plot coordinates, that is, the `coord.change.function` has been applied.

Value

Returns a list with four elements (`x0`, `x1`, `y0` and `y1`), each of them an integer with the plot coordinates for the data.panel

Note

A user is not expected to need this function. It is mainly used by plotting functions, specially when clipping the plot in a zoomed region.

See Also

[plotKaryotype](#), [kpDataBackground](#)

Examples

```
kp <- plotKaryotype(plot.type=2)  
dp1 <- getDataPanelBoundingBox(kp, 1)
```

getDefaultPlotParams *getDefaultParameters*

Description

Returns the default parameters for the given plot.type

Usage

```
getDefaultPlotParams(plot.type)
```

Arguments

plot.type (integer) the required plot type. can be any valid plot type (see [plotKaryotype](#))

Details

Given a plot.type, this function returns a list suitable as a valid plot.params object. The user can then proceed to change the parameter values as needed and supply the modified list to the plotKaryotype function.#'

Value

A valid plot.params object with the default values for the plotting parameters and ready to be used in the plotKaryotype

See Also

[plotKaryotype](#)

Examples

```
pp <- getDefaultPlotParams(plot.type=2)
pp

#Change the ideogramheight param to create thicker ideograms
pp$ideogramheight <- 150

plotKaryotype(genome="hg19", plot.type=2, plot.params=pp)
```

```
getMainTitleBoundingBox  
    getMainTitleBoundingBox
```

Description

Return the regions where the chromosome names should be placed

Usage

```
getMainTitleBoundingBox(karyoplot)
```

Arguments

karyoplot a karyoplot object returned by a call to `plotKaryotype`

Details

Given a `KaryoPlot` object, return the regions where the main plot should be placed. The position will depend on the plot type used.

Value

Returns a list with four elements (x0, x1, y0 and y1), each of them an integer with the coordinates for the main title

Note

In general, this function is automatically called by `karyoploteR` and the user never needs to call it.

See Also

[plotKaryotype](#), [kpAddMainTitle](#)

Examples

```
kp <- plotKaryotype()  
bb <- getMainTitleBoundingBox(kp)
```

getTextSize	<i>getTextSize</i>
-------------	--------------------

Description

Returns the size of character strings in bases and r's

Usage

```
getTextSize(karyoplot, labels, cex=1, data.panel="1")
```

Arguments

karyoplot	(KaryoPlot) A KaryoPlot object representing the current plot
labels	(character) The character strings to measure
cex	(numeric) The cex value used to plot the text (defaults to 1)
data.panel	(data panel identifier) The name of the data panel on which text was plotted. (defaults to "1")

Details

Small utility function to get the size of text labels in usable units for karyoplotR: bases for the width and r's for the height. The r units are the ones passed to r0 and r1 and take into account that a data panel has always total height of 1 r (from r0=0 to r1=1)

Value

Returns a list with two elements: width and height. Each of them is a numeric vector of the same length as "labels" with the width in bases of each label and the height in r units of each label.

Examples

```
pp <- getDefaultPlotParams(plot.type=2)
pp$data2height <- 50

kp <- plotKaryotype(chromosomes="chr1", plot.type=2, plot.params=pp)

label <- "Looooooooong label"
kpText(kp, chr="chr1", x=70e6, y=0.5, labels=label)
text.size <- getTextSize(kp, labels=label)
kpRect(kp, chr="chr1", x0=70e6-text.size$width/2, x1=70e6+text.size$width/2,
       y0=0.5-text.size$height/2, y1=0.5+text.size$height/2)

label <- "SHORT"
text.size <- getTextSize(kp, labels=label, cex=3)
kpRect(kp, chr="chr1", x0=170e6-text.size$width/2, x1=170e6+text.size$width/2,
       y0=0.2-text.size$height/2, y1=0.2+text.size$height/2, col="gold")
kpText(kp, chr="chr1", x=170e6, y=0.2, labels=label, cex=3)

label <- c("two_labels", "in a small data.panel=2")
kpText(kp, chr="chr1", x=c(100e6, 170e6), y=c(0.4, 0.2), labels=label, cex=0.6, data.panel=2)
```



```
text.size <- getTextSize(kp, labels=label, cex=0.6, data.panel=2)
kpRect(kp, chr="chr1", x0=c(100e6, 170e6)-text.size$width/2, x1=c(100e6, 170e6)+text.size$width/2,
       y0=c(0.4, 0.2)-text.size$height/2, y1=c(0.4, 0.2)+text.size$height/2, data.panel=2)
```

getVariantsColors *getVariantsColors*

Description

Given the reference and alternative for a set of variants, assigns a color to each of them

Usage

```
getVariantsColors(ref, alt, color.table=NULL, color.schema=c("cell21breast"))
```

Arguments

ref	(character vector) The reference nucleotides of the variants. It has to have the same length as alt.
alt	(character vector) The alternative nucleotides of the variants. It has to have the same length as ref
color.table	(named character vector) if present, its used to assign colors to the nucleotide substitutions.
color.schema	(character) The name of the color schema to use: cell21breast (the color schema used in "Mutational Processes Molding the Genomes of 21 Breast Cancers" by S. Nik-Zainal, Cell, 2012). (defaults to cell21breast)

Details

The function creates an nucleotide substitution identifier with for each variant and uses it to query the color.table lookup table. If color.table is NULL, a color.table based in the selected color.schema is used. All unkwonwn nucleotide substitutions are assigned a gray color. Color table needs to have entries for C>A, C>G, C>T, T>A, T>C and T>G (and optionally "others"), since other changes can be reverse complemented to these.

Value

a named character vector with the colors associated to each variant

See Also

[plotKaryotype](#), [kpPlotRainfall](#)

Examples

```
ref <- c("A", "A", "C", "T", "G", "A")
alt <- c("G", "C", "T", "A", "A", "-")
getVariantsColors(ref, alt)
```

```
col.table <- c("C>A"="#FF0000", "C>G"="#000000", "C>T"="#00FF00", "T>A"="#0000FF", "T>C"="#BB00BB", "T>G"="#000000")
getVariantsColors(ref, alt, col.table)
```

is.color

is.color

Description

Test if something is a valid color

Usage

```
is.color(x)
```

Arguments

x The element to test

Details

This function tests if something is a valid color. Returns TRUE or FALSE. The function is vectorised.

Value

TRUE is x is a valid color, FALSE otherwise

Examples

```
is.color("red")
is.color("#333333")
is.color(NA)
is.color(NULL)
is.color("not_a_color")
is.color(3)

is.color(c("not_a_color", "red", 3, "#FF0000"))
```

kpAbline	<i>kpAbline</i>
----------	-----------------

Description

This is the KaryoploteR version of the [abline](#) function to add horizontal or vertical lines to the plot.

Usage

```
kpAbline(karyoplot, chr=NULL, h=NULL, v=NULL, ymin=NULL, ymax=NULL, data.panel=1, r0=NULL, r1=NULL, ...)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
chr	(a character vector) A vector of chromosome names specifying the chromosomes where the lines will be plotted. If NULL, the lines will be plotted in all chromosomes. (defaults to NULL)
h	(a numeric vector) A numeric vector with the heights where the horizontal lines will be plotted. If h is NULL, no horizontal lines will be plotted. (defaults to NULL)
v	(a numeric vector) A numeric vector with the positions (in base pairs) where the vertical lines will be plotted. If v is NULL, no vertical lines will be plotted. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

As with all other base-inspired low-level plotting functions in karyoploteR, the function has been designed to accept mostly the same parameters as the base one (see the package vignette for more information). In this case, however, the interface has been reduced and it is only possible to plot vertical and horizontal lines and it's not possible to provide an intercept and slope. In addition, the function accepts graphical parameters that are valid for the base function [segments](#).

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpSegments](#), [kpLines](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=1000, mask=NA))
mcols(data.points) <- data.frame(y=rnorm(1000, mean = 0.5, sd = 0.1))

kp <- plotKaryotype("hg19", plot.type=1, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)

kpPoints(kp, data=data.points, pch=".", col="#2222FF", cex=3)

#Add horizontal lines at mean
kpAblines(kp, h=0.5, col="red")

#and at the 1 sd
kpAblines(kp, h=c(0.4, 0.6), col="orange", lwd=0.5)
#and 2 sd's
kpAblines(kp, h=c(0.3, 0.7), col="orange", lwd=0.5, lty=2)

#And add two vertical lines at specific chromosomal locations
kpAblines(kp, v=c(67000000, 190000000), chr="chr1")
```

kpAddBaseNumbers

kpAddBaseNumbers

Description

Plots the base numbers along the chromosome ideograms

Usage

```
kpAddBaseNumbers(karyoplot, tick.dist=20000000, tick.len=5, add.units=FALSE, digits=2, minor.ticks)
```

Arguments

karyoplot	(karyoplot object) A valid karyoplot object created by a call to plotKaryotype
tick.dist	(numeric) The distance between the major numbered tick marks in bases (defaults to 20 millions, one major tick every 20Mb)
tick.len	(numeric) The length of the major tick marks in plot coordinates (defaults to 5)
add.units	(boolean) Add the units (Mb, Kb...) to the tick labels. (Defaults to FALSE)
digits	(integer) The maximum number of digits after the decimal point in labels. (defaults to 2)
minor.ticks	(boolean) Whether to add unlabeled minor ticks between the major ticks (defaults to TRUE)
minor.tick.dist	(numeric) The distance between the minor ticks in bases (defaults to 5 millions, a minor tick mark every 5Mb)
minor.tick.len	(numeric) The length of the minor tick marks in plot coordinates (defaults to 2)
cex	(numeric) The cex parameter for the major ticks label (defaults to 0.5)
tick.col	(color) If specified, the color to plot the major ticks. Otherwise the default color or, if given, the col parameter will be used. (Defaults to NULL)
minor.tick.col	(color) If specified, the color to plot the minor ticks. Otherwise the default color or, if given, the col parameter will be used. (Defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	Any other parameter to be passed to internal function calls. Specially useful for graphic parameters.

Details

This function can be used to add the base numbers scale to the chromosome ideograms. The base numbers and ticks will be drawn next to the ideograms and not on a separate independent x axis. It is possible to control the number and position of the tick marks and labels

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#)

Examples

```
kp <- plotKaryotype()
kpAddBaseNumbers(kp)

kp <- plotKaryotype(chromosomes="chr17")
kpAddBaseNumbers(kp, tick.dist=10000000, minor.tick.dist=1000000)
```

kpAddChromosomeNames *kpAddChromosomeNames*

Description

Plots the chromosome names in the karyoplot

Usage

```
kpAddChromosomeNames(karyoplot, xoffset=0, yoffset=0, ...)
```

Arguments

karyoplot	a karyoplot object returned by a call to plotKaryotype
xoffset	(numeric) a number of units to move the the chromosome names on the x axis with respect to their standard position (defaults to 0)
yoffset	(numeric) a number of units to move the the chromosome names on the y axis with respect to their standard position (defaults to 0)
...	any additional parameter to be passed to the text plotting. All R base graphics params are passed along.

Details

Given a KaryoPlot object, plot the names of the depicted chromosomes. This function is usually automatically called by plotKaryotype unless labels.plotter is NULL.

Value

invisibly returns the given karyoplot object

See Also

[plotKaryotype](#), [getChromosomeNamesBoundingBox](#)

Examples

```
kp <- plotKaryotype(labels.plotter = NULL)
kpAddChromosomeNames(kp, col="red", srt=30)
```

kpAddChromosomeSeparators
kpAddChromosomeSeparators

Description

Plots between the chromosomes

Usage

```
kpAddChromosomeSeparators(karyoplot, col="gray", lty=3, data.panel="all", ...)
```

Arguments

karyoplot	a karyoplot object returned by a call to plotKaryotype
col	(color) The color of the separator lines (defaults to "gray")
lty	(integer) The line type of the separators (defaults to 3, dashed lines)
data.panel	(data panel specification) For vertical lines, the span of the separator lines. Ignored for horizontal lines. (defaults to "all")
...	any additional parameter to be passed to the text plotting. All R base graphics params are passed along.

Details

Depending on the plot type it will draw vertical lines (if all chromosomes are in a one line (3,4,5,7)) or horizontal lines (1,2,6)

By default the lines will occupy the whole chromosome extent (data.panel="all") but using the data.panel parameter it can be tuned.

Value

invisibly returns the given karyoplot object

See Also

[plotKaryotype](#)

Examples

```
kp <- plotKaryotype(plot.type=4)
kpAddChromosomeSeparators(kp)

kp <- plotKaryotype(plot.type=5, ideogram.plotter=NULL)
kpAddChromosomeSeparators(kp)

kp <- plotKaryotype(plot.type=2)
kpAddChromosomeSeparators(kp, col="red")
```

kpAddCytobandLabels *kpAddCytobandLabels*

Description

Plots the base numbers along the chromosome ideograms

Usage

```
kpAddCytobandLabels(karyoplot, cex=0.5, force.all=FALSE, clipping=TRUE, ...)
```

Arguments

karyoplot	(karyoplot object) A valid karyoplot object created by a call to plotKaryotype
cex	(numeric) The cex parameter for the cytoband labels
force.all	(boolean) If true, all cytoband labels are plotted, even if they do not fit into the cytobands (Defaults to FALSE)
clipping	(boolean) Only used if zooming is active. If TRUE, the name will be not drawn out of the drawing are (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the labels may overflow into the margins of the plot. (defaults to TRUE)
...	Any other parameter to be passed to internal function calls. Specially useful for graphic parameters.

Details

This function can be used to add labels identifying the cytobands. It gets the labels from the cytobands information stored in the karyoplot object and it will only plot the labels that fit inside the available space. This means than in some cases (such as when plotting a complete genome with default parameters) it is possible that no labels at all are added.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#)

Examples

```
kp <- plotKaryotype()
kpAddBaseNumbers(kp)
kpAddCytobandLabels(kp)

kp <- plotKaryotype(chromosomes="chr17")
kpAddBaseNumbers(kp, tick.dist=10000000, minor.tick.dist=1000000)
kpAddCytobandLabels(kp)
```

kpAddCytobands	<i>kpAddCytobands</i>
----------------	-----------------------

Description

Plots the chromosome cytobands in a karyoplot

Usage

```
kpAddCytobands(karyoplot, color.table=NULL, color.schema=c("circos", "biovizbase", "only.centromeres"))
```

Arguments

karyoplot	a karyoplot object returned by a call to plotKaryotype
color.table	(named character vector) a table specifying the colors to plot the cytobands. If NULL, it gets the colors calling getCytobandColors. (defaults to NULL)
color.schema	(character) The name of the color schema to use: circos, biovizBase, only.centromeres (everything in gray, except for centromeres in red). (defaults to circos)
clipping	(boolean) Only used if zooming is active. If TRUE, cytoband representation will be not drawn out of the drawing are (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the cytobands representation may overflow into the margins of the plot. (defaults to TRUE)
...	any additional parameter to be passed to the functions called from kpAddCytobands.

Details

Plots the cytobands representing the chromosome structure in a karyoplot. It extracts the cytobands from the karyoplot object it receives as a parameter. It is possible to specify the colors used to plot the cytobands.

Value

invisibly returns the given karyoplot object

Note

In general, this function is automatically called by plotKaryotype and the user never needs to call it.

See Also

[plotKaryotype](#), [getCytobandColors](#), [kpAddBaseNumbers](#), [kpAddCytobandLabels](#)

Examples

```
kp <- plotKaryotype(ideogram.plotter = NULL)
kpAddCytobands(kp)
```

kpAddCytobandsAsLine *kpAddCytobandsAsLine*

Description

Plots the chromosome cytobands in a karyoplot as a line

Usage

```
kpAddCytobandsAsLine(karyoplot, color.table=NULL, color.schema='only.centromeres', lwd=3, lend=1,
```

Arguments

karyoplot	a karyoplot object returned by a call to plotKaryotype
color.table	(named character vector) a table specifying the colors to plot the cytobands. If NULL, it gets the colors calling getCytobandColors. (defaults to NULL)
color.schema	(character: 'only.centromeres', 'circo', 'biovizbase') The name of the color schema to use. It is directly passed along to getCytobandColors . color.table takes precedence over color.schema. (defaults to 'only.centromeres')
lwd	(integer) The width of the line used to represent the ideogram (defaults to 3)
lend	(0, 1 or 2) The type of line end. (defaults to 1, "butt")
clipping	(boolean) Only used if zooming is active. If TRUE, cytoband representation will be not drawn out of the drawing are (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the cytobands representation may overflow into the margins of the plot. (defaults to TRUE)
...	any additional parameter to be passed to the functions called from kpAddCytobands.

Details

Plots the cytobands representing the chromosome structure in a karyoplot. It extracts the cytobands from the karyoplot object it receives as a parameter. It is possible to specify the colors used to plot the cytobands. In contrast to [kpAddCytobands](#) it represents the chromosomes as a thin line

Value

invisibly returns the given karyoplot object

Note

In general, this function is automatically called by plotKaryotype and the user never needs to call it.

See Also

[plotKaryotype](#), [getCytobandColors](#), [kpAddBaseNumbers](#), [kpAddCytobandLabels](#)

Examples

```
kp <- plotKaryotype(ideogram.plotter = NULL)
kpAddCytobandsAsLine(kp)

kp <- plotKaryotype(ideogram.plotter = NULL, plot.type=2)
kpAddCytobandsAsLine(kp)
```

kpAddLabels

*kpAddLabels***Description**

Add labels to identify the data in the plot

Usage

```
kpAddLabels(karyoplot, labels, label.margin=0.01, side="left", pos=NULL, offset=0, r0=NULL, r1=NULL)
```

Arguments

karyoplot	a karyoplot object returned by a call to plotKaryotype
labels	(character) the text on the labels
label.margin	(numeric) the additional the margin between the labels the first base of the chromosome. In plot coordinates. Usual value might be 0.05. Can be negative. (defaults to 0.01)
side	("left" or "right") The side of the plot where to plot the labels. (defaults to "left")
pos	(numeric) The standard graphical parameter. See text . If NULL, pos will be selected automatically based on "side" (Defaults to NULL)
offset	(numeric) The standard graphical parameter. See text . (Defaults to 0)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to position the label. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to position the label. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the labels are to be added. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
...	any additional parameter to be passed to the text plotting. All R base graphics params are passed along.

Details

Given a KaryoPlot object, plot labels on the side of the data panels to help identify the different types of data plotted

Value

invisibly returns the given karyoplot object

See Also

[plotKaryotype](#)

Examples

```
plot.params <- getDefaultPlotParams(plot.type=2)
plot.params$leftmargin <- 0.2
plot.params$rightmargin <- 0.2
kp <- plotKaryotype("hg19", chromosomes=c("chr1", "chr2"), plot.type=2, plot.params = plot.params)
#data panel 1
kpDataBackground(kp, r0=0, r1=0.5, col="#FFDDDD")
kpDataBackground(kp, r0=0.5, r1=1, col="#DDFFDD")
kpAddLabels(kp, "Everything", label.margin = 0.12, srt=90, pos=3, cex=0.8)
kpAddLabels(kp, "Red", r0=0, r1=0.5, cex=0.6)
kpAddLabels(kp, "Green", r0=0.5, r1=1, cex=0.6)
#data panel 2
kpDataBackground(kp, col="#DDDDFF", data.panel = 2)
kpAddLabels(kp, "BLUE", data.panel=2)

#Plot on the right
#data panel 1
kpAddLabels(kp, "Everything", label.margin = 0.12, srt=90, pos=1, cex=0.8, side="right")
kpAddLabels(kp, "Red", r0=0, r1=0.5, cex=0.6, side="right")
kpAddLabels(kp, "Green", r0=0.5, r1=1, cex=0.6, side="right")
```

`kpAddMainTitle`

kpAddMainTitle

Description

Plots the chromosome names in the karyoplot

Usage

```
kpAddMainTitle(karyoplot, main=NULL, ...)
```

Arguments

<code>karyoplot</code>	a karyoplot object returned by a call to <code>plotKaryotype</code>
<code>main</code>	(character) the main title of the plot
<code>...</code>	any additional parameter to be passed to the text plotting. All R base graphics params are passed along.

Details

Given a KaryoPlot object and a character string, plot the character strings as the main title of the plot. This function is usually automatically called by plotKaryotype unless.

Value

invisibly returns the given karyoplot object

See Also

[plotKaryotype](#), [getMainTitleBoundingBox](#)

Examples

```
kp <- plotKaryotype(labels.plotter = NULL)
kpAddMainTitle(kp, col="red", srt=30)
```

kpArea

kpArea

Description

Plots a line joining the data points along the genome and fills the area below the line.

Usage

```
kpArea(karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, base.y=0, ymin=NULL, ymax=NULL, data.panel=)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If data is not NULL, x is ignored. (defaults to NULL)
y	(a numeric vector) A numeric vector with the values of the data points. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
base.y	(numeric) The y value at which the polygon will be closed. (defaults to 0)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the minimum value of the selected data panel. (defaults to NULL)

ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
col	(color) The fill color of the area. If NULL the color will be assigned automatically, either a lighter version of the color used for the outer line or gray if the line color is not defined. If NA no area will be drawn. (defaults to NULL)
border	(color) The color of the line enclosing the area. If NULL the color will be assigned automatically, either a darker version of the color used for the area or black if col=NA. If NA no border will be drawn. (Defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is a karyoploteR low-level plotting functions. Given a set of positions on the genome (chromosome and base) and a value (y) for each of them, it plots a line joining them and shades the area below them. Data can be provided via a GRanges object (data), independent parameters for chr, x and y or a combination of both. A number of parameters can be used to define exactly where and how the line and area are drawn. In addition, via the ellipsis operator (...), kpArea accepts any parameter valid for [lines](#) and [polygon](#) (e.g. lwd, lty, col, density...) The lines are drawn in a per chromosome basis, so it is not possible to draw lines encompassing more than one chromosome.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpLines](#), [kpText](#), [kpPlotRibbon](#)

Examples

```
set.seed(1000)
```

```

data.points <- sort(createRandomRegions(nregions=500, mask=NA))
mcols(data.points) <- data.frame(y=runif(500, min=0, max=1))

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpArea(kp, data=data.points)
kpArea(kp, data=data.points, col="lightgray", border="red", lty=2, r0=0, r1=0.5)
kpArea(kp, data=data.points, border="red", data.panel=2, r0=0, r1=0.5)
kpArea(kp, data=data.points, border="blue", data.panel=2, r0=0, r1=0.5, base.y=1)

kpArea(kp, data=data.points, border="gold", data.panel=2, r0=0.5, r1=1, base.y=0.5)

```

kpArrows

*kpArrows***Description**

Plots segments at the specified genomic positions.

Usage

```
kpArrows(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=NULL, y0=NULL, y1=NULL, ymin=NULL, ymax=NULL,
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data), x0 to start(data) and x1 to end(data). If no parameter y0 is specified and data has a column named y0, this column will be used. The same for y1. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(a numeric vector) A numeric vector of x left positions (in base pairs). If data is not NULL, x0. (defaults to NULL)
x1	(a numeric vector) A numeric vector of x right positions (in base pairs). If data is not NULL, x1. (defaults to NULL)
y0	(a numeric vector) A numeric vector of y bottom positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
y1	(a numeric vector) A numeric vector of y top positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)

y max	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data. panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r 0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r 1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from `karyoploteR` implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome, `x0` and `x1`) and values (`y0` and `y1`) for each of them, it plots arrows going from (`x0`, `y0`) to (`x1`, `y1`). Data can be provided via a `GRanges` object (`data`), independent parameters for `chr`, `x0`, `x1`, `y0` and `y1`, or a combination of both. A number of parameters can be used to define exactly where and how the arrows are drawn. In addition, via the ellipsis operator (`...`), `kpSegments` accepts any parameter valid for segments (e.g. `code`, `lwd`, `lty`, `col`, ...)

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpRect](#), [kpPoints](#),
[kpPlotRegions](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=500, length.mean=2000000, mask=NA))
y <- runif(500, min=0, max=0.8)
mcols(data.points) <- data.frame(y0=y, y1=y+0.2)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
```



```
kpDataBackground(kp, data.panel=2)
```

```
kpArrows(kp, data=data.points, col="black", lwd=2, length=0.04)
```

```
kpArrows(kp, data=data.points, y0=0, y1=1, r0=0.2, r1=0.8, col="lightblue", data.panel=2)
```

kpAxis

kpAxis

Description

Plot axis at the sides of the data panels

Usage

```
kpAxis(karyoplot, ymin=NULL, ymax=NULL, r0=NULL, r1=NULL, side=1, numticks=3, labels=NULL, tick.pos
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotER. A KaryoPlot object referring to the currently active plot.
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
side	(numeric) In which side of the data panel should the axis be plotted. 1 - plot it on the right of the data panel. 2 - Plot it on the left. (defaults to 1)
numticks	(numeric) the number of ticks (and labels) of the axis. If tick.pos is present, it takes precedence over num.ticks and num.ticks is ignored. (defaults to 3)
labels	(character) the labels to be placed next to the ticks. If the number of labels is lower than the number of ticks, the labels will be reused. If NULL, the numeric values of the ticks will be used. (defaults to NULL)
tick.pos	(numeric) the places in the axis where a tick should be drawn. If present, num.ticks is ignored. If NULL, ticks are placed equidistant. (defaults to NULL)

tick.len	(numeric) the length of the ticks to be drawn measured in base pairs. If NULL, tick length is 0.01 times the length in bases of the longest chromosome. (defaults to NULL)
label.margin	(numeric) the additional the margin between the labels and ticks. Can be negative. If NULL, the default margin is used. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
text.col	(color) The color of the text elements (defaults to "black")
col	(color) The color of the axis lines (defaults to "black")
chromosomes	(character) To which chromosomes should we add the axis: "first", "last", "auto", "all" or a vector of chromosome names. With auto, the chromosomes will depend on the plot type and side of axis plotting. (defaults to "auto")
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

kpAxis plots axis at the sides of the data panels. It is possible to control the number of ticks and their labels, the placement of the plots and whether they span the whole data panel or just part of it. To do that they use the same placement parameters used by other karyoploteR functions (`r0` and `r1`). This function does not have a `chr` option: axis are always plotted for all chromosomes.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpDataBackground](#), [kpAbline](#)

Examples

```
kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))

#Prepare data panel 1
kpDataBackground(kp, data.panel=1)
kpAxis(kp, data.panel = 1)
kpAxis(kp, data.panel = 1, ymin = 0, ymax=10, numticks = 11, side = 2, cex = 0.4, col="red")

#Prepare data panel 2
#Data panel 2 is conceptually split into two parts and the second part is "inverted"
kpDataBackground(kp, data.panel=2, r0 = 0, r1 = 0.45, color = "#EEEEFF")
kpAxis(kp, data.panel = 2, r0=0, r1=0.45, ymin = 0, ymax = 1, cex=0.5,
       tick.pos = c(0.3, 0.5, 0.7), labels = c("-1 sd", "mean", "+1 sd"))
kpAxis(kp, data.panel = 2, r0=0, r1=0.45, ymin = 0, ymax = 1, cex=0.5, side=2)

kpDataBackground(kp, data.panel=2, r0 = 0.55, r1 = 1, color = "#EEFFEE")
kpAxis(kp, data.panel = 2, r0=1, r1=0.55, ymin = 0, ymax = 1, side=1, cex=0.5)
kpAxis(kp, data.panel = 2, r0=1, r1=0.55, ymin = 0, ymax = 1, side=2, cex=0.5)
```

```

#Customizing the axis appearance
pp <- getDefaultPlotParams(plot.type=4)
pp$leftmargin <- 0.2
pp$rightmargin <- 0.2
kp <- plotKaryotype("hg19", plot.type=4, chromosomes=c("chr1", "chr2"), plot.params=pp)

#Prepare data panel 1
kpDataBackground(kp, data.panel=1)
kpAxis(kp, data.panel = 1, text.col="red", cex=1.6, srt=45)
kpAxis(kp, data.panel = 1, ymin = 0, ymax=10, numticks = 11, side = 2,
       cex = 0.7, col="red", text.col="gold", tick.len=30e6, )

```

kpBars

*kpBars***Description**

Plot bars along the genome

Usage

```
kpBars(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=x0, y1=NULL, y0=NULL, ymin=NULL, ymax=NULL, data)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data), x0 to start(data) and x1 to end(data). If no parameter y0 is specified and data has a column named y0, this column will be used. The same for y1. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(a numeric vector) A numeric vector of x left positions (in base pairs). If data is not NULL, x0. (defaults to NULL)
x1	(a numeric vector) A numeric vector of x right positions (in base pairs). If data is not NULL, x1. (defaults to NULL)
y1	(a numeric vector) A numeric vector of y top positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
y0	(a numeric vector) A numeric vector of y bottom positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)

ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

kpBars plots bars (rectangles) along the genome. It is very similar to [kpRect](#) except that if y0 is missing, it's automatically set to ymin so all bars start from the base of the plotting region.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpRect](#), [kpLines](#)

Examples

```
set.seed(1000)

data <- toGRanges(data.frame(chr="chr1", start=10000000*(0:23), end=10000000*(1:24)))
y1 <- ((sin(start(data)) + rnorm(n=24, mean=0, sd=0.1))/5)+0.5
y0 <- y1 - rnorm(n=24, mean = 0, sd = 0.15)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))

#We can specify all data values separately. If missing y0, it defaults to ymin
kpBars(kp, chr=as.character(seqnames(data)), x0=start(data), x1=end(data), y1=y1,
       col="#FFBBBB", border="#EEAAAA")
kpLines(kp, data=data, y=y1, col="red")
```

```
#or we can provide all data into a single GRanges object
mcols(data) <- data.frame(y0=y0, y1=y1)
kpBars(kp, data[data$y0>data$y1], col="orange", border="orange", data.panel=2)
kpBars(kp, data[data$y0<=data$y1], col="purple", border="purple", data.panel=2)

kpLines(kp, data, y=data$y1, data.panel=2, col="red")
kpLines(kp, data, y=data$y0, data.panel=2, col="blue")

kpAxis(kp, data.panel = 1, cex=0.8, numticks = 5, col="#777777")
kpAxis(kp, data.panel = 2, cex=0.8, numticks = 5, col="#777777")
```

kpDataBackground	<i>kpDataBackground</i>
------------------	-------------------------

Description

Draws a solid rectangle delimiting the plotting area

Usage

```
kpDataBackground(karyoplot, r0=NULL, r1=NULL, data.panel=1, color="gray90", clipping=TRUE, ...)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotER. A KaryoPlot object referring to the currently active plot.
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
color	(color) a valid color specification
clipping	(boolean) Only used if zooming is active. If TRUE, the data background will be not drawn out of the drawing area (i.e. in margins, etc) even if it overflows the visible drawing area. If FALSE, the data background representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This function is used to add a background color to delimit the plotting area. It can either delimit the whole plotting area or part of it so different data plotting regions can be seen.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpAxis](#)

Examples

```
kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))

#Prepare data panel 1
kpDataBackground(kp, data.panel=1)
kpAxis(kp, data.panel = 1)
kpAxis(kp, data.panel = 1, ymin = 0, ymax=10, numticks = 11, side = 2, cex = 0.4, col="red")

#Prepare data panel 2
#Data panel 2 is conceptually split into two parts and the second part is "inverted"
kpDataBackground(kp, data.panel=2, r0 = 0, r1 = 0.45, color = "#EEEEFF")
kpAxis(kp, data.panel = 2, r0=0, r1=0.45, ymin = 0, ymax = 1, cex=0.5,
       tick.pos = c(0.3, 0.5, 0.7), labels = c("-1 sd", "mean", "+1 sd"))
kpAxis(kp, data.panel = 2, r0=0, r1=0.45, ymin = 0, ymax = 1, cex=0.5, side=2)

kpDataBackground(kp, data.panel=2, r0 = 0.55, r1 = 1, color = "#EEFFEE")
kpAxis(kp, data.panel = 2, r0=1, r1=0.55, ymin = 0, ymax = 1, side=1, cex=0.5)
kpAxis(kp, data.panel = 2, r0=1, r1=0.55, ymin = 0, ymax = 1, side=2, cex=0.5)
```

kpHeatmap

kpHeatmap

Description

Plots the given data as a heatmap along the genome

Usage

```
kpHeatmap(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=x0, y=NULL, ymax=NULL, ymin=NULL, r0=NULL, r1=1)
```

Arguments

karyoplot (a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.

data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(numeric) the position (in base pairs) where the data region starts
x1	(numeric) the position (in base pairs) where the data region ends
y	(a numeric vector) A numeric vector with the values of the data points. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the maximum value of the selected data panel. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the minimum value of the selected data panel. (defaults to NULL)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
colors	(colors) A set of colors used to determine the color associated with each value. Internally, it uses colorRamp . (defaults to c("blue", "white", "yellow"))
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

Given regions of the genome with a start, end and a value, draws a heatmap-like representation, with the color of the region determined by its value. It is important to note that kpHeatmap will not extend the regions in any way, so if regions are not contiguous, they will appear as a series of rectangles and not as a continuous plot.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpRect](#), [kpLines](#)

Examples

```
dd <- toGRanges(data.frame(chr="chr1", start=4980000*(0:49), end=4980000*(1:50)))
y <- sin(x=c(1:length(dd))/2)

kp <- plotKaryotype("hg19", plot.type=1, chromosomes=c("chr1", "chr2"))

kpLines(kp, dd, y=y, r0=0.4, r1=0.6, ymin=-1, ymax=1)
kpAxis(kp, r0=0.4, r1=0.6, ymin=-1, ymax=1, cex=0.5)

kpHeatmap(kp, dd, y=y, colors = c("red", "black", "green"), r0=0, r1=0.2)
kpHeatmap(kp, dd, y=y, colors = c("green", "black", "red"), r0=0.2, r1=0.4)

#or we can provide all data into a single GRanges object
mcols(dd) <- data.frame(y=y)

kpHeatmap(kp, dd, r0=0.6, r1=0.8)
#non-contiguous regions appear as solitary rectangles
kpHeatmap(kp, sample(x = dd, 10), r0=0.8, r1=1, color=c("orange", "black", "purple", "green"))
```

kpLines

kpLines

Description

Plots a line joining the data points along the genome.

Usage

```
kpLines(karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, ymin=NULL, ymax=NULL, data.panel=1, r0=NULL)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If data is not NULL, x is ignored. (defaults to NULL)

<code>y</code>	(a numeric vector) A numeric vector with the values of the data points. If <code>y</code> is not <code>NULL</code> , it is used instead of any data column in <code>data</code> . (defaults to <code>NULL</code>)
<code>ymin</code>	(numeric) The minimum value of <code>y</code> to be plotted. If <code>NULL</code> , it is set to the min value of the selected data panel. (defaults to <code>NULL</code>)
<code>ymax</code>	(numeric) The maximum value of <code>y</code> to be plotted. If <code>NULL</code> , it is set to the max value of the selected data panel. (defaults to <code>NULL</code>)
<code>data.panel</code>	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
<code>r0</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>r1</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>clipping</code>	(boolean) Only used if zooming is active. If <code>TRUE</code> , the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If <code>FALSE</code> , the data representation may overflow into the margins of the plot. (defaults to <code>TRUE</code>)
<code>...</code>	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from `karyoploteR` implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome and base) and a value (`y`) for each of them, it plots a line joining them. Data can be provided via a `GRanges` object (`data`), independent parameters for `chr`, `x` and `y` or a combination of both. A number of parameters can be used to define exactly where and how the lines are drawn. In addition, via the ellipsis operator (`...`), `kpLines` accepts any parameter valid for `lines` (e.g. `lwd`, `lty`, `col`, ...) The lines are drawn in a per chromosome basis, so it is not possible to draw lines encompassing more than one chromosome.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpLines](#), [kpText](#), [kpPlotRegions](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=500, mask=NA))
mcols(data.points) <- data.frame(y=runif(500, min=0, max=1))
```

```

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpLines(kp, data=data.points, col="red")

#Three ways of specifying the exact same data.points
kpPoints(kp, data=data.points)
kpPoints(kp, data=data.points, y=data.points$y, pch=16, col="#CCCCCCF", cex=0.6)
kpPoints(kp, chr=as.character(seqnames(data.points)),
          x=(start(data.points)+end(data.points))/2, y=data.points$y, pch=".",
          col="black", cex=1)

#plotting in the data.panel=2 and using r0 and r1, ymin and ymax
kpLines(kp, data=data.points, col="red", r0=0, r1=0.3, data.panel=2)
kpPoints(kp, data=data.points, r0=0, r1=0.3, data.panel=2, pch=".", cex=3)

kpLines(kp, data=data.points, col="blue", r0=0.4, r1=0.7, data.panel=2)
kpLines(kp, data=data.points, col="blue", y=-1*(data.points$y),
        ymin=-1, ymax=0, r0=0.7, r1=1, data.panel=2)
#It is also possible to "flip" the data by giving an r0 > r1
kpPoints(kp, data=data.points, col="red", y=(data.points$y),
        r0=1, r1=0.7, data.panel=2, pch=".", cex=2)

```

kpPlotBAMCoverage *kpPlotBAMCoverage*

Description

Plots the coverage of a BAM file along the genome

Usage

```
kpPlotBAMCoverage(karyoplot, data=NULL, max.valid.region.size=1e6, ymin=NULL, ymax=NULL, data.panel=1)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotR. A KaryoPlot object referring to the currently active plot.
data	(a character) The path to a bam file (must be indexed).
max.valid.region.size	(numeric) If the length of plotted region exceeds this number, nothing will be plotted. It's a safety mechanism to from excessive memory usage. (Defaults to 1e6, 1 million bases)
ymin	(numeric) The minimum value to be plotted on the data panel. If NULL, it is set to 0. (deafults to NULL)
ymax	(numeric) The maximum value to be plotted on the data.panel. If NULL the maximum density is used. (defaults to NULL)

<code>data.panel</code>	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
<code>r0</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>r1</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>col</code>	(color) The fill color to plot. If <code>NULL</code> the color will be assigned automatically, either a lighter version of the color used for the outer line or gray if the line color is not defined. If <code>NA</code> no area will be drawn. (defaults to <code>NULL</code>)
<code>border</code>	(color) The color to use to plot the borders of the bars. If <code>NULL</code> , it will be a darker version of <code>'col'</code> . If <code>NA</code> , no border will be plotted. (Defaults to <code>NA</code>)
<code>clipping</code>	(boolean) Only used if zooming is active. If <code>TRUE</code> , the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If <code>FALSE</code> , the data representation may overflow into the margins of the plot. (defaults to <code>TRUE</code>)
<code>...</code>	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions. In particular <code>col</code> and <code>border</code> can be used to set the colors used.

Details

`kpPlotBAMCoverage` plots the read coverage of a BAM file, that is, the number of reads overlapping each position. It uses the [bamsignals](#) package to efficiently access the BAM file. The BAM file must be indexed. This function is only recommended when plotting small parts of the genome. For larger plots consider using [kpPlotBAMDensity](#).

Value

Returns the original karyoplot object with the data computed (max.coverage) stored at `karyoplot$latest.plot`

Note

Since the plotting the exact coverage for large regions of the genome may be unfeasible, it includes a safety mechanism causing it to raise a warning and do nothing if the region is larger than a threshold specified by `max.valid.region.size`.

See Also

[kpPlotBAMDensity](#), [kpPlotCoverage](#)

Examples

```

library(pasillaBamSubset) #A package with 2 example bam files
un1.bam.file <- untreated1_chr4() # get the name of the first bam
un3.bam.file <- untreated3_chr4() #and the name of the second

kp <- plotKaryotype(genome="dm6", chromosomes="chr4") #The pasilla data comes from drosophila
kp <- kpAddBaseNumbers(kp, tick.dist = 1e5)
kp <- kpPlotBAMCoverage(kp, data = un1.bam.file) #Warning and does not plot. region too large.
kp <- kpPlotBAMCoverage(kp, data = un1.bam.file, max.valid.region.size=2000000)

#Use zoom to plot a smaller region to see the coverage with more detail
kp <- plotKaryotype(genome="dm6", zoom=toGRanges("chr4", 340000, 350000))
kp <- kpAddBaseNumbers(kp, tick.dist = 1e3)
kp <- kpPlotBAMCoverage(kp, data = un1.bam.file)

#Change the colors and borders and compare two bams
kp <- plotKaryotype(genome="dm6", zoom=toGRanges("chr4", 340000, 350000))
kp <- kpAddBaseNumbers(kp, tick.dist = 1e3)
kp <- kpPlotBAMCoverage(kp, data = un1.bam.file, r0=0.5, r1=1, border="orange")
kp <- kpPlotBAMCoverage(kp, data = un3.bam.file, r0=0.5, r1=0, border="darkgreen") #r1 < r0 will flip the plot
kpAbline(kp, h=0.5, col="darkgray")

```

kpPlotBAMDensity

*kpPlotBAMDensity***Description**

Plots the density of features along the genome

Usage

```
kpPlotBAMDensity(karyoplot, data=NULL, window.size=1e6, normalize=FALSE, ymin=NULL, ymax=NULL, dat
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a BamFile or character) The path to a bam file (must be indexed) or a BamFile object.
window.size	(numeric) The size of the windows for wich the density is computed. (Defaults to 1e6, one megabase windows)
normalize	(boolean) Specifies if the density values should be normalized by the total number of mapped reads in the bam file. (Defaults to FALSE)
ymin	(numeric) The minimum value to be plotted on the data panel. If NULL, it is set to 0. (deafults to NULL)
ymax	(numeric) The maximum value to be plotted on the data.panel. If NULL the maximum density is used. (defaults to NULL)

<code>data.panel</code>	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
<code>r0</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>r1</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>col</code>	(color) The background color to plot. If <code>NULL</code> , it will be a lighter version of 'border' or 'black' if border is null. (Defaults to "gray80")
<code>border</code>	(color) The color to use to plot the borders of the bars. If <code>NULL</code> , it will be a darker version of 'col'. If <code>NA</code> , no border will be plotted. (Defaults to <code>NULL</code>)
<code>clipping</code>	(boolean) Only used if zooming is active. If <code>TRUE</code> , the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If <code>FALSE</code> , the data representation may overflow into the margins of the plot. (defaults to <code>TRUE</code>)
<code>...</code>	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions. In particular <code>col</code> and <code>border</code> can be used to set the colors used.

Details

`kpPlotBAMDensity` plots the read density of a BAM file. It does not plot the coverage but the read density as the number of reads overlapping a every window. It uses [Rsamtools](#) to efficiently access the BAM file. The BAM file must be indexed.

Value

Returns the original karyoplot object with the data computed (windows and density) stored at `karyoplot$latest.plot`

See Also

[plotKaryotype](#), [kpPlotRibbon](#), [kpPlotCoverage](#)

Examples

```
library(pasillaBamSubset) #A package with 2 example bam files
un1.bam.file <- untreated1_chr4() # get the name of the first bam
un3.bam.file <- untreated3_chr4() #and the name of the second

window.size <- 1e4 #compute the density with 10kb windows

kp <- plotKaryotype(genome="dm6", chromosomes="chr4") #The pasilla data comes from drosophila
kp <- kpAddBaseNumbers(kp, tick.dist = 1e5)
```

```

kp <- kpPlotBAMDensity(kp, data = un1.bam.file, window.size = window.size, r0=0.5, r1=1, ymax=50000, col="darkred")
kp <- kpPlotBAMDensity(kp, data = un3.bam.file, window.size = window.size, r0=0.5, r1=0, ymax=50000, col="darkred")
kpAxis(kp, ymin=0, ymax=50000, r0=0.5, r1=1, labels = c("0", "25K", "50K"))
kpAxis(kp, ymin=0, ymax=50000, r0=0.5, r1=0, labels = c("0", "25K", "50K"))

kpText(kp, chr = "chr4", x=7e5, y=0.85, labels = paste0("Untreated 1 (reads per ", window.size, " bases)")
kpText(kp, chr = "chr4", x=7e5, y=0.15, labels = paste0("Untreated 3 (reads per ", window.size, " bases)")

#Or normalizing by the number of mapped reads
kp <- plotKaryotype(genome="dm6", chromosomes="chr4") #The pasilla data comes from drosophila
kp <- kpAddBaseNumbers(kp, tick.dist = 1e5)
kp <- kpPlotBAMDensity(kp, data = un1.bam.file, window.size = window.size, normalize=TRUE, r0=0.5, r1=1, ymax=50000)
kp <- kpPlotBAMDensity(kp, data = un3.bam.file, window.size = window.size, normalize=TRUE, r0=0.5, r1=0, ymax=50000)

```

kpPlotBigWig

kpPlotBigWig

Description

Plots the wiggle values in a BigWig file. This function does not work on windows.

Usage

```
kpPlotBigWig(karyoplot, data, ymin=NULL, ymax="global", data.panel=1, r0=NULL, r1=NULL, col=NULL, b
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotER. A KaryoPlot object referring to the currently active plot.
data	(a BigWigFile or character) The path to a bigwig file (either local or a URL to a remote file) or a BigWigFile object.
ymin	(numeric) The minimum value to be plotted on the data panel. If NULL, the minimum between 0 and the minimum value in the WHOLE GENOME will be used. (defaults to NULL)
ymax	(numeric or c("global", "per.chr", "visible.region")) The maximum value to be plotted on the data.panel. It can be either a numeric value or one of c("global", "per.chr", "per.region"). "Global" will set ymax to the maximum value in the whole data file. "per.chr" will set ymax to the maximum value in each chromosome. "visible.region" will set ymax to the maximum value in the visible region. (defaults to "global")
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)

r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
col	(color) The fill color of the area. If NULL the color will be assigned automatically, either a lighter version of the color used for the outer line or gray if the line color is not defined. If NA no area will be drawn. (defaults to NULL)
border	(color) The color of the line enclosing the area. If NULL the color will be assigned automatically, either a darker version of the color used for the area or black if col=NA. If NA no border will be drawn. (Defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

kpPlotBigWig plots the data contained in a binary file format called BigWig. BigWig are used to efficiently store numeric values computed for windows covering the whole genome, usually the coverage from an NGS experiment such as ChIP-seq. Only data required for the plotted region is loaded, and when more than one chromosome is visible, it will load the data for one chromosome at a time. The function accepts either a [BigWigFile](#) object or a character with the path to a valid big wig file. The character can also be a URL to a remote server. In this case data will be loaded transparently using the `import` function from `rtracklayer`. The data is plotted using `kpArea` and therefore it is possible to plot as a single line, a line with shaded area below or as a shaded area only adjusting the `col` and `border` parameters.

Value

Returns the original karyoplot object with the data computed (ymax and ymin values used) stored at `karyoplot$latest.plot`

Note

Since this function uses `rtracklayer` BigWig infrastructure and it does not work on windows, this function won't work on windows either.

See Also

[plotKaryotype](#), [kpArea](#), [kpPlotBAMDensity](#)

Examples

```
if (.Platform$OS.type != "windows") {
  bigwig.file <- system.file("extdata", "BRCA.genes.hg19.bw", package = "karyoploteR")
  brca.genes.file <- system.file("extdata", "BRCA.genes.hg19.txt", package = "karyoploteR")
  brca.genes <- toGRanges(brca.genes.file)
  seqlevelsStyle(brca.genes) <- "UCSC"
```

```

kp <- plotKaryotype(zoom = brca.genes[1])
kp <- kpPlotBigWig(kp, data=bigwig.file, r0=0, r1=0.2)
kp <- kpPlotBigWig(kp, data=bigwig.file, r0=0.25, r1=0.45, border="red", lwd=2)
kp <- kpPlotBigWig(kp, data=bigwig.file, r0=0.5, r1=0.7, ymin=0, ymax=1000, border="gold", col=NA)
kpAxis(kp, r0=0.5, r1=0.7, ymin=0, ymax=1000)
kp <- kpPlotBigWig(kp, data=bigwig.file, r0=0.75, r1=0.95, ymin=0, ymax="visible.region", border="orchid", col="orchid")
kpAxis(kp, r0=0.75, r1=0.95, ymin=0, ymax=kp$latest.plot$computed.values$ymax)
}

```

kpPlotCoverage

*kpCoverage***Description**

Given a GRanges object, plot the coverage along the genome.

Usage

```
kpPlotCoverage(karyoplot, data, show.0.cov=TRUE, data.panel=1, r0=NULL, r1=NULL, col="#0e87eb", ym
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotER. A KaryoPlot object referring to the currently active plot.
data	(a GRanges or a coverage object) A GRanges object from which the coverage will be computed or a SimpleRleList result of computing the coverage.
show.0.cov	(boolean) Whether to plot a thin line representing the regions with no coverage at all. (defaults to TRUE, plot the line)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
col	(color) The background color of the regions. (defaults to "#0e87eb")
ymax	(numeric) The maximum value to be plotted on the data panel. If NULL the maximum coverage is used. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)

... The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the high-level, or specialized, plotting functions of karyoploteR. It takes a GRanges object and plots its coverage, that is, the number of regions overlapping each genomic position. The input can also be a SimpleRleList resulting from computing the coverage with coverage(data). In contrast with the low-level functions such as [kpRect](#), it is not possible to specify the data using independent numeric vectors and the function only takes in the expected object types.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpPlotRegions](#), [kpBars](#)

Examples

```
set.seed(1000)

#Example 1: create 20 sets of non-overlapping random regions and plot them all. Add a coverage plot on top.
kp <- plotKaryotype("hg19", plot.type=1, chromosomes=c("chr1", "chr2"))

all.regs <- GRanges()

nreps <- 20
for(i in 1:nreps) {
  regs <- createRandomRegions(nregions = 100, length.mean = 10000000, length.sd = 1000000,
                             non.overlapping = TRUE, genome = "hg19", mask=NA)
  all.regs <- c(all.regs, regs)
  kpPlotRegions(kp, regs, r0 = (i-1)*(0.8/nreps), r1 = (i)*(0.8/nreps), col="#AAAAAA")
}

kpPlotCoverage(kp, all.regs, ymax = 20, r0=0.8, r1=1, col="#CCCCFF")
kpAxis(kp, ymin = 0, ymax= 20, numticks = 2, r0 = 0.8, r1=1)

#Example 2: Do the same with a single bigger set of possibly overlapping regions

kp <- plotKaryotype("hg19", plot.type=1, chromosomes=c("chr1", "chr2"))

regs <- createRandomRegions(nregions = 1000, length.mean = 10000000, length.sd = 1000000,
                           non.overlapping = FALSE, genome = "hg19", mask=NA)
kpPlotRegions(kp, regs, r0 = 0, r1 = 0.8, col="#AAAAAA")

kpPlotCoverage(kp, regs, ymax = 20, r0=0.8, r1=1, col="#CCCCFF")
kpAxis(kp, ymin = 0, ymax= 20, numticks = 2, r0 = 0.8, r1=1)
```

kpPlotDensity	<i>kpPlotDensity</i>
---------------	----------------------

Description

Plots the density of features along the genome

Usage

```
kpPlotDensity(karyoplot, data=NULL, window.size=1e6, ymin=NULL, ymax=NULL, data.panel=1, r0=NULL,
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotER. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object from which the density will be computed.
window.size	(numeric) The size of the windows for which the density is computed. (Defaults to 1e6, one megabase windows)
ymin	(numeric) The minimum value to be plotted on the data panel. If NULL, it is set to 0. (defaults to NULL)
ymax	(numeric) The maximum value to be plotted on the data panel. If NULL the maximum density is used. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions. In particular col and border can be used to set the colors used.

Details

kpPlotDensity plots the density of a set of features represented by a GRanges object along the genome. It creates a non-overlapping tiling of the genome and computes the number of features per window. It's possible to specify the window size.

Value

Returns the original karyoplot object with the data computed (windows and density) stored at `karyoplot$latest.plot`

See Also

[plotKaryotype](#), [kpPlotRibbon](#), [kpPlotCoverage](#)

Examples

```
set.seed(1000)

data <- createRandomRegions(nregions=20000)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes="chr1")

kp <- kpPlotDensity(kp, data)
kpAxis(kp, ymin = 0, ymax=kp$latest.plot$computed.values$max.density)

kp <- kpPlotDensity(kp, data, data.panel=2, col="#CCCCFF", ymax=20, lwd=2)
kpAxis(kp, ymin = 0, ymax=20, data.panel=2)

kp <- kpLines(kp, data=kp$latest.plot$computed.values$windows, y=kp$latest.plot$computed.values$density, col=
```

kpPlotGenes

kpPlotGenes

Description

Plot genes and transcripts in the genome. Can get the genes and transcripts information from TxDb or from custom objects.

Usage

```
kpPlotGenes(karyoplot, data, gene.margin=0.3, gene.col=NULL, gene.border.col=NULL,
  add.gene.names=TRUE, gene.names=NULL, gene.name.position="top", gene.name.cex=1, g
  plot.transcripts=TRUE, transcript.margin=0.5, transcript.col=NULL, transcript.bor
  add.transcript.names=FALSE, transcript.names=NULL, transcript.name.position="left
  plot.transcripts.structure=TRUE,
  non.coding.exons.height=0.5,
  add.strand.marks=TRUE, mark.height=0.20, mark.width=1, mark.distance=4,
  coding.exons.col=NULL, coding.exons.border.col=NULL,
  non.coding.exons.col=NULL, non.coding.exons.border.col=NULL,
  introns.col=NULL, marks.col=NULL,
  data.panel=1, r0=NULL, r1=NULL, col="black",
  border=NULL, avoid.overlapping=TRUE, clipping=TRUE, ...)
```

Arguments

<code>karyoplot</code>	(a KaryoPlot object) This is the first argument to all data plotting functions of <code>karyoploteR</code> . A KaryoPlot object referring to the currently active plot.
<code>data</code>	(a TxDb object or a list with the required elements) A TxDb object with information on genes, transcripts and exons and their position on the genome.
<code>gene.margin</code>	(numeric) If whole genes (as opposed to transcripts) are plotted (<code>plot.transcripts=FALSE</code>), the vertical margin between overlapping genes. The value is with respect to the gene height. A value of 0.5 will create a space above the genes with half the height of the genes themselves. (defaults to 0.3)
<code>gene.col</code>	(color) If whole genes (as opposed to transcripts) are plotted (<code>plot.transcripts=FALSE</code>), the color used to fill the rectangles representing the genes. If NULL, the value of <code>col</code> will be used. (Defaults to NULL)
<code>gene.border.col</code>	(color) If whole genes (as opposed to transcripts) are plotted (<code>plot.transcripts=FALSE</code>), the color used in the border of the rectangles representing the genes. If NULL, the value of <code>col</code> will be used. If NA, no border is drawn. (Defaults to NULL)
<code>add.gene.names</code>	(boolean) Whether to add the names of the genes to the plot.
<code>gene.names</code>	(named character vector) A named character vector with the labels of the genes. If not NULL, it will be used as a dictionary, so gene ids should be names and desired labels the values. If NULL, if <code>genes.data\$genes\$name</code> exists, it will use it, otherwise it will use the <code>mcols(genes.data\$genes)[,1]</code> as labels. (defaults to NULL)
<code>gene.name.position</code>	(character) The position of the gene name text relative to the rectangle. Can be "left", "right", "top", "bottom" or "center". (Defaults to "top")
<code>gene.name.cex</code>	(numeric) The cex value to plot the gene names (defaults to 1)
<code>gene.name.col</code>	(color) The color of the gene labels. If NULL, it will use <code>col</code> . (defaults to NULL)
<code>plot.transcripts</code>	(boolean) Whether to plot the individual transcripts (TRUE) or a single rectangle to represent the whole gene (FALSE). (Defaults to TRUE)
<code>transcript.margin</code>	(numeric) If transcripts are plotted (<code>plot.transcripts=TRUE</code>), the vertical margin between overlapping transcripts. The value is with respect to the transcript height. A value of 0.5 will create a space above the transcripts with half the height of the transcripts themselves. (defaults to 0.5)
<code>transcript.col</code>	(color) If transcripts are plotted (<code>plot.transcripts=TRUE</code>), the color used to fill the rectangles representing the transcripts. If NULL, the value of <code>col</code> will be used. (Defaults to NULL)
<code>transcript.border.col</code>	(color) If transcripts are plotted (<code>plot.transcripts=TRUE</code>), the color used in the border the rectangles representing the transcripts. If NULL, the value of <code>col</code> will be used. If NA, no border will be drawn. (Defaults to NULL)
<code>add.transcript.names</code>	(boolean) Whether to add the names of the transcripts to the plot. (defaults to FALSE)
<code>transcript.names</code>	(named character) A named character vector with the labels of the transcripts. If not null, it will be used as a dictionary, so transcript ids should be names and desired labels the values. If NULL, the transcript ids will be used as labels. (defaults to null)

<code>transcript.name.position</code>	(character) The position of the transcript name text relative to the rectangle. Can be "left", "right", "top", "bottom" or "center". (Defaults to "left")
<code>transcript.name.cex</code>	(numeric) The cex value to plot the transcript names (defaults to 0.6)
<code>transcript.name.col</code>	(color) The color of the transcript labels. If NULL, it will use col. (defaults to NULL)
<code>plot.transcripts.structure</code>	(boolean) Whether to draw the transcripts as single rectangles (FALSE) or to show the complete transcript structure (introns and exons) (TRUE). (Defaults to TRUE)
<code>non.coding.exons.height</code>	(numeric) The height of the non.coding exons relative to the transcript height. For example, if 0.5, non-coding exons will have a height half the size of the coding ones. (default 0.5)
<code>add.strand.marks</code>	(boolean) Whether strand marks should be plotted or not. Strand marks are small arrows along the introns (or whole transcripts if <code>plot.transcript.structure=FALSE</code>). (defaults to TRUE)
<code>mark.height</code>	(numeric) The height of the strand marks in "coding exons heights", that is, if <code>mark.height</code> is 0.5, the mark will have a height of half the height of an exon. (defaults to 0.2)
<code>mark.width</code>	(numeric) The width of the strand marks, in mark heights. <code>mark.width=1</code> will produce arrow heads with a slope of 45 degrees. A value higher than 1 will produce smaller angles and a value below 1 larger angles with more vertical lines. (defaults to 1, 45 degrees)
<code>mark.distance</code>	(numeric) The distance between marks, in mark widths. A distance of 2, will add a space of $2 * \text{mark.width}$ between consecutive marks. (defaults to 4)
<code>coding.exons.col</code>	(color) The fill color of the rectangles representing the coding exons. If NULL, it will use col. (defaults to NULL)
<code>coding.exons.border.col</code>	(color) The color of the border of the coding exons. If NULL, it will use border. (defaults to NULL)
<code>non.coding.exons.col</code>	(color) The fill color of the rectangles representing the non-coding exons. If NULL, it will use col. (defaults to NULL)
<code>non.coding.exons.border.col</code>	(color) The color of the border of the non-coding exons. If NULL, it will use border. (defaults to NULL)
<code>introns.col</code>	(color) The color of the lines representing the introns. If NULL, it will use col. (defaults to NULL)
<code>marks.col</code>	(color) The color of the arrows representing the strand. If NULL, it will use col. (defaults to NULL)
<code>data.panel</code>	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)

<code>r0</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>r1</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>col</code>	(color) The color of the genes, transcripts and labels. It is possible to specify different colors for each element class (transcript names, exons, strand marks...). All elements with no explicit color will be plotted using <code>col</code> . (Defaults to "black")
<code>border</code>	(color) The color of the border of rectangles representing genes, transcripts and exons. Every element class may have its own specific color using the appropriate parameters. The ones with no explicit color will use <code>border</code> . At the same time, if <code>border</code> is <code>NULL</code> , it will default to <code>col</code> . (Defaults to <code>NULL</code>)
<code>avoid.overlapping</code>	(boolean) If two or more regions (genes, transcripts) overlap in the genome (even partially), they can be drawn in two different layers (<code>TRUE</code>) or in the same layer, with superposing representations (<code>FALSE</code>). (Defaults to <code>TRUE</code> , draw non-overlapping elements)
<code>clipping</code>	(boolean) Only used if zooming is active. If <code>TRUE</code> , the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If <code>FALSE</code> , the data representation may overflow into the margins of the plot. (defaults to <code>TRUE</code>)
<code>...</code>	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of karyoploteR's higher level functions. It takes a transcript database (TxDb) object or a custom object with a specific structure and plots the genes along the genome. It's possible to plot genes as a whole using rectangle for each gene or to plot each transcript independently. If transcripts are drawn, it's possible to plot them as single boxes or to plot the detailed structure, differentiating coding exons, non-coding exons and introns. Transcripts may have, in addition, little arrows to mark the transcript strand (plus or minus). These strand marks are plotted in introns if the transcript structure is shown or on the whole transcript length if transcripts are plotted as boxes. Finally, it's possible to add labels to genes and transcripts. By default genes and transcripts identifiers in the input data structure will be used as labels, but it's possible to provide named character vectors to be used as dictionaries to change id's to better names.

The genes and transcripts representations are customizable. It's possible to change the colors of the different elements individually (i.e. to have red coding exons, blue non-coding exons and green introns); it's possible to change the relative height of the non-coding exons and to change the slate and density of the strand marks.

The data stating the positions of genes, transcripts and exons in the genome and their relations (which transcripts belong to which genes) can be given as a standard transcript database (TxDb) object or as a custom list with the following elements: `genes`, `transcripts`, `coding.exons` and `non.coding.exons`.

Value

Returns the original karyoplot object, unchanged.

Note

Plotting transcripts, specially plotting their structure might get quite slow in comparison to the usual speed of plotting in karyoplotR. It is not advised to plot genes and transcripts on the whole genome or in large regions of it. These functions have been designed to work with zoomed in karyoplots.

See Also

[plotKaryotype](#), [kpRect](#), [kpSegments](#), [kpPlotTranscripts](#)

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene

zoom <- toGRanges("chr2", 47986268, 48147403)
gene.names <- c("2956"="MSH6", "80204"="FBX011")

kp <- plotKaryotype(genome="hg19", zoom=zoom)
kpPlotGenes(kp, data=txdb, add.transcript.names = FALSE, gene.names=gene.names, r1=0.6)

kp <- plotKaryotype(genome="hg19", zoom=zoom)
kpPlotGenes(kp, data=txdb, plot.transcripts=FALSE, gene.names=gene.names, r1=0.6)

kp <- plotKaryotype(genome="hg19", zoom=zoom)
kpPlotGenes(kp, data=txdb, plot.transcripts.structure=FALSE, add.transcript.names=FALSE, gene.names=gene.names)

library(TxDb.Mmusculus.UCSC.mm10.knownGene)
kp <- plotKaryotype(genome="mm10", zoom="chr1:10.5e6-12.5e6")
genes.data <- makeGenesDataFromTxDb(txdb=TxDb.Mmusculus.UCSC.mm10.knownGene, karyoplot=kp)
genes.data <- addGeneNames(genes.data)
genes.data <- mergeTranscripts(genes.data)
kpPlotGenes(kp, genes.data, r1=0.25, mark.height = 0.5, gene.name.position = "left")
```

kpPlotLinks

kpPlotLinks

Description

Given 2 GRanges objects, plot lines or ribbons between region pairs

Usage

```
kpPlotLinks(karyoplot, data, data2=NULL, y=0, arch.height=NULL, data.panel=1, r0=NULL, r1=NULL, ym=0)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with link start regions. If data2 is NULL, mcols(data) should be a bed-like structure with "link.chr", "link.start", "link.end" and optionally a "link.strand" columns. The first three columns can have any name and the strand information will be extracted from the first column with "strand" in its name.
data2	(a GRanges) A GRanges object with the link end regions. If null, the end of the regions will be extracted from mcols(data). (Defaults to NULL)
y	(numeric) The y value where the links should be plotted (Defaults to 0)
arch.height	(numeric) The approximate arch height in links in the same chromosome in "y" scale. If NULL, it defaults to the whole span of the data panel. Also affects the curvature of links between chromosomes (Defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
ymin	(numeric) The minimum value to be plotted on the data panel. If NULL, it is set to 0. (defaults to NULL)
ymax	(numeric) The maximum value to be plotted on the data panel. If NULL the maximum density is used. (defaults to NULL)
col	(color) The background color of the links. If NULL and border is specified, it defaults to a lighter version of border.
border	(color) The border color of the links. If NULL and col is specified, it defaults to a darker version of col.
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the high-level, or specialized, plotting functions of karyoploteR. It takes two GRanges objects (or a single specially crafted one) and plots links (either lines or ribbons) between region pairs. Links are plotted between the first region of both objects, between the second one, etc... and therefore both objects need to have the same length. Specifying a region as negative strand, will "flip" it, so the the start of a region can be linked to the end of its pair.

Value

Returns the original karyoplot object, unchanged.

Note

For a link to be plotted BOTH ends must be visible in the karyoplot. In particular, if a chromosome is not included in the plot (due to not being specified in chromosomes, for example) any link with an end on it will NOT be plotted. The same is true for zoomed in plots, where only intrachromosomal links will be visible. No warning or message will be generated.

See Also

[plotKaryotype](#), [kpPlotRibbon](#), [kpSegments](#)

Examples

```
set.seed(222)

starts <- sort(createRandomRegions(nregions = 15))
ends <- sort(createRandomRegions(nregions = 15))

kp <- plotKaryotype()
kpPlotLinks(kp, data=starts, data2=ends)

#Create larger regions, so they look like ribbons
starts <- sort(createRandomRegions(nregions = 15, length.mean = 8e6, length.sd = 5e6))
ends <- sort(createRandomRegions(nregions = 15, length.mean = 8e6, length.sd = 5e6))

kp <- plotKaryotype()
kpPlotLinks(kp, data=starts, data2=ends)

#flip some of them to represent inversions
strand(ends) <- sample(c("+", "-"), length(ends), replace = TRUE)

kp <- plotKaryotype()
kpPlotLinks(kp, data=starts, data2=ends)
```

kpPlotLoess

kpPlotLoess

Description

Plot a LOESS smoothed line with confidence intervals given a list of points.

Usage

```
kpPlotLoess(karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, conf.interval=0.95, span=0.5, data.pan
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If data is not NULL, x is ignored. (defaults to NULL)
y	(a numeric vector) A numeric vector with the values of the data points. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
conf.interval	The confidence interval to plot. If a number in (0,1), the confidence interval is plotted. Else, no confidence interval is plotted. (defaults to 0.95)
span	A parameter to control the smoothing level. It is passed to underlying function loess . (defaults to 0.5)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
col	The color of the fitting line. (defaults to "black")
lty	The line type (dashed, dotted...) of the fitting line (defaults to 1, solid)
lwd	The line width of the fitting line (defaults to 1)
ci.col	The color of the area representing the confidence interval. If NA no CI is plotted. (defaults to #888888AA, transparent gray)
ci.border	The color of line marking the border of the confidence interval. If NA, it's not plotted. (defaults to NA)
ci.border.lty	The line type of line marking the border of the confidence interval. (defaults to 1, solid)
ci.border.lwd	The line width of line marking the border of the confidence interval. (defaults to 1)

clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

Given a set of data points (specified in any way accepted by [kpPoints](#)), plot a LOESS smoothed line with optional confidence intervals. LOESS is computed independently per each chromosome and data points are sorted before fitting. It is possible to adjust the confidence interval with `conf.interval` and setting it to NULL or NA will plot no CI. It is also possible to control the smoothing level with `span`. In addition to the standard plotting parameters, it is possible to control independently the color of the fitting line and CI area and CI borders. It is also possible to adjust the line type and line width of the fitting line and CI border.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpPoints](#), [kpLines](#), [kpPlotRibbon](#)

Examples

```
set.seed(1000)

dd <- data.frame(chr="chr1", x=1:48*5e6, y=rnorm(n=48, 0.5, 0.1 ))

kp <- plotKaryotype(chromosomes="chr1")
kpPoints(kp, chr=dd$chr, x=dd$x, y=dd$y)
kpPlotLoess(kp, chr=dd$chr, x=dd$x, y=dd$y, col="red", conf.interval = 0.99, ci.col = "#FAAAAAA")
```

kpPlotMarkers

kpPlotMarkers

Description

Plots markers on the genome as a line with a label on top.

Usage

```
kpPlotMarkers(karyoplot, data=NULL, chr=NULL, x=NULL, y=0.75, labels=NULL,
              adjust.label.position=TRUE, ignore.chromosome.ends=FALSE,
              label.margin=0.001, max.iter=150, label.dist=0.001,
              marker.parts = c(0.8,0.1, 0.1), text.orientation = "vertical",
              ymin=NULL, ymax=NULL, data.panel=1, r0=NULL, r1=NULL,
              line.color="black", label.color="black",
              pos=NULL, srt=NULL, offset=NULL, clipping=TRUE, ...)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If data is not NULL, x is ignored. (defaults to NULL)
y	(a numeric vector) A numeric vector with the values of the data points. If y is not NULL, it is used instead of any data column in data. (defaults to 0.75)
labels	(a character vector) The labels to be plotted. (defaults to NULL)
adjust.label.position	(logical) whether to adjust the label positions to avoid label overlapping (defaults to TRUE)
ignore.chromosome.ends	(logical) If TRUE, when adjusting label position marker labels can move beyond the chromosome ends. (defaults to FALSE, do not move out of origin chromosome)
label.margin	(numeric) The vertical margin to leave between the ends of the marker line and the marker label. In plot coordinates. (defaults to 0.001)
max.iter	(numeric) The maximum number of iterations in the iterative algorithm to adjust the label positioning. (defaults to 150)
label.dist	(numeric) The minimum distance between labels to consider them as non-overlapping (defaults to 0.001)
marker.parts	(numeric vector of three elements) The portion of the distance between 0 and y to be filled with a: vertical, diagonal of vertical part of the marker line. (defaults to c(0.8,0.1,0.1), long vertical stem, small diagonal and small vertical on top)
text.orientation	("vertical" or "horizontal") How should the text be plotted. Forced values of srt and pos take precedence. (defaults to "vertical")
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the minimum value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the maximum value of the selected data panel. (defaults to NULL)

<code>data.panel</code>	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
<code>r0</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>r1</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
<code>line.color</code>	(color) The color of marker line. (defaults to "black")
<code>label.color</code>	(color) The color of the label (defaults to "black")
<code>pos</code>	(1,2,3,4) The standard <code>pos</code> graphical parameter. If <code>NULL</code> , it's automatically set depending on "text.orientation". (defaults to <code>NULL</code>)
<code>srt</code>	(numeric) The standard <code>srt</code> graphical parameter. If <code>NULL</code> , it's automatically set depending on "text.orientation". (defaults to <code>NULL</code>)
<code>offset</code>	(numeric) The standard <code>offset</code> graphical parameter. If <code>NULL</code> , it's automatically set depending on "text.orientation". (defaults to <code>NULL</code>)
<code>clipping</code>	(boolean) Only used if zooming is active. If <code>TRUE</code> , the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If <code>FALSE</code> , the data representation may overflow into the margins of the plot. (defaults to <code>TRUE</code>)
<code>...</code>	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This function plots markers on the genome. It implements an iterative algorithm to avoid overlapping between the labels of different markers. Since labels might be plotted in a different position than the original points, a line with three parts (a vertical, a diagonal and another vertical) is plotted to link the label with the original position. It is possible to plot labels in horizontal or vertical text and to specify different colors for the marker line and label.

Value

Returns the original karyoplot object with the data computed (adjusted label positioning) stored at `karyoplot$latest.plot`

Note

The iterative algorithm is not guaranteed to succeed and might end up with overlapping labels if labels are too dense or if too few iterations allowed. With many markers, the algorithm might be slow.

See Also

[plotKaryotype](#), [kpLines](#), [kpText](#)

Examples

```

data <- toGRanges(data.frame(c("chr1", "chr1", "chr1"), c(20e6, 21e6, 22e6), c(20.01e6, 21.01e6, 22.01e6), lab

kp <- plotKaryotype("hg19", plot.type=1, chromosomes = "chr1", main="Default markers")
kpPlotMarkers(kp, data)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes = "chr1", main="Markers Horizontal")
kpPlotMarkers(kp, data, text.orientation = "horizontal")
kpPlotMarkers(kp, data, text.orientation = "horizontal", label.dist = 0.02, data.panel=2)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes = "chr1", main="Different Marker parts")
kpPlotMarkers(kp, data, text.orientation = "horizontal", marker.parts=c(0, 1, 0), line.color="red")
kpPlotMarkers(kp, data, text.orientation = "horizontal", marker.parts=c(0.1, 0.2, 0.4), label.dist = 0.02, dat

```

kpPlotNames

*kpPlotNames***Description**

Plots text labels with positioning relative to rectangles along the genome.

Usage

```
kpPlotNames(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=x0, y0=NULL, y1=NULL, labels=NULL, position
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data), x0 to start(data) and x1 to end(data). If no parameter y0 is specified and data has a column named y0, this column will be used. The same for y1. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(a numeric vector) A numeric vector of x left positions (in base pairs). If data is not NULL, x0. (defaults to NULL)
x1	(a numeric vector) A numeric vector of x right positions (in base pairs). If data is not NULL, x1. (defaults to NULL)
y0	(a numeric vector) A numeric vector of y bottom positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
y1	(a numeric vector) A numeric vector of y top positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)


```

end=c(40e6, 170e6, 210e6),
y0=c(0.1, 0.5, 0.7),
y1=c(0.5, 0.6, 0.95))

kp <- plotKaryotype(genome="hg19", chromosomes="chr1")
kpRect(kp, data=regs)

kpPlotNames(kp, data=regs, labels=c("R1", "R2", "R3"))
kpPlotNames(kp, data=regs, labels=c("R1", "R2", "R3"), position="top", cex=2)
kpPlotNames(kp, data=regs, labels=c("R1", "", "R3"), position="right", col="red")
kpPlotNames(kp, data=regs, labels="bottom", position="bottom", col=rainbow(3))
kpPlotNames(kp, data=regs, labels="o", position="center", col=rainbow(3), cex=1)

```

kpPlotRainfall

*kpPlotRainfall***Description**

Creates a rainfall plot showing the distances between features in the genome. Usually used to plot the distance between somatic mutations to identify kataegis.

Usage

```
kpPlotRainfall(karyoplot, data=NULL, col=NULL, ymin=NULL, ymax=7, data.panel=1, r0=NULL, r1=NULL, c
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the features to be plotted.
col	(a color vector) The colors to use to draw the points. If the length of the vector is lower than the length of data, it will be recycled. If NULL, points will be plotted in black. (defaults to NULL)
ymin	(numeric) The minimum value to be plotted on the data panel. If NULL, it is set to 0. (defaults to NULL)
ymax	(numeric) The maximum value to be plotted on the data.panel. (defaults to 7, (equivalent to 10Mb between consecutive features))
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)

clipping (boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)

... The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions. In particular col and border can be used to set the colors used.

Details

kpPlotRainfall plots the distances between a feature and the next one in a log scale along the genome. It is usually used to plot the distance between somatic mutations in order to identify regions with an accumulation of close mutations.

Value

Returns the original karyoplot object with the data computed (distances) stored at `karyoplot$latest.plot`

See Also

[plotKaryotype](#), [kpPlotDensity](#), [kpPlotCoverage](#)

Examples

```
set.seed(1000)

data <- createRandomRegions(nregions=2000)

kp <- plotKaryotype("hg19", plot.type=4)
kp <- kpPlotRainfall(kp, data)
kpAxis(kp, ymax=7, tick.pos=c(0:7))
```

kpPlotRegions

kpPlotRegions

Description

Plots rectangles along the genome representing the regions (or intervals) specified by a GRanges object

Usage

```
kpPlotRegions(karyoplot, data, data.panel=1, r0=NULL, r1=NULL, col="black", border=NULL, avoid.ove
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges or equivalent) It can be any of the formats accepted by the toGRanges function from the package regioneR .
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
col	(color) The background color of the regions. (defaults to black)
border	(color) The color used to draw the border of the regions. If NULL, no border is drawn. (defaults to NULL)
avoid.overlapping	(boolean) Whether overlapping regions should be drawn as stacks (TRUE) or drawing one occluding the other in a single layer (FALSE). (defaults to TRUE)
num.layers	(numeric) The number of layers the plotting space should be divided into to allow for plotting overlapping regions. The plotting region will be divided into this many pieces regardless if any overlapping regions actually exist. If NULL, the maximum number of regions overlapping a single point in the genome. (defaults to NULL)
layer.margin	(numeric) The blank space left between layers of regions. (defaults to 0.05)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the high-level, or specialized, plotting functions of karyoploteR. It takes a GRanges object and plots its content. Overlapping regions can be stacked and the number of layers for overlapping regions can be set. In contrast with the low-level functions such as [kpRect](#), it is not possible to specify the data using independent numeric vectors and the function only takes in GRanges.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpRect](#), [kpSegments](#)

Examples

```
set.seed(1000)

#Example 1: create 20 sets of non-overlapping random regions and plot them all. Add a coverage plot on top.
kp <- plotKaryotype("hg19", plot.type=1, chromosomes=c("chr1", "chr2"))

all.regs <- GRanges()

nreps <- 20
for(i in 1:nreps) {
  regs <- createRandomRegions(nregions = 100, length.mean = 10000000, length.sd = 1000000,
                             non.overlapping = TRUE, genome = "hg19", mask=NA)
  all.regs <- c(all.regs, regs)
  kpPlotRegions(kp, regs, r0 = (i-1)*(0.8/nreps), r1 = (i)*(0.8/nreps), col="#AAAAAA")
}

kpPlotCoverage(kp, all.regs, ymax = 20, r0=0.8, r1=1, col="#CCCCFF")
kpAxis(kp, ymin = 0, ymax= 20, numticks = 2, r0 = 0.8, r1=1)

#Example 2: Do the same with a single bigger set of possibly overlapping regions

kp <- plotKaryotype("hg19", plot.type=1, chromosomes=c("chr1", "chr2"))

regs <- createRandomRegions(nregions = 1000, length.mean = 10000000, length.sd = 1000000,
                           non.overlapping = FALSE, genome = "hg19", mask=NA)

kpPlotRegions(kp, regs, r0 = 0, r1 = 0.8, col="#AAAAAA")

kpPlotCoverage(kp, regs, ymax = 20, r0=0.8, r1=1, col="#CCCCFF")
kpAxis(kp, ymin = 0, ymax= 20, numticks = 2, r0 = 0.8, r1=1)
```

kpPlotRibbon

kpPlotRibbon

Description

A variable width ribbon

Usage

```
kpPlotRibbon(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=NULL, y0=NULL, y1=NULL, ymin=NULL, ymax=NULL)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data), x0 to start(data) and x1 to end(data). If no parameter y0 is specified and data has a column named y0, this column will be used. The same for y1. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(a numeric vector) A numeric vector of x left positions (in base pairs). If data is not NULL, x0. (defaults to NULL)
x1	(a numeric vector) A numeric vector of x right positions (in base pairs). If data is not NULL, x1. (defaults to NULL)
y0	(a numeric vector) A numeric vector of y bottom positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
y1	(a numeric vector) A numeric vector of y top positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to <code>plotKaryotype</code> . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
col	(color) The background color to plot. If NULL, it will be a lighter version of 'border' or 'black' if border is null. (Defaults to "gray80")
border	(color) The color to use to plot the borders of the bars. If NULL, it will be a darker version of 'col'. If NA, no border will be plotted. (Defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

kpPlotRibbon plots a variable width ribbon along the genome. It can be used, for example, to plot the sd region around a line representing a mean. It can also be used as a replacement for [kpBars](#) creating a smoother plot without the the actual individual bars. kpPlotRibbon has three additional parameters controlling the smoothing of the lines and their colors.

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpBars](#), [kpLines](#)

Examples

```
set.seed(1000)

data <- toGRanges(data.frame(chr="chr1", start=1e6*(0:239), end=1e6*(1:240)))
y <- ((sin(start(data))/5 + rnorm(n=24, mean=0, sd=0.1))/5)+0.5

kp <- plotKaryotype("hg19", plot.type=2, chromosomes="chr1")

kpPlotRibbon(kp, data, y0=y-0.3, y1=y+0.3, border="red", col=lighter("red"))
kpPlotRibbon(kp, data, y0=y-0.1, y1=y+0.1, border="blue", col=lighter("blue"))
kpLines(kp, data, y=y, col="green")
kpPlotRibbon(kp, data, y0=0.5+(y-min(y)), y1=0.5-(y-min(y)), data.panel=2)
```

kpPlotTranscripts *kpPlotTranscripts*

Description

Plot gene transcripts on the genome, with options to add strand markers and to differentiate between coding and non-coding exons.

Usage

```
kpPlotTranscripts(karyoplot, data, y0=NULL, y1=NULL, non.coding.exons.height=0.5,
  detail.level=2,
  add.strand.marks=TRUE, mark.height=0.20, mark.width=1, mark.distance=4,
  add.transcript.names=TRUE, transcript.names=NULL, transcript.name.position="left", transcript.names.col="black",
  border=NULL, coding.exons.col=NULL, coding.exons.border.col=NULL,
  non.coding.exons.col=NULL, non.coding.exons.border.col=NULL,
  introns.col=NULL, marks.col=NULL, transcript.name.col=NULL,
  ymax=NULL, ymin=NULL, r0=NULL, r1=NULL,
  data.panel=1, clipping=TRUE, ...)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoplotER. A KaryoPlot object referring to the currently active plot.
data	(a list) data must be a list with an element called 'transcripts' with a GRanges with all transcripts to be plotted. Additionally, to plot the transcript structure it needs two other elements, 'coding.exons' and 'non.coding.exons', each a list with an element for every transcript with GRanges objects representing the transcript exons. An example of the data structure needed can be seen in the function examples.
y0	(numeric) The bottom of the transcripts in the y axis. It can have a different value for each transcript and values will be recycled if needed. If null, it will be set to the minimum y value in the data.panel, usually 0. (Defaults to NULL)
y1	(numeric) The top of the transcripts in the y axis. It can have a different value for each transcript and values will be recycled if needed. If null, it will be set to the maximum y value in the data.panel, usually 1. (Defaults to NULL)
non.coding.exons.height	(numeric) The height of the non.coding exons relative to the transcript height. For example, if 0.5, non-coding exons will have a height half the size of the coding ones. (default 0.5)
detail.level	(numeric: 1 or 2) The detail level of the transcript representation: 1 will plot only boxes representing the transcripts, 2 will plot detailed structure of the transcripts (coding and non-coding exons and introns). (Defaults to 2)
add.strand.marks	(boolean) Whether strand marks should be plotted or not. Strand marks are small arrows along the introns (or whole transcripts if detail level=1). (defaults to TRUE)
mark.height	(numeric) The height of the strand marks in "coding exons heights", that is, if mark.height is 0.5, the mark will have a height of half the height of an exon. (defaults to 0.2)
mark.width	(numeric) The width of the strand marks, in mark heights. mark.width=1 will produce arrow heads with a slope of 45 degrees. A value higher than 1 will produce smaller angles and a value below 1 larger angles with more vertical lines. (defaults to 1, 45 degrees)
mark.distance	(numeric) The distance between marks, in mark widths. A distance of 2, will add a space of 2*mark.width between consecutive marks. (defaults to 4)
add.transcript.names	(boolean) Whether to add transcript names to the plot (defaults to TRUE)
transcript.names	(named character) A named character vector with the labels of the transcripts. If not null, it will be used as a dictionary, so transcript ids should be names and desired labels the values. If NULL, the transcript ids will be used as labels. (defaults to null)
transcript.name.position	(character) The position of the text relative to the rectangle. Can be "left", "right", "top", "bottom" or "center". (Defaults to "left")
transcript.name.cex	(numeric) The cex value to plot the transcript labels. (defaults to 1)

<code>col</code>	(color) The color of the transcripts and labels. It is possible to specify different colors for each element class (transcript names, exons, strand marks...). All elements with no explicit color will be plotted using <code>col</code> . (defaults to "black")
<code>border</code>	(color) The color of the border of rectangles representing genes, transcripts and exons. Every element class may have its own specific color using the appropriate parameters. The ones with no explicit color will use <code>border</code> . At the same time, if <code>border</code> is NULL, it will default to <code>col</code> . (results to NULL)
<code>coding.exons.col</code>	(color) The fill color of the rectangles representing the coding exons. If NULL, it will use <code>col</code> . (defaults to NULL)
<code>coding.exons.border.col</code>	(color) The color of the border of the coding exons. If NULL, it will use <code>border</code> . (defaults to NULL)
<code>non.coding.exons.col</code>	(color) The fill color of the rectangles representing the non-coding exons. If NULL, it will use <code>col</code> . (defaults to NULL)
<code>non.coding.exons.border.col</code>	(color) The color of the border of the non-coding exons. If NULL, it will use <code>border</code> . (defaults to NULL)
<code>introns.col</code>	(color) The color of the lines representing the introns. If NULL, it will use <code>col</code> . (defaults to NULL)
<code>marks.col</code>	(color) The color of the arrows representing the strand. If NULL, it will use <code>col</code> . (defaults to NULL)
<code>transcript.name.col</code>	(color) The color of the transcript labels. If NULL, it will use <code>col</code> . (defaults to NULL)
<code>ymin</code>	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
<code>ymax</code>	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
<code>r0</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
<code>r1</code>	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
<code>data.panel</code>	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to <code>plotKaryotype</code> . (defaults to 1)
<code>clipping</code>	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
<code>...</code>	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the high-level, or specialized, plotting functions of karyoploteR. It takes a list with the transcripts, coding and non-coding exons and creates a traditional boxes and line representation of the transcripts. With `y0` and `y1`, it is possible to specify a different vertical position and different height for each transcript. It can add little arrows, strand marks, along the introns to show the transcript strand. The marks appearance can be customized using 4 different parameters specifying the height (relative to the height of the transcript), width of each mark (relative to the height), distance between marks (relative to the width) and color of the marks. Marks are centered on the space they have available and if the available space is too tight for a single mark, no mark will be plotted. The direction of the marks is based on the transcript strand as specified in `data$transcripts` object. Two detail levels are available: `detail.level=1` will represent transcripts as solid boxes (optionally with strand marks along the whole transcript); `detail.level=2` will represent the internal structure of the transcripts -coding and non coding exons, introns, and optionally the strand marks only in the introns.

Value

Returns the original karyoplot object, unchanged.

Note

IMPORTANT: The direction of the strand marks is taken from the strand information in the `data$transcripts` object. If transcripts have no strand information there (they have `strand="*"`), no marks will be drawn.

See Also

[kpPlotGenes](#)

Examples

```
#Build the data object expected by transcripts

transcripts <- c(toGRanges("chr1", 100, 1000),
                toGRanges("chr1", 1500, 3000))
names(transcripts) <- c("T1", "T2")
strand(transcripts) <- c("+", "-")

coding.exons <- list("T1"=c(toGRanges("chr1", 200, 300),
                           toGRanges("chr1", 500, 800),
                           toGRanges("chr1", 900, 950)),
                    "T2"=c(toGRanges("chr1", 2200, 2300),
                           toGRanges("chr1", 2500, 2510),
                           toGRanges("chr1", 2700, 2800)))

non.coding.exons <- list("T1"=c(toGRanges("chr1", 100, 199),
                               toGRanges("chr1", 951, 1000)),
                        "T2"=c(toGRanges("chr1", 1500, 1700),
                               toGRanges("chr1", 1900, 1950),
                               toGRanges("chr1", 2100, 2199),
                               toGRanges("chr1", 2801, 3000)))

data <- list(transcripts=transcripts, coding.exons=coding.exons, non.coding.exons=non.coding.exons)
```



```

#Create a simple example plot
karyoplot <- plotKaryotype(zoom=toGRanges("chr1", 0, 3200))
kpAddBaseNumbers(karyoplot, tick.dist = 400)
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0, r1=0.1)

#Create a plot with different variants of the transcripts
karyoplot <- plotKaryotype(zoom=toGRanges("chr1", 0, 3200))
kpAddBaseNumbers(karyoplot, tick.dist = 400)
#Standard
kpPlotTranscripts(karyoplot, data=data, r0=0, r1=0.1)
#Customize colors
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0.11, r1=0.21, transcript.name.position = "right", non
#Change vertical position and transcript height
kpPlotTranscripts(karyoplot, data=data, y0=c(0, 0.4), y1=c(0.2, 1), r0=0.25, r1=0.8, add.transcript.names = TR
#Change detail level, colors and transcript names
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0.9, r1=1, detail.level = 1, add.transcript.names = TRU

#Create a plot with different variants of the strand marks
karyoplot <- plotKaryotype(zoom=toGRanges("chr1", 0, 3200))
kpAddBaseNumbers(karyoplot, tick.dist = 400)
#Standard
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0, r1=0.1)
#No marks
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0.15, r1=0.25, add.strand.marks=FALSE)
#Change the strand marks height
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0.3, r1=0.4, mark.height=1)
#Change the mark width
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0.45, r1=0.55, mark.width=2)
#Change the mark distance
kpPlotTranscripts(karyoplot, data=data, y0=0, y1=1, r0=0.6, r1=0.7, mark.distance=1.5)

```

kpPoints

*kpPoints***Description**

Plots data points along the genome.

Usage

```
kpPoints(karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, ymin=NULL, ymax=NULL, data.panel=1, r0=NULL)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)

chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If <code>data</code> is not <code>NULL</code> , <code>chr</code> is ignored. (defaults to <code>NULL</code>)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If <code>data</code> is not <code>NULL</code> , <code>x</code> is ignored. (defaults to <code>NULL</code>)
y	(a numeric vector) A numeric vector with the values of the data points. If <code>y</code> is not <code>NULL</code> , it is used instead of any data column in <code>data</code> . (defaults to <code>NULL</code>)
ymin	(numeric) The minimum value of <code>y</code> to be plotted. If <code>NULL</code> , it is set to the min value of the selected data panel. (defaults to <code>NULL</code>)
ymax	(numeric) The maximum value of <code>y</code> to be plotted. If <code>NULL</code> , it is set to the max value of the selected data panel. (defaults to <code>NULL</code>)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to <code>plotKaryotype</code> . (defaults to 1)
r0	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
r1	(numeric) <code>r0</code> and <code>r1</code> define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If <code>NULL</code> , they are set to the min and max of the data panel, it is, to use all the available space. (defaults to <code>NULL</code>)
clipping	(boolean) Only used if zooming is active. If <code>TRUE</code> , the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If <code>FALSE</code> , the data representation may overflow into the margins of the plot. (defaults to <code>TRUE</code>)
pch	(numeric) the glyph to represent the points as specified in <code>par</code> . (defaults to 16, a solid circle)
cex	(numeric) the relative size of the glyphs as defined at <code>par</code> . (defaults to 0.5)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from `karyoploteR` implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome and base) and a value (`y`) for each of them, it plots the set of points representing them. Data can be provided via a `GRanges` object (`data`), independent parameters for `chr`, `x` and `y` or a combination of both. A number of parameters can be used to define exactly where and how the points are drawn. In addition, via the ellipsis operator (`...`), `kpPoints` accepts any parameter valid for points (e.g. `pch`, `cex`, `col`, ...)

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpLines](#), [kpText](#)

[kpPlotRegions](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=500, mask=NA))
mcols(data.points) <- data.frame(y=runif(500, min=0, max=1))

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpLines(kp, data=data.points, col="red")

#Three ways of specifying the exact same data.points
kpPoints(kp, data=data.points, cex=0.5)
kpPoints(kp, data=data.points, y=data.points$y, pch=16, col="#CCCCCCF", cex=0.6)
kpPoints(kp, chr=as.character(seqnames(data.points)),
          x=(start(data.points)+end(data.points))/2,
          y=data.points$y, pch=".", col="black", cex=1)

#plotting in the data.panel=2 and using r0 and r1, ymin and ymax
kpLines(kp, data=data.points, col="red", r0=0, r1=0.3, data.panel=2)
kpPoints(kp, data=data.points, r0=0, r1=0.3, data.panel=2, pch=".", cex=3)

kpLines(kp, data=data.points, col="blue", r0=0.4, r1=0.7, data.panel=2)
kpLines(kp, data=data.points, col="blue", y=-1*(data.points$y),
          ymin=-1, ymax=0, r0=0.7, r1=1, data.panel=2)
#It is also possible to "flip" the data by giving an r0 > r1
kpPoints(kp, data=data.points, col="red", y=(data.points$y),
          r0=1, r1=0.7, data.panel=2, pch=".", cex=2)
```

kpPolygon

kpPolygon

Description

Plots the the given polygons along the genome

Usage

```
kpPolygon(karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, ymin=NULL, ymax=NULL, data.panel=1, r0=NU
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If data is not NULL, x is ignored. (defaults to NULL)
y	(a numeric vector) A numeric vector with the values of the data points. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from karyoploteR implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome, base and y), it plots the polygons defined by taking these positions as vertices. Data can be provided via a GRanges object (data), independent parameters for chr, x and y or a combination of both. A number of parameters can be used to define exactly where and how the polygon is drawn. In addition, via the ellipsis operator (...), kpPolygon accepts any parameter valid for polygon (e.g. border, density, fillOddEven, ...)

Value

Returns the original karyoplot object, unchanged.

Note

IMPORTANT: kpPolygon allows the creation of polygons encompassing multiple chromosomes. In some cases, when plotting only some of the chromosomes or when zooming, the default data filtering automatically discards some points before plotting, altering the polygon shape. See example below.

See Also

[plotKaryotype](#), [kpLines](#), [kpPoints](#)
[kpPlotRegions](#)

Examples

```
set.seed(1000)
x <- c(1,2,5,9,13,20,15,11,7,3)*10000000
y <- c(0,1,0.8,0.2,0.5,0.2,1,0.3,0.1,0.2)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpPolygon(kp, chr="chr1", x=x, y=y, col="red")
kpPolygon(kp, chr="chr1", x=x, y=y, col="orange", r0=0.2, r1=0.8, density=30)
#use kpPolygon to draw triangles at the specified positions
chr2.x <- c(1,3,7,26,48,79,120, 124, 128)*1000000
for(x in chr2.x) {
  kpPolygon(kp, chr="chr2", x=c(x-2000000, x+2000000, x), y=c(1,1,0), r0=0, r1=0.3, col="lightblue")
}

#Effect of data filtering

dp <- toGRanges(data.frame(rep(paste0("chr", (1:2)), 3), 10e6*1:6, 10e6*1:6+5e5, y=c(0,0,1,1,0,0)))
kp <- plotKaryotype(chromosomes=c("chr1", "chr2"))
kpPolygon(kp, dp)

kp <- plotKaryotype(chromosomes=c("chr2"))
kpPolygon(kp, dp)
```

kpRect

kpRect

Description

Plots rectangles at the specified genomic positions.

Usage

```
kpRect(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=x0, y0=NULL, y1=NULL, ymax=NULL, ymin=NULL, r0=N
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data), x0 to start(data) and x1 to end(data). If no parameter y0 is specified and data has a column named y0, this column will be used. The same for y1. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(a numeric vector) A numeric vector of x left positions (in base pairs). If data is not NULL, x0. (defaults to NULL)
x1	(a numeric vector) A numeric vector of x right positions (in base pairs). If data is not NULL, x1. (defaults to NULL)
y0	(a numeric vector) A numeric vector of y bottom positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
y1	(a numeric vector) A numeric vector of y top positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from karyoploteR implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome, x0 and x1) and values (y0 and y1) for each of them, it plots rectangles going from (x0, y0) to (x1, y1). Data can be provided via a GRanges object (*data*), independent parameters for chr, x0, x1, y0 and y1, or a combination of both. A number of parameters can be used to define exactly where and how the rectangles are drawn. In addition, via the ellipsis operator (...), kpRect accepts any parameter valid for rect (e.g. border, col, ...)

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpLines](#), [kpPoints](#)

[kpPlotRegions](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=500, length.mean=2000000, mask=NA))
y <- runif(500, min=0, max=0.8)
mcols(data.points) <- data.frame(y0=y, y1=y+0.2)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpRect(kp, data=data.points, col="black")
kpRect(kp, data=randomizeRegions(data.points, mask=NA), y0=0, y1=1, r0=0, r1=0.2, border=NA, col="lightblue")
kpRect(kp, data=randomizeRegions(data.points, mask=NA), y0=0, y1=1, r0=0.3, r1=0.5, border=NA, col="lightgreen")
kpRect(kp, data=randomizeRegions(data.points, mask=NA), y0=0, y1=1, r0=0.6, r1=0.8, border=NA, col="purple")
```

kpSegments

kpSegments

Description

Plots segments at the specified genomic positions.

Usage

```
kpSegments(karyoplot, data=NULL, chr=NULL, x0=NULL, x1=NULL, y0=NULL, y1=NULL, ymin=NULL, ymax=NULL)
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data), x0 to start(data) and x1 to end(data). If no parameter y0 is specified and data has a column named y0, this column will be used. The same for y1. (defaults to NULL)
chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x0	(a numeric vector) A numeric vector of x left positions (in base pairs). If data is not NULL, x0. (defaults to NULL)
x1	(a numeric vector) A numeric vector of x right positions (in base pairs). If data is not NULL, x1. (defaults to NULL)
y0	(a numeric vector) A numeric vector of y bottom positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
y1	(a numeric vector) A numeric vector of y top positions. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from karyoploteR implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome, x0 and x1) and values (y0 and y1) for each of them, it plots segments going from (x0, y0) to (x1,

y1). Data can be provided via a GRanges object (data), independent parameters for chr, x0, x1, y0 and y1, or a combination of both. A number of parameters can be used to define exactly where and how the segments are drawn. In addition, via the ellipsis operator (...), kpSegments accepts any parameter valid for segments (e.g. lwd, lty, col, ...)

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpRect](#), [kpPoints](#)

[kpPlotRegions](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=500, length.mean=2000000, mask=NA))
y <- runif(500, min=0, max=0.8)
mcols(data.points) <- data.frame(y0=y, y1=y+0.2)

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpRect(kp, data=data.points, col="black")
kpSegments(kp, data=data.points, col="white")

kpSegments(kp, data=data.points, y0=0, y1=1, r0=0.2, r1=0.8, col="lightblue", data.panel=2)
kpSegments(kp, data=data.points, y0=0, y1=1, r0=0.8, r1=0.2, col="lightgreen", data.panel=2)
```

kpText

kpText

Description

Plots the text given in labels at the positions defined by chr, x and y along the genome.

Usage

```
kpText(karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, labels=NULL, ymin=NULL, ymax=NULL, data.pane
```

Arguments

karyoplot	(a KaryoPlot object) This is the first argument to all data plotting functions of karyoploteR. A KaryoPlot object referring to the currently active plot.
data	(a GRanges) A GRanges object with the data. If data is present, chr will be set to seqnames(data) and x to the midpoints of the ranges in data. If no parameter y is specified and data has a column named y or value this column will be used to define the y value of each data point. (defaults to NULL)

chr	(a character vector) A vector of chromosome names specifying the chromosomes of the data points. If data is not NULL, chr is ignored. (defaults to NULL)
x	(a numeric vector) A numeric vector with the positions (in base pairs) of the data points in the chromosomes. If data is not NULL, x is ignored. (defaults to NULL)
y	(a numeric vector) A numeric vector with the values of the data points. If y is not NULL, it is used instead of any data column in data. (defaults to NULL)
labels	(a character vector) The labels to be plotted. (defaults to NULL)
ymin	(numeric) The minimum value of y to be plotted. If NULL, it is set to the min value of the selected data panel. (defaults to NULL)
ymax	(numeric) The maximum value of y to be plotted. If NULL, it is set to the max value of the selected data panel. (defaults to NULL)
data.panel	(numeric) The identifier of the data panel where the data is to be plotted. The available data panels depend on the plot type selected in the call to plotKaryotype . (defaults to 1)
r0	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
r1	(numeric) r0 and r1 define the vertical range of the data panel to be used to draw this plot. They can be used to split the data panel in different vertical ranges (similar to tracks in a genome browser) to plot different data. If NULL, they are set to the min and max of the data panel, it is, to use all the available space. (defaults to NULL)
clipping	(boolean) Only used if zooming is active. If TRUE, the data representation will be not drawn out of the drawing area (i.e. in margins, etc) even if the data overflows the drawing area. If FALSE, the data representation may overflow into the margins of the plot. (defaults to TRUE)
...	The ellipsis operator can be used to specify any additional graphical parameters. Any additional parameter will be passed to the internal calls to the R base plotting functions.

Details

This is one of the functions from karyoploteR implementing the adaptation to the genome context of basic plot functions from R base graphics. Given a set of positions on the genome (chromosome and base), a value (y) for each of them and a label, it plots the label at the position specified by the data point. Data can be provided via a GRanges object (data), independent parameters for chr, x and y or a combination of both. A number of parameters can be used to define exactly where and how the text is drawn. In addition, via the ellipsis operator (...), kpText accepts any parameter valid for text (e.g. cex, col, ...)

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#), [kpLines](#), [kpPoints](#)
[kpPlotRegions](#)

Examples

```
set.seed(1000)
data.points <- sort(createRandomRegions(nregions=500, mask=NA))
mcols(data.points) <- data.frame(y=runif(500, min=0, max=1))

kp <- plotKaryotype("hg19", plot.type=2, chromosomes=c("chr1", "chr2"))
kpDataBackground(kp, data.panel=1)
kpDataBackground(kp, data.panel=2)

kpLines(kp, data=data.points, col="red")

#Three ways of specifying the exact same data.points
kpPoints(kp, data=data.points)
kpPoints(kp, data=data.points, y=data.points$y, pch=16, col="#CCCCCCF", cex=0.6)
kpPoints(kp, chr=as.character(seqnames(data.points)),
         x=(start(data.points)+end(data.points))/2,
         y=data.points$y, pch=".", col="black", cex=1)

#plotting in the data.panel=2 and using r0 and r1, ymin and ymax
kpLines(kp, data=data.points, col="red", r0=0, r1=0.3, data.panel=2)
kpText(kp, data=data.points, labels=as.character(1:500), r0=0, r1=0.3, data.panel=2, pch=".", cex=3)

kpLines(kp, data=data.points, col="blue", r0=0.4, r1=0.7, data.panel=2)
kpLines(kp, data=data.points, col="blue", y=-1*(data.points$y), ymin=-1, ymax=0, r0=0.7, r1=1, data.panel=2)
#It is also possible to "flip" the data by giving an r0 > r1
kpPoints(kp, data=data.points, col="red", y=(data.points$y), r0=1, r1=0.7, data.panel=2, pch=".", cex=2)
```

lighter

*lighter***Description**

Given a color, return a lighter one

Usage

```
lighter(col, amount=150)
```

Arguments

col	(color) The original color. Might be specified as a color name or a "#RRGGBB(AA)" hex color definition.
amount	(integer, [0-255]) The fixed amount to add to each RGB channel (Defaults to 150).

Details

Very simple utility function to create lighter colors. Given a color, it transforms it to rgb space, adds a set amount to all channels and transforms it back to a color.

Value

A lighter color

See Also

[darker](#)

Examples

```
lighter("red")
lighter("#333333")
lighter(c("red", 3, "#FF00FF"))
```

makeGenesDataFromTxDb *makeGenesDataFromTxDb*

Description

This is a utility function that transforms a TxDb object into a custom object valid as input for [kpPlotGenes](#).

Usage

```
makeGenesDataFromTxDb(txdb, karyoplot=NULL, plot.transcripts=TRUE, plot.transcripts.structure=TRUE)
```

Arguments

txdb	(a TxDb object) The transcript database object from which the data will be extracted.
karyoplot	(karyoplot object) A valid karyoplot object created by a call to plotKaryotype . If present, genes data will be restricted to the visible region in the plot. If NULL, all genes will be included. (defaults to NULL)
plot.transcripts	(boolean) TRUE if transcripts are needed in addition to the genes. (defaults to TRUE)
plot.transcripts.structure	(boolean) TRUE if the coding and non-coding exons are needed in addition to the genes and transcripts. (defaults to TRUE)

Details

This function creates a valid data object for [kpPlotGenes](#) starting from a TxDb object. The resulting object will contain only the genes and transcripts overlapping the plot region of the given Karyoplot object.

Value

Returns a list with at least one element called `genes`, a `GRanges` with all genes overlapping karyoplot. If `plot.transcripts` is `TRUE`, the returned list will have a `transcript` element, a list of `GRanges` objects, one per gene (named with the gene ids), with the transcripts of that gene. If `plot.transcripts.structure` is `TRUE`, two more elements are present: `coding.exons` and `non.coding.exons`, each a list with one element per transcript (named with the transcript id), and each element the coding or non-coding exons of that transcript.

Note

[kpPlotGenes](#) accepts `TxDb` objects directly. This function is only expected to be used when the user want to manipulate the results somehow (i.e. removing some of the genes).

See Also

[kpPlotGenes](#)

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)

zoom <- toGRanges("chr17", 32.6e6, 33.2e6)
kp <- plotKaryotype(genome="hg19", zoom=zoom)

genes.data <- makeGenesDataFromTxDb(TxDb.Hsapiens.UCSC.hg19.knownGene,
                                   karyoplot=kp, plot.transcripts=TRUE,
                                   plot.transcripts.structure=TRUE)
```

mergeTranscripts

mergeTranscripts

Description

Merges the transcripts of each gene and creates one transcript per gene with all exons and UTR regions combined

Usage

```
mergeTranscripts(genes.data)
```

Arguments

`genes.data` (GenesData object) A valid `genes.dat` object like the ones obtained by [makeGenesDataFromTxDb](#)

Details

This function takes a valid data object and merges all transcripts from each gene into a single transcript. This is useful to reduce the plot complexity while keeping partial information on transcript structure. In this transcript, any region that is a coding exon in any transcript, will be an exon, any region that is a non-coding exon in any transcript and is not an exon in any transcript, will be a non-coding exon. Anything between coding and non-coding exons will be introns.

Value

The original GenesData object with a single transcript per gene `GenesData$genes$names`.

See Also

[kpPlotGenes](#), [makeGenesDataFromTxDb](#)

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)

zoom <- toGRanges("chr17:29.4e6-29.8e6")
kp <- plotKaryotype(genome="hg19", zoom=zoom)
genes.data <- makeGenesDataFromTxDb(TxDb.Hsapiens.UCSC.hg19.knownGene, karyoplot=kp)
genes.data <- addGeneNames(genes.data)
kpPlotGenes(kp, data=genes.data, r1=0.5, plot.transcripts=TRUE, gene.name.position = "left")
genes.data.merged <- mergeTranscripts(genes.data)
kpPlotGenes(kp, data=genes.data.merged, r0=0.6, r1=0.8, plot.transcripts=TRUE, gene.name.position = "left")
```

`plotDefaultPlotParams` *plotDefaultPlotParameters*

Description

Creates a karyoplot with the default parameters drawn.

Usage

```
plotDefaultPlotParams(plot.type=2, plot.params=NULL, ...)
```

Arguments

<code>plot.type</code>	(numeric) plot the params of this plot type. Currently, only plot types 2 and 3 are accepted. (defaults to 2)
<code>plot.params</code>	(a plot params object) a plot params object such the one returned by getDefaultPlotParams . If specified, it will be used to create the plots.
<code>...</code>	The ellipsis operator can be used to pass any additional graphics parameter

Details

Given a `plot.type`, this function creates a new karyoplot with lines and arrows showing the meaning and values of the `plot.params`

Value

Returns the original karyoplot object, unchanged.

See Also

[plotKaryotype](#)

Examples

```
kp <- plotDefaultPlotParams(plot.type=2)
```

plotKaryotype	<i>plotKaryotype</i>
---------------	----------------------

Description

Create a new empty plot with a karyotype (the chromosome ideograms and chromosome names).

Usage

```
plotKaryotype(genome="hg19", plot.type=1, ideogram.plotter=kpAddCytobands, labels.plotter=kpAddCh
```

Arguments

genome	The genome to plot. It can be either a UCSC style genome name (hg19, mm10, etc), a GRanges object with the chromosomes as ranges or in general any genome specification accepted by getGenomeAndMask . (defaults to "hg19")
plot.type	The orientation of the ideogram and placing of the data panels. Values explained above.. (defaults to 1)
ideogram.plotter	The function to be used to plot the ideograms. Only one function is included with the package, kpAddCytobands, but it is possible to create custom ones. If NULL, no ideograms are plotted. (defaults to kpAddCytobands)
labels.plotter	The function to be used to plot the labels identifying the chromosomes. Only one function is included with the package, kpAddChromosomeNames, but it is possible to create custom ones. If NULL, no labels are plotted. (defaults to kpAddChromosomeNames)
chromosomes	The chromosomes to plot. Can be either a vector of chromosome names or a chromosome group name ("canonical", "autosomal", "all"). Setting it to "auto" will select canonical for named genomes and no filtering for custom genomes. (defaults to "auto")
zoom	A GRanges object specifying a single region to zoom in or any format accepted by regionER::toGRanges . If not NULL, it takes precedence over chromosome and only the zoomed in region is represented. If more than one region is present in the GRanges, only the first one is used. (defaults to NULL, do not zoom in and show the whole plot as specified by genome and chromosomes)
cytobands	A GRanges object (or anything accepted by toGRanges function: bed file, data.frame...) specifying the positions and types of the cytobands. The type of the cytobands MUST be in a column named "gieStain" (as used by UCSC) with values such as 'gneg', 'gpos50', 'stalk', 'acen'... If NULL, the cytobands are recovered from the package cache or downloaded from UCSC if possible (it's not possible for custom genomes). If empty, no cytobands will be plotted. (defaults to NULL)
plot.params	An object obtained from getDefaultPlotParams and possibly modified, containing the basic plotting parameters. If NULL, the default parameters will be used. (defaults to NULL)

use.cache	karyoploteR has a small cache with the chromosome names and lengths and the cytobands for a handful of organisms so it's not needed to retrieve them from databases or BSGenomes objects. Set this parameter to FALSE to ignore the cache. (defaults to TRUE, use the cache)
main	The text to be used as the title of the plot. NULL produces no title. (defaults to NULL)
...	The ellipsis can be used to pass in any additional parameter accepted by the internal functions used.

Details

This is the main function of karyoploteR. It creates the basic empty plot with the chromosome ideograms and returns the karyoplot object needed for all other plotting functions. Both the basic plotting parameters (margins, sizes, etc.) and the specific plotting functions for the ideograms and chromosome labels are customizable. In particular, passing in a `plot.params` object specifies the basic plotting parameters to use and the `ideogram.plotter` and `labels.plotter` parameters can be used to specify custom plotting functions for the ideogram and the chromosome labels. It is also possible to specify the genome and a list with the chromosomes to be plotted.

The `plot.type` parameter specifies the type of karyoplot to create: the number and positions of the data panels respect to the ideograms:

- `plot.type=1` Horizontal ideograms with a single data panel above them
- `plot.type=2` Horizontal ideograms with two data panels, one above and one below them
- `plot.type=3` Horizontal ideograms with all chromosomes in a single line with two data panels, one above and one below them
- `plot.type=4` Horizontal ideograms with all chromosomes in a single line with one data panel above
- `plot.type=5` Horizontal ideograms with all chromosomes in a single line with one data panel below them
- `plot.type=6` Horizontal ideograms with NO data panels. Only plotting in the ideograms is possible.
- `plot.type=7` Horizontal ideograms with all chromosomes in a single line with NO data panels. Only plotting in the ideograms is possible.

Value

The KaryoPlot object needed by the plotting functions.

See Also

[getDefaultPlotParams](#), [kpPoints](#)

Examples

```
set.seed(1000)

rand.data <- createRandomRegions(genome="hg19", nregions=10000, length.mean=1,
                                length.sd=0, mask=NA, non.overlapping=TRUE)
mcols(rand.data) <- data.frame(y=rnorm(n=10000, mean = 0.5, sd=0.1))

#The simplest way, with all default parameters
```



```

kp <- plotKaryotype()
kpPoints(kp, rand.data, pch=".")

#Or we can plot only a few chromosomes, with 2 data panels
kp <- plotKaryotype(chromosomes = c("chr1", "chr2"), plot.type = 2)
kpDataBackground(kp, data.panel = 1, color = "lightgreen")
kpDataBackground(kp, data.panel = 2, color = "lightblue")
kpPoints(kp, rand.data, pch=".", data.panel = 1)
kpPoints(kp, rand.data, pch=".", data.panel = 2)

#Or we can use a different organism,
kp <- plotKaryotype(genome = "mm10")
kp <- plotKaryotype(genome = "dm6")

# Or we can change the plotting parameters. In this case, to create a smaller ideogram
# and smaller data panel below it
plot.params <- getDefaultPlotParams(plot.type=2)
plot.params$ideogramheight <- 5
plot.params$data2height <- 50

kp <- plotKaryotype(chromosomes = c("chr1", "chr2"), plot.type = 2, plot.params = plot.params)
kpDataBackground(kp, data.panel = 1, color = "lightgreen")
kpDataBackground(kp, data.panel = 2, color = "lightblue")
kpPoints(kp, rand.data, pch=".", data.panel = 1)
kpPoints(kp, rand.data, pch=".", data.panel = 2)

#Or we can remove the cytobands, passing an empty GRanges object
kp <- plotKaryotype(cytobands = GRanges())

#Or remove the chromosome labels
kp <- plotKaryotype(labels.plotter = NULL)
kpPoints(kp, rand.data, pch=".")

#In addition, it's possible to use maggritr piping to chain the plotting calls
library(maggritr)
kp <- plotKaryotype() %>%
  kpDataBackground(color = "lightgreen") %>%
  kpPoints(rand.data, pch=".")

```

```
prepareParameters2    prepareParameters2
```

Description

Prepare and normalize the parameters for functions with x and y parameters

Usage

```
prepareParameters2(function.name, karyoplot, data=NULL, chr=NULL, x=NULL, y=NULL, ymax=NULL, ymin=
```

Arguments

function.name	(character) The name of the function calling prepareParameters2. Only user for error reporting.
karyoplot	(KaryoPlot) A karyoplot object.
data	A GRanges. It can be NULL or a GRanges.
chr	A character representing the chromosome names.
x	The position in the chromosome in number of bases.
y	The value to be plotted.
ymin	The minimum value of y
ymax	The maximum value of y
r0	The start of the range to use for plotting
r1	The end of the range to use for plotting
data.panel	The data panel to use
filter.data	A boolean indicating if data should be filtered so only data in visible chromosomes is kept. (defaults to TRUE, filter data)
...	Any additional parameter

Details

This function prepares and normalizes the parameters for plotting functions with x and y parameters (as opposed to x0, x1, y0 and y1) so functions can offer a richer interface while internally dealing only with standard and simple code. It extracts the positions from data if available and applies the r0 and r1 scaling. It returns the ready to plot values in a list with only chr, x and y. Individual parameters (chr, x and y) take precedence over data. All parameters are interpreted and used as explained in [kpPoints](#). It also filters out any data points corresponding to chromosomes not present in the current karyoplot.

Value

A list with three values: chr, x and y. Each of them a vector of the same length with the normalized values to plot.

Note

This function is only useful when creating custom plotting functions. It is not intended to the general user.

For detailed documentation on the parameters, see [kpPoints](#)

See Also

[kpPoints](#)

Examples

```
kp <- plotKaryotype()
prepareParameters2("TestFunc", kp, data=NULL, chr="chr1", x=c(10, 20, 30), y=c(0, 1, 2), r0=0, r1=0.5, ymin=0,
```

```
prepareParameters4    prepareParameters4
```

Description

Prepare and normalize the parameters for functions with x0, x1 and y0, y1 parameters

Usage

```
prepareParameters4(function.name, karyoplot, data=NULL, chr=NULL, x0=NULL, x1=NULL, y0=NULL, y1=NULL, ...)
```

Arguments

function.name	(character) The name of the function calling prepareParameters4. Only user for error reporting.
karyoplot	(KaryoPlot) A karyoplot object.
data	A GRanges
chr	A character representing the chromosome names.
x0	The position in the chromosome in number of bases.
x1	The position in the chromosome in number of bases.
y0	The value to be plotted.
y1	The value to be plotted.
ymin	The maximum value of y
ymax	The minimum value of y
r0	The start of the range to use for plotting
r1	The end of the range to use for plotting
data.panel	The data panel to use
filter.data	A boolean indicating if data should be filtered so only data in visible chromosomes is kept. (defaults to TRUE, filter data)
...	Any additional parameter

Details

This function prepares and normalizes the parameters for plotting functions with x0, x1, y0 and y1 parameters (as opposed to x and y) so functions can offer a richer interface while internally dealing only with standard and simple code. It extracts the positions from data if available and applies the r0 and r1 scaling. It returns the ready to plot values in a list with only chr, x0, x1, y0 and y1. Individual parameters (chr, x0, x1, y0 and y1) are interpreted and used as explained in [kpRect](#). It also filters out any data points corresponding to chromosomes not present in the current karyoplot.

Value

A list with five values: chr, x0, x1, y0 and y1. Each of them a vector of the same length with the normalized values to plot.

Note

This function is only useful when creating custom plotting functions. It is not intended to the general user.

For detailed documentation on the parameters, see [kpRect](#)

See Also

[kpRect](#)

Examples

```
kp <- plotKaryotype()
prepareParameters4("TestFunc", kp, data=NULL, chr="chr1", x0=c(10, 20, 30), x1=c(20, 30, 40), y0=c(0, 1, 2), y1=c(10, 20, 30))
```

processClipping	<i>processClipping</i>
-----------------	------------------------

Description

Sets image clipping if needed

Usage

```
processClipping(karyoplot, clipping, data.panel)
```

Arguments

karyoplot	(KaryoPlot) A KaryoPlot object representing the current plot
clipping	(logical) Whether clipping should be activated or not
data.panel	(data panel identifier) The name of the data panel on which the plot should be allowed. Anything plotted outside it will be hidden (if clipping==TRUE and the plot is a zoom plot)

Details

Small utility function to help manage clipping. If the current plot is a zoomed plot and clipping is TRUE, activate the clip to the current data.panel. This will hide any plotting occurring out of the data.panel region.

Value

Returns the original karyoplot object, unchanged.

Note

Users wont usually use this function. It is used by the plotting functions to set the clipping if needed

Examples

```
kp <- plotKaryotype()
processClipping(kp, TRUE, 1)
```

transparent	<i>transparent</i>
-------------	--------------------

Description

Given a color, return a transparent one

Usage

```
transparent(col, amount=0.5)
```

Arguments

col	(color) The original color. Might be specified as a color name or a "#RRGGBB(AA)" hex color definition.
amount	(number, [0-1]) The amount of transparency. 0 for completely visible, 1 for completely transparent. (Defaults to 0.5).

Details

Very simple utility function to create transparent colors. Given a color, it transforms it to rgb space, adds a set amount to all channels and transforms it back to a color.

Value

A transparent color

See Also

[lighter](#)

Examples

```
transparent("red")
transparent("#333333")
```

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