Package ‘plotgardener’

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Title  Coordinate-Based Genomic Visualization Package for R
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Description  Coordinate-based genomic visualization package for R. It grants users the ability to programmatically produce complex, multi-paneled figures. Tailored for genomics, plotgardener allows users to visualize large complex genomic datasets and provides exquisite control over how plots are placed and arranged on a page.
Depends  R (>= 4.1.0)
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annoDomains

Annotate domains in a Hi-C plot

Description

Annotate domains in a Hi-C plot

Usage

annoDomains(
  plot,
  data,
  half = "inherit",
  linecolor = "black",
  params = NULL,
  ...
)

Arguments

plot  Hi-C plot object from plotHicSquare or plotHicTriangle on which to annotate pixels.

data  A string specifying the BED file path, a dataframe in BED format, or a GRanges object specifying domain ranges.
half

Character value specifying which half of hic plots to annotate. Triangle Hi-C plots will always default to the entirety of the triangular plot. Default value is half = "inherit". Options are:
- "inherit": Domains will be annotated on the half inherited by the input Hi-C plot.
- "both": Domains will be annotated on both halves of the diagonal of a square Hi-C plot.
- "top": Domains will be annotated on the upper diagonal half of a square Hi-C plot.
- "bottom": Domains will be annotated on the bottom diagonal half of a square Hi-C plot.

linecolor

A character value specifying the color of the domain annotations. Default value is linecolor = "black".

params

An optional pgParams object containing relevant function parameters.

Value

Returns a domain object containing relevant genomic region, placement, and grob information.

Examples

```r
### Define a GRanges object with TAD ranges
library(GenomicRanges)
library(IRanges)
domains <- GRanges("chr21",
ranges = IRanges(
  start = c(28210000, 29085000, 29430000, 29700000),
  end = c(29085000, 29430000, 29700000, 30125000)
)
)

### Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

### Create page
pageCreate(width = 4.5, height = 4, default.units = "inches")

### Plot and place a square Hi-C plot
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, resolution = 10000,
zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30000000,
  assembly = "hg19",
x = 0.5, y = 0.5, width = 3, height = 3,
  just = c("left", "top"),
  default.units = "inches"
)
```
## Annotate domains on bottom half of Hi-C plot
annoDomains(
    plot = hicPlot, data = domains,
    half = "bottom", linecolor = "red"
)

## Annotate heatmap legend
annoHeatmapLegend(
    plot = hicPlot,
    x = 3.6, y = 0.5, width = 0.12, height = 1.2,
    just = c("left", "top"), default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(
    plot = hicPlot, x = 0.5, y = 3.53, scale = "Mb",
    just = c("left", "top")
)

## Hide page guides
pageGuideHide()

---

**annoGenomeLabel**  
*Annotate genomic coordinates along the x or y-axis of a plot*

### Description
Annotate genomic coordinates along the x or y-axis of a plot

### Usage

```r
annoGenomeLabel(
    plot, fontsize = 10, fontcolor = "black",
    linecolor = "black", margin = unit(1, "mm"), scale = "bp",
    commas = TRUE, sequence = TRUE, boxWidth = 0.5,
    axis = "x", at = NULL, tcl = 0.5, x, y,
    just = c("left", "top"), default.units = "inches",
```
annoGenomeLabel

params = NULL,
...)

Arguments

plot  Input plot to annotate genomic coordinates. Genomic coordinates and assembly will be inherited from plot.

fontsize A numeric specifying text fontsize in points. Default value is fontsize = 10.

fontcolor A character value indicating the color for text. Default value is fontcolor = "black".

linecolor A character value indicating the color of the genome label axis. Default value is linecolor = "black".

margin A numeric or unit vector specifying space between axis and coordinate labels. Default value is margin = unit(1, "mm").

scale A character value indicating the scale of the coordinates along the genome label. Default value is scale = "bp". Options are:
- "bp": base pairs.
- "Kb": kilobase pairs. 1 kilobase pair is equal to 1000 base pairs.
- "Mb": megabase pairs. 1 megabase pair is equal to 1000000 base pairs.

commas A logical value indicating whether to include commas in start and stop labels. Default value is commas = TRUE.

sequence A logical value indicating whether to include sequence information above the label of an x-axis (only at appropriate resolutions).

boxWidth A numeric value indicating the width of the boxes representing sequence information at appropriate resolutions. Default value is boxWidth = 0.5.

axis A character value indicating along which axis to add genome label. Sequence information will not be displayed along a y-axis. Default value is axis = "x". Options are:
- "x": Genome label will be plotted along the x-axis.
- "y": Genome label will be plotted along the y-axis. This is typically used for a square Hi-C plot made with plotHicSquare.

at A numeric vector of x-value locations for tick marks.

tcl A numeric specifying the length of tickmarks as a fraction of text height. Default value is tcl = 0.5.

x A numeric or unit object specifying genome label x-location.

y A numeric, unit object, or character containing a "b" combined with a numeric value specifying genome label y-location. The character value will place the genome label y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

just Justification of genome label relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
annoGenomeLabel

- default.units: A string indicating the default units to use if x or y are only given as numerics. Default value is default.units = "inches".
- params: An optional pgParams object containing relevant function parameters.
- ...: Additional grid graphical parameters or digit specifications. See gpar and formatC.

Value

Returns a genomeLabel object containing relevant genomic region, placement, and grob information.

Examples

```r
## Load hg19 genomic annotation packages
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
library("org.Hs.eg.db")

## Create page
pageCreate(width = 5, height = 2, default.units = "inches")

## Plot and place gene track on page
genesPlot <- plotGenes(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19", fill = c("grey", "grey"),
  fontcolor = c("grey", "grey"),
  x = 0.5, y = 0.25, width = 4, height = 1,
  just = c("left", "top"),
  default.units = "inches"
)

## Annotate x-axis genome labels at different scales
annoGenomeLabel(
  plot = genesPlot, scale = "Mb",
  x = 0.5, y = 1.25, just = c("left", "top"),
  default.units = "inches"
)
annoGenomeLabel(
  plot = genesPlot, scale = "Kb",
  x = 0.5, y = 1.5, just = c("left", "top"),
  default.units = "inches"
)
annoGenomeLabel(
  plot = genesPlot, scale = "bp",
  x = 0.5, y = 1.75, just = c("left", "top"),
  default.units = "inches"
)

## Hide page guides
pageGuideHide()
```
annoHeatmapLegend  Add a color scale legend for heatmap-style plots

Description
Add a color scale legend for heatmap-style plots

Usage
annoHeatmapLegend(
plot, orientation = "v",
fontsize = 8,
fontcolor = "dark grey",
scientific = FALSE,
digits = 1,
ticks = FALSE,
bbreaks = NULL,
border = FALSE,
x,
y,
width,
height,
just = c("left", "top"),
default.units = "inches",
params = NULL,
...)

Arguments
plot Heatmap-style plot object to add heatmap legend for.
orientation A string specifying legend orientation. Default value is orientation = "v". Options are:
  • "v": Vertical legend orientation.
  • "h": Horizontal legend orientation.
fontsize A numeric specifying text fontsize in points. Default value is fontsize = 8.
fontcolor Character value specifying text fontcolor. Default value is fontcolor = "dark grey".
scientific Logical value specifying if numeric color value labels should be encoded in scientific format. Default value is scientific = FALSE.
digits Numeric specifying how many significant digits to include of numeric color value labels. Default value is digits = 1.
ticks Logical value specifying if tick marks on the heatmap colorbar should be visible. Default value is ticks = FALSE.
annoHeatmapLegend

breaks A numeric vector specifying tick breaks. Default value is breaks = NULL.
border Logical value indicating whether to add a border around heatmap legend. Default value is border = FALSE.
x A numeric or unit object specifying x-location of legend.
y A numeric, unit object, or character containing a "b" combined with a numeric value specifying y-location of legend. The character value will place the legend y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
width A numeric or unit object specifying width of legend.
height A numeric or unit object specifying height of legend.
just Justification of heatmap legend relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
params An optional pgParams object containing relevant function parameters.
...

Value
Returns a heatmapLegend object with relevant color value, placement, and grob information.

Examples

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create page
pageCreate(width = 4, height = 3.5, default.units = "inches")

## Plot and place a square Hi-C plot
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  x = 0.5, y = 0.5, width = 2.5, height = 2.5,
  just = c("left", "top"),
  default.units = "inches"
)

## Add heatmap legend
annoHeatmapLegend(
  plot = hicPlot,
)```
x = 3.2, y = 0.5, width = 0.12, height = 1.2,
just = c("left", "top"), default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(
    plot = hicPlot, x = 0.5, y = 3.03, scale = "Mb",
    just = c("left", "top")
)

## Hide page guides
pageGuideHide()

---

**annoHighlight**

Annotates a highlight box around a specified genomic region of a plot

### Description

Annotates a highlight box around a specified genomic region of a plot

### Usage

```r
annoHighlight(
    plot,
    chrom,
    chromstart = NULL,
    chromend = NULL,
    fill = "grey",
    linecolor = NA,
    alpha = 0.4,
    y,
    height,
    just = c("left", "top"),
    default.units = "inches",
    params = NULL,
    ...
)
```

### Arguments

- **plot**: Input plot on which to annotate genomic region.
- **chrom**: Chromosome of region to be highlighted, as a string.
- **chromstart**: Integer start position on chromosome to be highlighted.
- **chromend**: Integer end position on chromosome to be highlighted.
- **fill**: A character value specifying highlight box fill color. Default value is `fill = "grey"`. 
linecolor  A character value specifying highlight box line color. Default value is `linecolor = NA`.

alpha    Numeric value specifying color transparency. Default value is `alpha = 0.4`.

y        A numeric, unit object, or character containing a "b" combined with a numeric value specifying square highlight box y-location. The character value will place the highlight box y relative to the bottom of the most recently plotted plot according to the units of the `plotgardener` page.

height   A numeric or unit object specifying highlight box height.

just     Justification of highlight box relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is `just = c("left", "top")`.

default.units A string indicating the default units to use if y or height are only given as numerics or numeric vectors. Default value is `default.units = "inches"`.

params   An optional `pgParams` object containing relevant function parameters.

...      Additional grid graphical parameters. See `gpar`.

Value

Returns a highlight object containing relevant genomic region, placement, and `grob` information.

Examples

```r
## Create a page
pageCreate(width = 7.5, height = 1.5, default.units = "inches")

## Plot and place a signal plot
library(plotgardenerData)
data("IMR90_ChIP_H3K27ac_signal")
region <- pgParams(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  range = c(0, 45)
)
signalPlot <- plotSignal(
  data = IMR90_ChIP_H3K27ac_signal, params = region,
  x = 0.5, y = 0.25, width = 6.5, height = 0.65,
  just = c("left", "top"),
  default.units = "inches"
)

## Highlight genomic region on signal plot
annoHighlight(
  plot = signalPlot,
  chrom = "chr21",
  chromstart = 29000000, chromend = 29125000,
  y = 0.25, height = 1, just = c("left", "top"),
  default.units = "inches"
)
```
annoPixels

Annotate pixels in a Hi-C plot

Description

Annotate pixels in a Hi-C plot

Usage

annoPixels(
  plot,
  data,
  type = "box",
  half = "inherit",
  shift = 4,
  params = NULL,
  quiet = FALSE,
...
)

Arguments

plot
  Hi-C plot object from `plotHicSquare` or `plotHicTriangle` on which to annotate pixels.

data
  A string specifying the BEDPE file path, a dataframe in BEDPE format specifying pixel positions, or a `GInteractions` object specifying pixel positions.

type
  Character value specifying type of annotation. Default value is `type = "box"`. Options are:
  • "box": Boxes are drawn around each pixel.
annoPixels

- "circle": Circles are drawn around each pixel.
- "arrow": Arrows are drawn pointing to each pixel.

half

Character value specifying which half of hic plots to annotate. Triangle Hi-C plots will always default to the entirety of the triangular plot. Default value is half = "inherit". Options are:

- "inherit": Pixels will be annotated on the half inherited by the input Hi-C plot.
- "both": Pixels will be annotated on both halves of the diagonal of a square Hi-C plot.
- "top": Pixels will be annotated on the upper diagonal half of a square Hi-C plot.
- "bottom": Pixels will be annotated on the bottom diagonal half of a square Hi-C plot.

shift

Numeric specifying the number of pixels on either end of main pixel in a box or circle. Numeric specifying number of pixels for the length of an arrow.

params

An optional pgParams object containing relevant function parameters.

quiet

A logical indicating whether or not to print messages.

...

Additional grid graphical parameters. See gpar.

Value

Returns a pixel object containing relevant genomic region, placement, and grob information.

Examples

```r
## Load Hi-C data and BEDPE data
library(plotgardenerData)
data("IMR90_HiC_10kb")
data("IMR90_DNAloops_pairs")

## Create page
pageCreate(width = 4.5, height = 4, default.units = "inches")

## Plot and place a square Hi-C plot
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  x = 0.5, y = 0.5, width = 3, height = 3,
  just = c("left", "top"),
  default.units = "inches"
)

## Annotate loops of both sides of Hi-C plot with squares
pixels <- annoPixels(
  plot = hicPlot, data = IMR90_DNAloops_pairs, type = "box",
)```
## Annotate loops on one side of Hi-C plot with arrows and the other side with circles

```r
pagePlotRemove(plot = pixels)
pixels1 <- annoPixels(
  plot = hicPlot, data = IMR90_DNAloops_pairs,
  type = "arrow", half = "top", shift = 8
)
pixels2 <- annoPixels(
  plot = hicPlot, data = IMR90_DNAloops_pairs,
  type = "circle", half = "bottom"
)
```

## Annotate heatmap legend

```r
annoHeatmapLegend(
  plot = hicPlot,
  x = 3.6, y = 0.5, width = 0.12, height = 1.2,
  just = c("left", "top"), default.units = "inches"
)
```

## Annotate genome label

```r
annoGenomeLabel(
  plot = hicPlot, x = 0.5, y = 3.53, scale = "Mb",
  just = c("left", "top")
)
```

## Hide page guides

```r
pageGuideHide()
```

### annoSegments

**Annotates a line segment within a plot**

---

**Description**

Annotates a line segment within a plot

**Usage**

```r
annoSegments(
  x0, y0, x1, y1, plot, default.units = "native",
  linecolor = "black", lwd = 1,
)```
annoSegments

\[
\begin{align*}
\text{lty} &= 1, \\
\text{lineend} &= \text{"butt"}, \\
\text{linejoin} &= \text{"mitre"}, \\
\text{arrow} &= \text{NULL}, \\
\text{params} &= \text{NULL}, \\
\ldots
\end{align*}
\]

Arguments

- **x0**: A numeric vector or unit object indicating the starting x-values of the line segments.
- **y0**: A numeric vector or unit object indicating the starting y-values of the line segments.
- **x1**: A numeric vector or unit object indicating the stopping x-values of the line segments.
- **y1**: A numeric vector or unit object indicating the stopping y-values of the line segments.
- **plot**: Input plotgardener plot to internally plot line segments relative to.
- **default.units**: A string indicating the default units to use if x0, y0, x1, or y1 are only given as numeric vectors. Default value is default.units = "native".
- **linecolor**: A character value specifying segment line color. Default value is linecolor = "black".
- **lwd**: A numeric specifying segment line width. Default value is lwd = 1.
- **lty**: A numeric specifying segment line type. Default value is lty = 1.
- **lineend**: A character value specifying line end style. Default value is lineend = "butt". Options are:
  - "round": Segment ends are rounded.
  - "butt": Segment ends end exactly where ended.
  - "square": Segment ends are squared.
- **linejoin**: A character value specifying line join style. Default value is linejoin = "mitre". Options are:
  - "round": Line joins are rounded.
  - "mitre": Line joins are sharp corners.
  - "bevel": Line joins are flattened corners.
- **arrow**: A list describing arrow heads to place at either end of the line segments, as produced by the arrow function.
- **params**: An optional pgParams object containing relevant function parameters.
- **...**: Additional grid graphical parameters. See gpar.

Value

Returns a segments object containing relevant placement and grob information.
See Also

grid.segments, arrow

Examples

library(grid)
## Create a page
pageCreate(width = 7.5, height = 2.5, default.units = "inches")

## Plot a Manhattan plot
library(plotgardenerData)
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
data("hg19_insulin_GWAS")
manhattanPlot <- plotManhattan(
  data = hg19_insulin_GWAS, assembly = "hg19",
  fill = c("grey", "#37a7db"),
  sigLine = TRUE,
  col = "grey", lty = 2, range = c(0, 14),
  x = 0.5, y = 0, width = 6.5, height = 2,
  just = c("left", "top"),
  default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(
  plot = manhattanPlot, x = 0.5, y = 2, fontsize = 8,
  just = c("left", "top"),
  default.units = "inches"
)
plotText(
  label = "Chromosome", fontsize = 8,
  x = 3.75, y = 2.20, just = "center", default.units = "inches"
)

## Annotate y-axis
annoYaxis(
  plot = manhattanPlot, at = c(0, 2, 4, 6, 8, 10, 12, 14),
  axisLine = TRUE, fontsize = 8
)

## Annotate a line segment for an additional significance line of
## the Manhattan plot
annoSegments(
  x0 = unit(0, "npc"), y0 = 10,
  x1 = unit(1, "npc"), y1 = 10,
  plot = manhattanPlot, default.units = "native",
  linecolor = "red", lty = 2
)

## Plot y-axis label
plotText(
  label = "-log10(p-value)", x = 0.15, y = 1, rot = 90,
annoText

## Hide page guides

pageGuideHide()

annoText

Annotates text within a plot

### Description

Annotates text within a plot

### Usage

```
annoText(
  label,
  fontcolor = "black",
  fontsize = 12,
  rot = 0,
  check.overlap = FALSE,
  plot,
  x,
  y,
  just = "center",
  default.units = "native",
  params = NULL,
  ...
)
```

### Arguments

- **label**: Character or expression of text to be plotted.
- **fontcolor**: A character value specifying text fontcolor. Default value is `fontcolor = "black"`. 
- **fontsize**: A numeric specifying text fontsize in points. Default value is `fontsize = 12`. 
- **rot**: A numeric specifying the angle to rotate the text. Default value is `rot = 0`. 
- **check.overlap**: A logical value to indicate whether to check for and omit overlapping text. Default value is `check.overlap = FALSE`. 
- **plot**: Input plotgardener plot to internally place text relative to. 
- **x**: A numeric vector or unit object specifying text x-location. 
- **y**: A numeric vector or unit object specifying text y-location. 
- **just**: Justification of text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is `just = "center"`. 

...
annoXaxis

Add an x-axis to a plot

Description

Add an x-axis to a plot

default.units  A string indicating the default units to use if x or y are only given as numerics or numeric vectors. Default value is default.units = "native".

params  An optional pgParams object containing relevant function parameters.

...  Additional grid graphical parameters. See gpar.

Value

Returns a text object containing relevant placement and grob information.

See Also

gird.text

Examples

## Create a page
pageCreate(width = 4, height = 4, default.units = "inches")

## Plot text relative to a plotgardener plot
library(plotgardenerData)
data("IMR90_HiC_10kb")
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, chrom = "chr21",
  chromstart = 28000000, chromend = 29500000,
  assembly = "hg19",
  zrange = c(0, 70),
  x = 0.5, y = 0.5, width = 3, height = 3,
  just = c("left", "top"),
  default.units = "inches"
)
annoGenomeLabel(
  plot = hicPlot, x = 0.5, y = 3.55, scale = "Mb",
  just = c("left", "top"), default.units = "inches"
)

annoText(
  label = "Loop", fontsize = 8, plot = hicPlot,
  x = 29075000, y = 28150000,
  just = "center", default.units = "native"
)

## Hide page guides
pageGuideHide()
annoXaxis

Usage

annoXaxis(
  plot, 
  at = NULL, 
  label = TRUE, 
  main = TRUE, 
  scipen = 999, 
  axisLine = FALSE, 
  params = NULL, 
  ...
)

Arguments

plot  Plot object to annotate with x-axis.
at  A numeric vector of x-value locations for tick marks.
label  A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the at argument.
main  A logical value indicating whether to draw the x-axis at the bottom of the plot. Default value is main = TRUE. Options are:
  • TRUE: x-axis is drawn at the bottom of the plot.
  • FALSE: x-axis is drawn at the top of the plot.
scipen  An integer indicating the penalty to be applied when deciding to print numeric values in fixed or exponential notation. Default value is scipen = 999.
axisLine  A logical value indicating whether to show the axis line. Default value is axisLine = FALSE.
params  An optional pgParams object containing relevant function parameters.
...  Additional grid graphical parameters. See gpar.

Value

Returns a xaxis object containing relevant grob information.

Examples

```r
## Load transcript information
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
library("org.Hs.eg.db")

## Create page
pageCreate(width = 7.5, height = 4.5, default.units = "inches")

## Plot gene transcripts
transcriptPlot <- plotTranscripts(
  chrom = "chr1",
  chromstart = 1000000,
```
annoYaxis

Add a y-axis to a plot

Description

Add a y-axis to a plot

Usage

annoYaxis(
plot, at = NULL, label = TRUE, main = TRUE, scipen = 999, axisLine = FALSE, params = NULL, ...
)

Arguments

plot Plot object to annotate with y-axis.
at A numeric vector of y-value locations for tick marks.
label A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the at argument.
annoYaxis

main A logical value indicating whether to draw the y-axis at the left of the plot. Default value is main = TRUE. Options are:
- TRUE: y-axis is drawn at the left of the plot.
- FALSE: y-axis is drawn at the right of the plot.

scipen An integer indicating the penalty to be applied when deciding to print numeric values in fixed or exponential notation. Default value is scipen = 999.

axisLine A logical value indicating whether to show the axis line. Default value is axisLine = FALSE.

params An optional pgParams object containing relevant function parameters.

Value

Returns a yaxis object containing relevant grob information.

Examples

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create page
pageCreate(width = 4, height = 3.5, default.units = "inches")

## Plot and place a square Hi-C plot
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  x = 1, y = 0.5, width = 2.5, height = 2.5,
  just = c("left", "top"),
  default.units = "inches"
)

## Add standard y-axis to Hi-C plot
annoYaxis(
  plot = hicPlot, at = c(28000000, 29000000, 30300000),
  fontsize = 10
)

## Annotate genome label on x-axis
annoGenomeLabel(plot = hicPlot, x = 1, y = 3.03)

## Annotate heatmap legend
annoHeatmapLegend(
  plot = hicPlot,
  x = 3.6, y = 0.5, width = 0.12, height = 1.2
)
```
annoZoomLines

Annotates zoom lines for a specified genomic region of a plot

Description

Annotates zoom lines for a specified genomic region of a plot

Usage

annoZoomLines(
  plot,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  y0,
  x1 = NULL,
  y1,
  extend = 0,
  default.units = "inches",
  linecolor = "grey",
  lty = 2,
  params = NULL,
  ...
)

Arguments

plot 		Input plot to annotate genomic region zoom lines from.
chrom 	Chromosome of region to draw zoom lines from, as a string.
chromstart 	Integer start position on chromosome to draw zoom lines from.
chromend 	Integer end position on chromosome to draw zoom lines from.
y0 	A numeric vector or unit object indicating the starting y-values of the zoom line segments. If two values are given, the first value will correspond to the left zoom line and the second value will correspond to the right zoom line.
x1 	A numeric vector or unit object indicating the stopping x-values of the zoom line segments. If two values are given, the first value will correspond to the left zoom line and the second value will correspond to the right zoom line. If NULL, straight lines from zoomed genomic region will be drawn.
y1 	A numeric vector or unit object indicating the stopping y-values of the zoom line segments. If two values are given, the first value will correspond to the left zoom line and the second value will correspond to the right zoom line.
annoZoomLines

extend A numeric vector or unit object indicating the length to extend straight lines from each end of the zoom line segments. If two values are given, the first value will correspond to the top extension length and the second value will correspond to the bottom extension length. Default value is extend = 0.

default.units A string indicating the default units to use if y0, x1, y1, or extend are only given as numerics or numeric vectors. Default value is default.units = "inches".

linecolor A character value specifying zoom line color. Default value is linecolor = "grey".

lty A numeric specifying zoom line type. Default value is lty = 2.

params An optional pgParams object containing relevant function parameters.

... Additional grid graphical parameters. See gpar.

Value

Returns a zoom object containing relevant genomic region, placement, and grob information.

Examples

```r
## Create a page
pageCreate(width = 7.5, height = 4.75, default.units = "inches")

## Plot and place a Manhattan plot
library(plotgardenerData)
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
data("hg19_insulin_GWAS")
manhattanPlot <- plotManhattan(
data = hg19_insulin_GWAS, assembly = "hg19",
fill = c("grey", "#37a7db"),
sigLine = FALSE,
col = "grey", lty = 2, range = c(0, 14),
x = 0.5, y = 0, width = 6.5, height = 2,
just = c("left", "top"),
default.units = "inches"
)
annoYaxis(
plot = manhattanPlot, at = c(0, 2, 4, 6, 8, 10, 12, 14),
axisLine = TRUE, fontsize = 8
)

## Annotate zoom lines for a region on chromosome 21
zoomRegion <- pgParams(
chrom = "chr21",
chromstart = 28000000, chromend = 30300000,
assembly = "hg19"
)
annoZoomLines(
plot = manhattanPlot, params = zoomRegion,
y0 = 2, x1 = c(0.5, 7), y1 = 2.5, extend = c(0, 1.1),
default.units = "inches",
lty = 3
)
```

## Annotate highlight region for zoom region

```r
annoHighlight(
  plot = manhattanPlot, params = zoomRegion,
  y = 2, height = 2, just = c("left", "bottom"),
  default.units = "inches",
  fill = "red", alpha = 0.8
)
```

## Plot Manhattan plot data and signal track under zoom lines

```r
manhattanPlotZoom <- plotManhattan(
  data = hg19_insulin_GWAS,
  fill = "grey",
  sigLine = FALSE,
  baseline = TRUE,
  params = zoomRegion, range = c(0, 14),
  x = 0.5, y = 2.6,
  width = 6.5, height = 1
)
```

```r
data("IMR90_ChIP_H3K27ac_signal")
```

```r
signalPlot <- plotSignal(
  data = IMR90_ChIP_H3K27ac_signal, params = zoomRegion,
  range = c(0, 45),
  x = 0.5, y = "b0.1",
  width = 6.5, height = 0.65,
  just = c("left", "top"),
  default.units = "inches"
)
```

## Plot genome label

```r
plotGenomeLabel(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  x = 0.5, y = 4.4, length = 6.5,
  default.units = "inches"
)
```

## Hide page guides

```r
pageGuideHide()
```

---

**assembly**

*Make a assembly object for alternate TxDb, OrgDb,and BSgenome genomic annotation packages*

**Description**

Make a assembly object for alternate TxDb, OrgDb,and BSgenome genomic annotation packages
Usage

```r
assembly(
  Genome,
  TxDb,
  OrgDb,
  gene.id.column = "ENTREZID",
  display.column = "SYMBOL",
  BSgenome = NULL
)
```

Arguments

- **Genome**: String indicating the name of the genome assembly.
- **TxDb**: String of existing TxDb package name or a TxDb object.
- **OrgDb**: String of the desired OrgDb package name.
- **gene.id.column**: String of the TxDb column name that refers to the given TxDb gene IDs. Default value is `gene.id.column = "ENTREZID"`. 
- **display.column**: String of the OrgDb column name that refers to the type of gene symbol to be displayed in plots. Default value is `display.column = "SYMBOL"`. 
- **BSgenome**: String of the desired BSgenome package name.

Value

Returns a `assembly` object containing all input parameters.

See Also

- `TxDb`, `OrgDb-class`, `BSgenome`

Examples

```r
## Create a custom `assembly` object for hg38/GRCh38 packages
newAssembly <- assembly(
  Genome = "hg38_GRCh38",
  TxDb = "TxDb.Hsapiens.UCSC.hg38.knownGene",
  OrgDb = "org.Hs.eg.db",
  BSgenome = "BSgenome.Hsapiens.NCBI.GRCh38"
)
```

---

**Combine multiple pgParams objects into a vector**

Description

Combine multiple pgParams objects into a vector
Usage

c(..., recursive = FALSE)

Arguments

... pgParams objects to be concatenated.
recursive logical. If recursive = TRUE, the function recursively descends through lists (and pairlists) combining all their elements into a vector.

Value

NULL or an expression or a vector of an appropriate mode. (With no arguments the value is NULL.)

Examples

## Define parameters
p1 <- pgParams(chrom = "chr1", assembly = "hg19")

## Define another set of parameters
p2 <- pgParams(fontsize = 10, assembly = "hg19")

## Combine parameters into one `pgParams` object
pTotal <- c(p1, p2)

calcSignalRange Calculate a score range for multiple signals

Description

Calculate a score range for multiple signals

Usage

calcSignalRange(
  data,
  chrom = NULL,
  chromstart = 1,
  chromend = .Machine$integer.max,
  assembly = "hg38",
  negData = FALSE)

Arguments

data List of data to be plotted as character values specifying multiple bigwig file paths, dataframes in BED format, or GRanges objects with metadata column score.
chrom Chromosome of data region range as a string, if range for a specific chromosome is desired.
**colorby**

Handle plotgardener color scaling parameters

**Description**

colorby should be used to create a set of parameters that specify color scaling for the functions plotPairs, plotPairsArches, and plotRanges.

**Usage**

colorby(column = NULL, palette = NULL, range = NULL, scalePerRegion = FALSE)

**Arguments**

column String specifying name of data column to scale colors by.

palette (optional) A function describing the color palette to use for color scaling.

range (optional) A numeric vector specifying the range of values to apply a color scale to.

**Value**

Returns a vector of length 2 with the calculated c(min, max) range.

**Examples**

```r
library("plotgardenerData")
data("GM12878_ChIP_CTCF_signal")
data("IMR90_ChIP_CTCF_signal")
data("GM12878_ChIP_H3K27ac_signal")
data("IMR90_ChIP_H3K27ac_signal")
calcSignalRange(data = list(GM12878_ChIP_CTCF_signal, GM12878_ChIP_H3K27ac_signal, IMR90_ChIP_CTCF_signal, IMR90_ChIP_H3K27ac_signal), chrom = "chr21", chromstart = 28150000, chromend = 29150000, assembly = "hg38", negData = FALSE)
```
scalePerRegion  A logical value indicating whether to adjust NULL range of numerical `colorby` values to subset of data in a plotted genomic region. Default value is `scalePerRegion = FALSE`.

Value

Returns a "colorby" object.

Examples

```r
## Load paired ranges data in BEDPE format
library(plotgardenerData)
data("IMR90_DNAloops_pairs")

## Add a length column
IMR90_DNAloops_pairs$length <-
(IMR90_DNAloops_pairs$start2 - IMR90_DNAloops_pairs$start1) / 1000

## Plot pairs with colorby object set for `length` column
bedpePlot <- plotPairs(
data = IMR90_DNAloops_pairs,
chrom = "chr21",
chromstart = 27900000, chromend = 30700000,
assembly = "hg19",
fill = colorby("length", palette =
colorRampPalette(c("dodgerblue2", "firebrick2"))),
lwd = 2, spaceHeight = .7,
)
```

defaultPackages

Display the default genomic annotation packages associated with a genome build

Description

Display the default genomic annotation packages associated with a genome build

Usage

```r
defaultPackages(Genome)
```

Arguments

Genome  String indicating the name of the genome assembly.

Value

Returns a list of the default data packages for a genome build.
## View default genomic annotation packages associated with "hg19"

defaultPackages(Genome = "hg19")

## View default genomic annotation packages associated with "mm9"

defaultPackages(Genome = "mm9")

---

### genomes

Display the included available default genome assemblies

### Description

Display the included available default genome assemblies

### Usage

genomes()

### Value

Returns the included available default genome assemblies

### Examples

genomes()

---

### mapColors

Maps a numeric or character vector to a color palette and returns the vector of colors

### Description

Maps a numeric or character vector to a color palette and returns the vector of colors

### Usage

mapColors(vector, palette, range = NULL)

### Arguments

- **vector**: Vector to map to color.
- **palette**: Color palette function.
- **range**: Range of values to map for a numerical value.
Details

This function allows for the manual mapping of a numerical or factor vector to a palette of colors. For a more automatic implementation of this functionality in plotgardener functions, `colorby` objects can be used.

Value

Returns a character vector of color values. If the input vector is numerical, this vector will have additional ‘palette’ and ‘range’ attributes.

See Also

colorby

Examples

```r
## Load paired ranges data in BEDPE format
library(plotgardenerData)
data("IMR90_DNAloops_pairs")

## Add a length column
IMR90_DNAloops_pairs$length <- (IMR90_DNAloops_pairs$start2 -
IMR90_DNAloops_pairs$start1) / 1000

## Map length column to a vector of colors
colors <- mapColors(vector = IMR90_DNAloops_pairs$length,
  palette = colorRampPalette(c("dodgerblue2", "firebrick2")))

## Pass color vector into bbPlotPairsArches
heights <- IMR90_DNAloops_pairs$length / max(IMR90_DNAloops_pairs$length)
pageCreate(width = 7.5, height = 2.1, default.units = "inches",
  showGuides = FALSE, xgrid = 0, ygrid = 0)
params <- pgParams(
  chrom = "chr21",
  chromstart = 27900000, chromend = 30700000,
  assembly = "hg19",
  width = 7
)

archPlot <- plotPairsArches(
  data = IMR90_DNAloops_pairs, params = params,
  fill = colors,
  linecolor = "fill",
  archHeight = heights, alpha = 1,
  x = 0.25, y = 0.25, height = 1.5,
  just = c("left", "top"),
  default.units = "inches"
)

annoGenomeLabel(plot = archPlot, x = 0.25, y = 1.78, scale = "Mb")
annoHeatmapLegend(
  plot = archPlot, fontcolor = "black",
)```
pageCreate

Create a page for a plotgardener layout

Description

Create a page for a plotgardener layout

Usage

pageCreate(
  width = 8.5,
  height = 11,
  default.units = "inches",
  bg = NA,
  xgrid = 0.5,
  ygrid = 0.5,
  showGuides = TRUE,
  params = NULL
)

Arguments

width A numeric or unit object specifying page width. Default value is width = 8.
height A numeric or unit object specifying page height. Default value is height = 11.
default.units A string indicating the default units to use if width or height are only given as numerics. Default value is default.units = "inches".
bg Character value indicating page background color. Default value is bg = NA.
xgrid A numeric indicating the increment by which to place vertical gridlines. Default value is xgrid = 0.5.
ygrid A numeric indicating the increment by which to place horizontal gridlines. Default value is ygrid = 0.5.
showGuides A logical value indicating whether to draw a black border around the entire page and guiding rulers along the top and left side of the page. Default value is showGuides = TRUE.
params An optional pgParams object containing relevant function parameters.
Details

width and height must be specified in the same units.

Value

None.

Examples

```r
## Create a 6-inch wide, 4.5-inch high page
pageCreate(width = 6, height = 4.5, default.units = "inches")

## Create a 14-cm wide, 10-cm high page
pageCreate(width = 14, height = 10, default.units = "cm")
```

Description

Remove guides from a plotgardener page

Usage

```r
pageGuideHide()
```

Note

Please note that due to the implementation of `grid` removal functions, using `pageGuideHide` within a `pdf` call will result in the rendering of a separate, new page with the plot guides removed. To avoid this artifact, hide guides in the `pageCreate` function call with `showGuides = FALSE`.

Examples

```r
## Make a page
pageCreate(width = 7, height = 4, default.units = "inches")

## Hide page guides
pageGuideHide()
```
pageGuideHorizontal

Description

Draw a horizontal guideline at a specified y-coordinate on a plotgardener page

Usage

pageGuideHorizontal(
  y,
  default.units = "inches",
  linecolor = "grey55",
  params = NULL,
  ...
)

Arguments

y A numeric or unit object specifying y-coordinate of guide.
default.units A string indicating the default units to use if y is only given as a numeric. Default value is default.units = "inches".
linecolor Character value indicating color of guideline. Default value is linecolor = "grey55".
params An optional pgParams object containing relevant function parameters.
... Additional grid graphical parameters. See gpar.

Value

None.

Examples

## Create a page
pageCreate(width = 6, height = 5, default.units = "inches")

## Add red horizontal guideline at y = 2.5 inches
pageGuideHorizontal(y = 2.5, linecolor = "red")
pageGuideShow  

Reshow guides drawn with pageCreate, pageGuideHorizontal, and pageGuideVertical

Description

Reshow guides drawn with pageCreate, pageGuideHorizontal, and pageGuideVertical

Usage

pageGuideShow()

Value

None.

See Also

pageCreate, pageGuideHorizontal, pageGuideVertical

Examples

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create a page
pageCreate(width = 3, height = 3, default.units = "inches")

## Add a page guide
pageGuideHorizontal(y = 0.5, default.units = "inches")

## Plot and place Hi-C plot
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  x = 0.5, y = 0.5, width = 2, height = 2,
  just = c("left", "top"),
  default.units = "inches"
)

## Hide page guides
pageGuideHide()

## Re-show page guides
pageGuideShow()

## Annotate genome label
```
pageGuideVertical

Draw a vertical guideline at a specified x-coordinate on a plotgardener page

Description

Draw a vertical guideline at a specified x-coordinate on a plotgardener page

Usage

pageGuideVertical(
  x,
  default.units = "inches",
  linecolor = "grey55",
  params = NULL,
  ...
)

Arguments

x
  A numeric or unit object specifying x-coordinate of guide.

default.units
  A string indicating the default units to use if x is only given as a numeric. Default value is default.units = "inches".

linecolor
  Character value indicating color of guideline. Default value is linecolor = "grey55".

params
  An optional pgParams object containing relevant function parameters.

...
  Additional grid graphical parameters. See gpar.

Value

None.

Examples

## Create a page
pageCreate(width = 6, height = 5, default.units = "inches")

## Add blue vertical guideline at x = 1.7 inches
pageGuideVertical(x = 1.7, linecolor = "blue")
pageLayoutCol

Generate column positions for a number of plot elements with a specified width and space between them

Description
Generate column positions for a number of plot elements with a specified width and space between them

Usage
pageLayoutCol(x, width, space, n, default.units = "inches")

Arguments
- x: A numeric or unit object specifying the starting column x-position.
- width: A numeric or unit object specifying the width of columns.
- space: A numeric or unit object specifying the space between columns.
- n: An integer specifying the number of elements to generate column positions for.
- default.units: A string indicating the default units to use if x, w, or s are only given as numerics. Default value is default.units = "inches"

Value
Returns a unit vector of page positions.

Examples
# Starting at 0.5 units, return a vector of positions for 3 objects that
# are 2 units in width with 0.1 units of space between them
pageLayoutCol(x = 0.5, width = 2, space = 0.1, n = 3,
               default.units = "inches")

pageLayoutRow

Generate row positions for a number of plot elements with a specified height and space between them

Description
Generate row positions for a number of plot elements with a specified height and space between them
Usage

```
pageLayoutRow(y, height, space, n, default.units = "inches")
```

Arguments

- `y` A numeric or unit object specifying the starting row y-position.
- `height` A numeric or unit object specifying the height of rows.
- `space` A numeric or unit object specifying the space between rows.
- `n` An integer specifying the number of elements to generate row positions for.
- `default.units` A string indicating the default units to use if `y`, `h`, or `s` are only given as numerics. Default value is `default.units = "inches"`.

Value

Returns a unit vector of page positions.

Examples

```r
# Starting at 0.5 units, return a vector of positions for 3 objects that
# are 2 units in height with 0.1 units of space between them
pageLayoutRow(y = 0.5, height = 2, space = 0.1, n = 3,
              default.units = "inches")
```

---

```r
pagePlotPlace

Place a plot that has been previously created but not drawn
```

---

Description

Place a plot that has been previously created but not drawn

Usage

```
pagePlotPlace(
  plot,
  x = NULL,
  y = NULL,
  width = NULL,
  height = NULL,
  just = c("left", "top"),
  default.units = "inches",
  draw = TRUE,
  params = NULL
)
```
Arguments

plot  Plot object to be placed, defined by the output of a plotgardener plotting function.

x  A numeric or unit object specifying plot x-location.

y  A numeric, unit object, or character containing a "b" combined with a numeric value specifying plot y-location. The character value will place the plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width  A numeric or unit object specifying plot width.

height  A numeric or unit object specifying plot height.

just  Justification of plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units  A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".

draw  A logical value indicating whether graphics output should be produced. Default value is draw = TRUE.

params  An optional pgParams object containing relevant function parameters.

Value

Function will update dimensions of an input plot and return an updated plot object.

Examples

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create, but do not plot, square Hi-C plot
hicPlot <- plotHicSquare(
    data = IMR90_HiC_10kb, resolution = 10000,
    zrange = c(0, 70),
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    draw = FALSE
)

## Create page
pageCreate(width = 3.75, height = 3.5, default.units = "inches")

## Place Hi-C plot on page
pagePlotPlace(
    plot = hicPlot,
    x = 0.25, y = 0.25, width = 3, height = 3,
    just = c("left", "top"),
    default.units = "inches", draw = TRUE
)```
## Annotate heatmap legend

```r
annoHeatmapLegend(
  plot = hicPlot,
  x = 3.4, y = 0.25, width = 0.12, height = 1.2,
  just = c("left", "top"), default.units = "inches"
)
```

## Hide page guides

```r
pageGuideHide()
```

---

### pagePlotRemove

Remove plotgardener plots and annotations

**Description**

Remove plotgardener plots and annotations

**Usage**

```r
pagePlotRemove(plot)
```

**Arguments**

- `plot` Plot object to be removed, defined by the output of a plotgardener plotting function.

**Value**

None.

**Examples**

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create page
pageCreate(width = 5.5, height = 4, default.units = "inches")

## Plot and place a square Hi-C plot
hicPlot <- plotHicSquare(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  x = 0.5, y = 0.5, width = 2.5, height = 2.5,
  just = c("left", "top"),
  default.units = "inches"
)
```
## Remove square Hi-C plot from page

```r
pagePlotRemove(plot = hicPlot)
```

---

**pgParams**

**pgParams: plotgardener parameters object**

### Description

Creates an object of class "pgParams" that can be used by plotgardener functions. pgParams can be used to set a set of parameters to be shared across multiple functions.

### Usage

```r
pgParams(assembly = "hg38", gene = NULL, geneBuffer = NULL, ...)
```

### Arguments

- **assembly**
  - String defining the genome build. Default value is `assembly = "hg38"`.

- **gene**
  - (optional) String naming a gene used to set the chrom, chromstart, and chromend arguments.

- **geneBuffer**
  - (optional) Integer base-pairs to extend the start and end of a gene defined by argument `gene`. Can be one integer or a vector of length 2, where the first integer will extend the start of the gene and the second integer will extend the end of the gene.

- **...**
  - This function will take any plotgardener function parameters and their values:
    - `alpha`
    - `altchrom`
    - `altchromend`
    - `altchromstart`
    - `archHeight`
    - `arrow`
    - `at`
    - `axis`
    - `axisLine`
    - `baseline`
    - `baseline.color`
    - `baseline.lwd`
    - `bg`
    - `binCap`
    - `binSize`
    - `border`
    - `boxHeight`
• boxWidth
• breaks
• BSgenome
• cex
• check.overlap
• chrom
• chromend
• chromstart
• clip
• collapse
• colorbyStrand
• colorTrans
• column
• commas
• curvature
• data
• default.units
• digits
• display.column
• draw
• extend
• file
• fill
• flip
• fontcolor
• fontsize
• geneBackground
• geneHighlights
• gene.id.column
• geneOrder
• Genome
• half
• height
• id
• id.lengths
• image
• interpolate
• just
• label
• labels
• leadSNP
• legend
• length
• limitLabel
• linecolor
• lineend
• linejoin
• lty
• lwd
• main
• margin
• matrix
• negData
• norm
• OrgDb
• orientation
• palette
• pch
• plot
• quiet
• r
• range
• resolution
• res_scale
• rot
• scale
• scientific
• scipen
• sequence
• shift
• showBands
• showGuides
• sigCol
• sigLine
• sigVal
• spaceHeight
• spaceWidth
• strand
• strandLabels
• strandSplit
• stroke
• style
• tcl
• ticks
Details

pgParams generates arguments from exported plotgardener functions at loading time of the package. Arguments defined in a pgParams object can be passed into the params argument of plotgardener functions. params arguments can be overridden from within plotgardener functions.

pgParams also provides an alternative region definition mechanism. Given a gene name and genome assembly, pgParams returns the appropriate "chrom", "chromstart", and "chromend" with a default buffer of (gene length) / 2 added to the ends of the gene coordinates. The buffer amount can be set manually with the geneBuffer parameter. Buffer extending beyond the length of the chromosome will be trimmed.

Value

Returns an object of class pgParams containing plotgardener function arguments.

Examples

```r
## Load hg19 genomic annotation packages
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
library("org.Hs.eg.db")

## Define parameters
p1 <- pgParams(gene = "IL1B", assembly = "hg19")

## Optionally add more parameters
p2 <- pgParams(fontsize = 10, assembly = "hg19")

## Combine parameters and pass them to a plotgardener function
plotGenes(params = c(p1, p2))
```
**plotCircle**

Plot a circle within a plotgardener layout

**Description**

Plot a circle within a plotgardener layout

**Usage**

```r
plotCircle(
  x, y, r,
  default.units = "inches",
  linecolor = "black",
  lwd = 1,
  lty = 1,
  fill = NA,
  alpha = 1,
  params = NULL,
  ...
)
```

**Arguments**

- `x` A numeric vector or unit object specifying circle x-locations relative to center.
- `y` A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying circle y-locations relative to center. The character vector will place circle y-locations relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
- `r` A numeric vector or unit object specifying radii.
- `default.units` A string indicating the default units to use if `r`, `x`, or `y` are only given as numerics or numeric vectors. Default value is `default.units = "inches"`. 
- `linecolor` A character value specifying circle line color. Default value is `linecolor = "black"`. 
- `lwd` A numeric specifying circle line width. Default value is `lwd = 1`. 
- `lty` A numeric specifying circle line type. Default value is `lty = 1`. 
- `fill` A character value specifying circle fill color. Default value is `fill = NA`. 
- `alpha` Numeric value specifying color transparency. Default value is `alpha = 1`. 
- `params` An optional `pgParams` object containing relevant function parameters.
- `...` Additional grid graphical parameters. See `gpar`. 

**Value**

Returns a `circle` object containing relevant placement and `grob` information.
plotgardener

See Also

grid.circle

Examples

```r
## Create a page
pageCreate(width = 2, height = 2, default.units = "inches")

## Plot two circles, one at a time
plotCircle(
  x = 0.6, y = 0.5, r = 0.1, fill = "black",
  default.units = "inches"
)
plotCircle(
  x = 1.4, y = 0.5, r = 0.1, fill = "black",
  default.units = "inches"
)

## Plot a vector of circles
xVals <- 1 + (0.5 * cos(seq(0, pi, pi / 8)))
yVals <- 1 + (0.5 * sin(seq(0, pi, pi / 8)))
plotCircle(x = xVals, y = yVals, r = 0.05, default.units = "inches")

## Hide page guides
pageGuideHide()
```

plotgardener

plotgardener: Coordinate-based Genomic Visualization Package for R

Description

plotgardener is a coordinate-based genomic visualization package for R. It grants users the ability to programatically produce complex, multi-paneled figures. Tailored for genomics, plotgardener allows users to visualize large complex genomic datasets and provides exquisite control over how plots are placed and arranged on a page.

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plotGenes

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• Michael Love <milove@email.unc.edu> [contributor]

See Also

Useful links:

• https://phanstiellab.github.io/plotgardener
• https://github.com/PhanstielLab/plotgardener

plotGenes

Plot a gene track for a specified genomic region

Description

Plot a gene track for a specified genomic region

Usage

plotGenes(
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
  fontsize = 8,
  fontcolor = c("#669fd9", "#abcc8e"),
  fill = c("#669fd9", "#abcc8e"),
  geneOrder = NULL,
  geneHighlights = NULL,
  geneBackground = "grey",
  strandLabels = TRUE,
  stroke = 0.1,
  bg = NA,
  x = NULL,
  y = NULL,
  width = NULL,
  height = unit(0.6, "inches"),
  just = c("left", "top"),
  default.units = "inches",
  draw = TRUE,
  params = NULL
)

### Arguments

- **chrom**
  Chromosome of region to be plotted, as a string.

- **chromstart**
  Integer start position on chromosome to be plotted.

- **chromend**
  Integer end position on chromosome to be plotted.

- **assembly**
  Default genome assembly as a string or a `assembly` object. Default value is `assembly = "hg38"`.

- **fontsize**
  A numeric specifying text fontsize in points. Default value is `fontsize = 8`.

- **fontcolor**
  A character value or vector of length 2 indicating the fontcolors for the plus strand and minus strand gene labels. The first value will color the plus strand gene labels and the second value will color the minus strand gene labels. Default value is `fontcolor = c("#669fd9", "#abcc8e")`.

- **fill**
  A character value or vector of length 2 indicating the strand fill colors for the plus strand and minus strand plot elements. The first value will color the plus strand plot elements and the second label will color the minus strand plot elements. Default value is `fill = c("#669fd9", "#abcc8e")`.

- **geneOrder**
  An ordered character vector of gene names to prioritize when labeling genes.

- **geneHighlights**
  A two-column dataframe with a column named "gene" containing gene names as strings to highlight and a named column "color" containing corresponding highlight colors.

- **geneBackground**
  If `geneHighlights` is given, a character value indicating the color for genes that are not highlighted.

- **strandLabels**
  A logical value indicating whether to include + and - strand labels to the left of the gene track.

- **stroke**
  A numeric value indicating the stroke width for gene body outlines. Default value is `stroke = 0.1`.

- **bg**
  Character value indicating background color. Default value is `bg = NA`.

- **x**
  A numeric or unit object specifying genes plot x-location.

- **y**
  A numeric, unit object, or character containing a "b" combined with a numeric value specifying genes plot y-location. The character value will place the genes plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

- **width**
  A numeric or unit object specifying genes plot width.

- **height**
  A numeric or unit object specifying genes plot height.

- **just**
  Justification of genes plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is `just = c("left", "top")`.

- **default.units**
  A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is `default.units = "inches"`.

- **draw**
  A logical value indicating whether graphics output should be produced. Default value is `draw = TRUE`.

- **params**
  An optional `pgParams` object containing relevant function parameters.
Details

A gene track can be placed on a page by providing plot placement parameters:

```r
plotGenes(chrom, chromstart = NULL, chromend = NULL,
          x, y, width, height, just = c("left", "top"),
          default.units = "inches")
```

This function can be used to quickly plot an unannotated gene track by ignoring plot placement parameters:

```r
plotGenes(chrom, chromstart = NULL, chromend = NULL)
```

Genomic annotation information is acquired through TxDb and OrgDb-class packages, as determined through the assembly parameter. To avoid overcrowding of gene name labels, plotted gene labels are by default prioritized according to citation counts.

Value

Returns a genes object containing relevant genomic region, placement, and grob information.

See Also

assembly, genomes, defaultPackages

Examples

```r
## Load hg19 genomic annotation packages
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
library("org.Hs.eg.db")

## Set genomic coordinates
paramsSmall <- pgParams(
  chrom = "chr8",
  chromstart = 1, chromend = 3000000,
  assembly = "hg19", width = 7
)
paramsBig <- pgParams(
  chrom = "chr8",
  chromstart = 1, chromend = 146364022,
  assembly = "hg19", width = 7
)

## Set colors
cols <- c("#41B6C4", "#225EA8")

## Create page
pageCreate(width = 7.5, height = 3.5, default.units = "inches")

## Plot genes big
genesPlotBig <- plotGenes(
  params = paramsBig, fill = cols,
  fontcolor = cols,
  )
```
### plotGenomeLabel

Plot genomic coordinates along the x or y-axis of a plotgardener plot

#### Description

Plot genomic coordinates along the x or y-axis of a plotgardener plot

#### Usage

```r
plotGenomeLabel(
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
  fontsize = 10,
  fontcolor = "black",
  linecolor = "black",
  x = 0.25, y = 0.25, height = 0.75,
  just = c("left", "top"),
  default.units = "inches"
)
```

```r
## Annotate genome label
annoGenomeLabel(
  plot = genesPlot, x = 0.25, y = 1.0,
  scale = "Mb", just = c("left", "top")
)
```

```r
## Plot genes small
genesPlot <- plotGenes(
  params = paramssmall,
  geneHighlights = data.frame(
    "gene" = c("DLGAP2"),
    "color" = c("#225EA8")
  ),
  geneBackground = "grey",
  x = 0.25, y = 2.25, height = 0.75,
  just = c("left", "top"), default.units = "inches"
)
```

```r
## Annotate genome label
annoGenomeLabel(
  plot = genesPlot, x = 0.25, y = 3.0, scale = "Mb",
  just = c("left", "top")
)
```

```r
## Hide page guides
pageGuideHide()
```
plotGenomeLabel

margin = unit(1, "mm"),
scale = "bp",
comas = TRUE,
sequence = TRUE,
boxWidth = 0.5,
axis = "x",
at = NULL,
tcl = 0.5,
x,
y,
length,
just = c("left", "top"),
default.units = "inches",
params = NULL,
...
)

Arguments

chrom   Chromosome of genome label, as a string, or a character vector of chromosomes for a whole genome Manhattan plot.
chromstart   Integer start of genome label.
chromend   Integer end of genome label.
assembly   Default genome assembly as a string or a assembly object.
fontsize   A numeric specifying text fontsize in points. Default value is fontsize = 10.
fontcolor   A character value indicating the color for text. Default value is fontcolor = "black".
linecolor   A character value indicating the color of the genome label axis. Default value is linecolor = "black".
margin   A numeric or unit vector specifying space between axis and coordinate labels. Default value is margin = unit(1, "mm"),
scale   A character value indicating the scale of the coordinates along the genome label. Default value is scale = "bp". Options are:
  • "bp": base pairs.
  • "Kb": kilobase pairs. 1 kilobase pair is equal to 1000 base pairs.
  • "Mb": megabase pairs. 1 megabase pair is equal to 1000000 base pairs.
comas   A logical value indicating whether to include commas in start and stop labels. Default value is commas = TRUE.
sequence   A logical value indicating whether to include sequence information above the label of an x-axis (only at appropriate resolutions).
boxWidth   A numeric value indicating the width of the boxes representing sequence information at appropriate resolutions. Default value is boxWidth = 0.5.
axis   A character value indicating along which axis to add genome label. Sequence information will not be displayed along a y-axis. Default value is axis = "x". Options are:
• "x": Genome label will be plotted along the x-axis.
• "y": Genome label will be plotted along the y-axis. This is typically used for a square Hi-C plot made with plotHicSquare.

at          A numeric vector of x-value locations for tick marks.
tcl          A numeric specifying the length of tickmarks as a fraction of text height. Default value is tcl = 0.5.
x            A numeric or unit object specifying genome label x-location.
y            A numeric, unit object, or character containing a "b" combined with a numeric value specifying genome label y-location. The character value will place the genome label y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
length       A numeric or unit object specifying length of genome label axis.
just         Justification of genome label relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
default.units A string indicating the default units to use if x, y, or length are only given as numerics. Default value is default.units = "inches".
params       An optional pgParams object containing relevant function parameters.
...          Additional grid graphical parameters or digit specifications. See gpar and formatC.

Value

Returns a genomeLabel object containing relevant genomic region, placement, and grob information.

Examples

## Load hg19 genomic annotation packages
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
library("org.Hs.eg.db")
library("BSgenome.Hsapiens.UCSC.hg19")

## Create page
pageCreate(width = 5, height = 3, default.units = "inches")

## Plot and place gene track on page
genesPlot <- plotGenes(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19", fill = c("grey", "grey"),
  fontcolor = c("grey", "grey"),
  x = 0.5, y = 0.25, width = 4, height = 1,
  just = c("left", "top"),
  default.units = "inches"
)
## Plot x-axis genome labels at different scales

```r
plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  scale = "Mb",
  x = 0.5, y = 1.25, length = 4, just = c("left", "top"),
  default.units = "inches"
)
```

```r
plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  scale = "Kb",
  x = 0.5, y = 1.5, length = 4, just = c("left", "top"),
  default.units = "inches"
)
```

```r
plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  scale = "bp",
  x = 0.5, y = 1.75, length = 4, just = c("left", "top"),
  default.units = "inches"
)
```

## Plot a different genomic label region, zooming in enough
## to see base pairs

```r
plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 1000050,
  assembly = "hg19",
  x = 0.25, y = 2.2, length = 4.5
)
```

```r
plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 1000020,
  assembly = "hg19",
  x = 0, y = 2.6, length = 5
)
```

## Hide page guides

```r
pageGuideHide()
```

---

**Description**

Plot a ggplot2 plot, gtable, or grob object in a plotgardener layout
Usage

plotGG(
  plot,
  x,
  y,
  width,
  height,
  just = c("left", "top"),
  default.units = "inches",
  params = NULL
)

Arguments

plot  ggplot, gtable, or grob object.
x     A numeric or unit object specifying ggplot x-location.
y     A numeric, unit object, or character containing a "b" combined with a numeric value specifying ggplot y-location. The character value will place the ggplot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
width A numeric or unit object specifying ggplot width.
height A numeric or unit object specifying ggplot height.
just  Justification of ggplot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
params An optional pgParams object containing relevant function parameters.

Value

Returns a pg_gg object containing relevant placement and grob information.

See Also

ggplot

Examples

## Create a plot using ggplot2
library(ggplot2)
p <- ggplot(mtcars) +
  geom_point(aes(mpg, disp))

## Create a page
pageCreate(width = 4, height = 4, default.units = "inches")
## Place ggplot in page
plotGG(
    plot = p, x = 0.5, y = 0.5, width = 3, height = 3,
    just = c("left", "top"), default.units = "inches"
)

## Add title
plotText(
    label = "mtcars", fontsize = 14, fontface = "bold",
    x = 1, y = 0.35
)

## Hide page guides
pageGuideHide()

---

**plotHicRectangle**  
*Plot a triangular Hi-C interaction matrix in a rectangular format*

### Description
Plot a triangular Hi-C interaction matrix in a rectangular format

### Usage
```r
plotHicRectangle(
    data,
    resolution = "auto",
    zrange = NULL,
    norm = "KR",
    matrix = "observed",
    chrom,
    chromstart = NULL,
    chromend = NULL,
    assembly = "hg38",
    palette = colorRampPalette(brewer.pal(n = 9, "YlGnBu")),
    colorTrans = "linear",
    flip = FALSE,
    bg = NA,
    x = NULL,
    y = NULL,
    width = NULL,
    height = NULL,
    just = c("left", "top"),
    default.units = "inches",
    draw = TRUE,
    params = NULL,
    quiet = FALSE
)
```
Arguments

data  Path to .hic file as a string or a 3-column dataframe of interaction counts in sparse upper triangular format.

resolution  A numeric specifying the width in basepairs of each pixel. For hic files, "auto" will attempt to choose a resolution based on the size of the region. For dataframes, "auto" will attempt to detect the resolution the dataframe contains.

zrange  A numeric vector of length 2 specifying the range of interaction scores to plot, where extreme values will be set to the max or min.

norm  Character value specifying hic data normalization method, if giving .hic file. This value must be found in the .hic file. Default value is norm = "KR".

matrix  Character value indicating the type of matrix to output. Default value is matrix = "observed". Options are:
- "observed": Observed counts.
- "oe": Observed/expected counts.
- "log2oe": Log2 transformed observed/expected counts.

chrom  Chromosome of region to be plotted, as a string.

chromstart  Integer start position on chromosome to be plotted.

chromend  Integer end position on chromosome to be plotted.

assembly  Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".

palette  A function describing the color palette to use for representing scale of interaction scores. Default value is palette = colorRampPalette(brewer.pal(n = 9, "YlGnBu")).

colorTrans  A string specifying how to scale Hi-C colors. Options are "linear", "log", "log2", or "log10". Default value is colorTrans = "linear".

flip  A logical indicating whether to flip the orientation of the Hi-C matrix over the x-axis. Default value is flip = FALSE.

bg  Character value indicating background color. Default value is bg = NA.

x  A numeric or unit object specifying rectangle Hi-C plot x-location.

y  A numeric, unit object, or character containing a "b" combined with a numeric value specifying rectangle Hi-C plot y-location. The character value will place the rectangle Hi-C plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width  A numeric or unit object specifying the width of the Hi-C plot rectangle.

height  A numeric or unit object specifying the height of the Hi-C plot rectangle.

just  Justification of rectangle Hi-C plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units  A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
draw A logical value indicating whether graphics output should be produced. Default value is `draw = TRUE`.

params An optional `pgParams` object containing relevant function parameters.

quiet A logical indicating whether or not to print messages.

Details

This function is similar to `plotHicTriangle` but will fill in additional pixels around the triangular portion of the plot to make a rectangle. The x-axis represents the genomic coordinates and the y-axis corresponds to distance in Hi-C bins.

A rectangle Hi-C plot can be placed on a plotgardener coordinate page by providing plot placement parameters:

```r
plotHicRectangle(data, chrom,
  chromstart = NULL, chromend = NULL,
  x, y, width, height, just = c("left", "top"),
  default.units = "inches")
```

This function can also be used to quickly plot an unannotated rectangle Hi-C plot by ignoring plot placement parameters:

```r
plotHicRectangle(data, chrom,
  chromstart = NULL, chromend = NULL)
```

Value

Returns a `hicRectangle` object containing relevant genomic region, Hi-C data, placement, and grob information.

See Also

`readHic`, `plotHicTriangle`

Examples

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create a page
pageCreate(width = 6, height = 3.5, default.units = "inches")

## Plot and place rectangle Hi-C plot
hicPlot <- plotHicRectangle(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28950000, chromend = 29800000,
  assembly = "hg19",
  x = 0.5, y = 0.5, width = 5, height = 2.5,
  just = c("left", "top"),
  default.units = "inches")
```
plotHicSquare

Plot a Hi-C interaction matrix in a square format

Description

Plot a Hi-C interaction matrix in a square format

Usage

plotHicSquare(
  data,
  resolution = "auto",
  zrange = NULL,
  norm = "KR",
  matrix = "observed",
  chrom,
  chromstart = NULL,
  chromend = NULL,
  altchrom = NULL,
  altchromstart = NULL,
  altchromend = NULL,
  assembly = "hg38",
  palette = colorRampPalette(brewer.pal(n = 9, "YlGnBu")),
  colorTrans = "linear",
  half = "both",
  yaxisDir = "increase",
  bg = NA,
  x = NULL,
  just = c("left", "top"),
  default.units = "inches"
)

## Annotate x-axis genome label
annoGenomeLabel(
  plot = hicPlot, scale = "Kb", x = 0.5, y = 3.03,
  just = c("left", "top")
)

## Annotate heatmap legend
annoHeatmapLegend(
  plot = hicPlot, x = 5.6, y = 0.5,
  width = 0.13, height = 1.5,
  just = c("left", "top")
)

## Hide page guides
pageGuideHide()
plotHicSquare

y = NULL,
width = NULL,
height = NULL,
just = c("left", "top"),
default.units = "inches",
draw = TRUE,
params = NULL,
quiet = FALSE
)

Arguments

data Path to .hic file as a string or a 3-column dataframe of interaction counts in sparse upper triangular format.
resolution A numeric specifying the width in basepairs of each pixel. For hic files, "auto" will attempt to choose a resolution based on the size of the region. For dataframes, "auto" will attempt to detect the resolution the dataframe contains.
zrange A numeric vector of length 2 specifying the range of interaction scores to plot, where extreme values will be set to the max or min.
norm Character value specifying hic data normalization method, if giving .hic file. This value must be found in the .hic file. Default value is norm = "KR".
matrix Character value indicating the type of matrix to output. Default value is matrix = "observed". Options are:
  • "observed": Observed counts.
  • "oe": Observed/expected counts.
  • "log2oe": Log2 transformed observed/expected counts.
chrom Chromosome of region to be plotted, as a string.
chromstart Integer start position on chromosome to be plotted.
chromend Integer end position on chromosome to be plotted.
altn chrom Alternate chromosome for off-diagonal plotting or interchromosomal plotting, as a string.
altn chromstart Alternate chromosome integer start position for off-diagonal plotting or interchromosomal plotting.
altn chromend Alternate chromosome integer end position for off-diagonal plotting or interchromosomal plotting.
assembly Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".
palette A function describing the color palette to use for representing scale of interaction scores. Default value is palette = colorRampPalette(brewer.pal(n = 9, "YlGnBu")).
colorTrans A string specifying how to scale Hi-C colors. Options are "linear", "log", "log2", or "log10". Default value is colorTrans = "linear".
plotHicSquare

half  A character value indicating which diagonal regions to plot. For intrachromosomal plotting, options are "both", "top", or "bottom". For off-diagonal or interchromosomal plotting, options are "top" or "bottom". Default value is half = "both".
  • "both": Both diagonal halves.
  • "top": Half above the diagonal.
  • "bottom": Half below the diagonal.

yaxisDir  A string specifying the genomic direction of the y-axis. Options are "increase", where the bottom left corner of the Hi-C map indicates the origin, and "decrease", where the top left corner of the Hi-C map indicates the origin. This will change the direction of the diagonal for intrachromosomal maps. Default value is yaxisDir = "increase".

bg  Character value indicating background color. Default value is bg = NA.

x  A numeric or unit object specifying square Hi-C plot x-location.

y  A numeric, unit object, or character containing a "b" combined with a numeric value specifying square Hi-C plot y-location. The character value will place the square Hi-C plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width  A numeric or unit object specifying square Hi-C plot width.

height  A numeric or unit object specifying square Hi-C plot height.

just  Justification of square Hi-C plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units  A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".

draw  A logical value indicating whether graphics output should be produced. Default value is draw = TRUE.

params  An optional pgParams object containing relevant function parameters.

quiet  A logical indicating whether or not to print messages.

Details

A square Hi-C plot can be placed on a plotgardener coordinate page by providing plot placement parameters:

plotHicSquare(data, chrom, 
  chromstart = NULL, chromend = NULL, 
  x, y, width, height, just = c("left", "top"), 
  default.units = "inches")

This function can be used to quickly plot an unannotated square Hi-C plot by ignoring plot placement parameters:

plotHicSquare(data, chrom, 
  chromstart = NULL, chromend = NULL)
Value

Returns a hicSquare object containing relevant genomic region, Hi-C data, placement, and grob information.

See Also

readHic

Examples

```r
## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create a page
pageCreate(width = 3, height = 3, default.units = "inches")

## Plot and place Hi-C plot
hicPlot <- plotHicSquare(
data = IMR90_HiC_10kb, resolution = 10000,
   zrange = c(0, 70),
   chrom = "chr21",
   chromstart = 28000000, chromend = 30300000,
   assembly = "hg19",
   x = 0.5, y = 0.5, width = 2, height = 2,
   just = c("left", "top"),
   default.units = "inches", bg = "black"
)

## Annotate heatmap legend
annoHeatmapLegend(
   plot = hicPlot, x = 2.6, y = 0.5,
   width = 0.12, height = 1.2,
   just = c("left", "top"), default.units = "inches"
)

## Annotate x-axis and y-axis genome labels
annoGenomeLabel(
   plot = hicPlot, scale = "Mb", axis = "x",
   x = 0.5, y = 2.53, just = c("left", "top")
)
annoGenomeLabel(
   plot = hicPlot, scale = "Mb", axis = "y",
   x = 0.47, y = 0.5, just = c("right", "top")
)

## Hide page guides
pageGuideHide()
```
**plotHicTriangle**

*Plot a Hi-C interaction matrix in a triangular format*

---

**Description**

Plot a Hi-C interaction matrix in a triangular format

**Usage**

```r
plotHicTriangle(
  data, 
  resolution = "auto", 
  zrange = NULL, 
  norm = "KR", 
  matrix = "observed", 
  chrom, 
  chromstart = NULL, 
  chromend = NULL, 
  assembly = "hg38", 
  palette = colorRampPalette(brewer.pal(n = 9, "YlGnBu")), 
  colorTrans = "linear", 
  flip = FALSE, 
  bg = NA, 
  x = NULL, 
  y = NULL, 
  width = NULL, 
  height = NULL, 
  just = c("left", "top"), 
  default.units = "inches", 
  draw = TRUE, 
  params = NULL, 
  quiet = FALSE
)
```

**Arguments**

- `data`: Path to .hic file as a string or a 3-column dataframe of interaction counts in sparse upper triangular format.
- `resolution`: A numeric specifying the width in basepairs of each pixel. For hic files, "auto" will attempt to choose a resolution based on the size of the region. For dataframes, "auto" will attempt to detect the resolution the dataframe contains.
- `zrange`: A numeric vector of length 2 specifying the range of interaction scores to plot, where extreme values will be set to the max or min.
- `norm`: Character value specifying hic data normalization method, if giving .hic file. This value must be found in the .hic file. Default value is `norm = "KR"`. 

---
matrix Character value indicating the type of matrix to output. Default value is matrix = "observed". Options are:

- "observed": Observed counts.
- "oe": Observed/expected counts.
- "log2oe": Log2 transformed observed/expected counts.

chrom Chromosome of region to be plotted, as a string.

chromstart Integer start position on chromosome to be plotted.

chromend Integer end position on chromosome to be plotted.

assembly Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".

palette A function describing the color palette to use for representing scale of interaction scores. Default value is palette = colorRampPalette(brewer.pal(n = 9, "YlGnBu")).

colorTrans A string specifying how to scale Hi-C colors. Options are "linear", "log", "log2", or "log10". Default value is colorTrans = "linear".

flip A logical indicating whether to flip the orientation of the Hi-C matrix over the x-axis. Default value is flip = FALSE.

bg Character value indicating background color. Default value is bg = NA.

x A numeric or unit object specifying triangle Hi-C plot x-location.

y A numeric, unit object, or character containing a "b" combined with a numeric value specifying triangle Hi-C plot y-location. The character value will place the triangle Hi-C plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width A numeric or unit object specifying the bottom width of the Hi-C plot triangle.

height A numeric or unit object specifying the height of the Hi-C plot triangle.

just Justification of triangle Hi-C plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".

draw A logical value indicating whether graphics output should be produced. Default value is draw = TRUE.

params An optional pgParams object containing relevant function parameters.

quiet A logical indicating whether or not to print messages.

Details

In this orientation, the x-axis represents the genomic coordinates and the y-axis corresponds to distance in Hi-C bins.

A triangle Hi-C plot can be placed on a plotgardener coordinate page by providing plot placement parameters:
plotHicTriangle[data, chrom,
              chromstart = NULL, chromend = NULL,
              x, y, width, height, just = c("left", "top"),
              default.units = "inches")

This function can also be used to quickly plot an unannotated triangle Hi-C plot by ignoring plot placement parameters:

plotHicTriangle(data, chrom,
                chromstart = NULL, chromend = NULL)

If height is < 0.5 * width, the top of the triangle will be cropped to the given height.

Value

Returns a hicTriangle object containing relevant genomic region, Hi-C data, placement, and grob information.

See Also

readHic

Examples

## Load Hi-C data
library(plotgardenerData)
data("IMR90_HiC_10kb")

## Create a page
pageCreate(width = 4, height = 2.5, default.units = "inches")

## Plot and place triangle Hi-C plot
hicPlot <- plotHicTriangle(
  data = IMR90_HiC_10kb, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  x = 2, y = 0.5, width = 3, height = 1.5,
  just = "top", default.units = "inches"
)

## Annotate x-axis genome label
annoGenomeLabel(
  plot = hicPlot, scale = "Mb", x = 0.5, y = 2.03,
  just = c("left", "top")
)

## Annotate heatmap legend
annoHeatmapLegend(
  plot = hicPlot, x = 3.5, y = 0.5,
  width = 0.13, height = 1.2,
just = c("right", "top")

## Hide page guides
draw = TRUE
params = NULL

plotIdeogram

Plot a chromosome ideogram with or without cytobands

Description

Plot a chromosome ideogram with or without cytobands

Usage

plotIdeogram(
  chrom,
  assembly = "hg38",
  data = NULL,
  orientation = "h",
  flip = FALSE,
  showBands = TRUE,
  fill = NULL,
  x = NULL,
  y = NULL,
  width = NULL,
  height = NULL,
  just = c("left", "top"),
  default.units = "inches",
  draw = TRUE,
  params = NULL
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chrom</td>
<td>Chromosome to be plotted, as a string.</td>
</tr>
<tr>
<td>assembly</td>
<td>Default genome assembly as a string or a assembly object. Default value is</td>
</tr>
<tr>
<td></td>
<td>assembly = &quot;hg38&quot;.</td>
</tr>
<tr>
<td>data</td>
<td>Custom cytoband data, as a dataframe with the following columns: &quot;seqnames&quot;,</td>
</tr>
<tr>
<td></td>
<td>&quot;start&quot;, &quot;end&quot;, &quot;width&quot;, &quot;strand&quot;, &quot;name&quot;, &quot;gieStain&quot;.</td>
</tr>
<tr>
<td>orientation</td>
<td>Character value indicating the orientation of the ideogram. Default value is</td>
</tr>
<tr>
<td></td>
<td>orientation = &quot;h&quot;. Options are:</td>
</tr>
<tr>
<td></td>
<td>• &quot;v&quot;: Vertical ideogram orientation.</td>
</tr>
<tr>
<td></td>
<td>• &quot;h&quot;: Horizontal ideogram orientation.</td>
</tr>
</tbody>
</table>
plotIdeogram

flip Logical value indicating whether to reverse the start and end positions of the ideogram. If flip = FALSE (default), the ideogram starts at the top/left and ends at the bottom/right. If flip = TRUE, the start and end positions are reversed, meaning the ideogram starts at the bottom/right and ends at the top/left.

showBands Logical value indicating whether to draw colored cytobands within ideogram. Default value is showBands = TRUE.

fill (optional) A vector specifying alternate colors for cytoband stains. To change specific gieStain values (i.e. gneg, gpos, etc.) to specific colors, this vector can be named. This vector must have the same number of colors as there are gieStain values for each genome assembly.

x A numeric or unit object specifying ideogram x-location.

y A numeric, unit object, or character containing a "b" combined with a numeric value specifying ideogram y-location. The character value will place the ideogram y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width A numeric or unit object specifying ideogram width.

height A numeric or unit object specifying ideogram height.

just Justification of ideogram relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".

draw A logical value indicating whether graphics output should be produced. Default value is draw = TRUE.

params An optional pgParams object containing relevant function parameters.

Details

An ideogram can be placed on a plotgardener coordinate page by providing plot placement parameters:

plotIdeogram(chrom, x, y, width, height, just = c("left", "top"), default.units = "inches")

This function can also be used to quickly plot an unannotated ideogram by ignoring plot placement parameters:

plotIdeogram(chrom)

If no data is provided, Giemsa stain band data will first try to fetch UCSC with AnnotationHub. The results are cached for faster access, but these cached items can be deleted. If no internet connection is available and AnnotationHub has not previously cached the data, custom Giemsa stain band data can be loaded with the 'data' parameter.
Value

Returns a ideogram object containing relevant genomic region, placement, and grob information.

See Also

AnnotationHub

Examples

```r
## Load Giemsa stain band information and genomic
## annotation data for hg19 genome assembly
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(AnnotationHub)

## Create page
pageCreate(width = 4.5, height = 1, default.units = "inches")

## Plot and place ideogram
ideogramPlot <- plotIdeogram(
  chrom = "chr2", assembly = "hg19",
  x = 0.25, y = 0.25, width = 4, height = 0.3,
  just = c("left", "top"),
  default.units = "inches"
)

## Plot text
plotText(
  label = "Chromosome 2", fontcolor = "dark grey",
  x = 4.25, y = 0.65, just = "right"
)

## Hide page guides
pageGuideHide()
```

---

`plotLegend`  
*Plot a legend*

Description

Plot a legend

Usage

```r
plotLegend(
  legend,
  fill = NULL,
  pch = NULL,
  lty = NULL,
  orientation = "v",
```
Arguments

legend A character or expression vector to appear in the legend.
fill If specified, this argument will produce boxes filled with the specified colors to appear beside the legend text.
pch The plotting symbols appearing in the legend, as a numeric vector.
lty The line types for lines appearing in the legend.
orientation A string specifying legend orientation. Default value is orientation = "v". Options are:
  • "v": Vertical legend orientation.
  • "h": Horizontal legend orientation.
title A character value giving a title to be placed at the top of the legend.
fontsize A numeric specifying text fontsize in points. Default value is fontsize = 10.
border Logical value indicating whether to add a border around heatmap legend. Default value is border = TRUE.
bg Character value indicating background color. Default value is bg = NA.
x A numeric or unit object specifying legend x-location.
y A numeric, unit object, or character containing a "b" combined with a numeric value specifying legend y-location. The character value will place the legend y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
width A numeric or unit object specifying legend width.
height A numeric or unit object specifying legend height.
just Justification of legend relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
plotLegend

- **draw**: A logical value indicating whether graphics output should be produced. Default value is `draw = TRUE`.
- **params**: An optional `pgParams` object containing relevant function parameters.
- **...**: Additional grid graphical parameters. See `gpar`.

**Value**

Returns a legend object containing relevant placement and `grob` information.

**Examples**

```r
## Load BED data
library(plotgardenerData)
data("IMR90_ChIP_CTCF_reads")

## Create page
pageCreate(width = 7.5, height = 4, default.units = "inches")

## Plot a pileup plot, coloring elements by strand
pileupPlot <- plotRanges(
data = IMR90_ChIP_CTCF_reads, chrom = "chr21",
chromstart = 29072500, chromend = 29075000,
assembly = "hg19",
fill = colorby("strand", palette =
  colorRampPalette(c("steel blue", "light salmon"))),
x = 0.5, y = 3.5, width = 6.5, height = 3.5,
just = c("left", "bottom"),
default.units = "inches")

## Add a legend depicting strand colors
legendPlot <- plotLegend(
  legend = c("- strand", "+ strand"),
  fill = c("steel blue", "light salmon"),
  border = FALSE,
x = 5, y = 0.5, width = 1.5, height = 0.7,
just = c("left", "top"),
default.units = "inches")

## Annotate genome label
annoGenomeLabel(
  plot = pileupPlot, x = 0.5, y = 3.5,
  just = c("left", "top")
)

## Hide page guides
pageGuideHide()
```
Description

Plot a Manhattan plot

Usage

plotManhattan(
  data,
  sigVal = 5e-08,
  chrom = NULL,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
  fill = "black",
  pch = 19,
  cex = 0.25,
  leadSNP = NULL,
  sigLine = FALSE,
  sigCol = NULL,
  trans = "-log10",
  range = NULL,
  yscale_reverse = FALSE,
  space = 0.01,
  bg = NA,
  baseline = FALSE,
  baseline.color = "grey",
  baseline.lwd = 1,
  x = NULL,
  y = NULL,
  width = NULL,
  height = NULL,
  just = c("left", "top"),
  flip = FALSE,
  default.units = "inches",
  draw = TRUE,
  params = NULL,
  ...
)

Arguments

data Data to be plotted, as a character value specifying a file path of GWAS data, a dataframe, or a GRanges object. Each of these data types must have the following columns:
- "chrom": Chromosome names. This column must be a character.
- "pos": Chromosomal position. This column must be an integer or numeric.
- "p": p-value or similar measure. This column must be numeric. Values will be converted according to the trans parameter.
- "snp" (optional): SNP name or rsid. This column should be a character.

sigVal
A numeric specifying the significance level of p-values. Along with data p-values, this value will be converted according to the trans parameter. Default value is sigVal = 5e-08.

chrom
Chromosome of region to be plotted, as a string. If left NULL, all chromosomes found in data will be plotted.

chromstart
Integer start position on chromosome to be plotted.

chromend
Integer end position on chromosome to be plotted.

assembly
Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".

fill
A single character value, a vector, or a colorby object specifying fill colors of data points. For a Manhattan plot with multiple chromosomes, a vector of colors will be used to color points of different chromosomes. Default value is fill = "black".

pch
A numeric value or numeric vector specifying point symbols. If colorby object is supplied for fill, point symbols will be mapped to colorby values. Default value is pch = 19.

cex
A numeric indicating the amount by which points should be scaled relative to the default. Default value is cex = 0.25.

leadSNP
A list specifying the lead SNP in the desired region and any associated aesthetic features of the lead SNP data point and text label. The lead SNP should be specified as a character with the name slot "snp" in the list. Accepted lead SNP aesthetic features in the list include fill, pch, cex, fontcolor, and fontsize.

sigLine
Logical value indicating whether to draw a line at the significance level indicated with sigVal. Default value is sigLine = FALSE.

sigCol
Single character value specifying the color of significant data points.

trans
Character value specifying the transformation to apply to the "p" column plotted along the y-axis. For no transformation, set value to the empty character "". Default value is trans = "-log10".

range
A numeric vector of length 2 specifying the y-range of p-values to plot (c(min, max)).

yscale_reverse
Logical value indicating whether to reverse the y-scale and order points from max to min.

space
A numeric value indicating the space between each chromosome as a fraction of the width of the plot, if plotting multiple chromosomes. Default value is space = 0.01.

bg
Character value indicating background color. Default value is bg = NA.

baseline
Logical value indicating whether to include a baseline along the x-axis. Default value is baseline = FALSE.
plotManhattan

baseline.color Baseline color. Default value is baseline.color = "grey".
baseline.lwd Baseline line width. Default value is baseline.lwd = 1.
x A numeric or unit object specifying Manhattan plot x-location.
y A numeric, unit object, or character containing a "b" combined with a numeric value specifying Manhattan plot y-location. The character value will place the Manhattan plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
width A numeric or unit object specifying Manhattan plot width.
height A numeric or unit object specifying Manhattan plot height.
just Justification of Manhattan plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
flip Logical value indicating whether to reflect Manhattan plot over the x-axis. Default value is flip = FALSE.
default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
draw A logical value indicating whether graphics output should be produced. Default value is draw = TRUE.
params An optional pgParams object containing relevant function parameters.
... Additional grid graphical parameters. See gpar.

Details

A Manhattan plot can be placed on a plotgardener coordinate page by providing plot placement parameters:

plotManhattan(data,    
            chrom = NULL,    
            chromstart = NULL, chromend = NULL,    
            x, y, width, height, just = c("left", "top"),    
            default.units = "inches")

This function can also be used to quickly plot an unannotated Manhattan plot by ignoring plot placement parameters:

plotManhattan(data,    
            chrom = NULL,    
            chromstart = NULL, chromend = NULL)

Value

Returns a manhattan object containing relevant genomic region, placement, and grob information.
Examples

```r
## Load genomic assembly information
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
## Load GWAS data
library(plotgardenerData)
data("hg19_insulin_GWAS")

## Create a page
pageCreate(width = 7.5, height = 4.5, default.units = "inches")

## Plot all GWAS data
manhattanPlot <- plotManhattan(
data = hg19_insulin_GWAS, assembly = "hg19",
fill = c("grey", "#37a7db"),
sigLine = TRUE,
trans = "-log10",
col = "grey", lty = 2, range = c(0, 14),
x = 0.5, y = 0, width = 6.5, height = 2,
just = c("left", "top"),
default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(
plot = manhattanPlot, x = 0.5, y = 2, fontsize = 8,
just = c("left", "top"),
default.units = "inches"
)

plotText(
label = "Chromosome", fontsize = 8,
x = 3.75, y = 2.20, just = "center", default.units = "inches"
)

## Annotate y-axis
annoYaxis(
plot = manhattanPlot, at = c(0, 2, 4, 6, 8, 10, 12, 14),
axisLine = TRUE, fontsize = 8
)

## Plot y-axis label
plotText(
label = "-log10(p-value)", x = 0.15, y = 1, rot = 90,
fontsize = 8, fontface = "bold", just = "center",
default.units = "inches"
)

## Plot GWAS data zooming in on chromosome 11
## highlighting a lead SNP, and coloring by LD score
hg19_insulin_GWAS$LD <- as.numeric(hg19_insulin_GWAS$LD)
## Group LD column into LD ranges
hg19_insulin_GWAS <- as.data.frame(dplyr::group_by(hg19_insulin_GWAS,
LDgrp = cut(
```

```r
plotManhattan
```
hg19_insulin_GWAS$LD, c(0, 0.2, 0.4, 0.6, 0.8, 1))))

hg19_insulin_GWAS$LDgrp <- addNA(hg19_insulin_GWAS$LDgrp)
leadSNP_p <- min(hg19_insulin_GWAS[chrom == "chr11"], ]$p)
leadSNP <- hg19_insulin_GWAS[which(hg19_insulin_GWAS$p == leadSNP_p), ]$snp

chr11_manhattanPlot <- plotManhattan(
  data = hg19_insulin_GWAS, chrom = "chr11",
  chromstart = 60000000,
  chromend = 130000000,
  assembly = "hg19",
  fill = colorby("LDgrp",
    palette = colorRampPalette(c("#1f4297",
      "#37a7db", "green",
      "orange", "red", "grey" ))),
  trans = "-log10",
  sigLine = TRUE, col = "grey",
  lty = 2, range = c(0, 16),
  leadSNP = list(
    snp = leadSNP,
    pch = 18,
    cex = 0.75,
    fill = "#7ecdbb",
    fontsize = 8
  ),
  x = 0.5, y = 2.5, width = 6.5,
  height = 1.5,
  just = c("left", "top"),
  default.units = "inches"
)

## Plot legend for LD scores
plotLegend(
  legend = c("LD Ref Var",
    paste("0.4", ">", "r^2",
      "", ">=", "0.2"),
    paste("0.2", ">", "r^2",
      "", ">=", "0"),
    "no LD data" ),
  fill = c("#7ecdbb", "#37a7db", "#1f4297", "grey"), cex = 0.75,
  pch = c(18, 19, 19, 19), border = FALSE, x = 7, y = 2.5,
  width = 1.5, height = 0.6, just = c("right", "top"),
  default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(
  plot = chr11_manhattanPlot, x = 0.5, y = 4.01,
Plot multiple signal tracks in line with each other

Description

Plot multiple signal tracks in line with each other

Usage

plotMultiSignal(data, binSize = NA, binCap = TRUE, negData = FALSE, chrom, chromstart = NULL, chromend = NULL, assembly = "hg38", linecolor = "#37a7db", fill = NA, ymax = 1, range = NULL, scale = FALSE, label = NULL, bg = NA, baseline = TRUE, baseline.color = "grey", baseline.lwd = 1)
plotMultiSignal

orientation = "h",
x = NULL,
y = NULL,
width = NULL,
height = NULL,
just = c("left", "top"),
gapdistance = .2,
default.units = "inches",
draw = TRUE,
params = NULL, ...
)

Arguments

data List of data to be plotted as character values specifying multiple bigwig file
paths, dataframes in BED format, or GRanges objects with metadata column
score.
binSize A numeric specifying the length of each data bin in basepairs. Default value is
binSize = NA.
binCap A logical value indicating whether the function will limit the number of data
bins to 8,000. Default value is binCap = TRUE.
negData A logical value indicating whether any of the data has both positive and nega-
tive scores and the y-axis of each signal track should be split. Default value is
negData = FALSE.
chrom Chromosome of region to be plotted, as a string.
chromstart Integer start position on chromosome to be plotted.
chromend Integer end position on chromosome to be plotted.
assembly Default genome assembly as a string or a assembly object. Default value is
assembly = "hg38".
linelcolor A character value or vector of character values specifying the line color(s) out-
lining the signal tracks. Default value is linelcolor = "#37a7db".
fill A character value or vector specifying the fill color(s) of the signal tracks. De-
fault value is fill = NA.
ymax A numeric specifying the fraction of the max y-value to set as the height of each
plot. Default value is ymax = 1.
range A numeric vector of length 2 specifying the y-range of data to plot (c(min, max))
in each signal track. If range = NULL, an optimal range for all signal tracks will
be calculated.
scale A logical value indicating whether to include a data scale label in the top left
corner of each plot. Default value is scale = FALSE.
label An optional character vector to conveniently add text labels to signal tracks. If
scale = TRUE, the labels will be drawn in the top right of the signal tracks. Other-
wise, the label will be drawn in the top left of the plot. For more customizable
labels, use plotText.
bg Character value indicating background color. Default value is bg = NA.


**baseline** Logical value indicating whether to include a baseline along the x-axis. Default value is `baseline = TRUE`.

**baseline.color** Baseline color. Default value is `baseline.color = "grey"`.

**baseline.lwd** Baseline line width. Default value is `baseline.lwd = 1`.

**orientation** A string specifying signal track orientations. Default value is `orientation = "h"`. Options are:
- "v": Vertical signal track orientations, where signal tracks will be stacked from left to right.
- "h": Horizontal signal track orientations, where signal tracks will be stacked from top to bottom.

**x** A numeric vector or unit object specifying the overall multisignal x-location.

**y** A numeric, unit object, or character containing a "b" combined with a numeric value specifying overall multisignal plot y-location. The character value will place the multisignal plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

**width** A numeric or unit object specifying overall multisignal plot width.

**height** A numeric or unit object specifying overall multisignal plot height.

**just** Justification of overall multisignal plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is `just = c("left", "top")`.

**gapdistance** A numeric or unit object specifying space between plots. Default value is `gapdistance = 0.2`.

**default.units** A string indicating the default units to use if x or y are only given as numerics. Default value is `default.units = "inches"`.

**draw** A logical value indicating whether graphics output should be produced. Default value `draw = TRUE`.

**params** An optional `pgParams` object containing relevant function parameters.

**...** Additional grid graphical parameters. See `gpar`.

**Value**

Returns a list of `signal` objects containing relevant genomic region, placement, and `grob` information for each signal track.

**Examples**

```r
library("plotgardenerData")
data("GM12878_ChIP_CTCF_signal")
data("IMR90_ChIP_CTCF_signal")
data("GM12878_ChIP_H3K27ac_signal")
data("IMR90_ChIP_H3K27ac_signal")
library("RColorBrewer")
```
## List of multiple signal datasets

```r
signalList <- list(GM12878_ChIP_CTCF_signal, GM12878_ChIP_H3K27ac_signal,
                   IMR90_ChIP_CTCF_signal, IMR90_ChIP_H3K27ac_signal)
```

## Create page

```r
pageCreate(width = 6.9, height = 3.5, default.units = "inches")
```

## Plot multiple signals

```r
multisignal <- plotMultiSignal(signalList, chrom = "chr21",
                                chromstart = 28150000, chromend = 29150000,
                                linecolor = c(brewer.pal(n = 9, "YlGnBu")[4],
                                               brewer.pal(n = 9, "YlGnBu")[5],
                                               brewer.pal(n = 9, "YlGnBu")[6],
                                               brewer.pal(n = 9, "YlGnBu")[7]),
                                label = c("GM12878 CTCF", "GM12878 H3K27ac",
                                          "IMR90 CTCF", "IMR90 H3K27ac"),
                                assembly = "hg19",
                                x = 0.2, y = 0.2,
                                width = 6.5, height = 3,
                                default.units = "inches",
                                gapdistance = 0.1)
```

## Plot genome label

```r
plotGenomeLabel(
    chrom = "chr21",
    chromstart = 28150000, chromend = 29150000,
    assembly = "hg19",
    scale = "Kb",
    x = 0.2, y = 3.25, length = 6.5,
    default.units = "inches"
)
```

## Hide page guides

```r
pageGuideHide()
```

---

### plotPairs

**Plot paired-end genomic range elements**

**Description**

Plot paired-end genomic range elements

**Usage**

```r
plotPairs(
  data,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
```
Arguments

- **data**: A string specifying the BEDPE file path, a dataframe in BEDPE format specifying data to be plotted, or a `GInteractions` object.
- **chrom**: Chromosome of region to be plotted, as a string.
- **chromstart**: Integer start position on chromosome to be plotted.
- **chromend**: Integer end position on chromosome to be plotted.
- **assembly**: Default genome assembly as a string or a `assembly` object. Default value is `assembly = "hg38"`.
- **fill**: A single character value, a vector, or a `colorby` object specifying fill colors of paired range elements. Default value is `fill = "#1f4297"`.
- **linecolor**: A single character value, a vector, or a `colorby` object specifying the color of the lines outlining paired range elements. Default value is `linecolor = NA`. Special options include:
  - `NA`: No line color.
  - "fill": Same color as `fill`.
- **bg**: Character value indicating background color. Default value is `bg = NA`.
- **boxHeight**: A numeric or unit object specifying height of boxes at either end of paired range elements. Default value is `boxHeight = unit(2, "mm")`.
- **spaceWidth**: A numeric specifying the width of spacing between paired range elements, as a fraction of the plot’s genomic range. Default value is `spaceWidth = 0.02`.
- **spaceHeight**: A numeric specifying the height of space between boxes of paired range elements on different rows. Default value is `spaceHeight = 0.3`.
limitLabel: A logical value indicating whether to draw a "+" when not all elements can be plotted in the plotting space. Default value is `limitLabel = TRUE`.

baseline: Logical value indicating whether to include a baseline along the x-axis. Default value is `baseline = FALSE`.

baseline.color: Baseline color. Default value is `baseline.color = "grey"`.

baseline.lwd: Baseline line width. Default value is `baseline.lwd = 1`.

x: A numeric or unit object specifying paired range plot x-location.

y: A numeric, unit object, or character containing a "b" combined with a numeric value specifying paired range plot y-location. The character value will place the paired range plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width: A numeric or unit object specifying paired range plot width.

height: A numeric or unit object specifying paired range plot height.

just: Justification of paired range plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is `just = c("left", "top")`.

default.units: A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is `default.units = "inches"`.

draw: A logical value indicating whether graphics output should be produced.

params: An optional `pgParams` object containing relevant function parameters.

...: Additional grid graphical parameters. See `gpar`.

Details

#' A paired ranges plot can be placed on a plotgardener coordinate page by providing plot placement parameters:

```r
plotPairs(data, chrom,
         chromstart = NULL, chromend = NULL,
         x, y, width, height, just = c("left", "top"),
         default.units = "inches")
```

This function can also be used to quickly plot an unannotated paired ranges plot by ignoring plot placement parameters:

```r
plotPairs(data, chrom,
          chromstart = NULL, chromend = NULL)
```

Value

Returns a `pairs` object containing relevant genomic region, placement, and `grob` information.
## Load paired ranges data in BEDPE format
library(plotgardenerData)
data("IMR90_DNAloops_pairs")

## Set the coordinates
params <- pgParams(
  chrom = "chr21",
  chromstart = 27900000, chromend = 30700000,
  assembly = "hg19",
  width = 7
)

## Create a page
pageCreate(width = 7.5, height = 2.1, default.units = "inches")

## Add a length column
IMR90_DNAloops_pairs$length <-
  (IMR90_DNAloops_pairs$start2 - IMR90_DNAloops_pairs$start1) / 1000

## Plot the data
bedpePlot <- plotPairs(
  data = IMR90_DNAloops_pairs, params = params,
  fill = colorby("length", palette =
    colorRampPalette(c("dodgerblue2", "firebrick2"))),
  lwd = 2, spaceHeight = .7,
  x = 0.25, y = 0.25, height = 1.5,
  just = c("left", "top"), default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(plot = bedpePlot, x = 0.25, y = 1.78, scale = "Mb")

## Add heatmap legend
annoHeatmapLegend(
  plot = bedpePlot, fontcolor = "black",
  x = 7.0, y = 0.25,
  width = 0.10, height = 1, fontsize = 10
)

## Add heatmap legend label
plotText(
  label = "Kb", rot = 90, x = 6.9, y = 0.75,
  just = c("center", "center"), fontsize = 10
)

## Hide page guides
pageGuideHide()
Description

Plot paired-end genomic range data in an arch style

Usage

plotPairsArches(
  data,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
  style = "2D",
  flip = FALSE,
  curvature = 5,
  archHeight = NULL,
  fill = "#1f4297",
  linecolor = NA,
  alpha = 0.4,
  bg = NA,
  clip = FALSE,
  clip.noAnchor = TRUE,
  range = NULL,
  baseline = FALSE,
  baseline.color = "grey",
  baseline.lwd = 1,
  x = NULL,
  y = NULL,
  width = NULL,
  height = NULL,
  just = c("left", "top"),
  default.units = "inches",
  draw = TRUE,
  params = NULL,
  ...
)

Arguments

data A string specifying the BEDPE file path, a dataframe in BEDPE format specifying data to be plotted, or a GInteractions object.

chrom Chromosome of region to be plotted, as a string.

chromstart Integer start position on chromosome to be plotted.

chromend Integer end position on chromosome to be plotted.

assembly Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".

style Character value describing the style of arches. Default value is style = "2D". Options are:
- "2D": Arches will be drawn in a 2-dimensional style.
- "3D": Arches will be drawn in a 3-dimensional style.

flip Logical value indicating whether to reflect arches over the x-axis. Default value is flip = FALSE.

curvature Numeric indicating the number of points along the arch curvature. Default value is curvature = 5.

archHeight Single numeric value, numeric vector, or column name in data specifying the arch heights. When NULL, all arches will be the same height, filling up the given plot area.

fill A single character value, a vector, or a colorby object specifying fill colors of arches. Default value is fill = "#1f4297".

linecolor A single character value, a vector, or a colorby object specifying the color of the lines outlining arches. Default value is linecolor = NA. Special options include:
- NA: No line color.
- "fill": Same color as fill.

alpha Numeric value specifying transparency. Default value is alpha = 0.4.

bg Character value indicating background color. Default value is bg = NA.

clip A logical value indicating whether to clip any arches that get cutoff in the given genomic region. Default value is clip = FALSE.

clip.noAnchor A logical value indicating whether to clip any arches that overlap the given genomic region but do not have an anchor in that region. Default value is clip.noAnchor = TRUE.

range A numeric vector of length 2 specifying the y-range of archHeight to plot (c(min, max)).

baseline Logical value indicating whether to include a baseline along the x-axis. Default value is baseline = FALSE.

baseline.color Baseline color. Default value is baseline.color = "grey".

baseline.lwd Baseline line width. Default value is baseline.lwd = 1.

x A numeric or unit object specifying pair arches plot x-location.

y A numeric, unit object, or character containing a "b" combined with a numeric value specifying BEDPE arches plot y-location. The character value will place the pair arches plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width A numeric or unit object specifying pair arches plot width.

height A numeric or unit object specifying pair arches plot height.

just Justification of pair arches plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
draw A logical value indicating whether graphics output should be produced. Default value is draw = TRUE.

params An optional pgParams object containing relevant function parameters.

Additional grid graphical parameters. See gpar.

Details
A pair arches plot can be placed on a plotgardener coordinate page by providing plot placement parameters:

```
plotPairsArches(data chrom,
chromstart = NULL, chromend = NULL,
x, y, width, height, just = c("left", "top"),
default.units = "inches")
```

This function can also be used to quickly plot an unannotated pair arches plot by ignoring plot placement parameters:

```
plotPairsArches(data, chrom,
chromstart = NULL, chromend = NULL)
```

Value
Returns a arches object containing relevant genomic region, placement, and grob information.

Examples
```r
## Load paired ranges data in BEDPE format
library(plotgardenerData)
data("IMR90_DNAloops_pairs")

## Set the coordinates
params <- pgParams(
  chrom = "chr21",
  chromstart = 27900000, chromend = 30700000,
  assembly = "hg19",
  width = 7
)

## Create a page
pageCreate(width = 7.5, height = 2.1, default.units = "inches")

## Add a length column to color by
IMR90_DNAloops_pairs$length <-
  (IMR90_DNAloops_pairs$start2 - IMR90_DNAloops_pairs$start1) / 1000

## Translate lengths into heights
IMR90_DNAloops_pairs$h <-
  IMR90_DNAloops_pairs$length / max(IMR90_DNAloops_pairs$length)

## Plot the data
archPlot <- plotPairsArches(
  data = IMR90_DNAloops_pairs, params = params,
  fill = colorby("length", palette =
    colorRampPalette(c("dodgerblue2", "firebrick2"))),
  linecolor = "fill",
  archHeight = "h", alpha = 1,
  x = 0.25, y = 0.25, height = 1.5,
  just = c("left", "top"),
  default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(plot = archPlot, x = 0.25, y = 1.78, scale = "Mb")

## Annotate heatmap legend
annoHeatmapLegend(
  plot = archPlot, fontcolor = "black",
  x = 7.0, y = 0.25,
  width = 0.10, height = 1, fontsize = 10
)

## Add the heatmap legend title
plotText(
  label = "Kb", rot = 90, x = 6.9, y = 0.75,
  just = c("center", "center"),
  fontsize = 10
)

## Hide page guides
pageGuideHide()

---

**plotPolygon**  
*Plot a polygon within a plotgardener layout*

**Description**

Plot a polygon within a plotgardener layout

**Usage**

```r
plotPolygon(
  x,
  y,
  default.units = "inches",
  linecolor = "black",
  lwd = 1,
  lty = 1,
  fill = NA,
)```
Arguments

x A numeric vector or unit object specifying polygon vertex x-locations.
y A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying polygon vertex y-locations. The character vector will place polygon vertex y-locations relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

default.units A string indicating the default units to use if x or y are only given as numeric vectors. Default value is default.units = "inches".

linecolor A character value specifying polygon line color. Default value is linecolor = "black".
lwd A numeric specifying polygon line width. Default value is lwd = 1.
lty A numeric specifying polygon line type. Default value is lty = 1.
fill A character value specifying polygon fill color. Default value is fill = NA.
alpha Numeric value specifying color transparency. Default value is alpha = 1.
id A numeric vector used to separate locations in x and y into multiple polygons. All locations with the same id belong to the same polygon.
id.lengths A numeric vector used to separate locations in x and y into multiple polygons. Specifies consecutive blocks of locations which make up separate polygons.
params An optional pgParams object containing relevant function parameters.
...

Value

Returns a polygon object containing relevant placement and grob information.

See Also

grid.polygon

Examples

## Create a page
pageCreate(width = 7.5, height = 6, default.units = "inches")

## Plot complex polygons one at a time
plotPolygon(
  x = c(2.6, 4.65, 4.75, 6.05, 1.4, 1.3),
  y = c(2.5, 3.1, 3.5, 4, 3.15, 2.8),
  fill = "#4a168e", linecolor = NA
plotRanges

Plot genomic range elements in a pileup or collapsed format

Description
Plot genomic range elements in a pileup or collapsed format

Usage
plotRanges(
  data,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
  fill = "#7ecdbb",
  linecolor = NA,
  order = "width",
  collapse = FALSE,
  boxHeight = unit(2, "mm"),
)
Arguments

data Data to be plotted; as a character value specifying a BED file path, a data frame in BED format, a character value specifying a .bam file path where a bam index file (.bam.bai) is in the same directory, or a GRanges object.

chrom Chromosome of region to be plotted, as a string.

chromstart Integer start position on chromosome to be plotted.

chromend Integer end position on chromosome to be plotted.

assembly Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".

fill A single character value, a vector, or a colorby object specifying fill colors of range elements. Default value is fill = "#7ecdbb".

linecolor A single character value, a vector, or a colorby object specifying the color of the lines outlining range elements. Default value is linecolor = NA. Special options include:

- NA: No line color.
- "fill": Same color as fill.

order A character value specifying how to order pileup data before assigning rows. Default value is order = "width". Options include:

- "width": Ordered by decreasing width of elements.
- "random": Ordered randomly in each function call.

collapse A logical value indicating whether to collapse range elements into a single row, or into two rows if strandSplit = TRUE. If collapse = TRUE, boxHeight will be ignored and elements will be the height of the entire plot if strandSplit =
plotRanges

FALSE or be the height of half of the entire plot if strandSplit = TRUE. Default value is collapse = FALSE.

boxHeight A numeric or unit object specifying height of range element boxes. Default value is boxHeight = unit(2, "mm").

spaceWidth A numeric value specifying the width of minimum spacing between range element boxes, as a fraction of the plot's genomic range. Default value is spaceWidth = 0.02.

spaceHeight A numeric value specifying the height of spacing between range element boxes on different rows, as a fraction of boxHeight. Default value is spaceHeight = 0.3.

limitLabel A logical value indicating whether to draw a "+" when not all elements can be plotted in the plotting space. Default value is limitLabel = TRUE.

strandSplit A logical value indicating whether plus and minus-stranded elements should be separated. Elements can only be split by strand if a strand column is found in data. Default value is strandSplit = FALSE.

bg Character value indicating background color. Default value is bg = NA.

baseline Logical value indicating whether to include a baseline along the x-axis. Default value is baseline = FALSE.

baseline.color Baseline color. Default value is baseline.color = "grey".

baseline.lwd Baseline line width. Default value is baseline.lwd = 1.

x A numeric or unit object specifying ranges plot x-location.

y A numeric, unit object, or character containing a "b" combined with a numeric value specifying ranges plot y-location. The character value will place the ranges plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width A numeric or unit object specifying ranges plot width.

height A numeric or unit object specifying ranges plot height.

just Justification of ranges plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").

default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".

draw A logical value indicating whether graphics output should be produced. Default value draw = TRUE.

params An optional pgParams object containing relevant function parameters.

... Additional grid graphical parameters. See gpar.

Details

A ranges plot can be placed on a plotgardener coordinate page by providing plot placement parameters:
plotRanges(data, chrom, chromstart = NULL, chromend = NULL, x, y, width, height, just = c("left", "top"), default.units = "inches")

This function can also be used to quickly plot an unannotated BED plot by ignoring plot placement parameters:

plotRanges(data, chrom, chromstart = NULL, chromend = NULL)

Value

Returns a ranges object containing relevant genomic region, coloring data, placement, and grob information.

Examples

```r
## Load ranges data in BED format
library(plotgardenerData)
data("IMR90_ChIP_CTCF_reads")

## Create page
pageCreate(width = 7.5, height = 5, default.units = "inches")

## Plot and place a pileup ranges plot
pileupPlot <- plotRanges(
data = IMR90_ChIP_CTCF_reads, chrom = "chr21",
chromstart = 29073000, chromend = 29074000,
assembly = "hg19",
order = "random",
fill = colorby("strand", palette =
  colorRampPalette(c("#7ecdbb", "#37a7db")),
strandSplit = TRUE,
x = 0.5, y = 0.25, width = 6.5, height = 4.25,
just = c("left", "top"), default.units = "inches"
)

## Annotate genome label
annoGenomeLabel(
  plot = pileupPlot, x = 0.5, y = 4.5,
  just = c("left", "top")
)

## Add text labels
plotText(
  label = "+ strand", fontcolor = "#37a7db", fontsize = 12,
  x = 0.5, y = 1.25, just = "left"
)
plotText(
  label = "- strand", fontcolor = "#7ecdbb", fontsize = 12,
  x = 0.5, y = 3.5, just = "left"
)
```
## Hide page guides

pageGuideHide()

---

### plotRaster

**Plot a raster object within a plotgardener layout**

**Description**

Plot a raster object within a plotgardener layout

**Usage**

```r
plotRaster(
  image,
  x,
  y,
  width,
  height,
  just = "center",
  default.units = "inches",
  interpolate = TRUE,
  params = NULL,
  ...  
)
```

**Arguments**

- **image**
  - Any R object that can be coerced to a raster object.

- **x**
  - A numeric vector or unit object specifying raster x-locations.

- **y**
  - A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying raster y-locations. The character vector will place raster y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

- **width**
  - A numeric vector or unit object specifying raster widths.

- **height**
  - A numeric vector or unit object specifying raster heights.

- **just**
  - Justification of text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = "center".

- **default.units**
  - A string indicating the default units to use if x, y, width, or height are only given as numerics or numeric vectors. Default value is default.units = "inches".

- **interpolate**
  - A logical value indicating whether to linearly interpolate the image. Default value is interpolate = TRUE.

- **params**
  - An optional `pgParams` object containing relevant function parameters.

- **...**
  - Additional grid graphical parameters. See `gpar`.
PlotRaster

Value

Returns a raster object containing relevant placement and grob information.

See Also

grid.raster

Examples

library(png)

## Load images

pg_type <- readPNG(system.file("images", "pg-wordmark.png", package = "plotgardener")
)

gene_gnome <- readPNG(system.file("images", "pg-gnome-hole-shadow.png", package = "plotgardener")
)

rlogo <- readPNG(system.file("images", "Rlogo.png", package = "plotgardener")
)

## Create page

pageCreate(width = 5, height = 6)

## Plot images

plotRaster(
  image = pg_type,
  x = 2.5, y = 0.25, width = 4, height = 1.5,
  just = "top"
)

plotRaster(
  image = gene_gnome,
  x = 2.5, y = 2.25, width = 3.5, height = 3.5,
  just = "top"
)

plotRaster(
  image = rlogo,
  x = 1, y = 1.5, width = 0.5, height = 0.45,
  just = c("left", "top")
)

## Hide page guides

pageGuideHide()
plotRect

Plot a rectangle within a plotgardener layout

Description

Plot a rectangle within a plotgardener layout

Usage

plotRect(
  x,
  y,
  width,
  height,
  just = "center",
  default.units = "inches",
  linecolor = "black",
  lwd = 1,
  lty = 1,
  fill = NA,
  alpha = 1,
  params = NULL,
  ...
)

Arguments

x A numeric vector or unit object specifying rectangle x-locations.
y A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying rectangle y-locations. The character vector will place rectangle y-locations relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
width A numeric vector or unit object specifying rectangle widths.
height A numeric vector or unit object specifying rectangle heights.
just Justification of rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = "center".
default.units A string indicating the default units to use if x, y, width, and height are only given as numerics or numeric vectors. Default value is default.units = "inches".
linecolor A character value specifying rectangle line color. Default value is linecolor = "black".
lwd A numeric specifying rectangle line width. Default value is lwd = 1.
lty A numeric specifying rectangle line type. Default value is lty = 1.
fill  A character value specifying rectangle fill color. Default value is fill = NA.
alpha Numeric value specifying color transparency. Default value is alpha = 1.
params An optional pgParams object containing relevant function parameters.
... Additional grid graphical parameters. See gpar.

Value

Returns a rect object containing relevant placement and grob information.

See Also

grid.rect

Examples

## Create a page
pageCreate(width = 7.5, height = 6, default.units = "inches")

## Plot one rectangle with no fill
plotRect(
  x = 0.5, y = 0.5, width = 3, height = 3,
  just = c("left", "top"), default.units = "inches",
  lwd = 2, fill = NA
)

## Plot two rectangles with same width and height at different locations
plotRect(
  x = 4, y = c(0.5, 2.25), width = 3, height = 1.25,
  just = c("left", "top"), default.units = "inches",
  fill = "#7ecdbb"
)

## Plot two rectangles with different widths, heights, 
## locations, and colors
plotRect(
  x = 3.75, y = c(4, 5.25), width = c(6.5, 4.5),
  height = c(1, 0.25),
  just = "top", default.units = "inches",
  fill = c("#7ecdbb", "#37a7db"), linecolor = NA, alpha = 0.4
)

## Hide page guides
pageGuideHide()
plotSegments

Draw a line segment within a plotgardener layout

Description

Draw a line segment within a plotgardener layout

Usage

plotSegments(
  x0, y0, x1, y1,
  default.units = "inches",
  linecolor = "black",
  lwd = 1,
  lty = 1,
  lineend = "butt",
  linejoin = "mitre",
  arrow = NULL,
  params = NULL,
  ...
)

Arguments

- **x0**: A numeric vector or unit object indicating the starting x-values of the line segments.
- **y0**: A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying starting y-values of the line segments. The character vector will place starting y-values relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
- **x1**: A numeric vector or unit object indicating the stopping x-values of the line segments.
- **y1**: A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying stopping y-values of the line segments. The character vector will place stopping y-values relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
- **default.units**: A string indicating the default units to use if x0, y0, x1, or y1 are only given as numeric vectors. Default value is default.units = "inches".
- **linecolor**: A character value specifying segment line color. Default value is linecolor = "black".
- **lwd**: A numeric specifying segment line width. Default value is lwd = 1.
- **lty**: A numeric specifying segment line type. Default value is lty = 1.
lineend A character value specifying line end style. Default value is lineend = "butt". Options are:
  • "round": Segment ends are rounded.
  • "butt": Segment ends end exactly where ended.
  • "square": Segment ends are squared.

linejoin A character value specifying line join style. Default value is linejoin = "mitre". Options are:
  • "round": Line joins are rounded.
  • "mitre": Line joins are sharp corners.
  • "bevel": Line joins are flattened corners.

arrow A list describing arrow heads to place at either end of the line segments, as produced by the arrow function.

params An optional pgParams object containing relevant function parameters.

Value

Returns a segments object containing relevant placement and grob information.

See Also

  grid.segments, arrow

Examples

library(grid)
# Create a page
pageCreate(width = 7.5, height = 6, default.units = "inches")

# Plot one line segment
plotSegments(
  x0 = 3.75, y0 = 0.25, x1 = 3.75, y1 = 5.75,
  default.units = "inches",
  lwd = 3, lty = 2
)

# Plot multiple line segments at different locations in different colors
plotSegments(
  x0 = 0.5, y0 = c(1, 3, 5), x1 = 3.25, y1 = c(1, 3, 5),
  default.units = "inches",
  lwd = 2, linecolor = c("#7ecdbb", "#37a7db", "grey")
)

# Plot a line segment with an arrowhead
plotSegments(
  x0 = 4.5, y0 = 0.5, x1 = 7, y1 = 3,
  default.units = "inches",
  arrow = arrow(type = "closed"), fill = "black"
)
## Plot lines with round lineends
```
plotSegments(
  x0 = c(4, 7), y0 = 3.5, x1 = 5.5, y1 = 4.5,
  default.units = "inches",
  lwd = 5, lineend = "round"
)
```

## Hide page guides
```
pageGuideHide()
```

---

**plotSignal**

*Plot any kind of signal track data for a single chromosome*

### Description

Plot any kind of signal track data for a single chromosome

### Usage

```
plotSignal(
  data,
  binSize = NA,
  binCap = TRUE,
  negData = FALSE,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg38",
  linecolor = "#37a7db",
  fill = NA,
  ymax = 1,
  range = NULL,
  scale = FALSE,
  label = NULL,
  bg = NA,
  baseline = TRUE,
  baseline.color = "grey",
  baseline.lwd = 1,
  orientation = "h",
  x = NULL,
  y = NULL,
  width = NULL,
  height = NULL,
  just = c("left", "top"),
  default.units = "inches",
  draw = TRUE,
  params = NULL,
)```
plotSignal

Arguments

- **data**: Data to be plotted as a character value specifying a bigwig file path, a dataframe in BED format, or a GRanges object with metadata column score. Either one data argument or a list of two can be provided, where the second data will be plotted below the x-axis if positive. The second data can also be negative data.

- **binSize**: A numeric specifying the length of each data bin in basepairs. Default value is binSize = NA.

- **binCap**: A logical value indicating whether the function will limit the number of data bins to 8,000. Default value is binCap = TRUE.

- **negData**: A logical value indicating whether the provided data has negative scores. Default value is negData = FALSE.

- **chrom**: Chromosome of region to be plotted, as a string.

- **chromstart**: Integer start position on chromosome to be plotted.

- **chromend**: Integer end position on chromosome to be plotted.

- **assembly**: Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".

- **linecolor**: A character value or vector of length 2 specifying the line color(s) outlining the signal track(s). Default value is linecolor = "#37a7db".

- **fill**: A character value or vector of length 2 specifying the fill color(s) of the signal track(s). Default value is fill = NA.

- **ymax**: A numeric specifying the fraction of the max y-value to set as the height of the plot. Default value is ymax = 1.

- **range**: A numeric vector of length 2 specifying the y-range of data to plot (c(min, max)).

- **scale**: A logical value indicating whether to include a data scale label in the top left corner of the plot. Default value is scale = FALSE.

- **label**: An optional character value to conveniently add a text label to the plot. If scale = TRUE, the label will be drawn in the top right of the plot. Otherwise, the label will be drawn in the top left of the plot. For more customizable labels, use plotText. Default value is label = NULL.

- **bg**: Character value indicating background color. Default value is bg = NA.

- **baseline**: Logical value indicating whether to include a baseline along the x-axis. Default value is baseline = TRUE.

- **baseline.color**: Baseline color. Default value is baseline.color = "grey".

- **baseline.lwd**: Baseline line width. Default value is baseline.lwd = 1.

- **orientation**: A string specifying signal track orientation. Default value is orientation = "h". Options are:
  - "v": Vertical signal track orientation.
  - "h": Horizontal signal track orientation.
plotSignal

x A numeric or unit object specifying signal plot x-location.
y A numeric, unit object, or character containing a "b" combined with a numeric value specifying signal plot y-location. The character value will place the signal plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width A numeric or unit object specifying signal plot width.
height A numeric or unit object specifying signal plot height.
just Justification of signal plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = c("left", "top").
default.units A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is default.units = "inches".
draw A logical value indicating whether graphics output should be produced. Default value draw = TRUE.
params An optional pgParams object containing relevant function parameters.
... Additional grid graphical parameters. See gpar.

Details

#A signal track can be placed on a plotgardener coordinate page by providing plot placement parameters:

plotSignal(data, chrom,
    chromstart = NULL, chromend = NULL,
    x, y, width, height, just = c("left", "top"),
    default.units = "inches")

This function can also be used to quickly plot an unannotated signal track by ignoring plot placement parameters:

plotSignal(data, chrom,
    chromstart = NULL, chromend = NULL)

Value

Returns a signal object containing relevant genomic region, placement, and grob information.

Examples

## Load signal data
library(plotgardenerData)
data("IMR90_ChIP_H3K27ac_signal")
data("GM12878_ChIP_H3K27ac_signal")

## Create a page
pageCreate(width = 7.5, height = 2.1, default.units = "inches")
''Define region
region <- pgParams(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  range = c(0, 45)
)
''

''Plot and place signal plots
signal1 <- plotSignal(
  data = IMR90_ChIP_H3K27ac_signal, params = region,
  x = 0.5, y = 0.25, width = 6.5, height = 0.65,
  just = c("left", "top"), default.units = "inches"
)

signal2 <- plotSignal(
  data = GM12878_ChIP_H3K27ac_signal, params = region,
  linecolor = "#7ecdbb",
  x = 0.5, y = 1, width = 6.5, height = 0.65,
  just = c("left", "top"), default.units = "inches"
)
''

''Plot genome label
plotGenomeLabel(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  assembly = "hg19",
  x = 0.5, y = 1.68, length = 6.5,
  default.units = "inches"
)
''

''Add text labels
plotText(
  label = "IMR90", fonsize = 10, fontcolor = "#37a7db",
  x = 0.5, y = 0.25, just = c("left", "top"),
  default.units = "inches"
)

plotText(
  label = "GM12878", fonsize = 10, fontcolor = "#7ecdbb",
  x = 0.5, y = 1, just = c("left", "top"),
  default.units = "inches"
)
''

''Hide page guides
pageGuideHide()

plotText

Description
Plot text within a plotgardener layout

Usage

plotText(
  label,
  fontcolor = "black",
  fontsize = 12,
  rot = 0,
  check.overlap = FALSE,
  x,
  y,
  just = "center",
  default.units = "inches",
  params = NULL,
  ...
)

Arguments

label Character or expression of text to be plotted.
fontcolor A character value specifying text fontcolor. Default value is fontcolor = "black".
fontsize A numeric specifying text fontsize in points. Default value is fontsize = 12.
rot A numeric specifying the angle to rotate the text. Default value is rot = 0.
check.overlap A logical value to indicate whether to check for and omit overlapping text. Default value is check.overlap = FALSE.
x A numeric vector or unit object specifying text x-location.
y A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying text y-locations. The character vector will place text y-locations relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.
just Justification of text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is just = "center".
default.units A string indicating the default units to use if x or y are only given as numerics or numeric vectors. Default value is default.units = "inches".
params An optional pgParams object containing relevant function parameters.
... Additional grid graphical parameters. See gpar.

Value
Returns a text object containing relevant placement and grob information.
plotTranscripts

Plot gene transcripts in a pileup style for a single chromosome

Description

Plot gene transcripts in a pileup style for a single chromosome

Usage

plotTranscripts(
  chrom,
  chromstart = NULL,
  chromend = NULL,
plotTranscripts

assembly = "hg38",
fill = c("#669fd9", "#abcc8e"),
colorbyStrand = TRUE,
strandSplit = FALSE,
boxHeight = unit(2, "mm"),
spaceWidth = 0.02,
spaceHeight = 0.3,
limitLabel = TRUE,
transcriptHighlights = NULL,
fontsize = 8,
labels = "transcript",
stroke = 0.1,
bg = NA,
x = NULL,
width = NULL,
height = NULL,
just = c("left", "top"),
default.units = "inches",
draw = TRUE,
params = NULL
}

Arguments

chrom     Chromosome of region to be plotted, as a string.
chromstart Integer start position on chromosome to be plotted.
chromend   Integer end position on chromosome to be plotted.
assembly   Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".
fill       Character value(s) as a single value or vector specifying fill colors of transcripts. Default value is fill = c("#669fd9", "#abcc8e").
colorbyStrand A logical value indicating whether to color plus and minus strands by the first two colors in a fill vector, where plus strand transcripts will be colored by the first fill color and minus strand transcripts will be colored by the second fill color. Default value is colorbyStrand = TRUE.
strandSplit A logical value indicating whether plus and minus-stranded transcripts should be separated, with plus strand transcripts plotted above the x-axis and minus strand transcripts plotted below the x-axis. Default value is strandSplit = FALSE.
boxHeight  A numeric or unit object specifying height of transcripts. Default value is boxHeight = unit(2, "mm").
spaceWidth  A numeric value specifying the width of minimum spacing between transcripts, as a fraction of the plot's genomic range. Default value is spaceWidth = 0.02.
spaceHeight A numeric value specifying the height of spacing between transcripts on different rows, as a fraction of boxHeight. Default value is spaceHeight = 0.3.
limitLabel A logical value indicating whether to draw a "+" when not all elements can be plotted in the plotting space. Default value is \text{limitLabel} = \text{TRUE}.

transcriptHighlights A two-column dataframe with a column named "transcript" or "gene" containing transcript names or their associated gene names as strings to highlight and a column named "color" containing corresponding highlight colors.

fontsize A numeric specifying text fontsize in points. Default value is \text{fontsize} = 8.

labels A character value describing the format of transcript text labels. Default value is \text{labels} = "transcript". Options are:
  - NULL: No labels.
  - "transcript": Transcript name labels.
  - "gene": Gene name labels.
  - "both": Combined transcript and gene name labels with the format "gene name:transcript name".

stroke A numeric value indicating the stroke width for transcript body outlines. Default value is \text{stroke} = 0.1.

bg Character value indicating background color. Default value is \text{bg} = \text{NA}.

x A numeric or unit object specifying transcript plot x-location.

y A numeric, unit object, or character containing a "b" combined with a numeric value specifying transcript plot y-location. The character value will place the transcript plot y relative to the bottom of the most recently plotted plot according to the units of the plotgardener page.

width A numeric or unit object specifying transcript plot width.

height A numeric or unit object specifying transcript plot height.

just Justification of transcript plot relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". Default value is \text{just} = c("left", "top").

default.units A string indicating the default units to use if \text{x}, \text{y}, \text{width}, or \text{height} are only given as numerics. Default value is \text{default.units} = "inches".

draw A logical value indicating whether graphics output should be produced. Default value is \text{draw} = \text{TRUE}.

params An optional \text{pgParams} object containing relevant function parameters.

Details

A transcripts plot can be placed on a plotgardener coordinate page by providing plot placement parameters:

\begin{verbatim}
plotTranscripts(chrom, chromstart = NULL, chromend = NULL,
               x, y, width, height, just = c("left", "top"),
               default.units = "inches")
\end{verbatim}
plotTranscripts

This function can also be used to quickly plot an unannotated transcripts plot by ignoring plot placement parameters:

plotTranscripts(chrom, chromstart = NULL, chromend = NULL)

Genomic annotation information is acquired through TxDb and OrgDb-class packages, as determined through the assembly parameter.

Value

Returns a transcripts object containing relevant genomic region, placement, and grob information.

See Also

assembly, genomes, defaultPackages

Examples

## Load hg19 genomic annotation packages
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
library("org.Hs.eg.db")

## Create page
pageCreate(width = 7.5, height = 3.5, default.units = "inches")

## Plot and place transcripts
plotTranscripts(
  chrom = "chr8", chromstart = 1000000, chromend = 2000000,
  assembly = "hg19", labels = "gene",
  x = 0.5, y = 0.5, width = 6.5, height = 2.5,
  just = c("left", "top"), default.units = "inches"
)

## Plot genome label
plotGenomeLabel(
  chrom = "chr8", chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  x = 0.5, y = 3.03, length = 6.5, default.units = "inches"
)

## Plot a legend
plotLegend(
  legend = c("+ strand", "- strand"),
  fill = c("#669fd9", "#abcc8e"), border = FALSE,
  x = 0.5, y = 1, width = 1, height = 0.5,
  just = c("left", "top")
)

## Hide page guides
pageGuideHide()
**readBigwig**  
*Read a bigWig file and return it as a data frame*

**Description**
Read a bigWig file and return it as a data frame

**Usage**

```r
readBigwig(
  file,
  chrom = NULL,
  chromstart = 1,
  chromend = .Machine$integer.max,
  strand = "*",
  params = NULL
)
```

**Arguments**
- **file** A character value specifying the path to the bigwig file.
- **chrom** Chromosome of data as a string, if data for a specific chromosome is desired.
- **chromstart** Integer start position on chromosome.
- **chromend** Integer end position on chromosome.
- **strand** A character value specifying strand. Default value is \texttt{strand = "}*". Options are:
  - \texttt{"+"}: Plus strand.
  - \texttt{"-"}: Minus strand.
  - \texttt{"*"}: Plus and minus strands.
- **params** An optional \texttt{pgParams} object containing relevant function parameters.

**Details**
This function does not work on Windows.

**Value**
Returns a 6-column dataframe of bigwig information.

**See Also**
- \texttt{import.bw}
Examples

```r
if (.Platform$OS.type != "windows"){
    bwFile <- system.file("extdata/test.bw", package="plotgardenerData")

    ## Read in entire file
    bwData <- readBigwig(file = bwFile)

    ## Read in specified region
    bwRegion <- readBigwig(file = bwFile,
                           chrom = "chr2",
                           chromstart = 1,
                           chromend = 1500)
}
```

---

**readHic**

*Read a .hic file and return Hi-C data as a dataframe*

**Description**

Read a .hic file and return Hi-C data as a dataframe

**Usage**

```r
readHic(
    file,
    chrom,
    chromstart = NULL,
    chromend = NULL,
    altchrom = NULL,
    altchromstart = NULL,
    altchromend = NULL,
    assembly = "hg38",
    resolution = "auto",
    res_scale = "BP",
    zrange = NULL,
    norm = "KR",
    matrix = "observed",
    params = NULL,
    quiet = FALSE
)
```

**Arguments**

- **file**: A character value specifying the path to the .hic file.
- **chrom**: Chromosome of data, as a string.
- **chromstart**: Integer start position on chromosome.
readHic

chromend Integer end position on chromosome.
altdchrom Alternate chromosome for interchromosomal data, as a string.
altdchromstart Alternate chromosome integer start position for interchromosomal data.
altdchromend Alternate chromosome integer end position for interchromosomal data.
assembly Default genome assembly as a string or a assembly object. Default value is assembly = "hg38".
resolution A numeric specifying the width of each pixel. "auto" will attempt to choose a resolution in basepairs based on the size of the region.
res_scale A character value specifying the resolution scale. Default value is res_scale = "BP". Options are:
  • "BP": Base pairs.
  • "FRAG": Fragments.
zrange A numeric vector of length 2 specifying the range of interaction scores, where extreme values will be set to the max or min.
norm Character value specifying hic data normalization method. This value must be found in the .hic file. Default value is norm = "KR".
matrix Character value indicating the type of matrix to output. Default value is matrix = "observed". Options are:
  • "observed": Observed counts.
  • "oe": Observed/expected counts.
  • "log2oe": Log2 transformed observed/expected counts.
params An optional pgParams object containing relevant function parameters.
quiet A logical indicating whether or not to print messages.

Value

Returns a 3-column dataframe in sparse upper triangular format with the following columns: chrom, altdchrom, counts.

See Also

straw

Examples

hicFile <- system.file("extdata/test_chr22.hic", package="plotgardenerData")

## Read in data for all chr22 file at 2.5Mb bp resolution
hicData <- readHic(file = hicFile, chrom = "22",
 assembly = "hg19",
 resolution = 2500000)

## Read in region `chr22:20000000-47500000` at 100 Kb resolution
hicData10Kb <- readHic(file = hicFile, chrom = "22",
 chromstart = 20000000, chromend = 47500000,
 assembly = "hg19",
 resolution = 100000)
resolution = 100000)
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