Package 'BentoBox'

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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, BentoBox 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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URL https://phanstiellab.github.io/BentoBox, https://github.com/PhanstielLab/BentoBox

Encoding UTF-8

RoxygenNote 7.1.1

Imports curl, data.table, dplyr, grDevices, grid, ggplotify, methods, plyranges, purrr, Rcpp, RColorBrewer, rlang, stats, strawr, tools, utils

biocViews Visualization, GenomeAnnotation, FunctionalGenomics, GenomeAssembly, HiC

LinkingTo Rcpp

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R topics documented:

`bbAnnoDomains` *Annotate domains in a Hi-C plot*

Description

Annotate domains in a Hi-C plot

Usage

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

Arguments

`plot`	Hi-C plot object from `bbPlotHicSquare` or `bbPlotHicTriangle` 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 ont 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 bbParams object containing relevant function parameters.

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

Value

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

Examples

```
## 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(BentoBoxData)
data("IMR90_HiC_10kb")

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

## Plot and place a square Hi-C plot
hicPlot <- bbPlotHicSquare(
    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 domains on bottom half 0f Hi-C plot
bbAnnoDomains(
    plot = hicPlot, data = domains,
    half = "bottom", linecolor = "red"
)

## Annotate heatmap legend
```

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

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

## Hide page guides
bbPageGuideHide()
```

---

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

Description

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

Usage

```
bbAnnoGenomeLabel(
    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",
    params = NULL,
    ...
)
```

Arguments

plot	Input BentoBox 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 bbPlotHicSquare.
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 BentoBox plot according to the units of the BentoBox 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").
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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters or digit specifications. See gpar and formatC.

Value

Returns a bb_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")

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

## Plot and place gene track on a BentoBox page
genesPlot <- bbPlotGenes(
    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
bbAnnoGenomeLabel(
    plot = genesPlot, scale = "Mb",
    x = 0.5, y = 1.25, just = c("left", "top"),
    default.units = "inches"
)
bbAnnoGenomeLabel(
    plot = genesPlot, scale = "Kb",
    x = 0.5, y = 1.5, just = c("left", "top"),
    default.units = "inches"
)
bbAnnoGenomeLabel(
    plot = genesPlot, scale = "bp",
    x = 0.5, y = 1.75, just = c("left", "top"),
    default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

---

bbAnnoHeatmapLegend *Add a color scale legend for heatmap-style plots*

Description

Add a color scale legend for heatmap-style plots

Usage

```
bbAnnoHeatmapLegend(
    plot,
    orientation = "v",
    fontsize = 8,
    fontcolor = "dark grey",
    scientific = FALSE,
    digits = 0,
    ticks = FALSE,
    breaks = 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 specfying 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 digits to include after decimal points of numeric color value labels. Default value is digits = 0.
ticks	Logical value specifying if tick marks on the heatmap colorbar should be visible. Default value is ticks = FALSE.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

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

Examples

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

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

## Plot and place a square Hi-C plot
hicPlot <- bbPlotHicSquare(
    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
bbAnnoHeatmapLegend(
    plot = hicPlot,
    x = 3.2, y = 0.5, width = 0.12, height = 1.2,
    just = c("left", "top"), default.units = "inches"
)

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

## Hide page guides
bbPageGuideHide()
```

bbAnnoHighlight *Annotates a highlight box around a specified genomic region of a BentoBox plot*

Description

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

Usage

```
bbAnnoHighlight(
    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 BentoBox 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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
`...`	Additional grid graphical parameters. See gpar.

Value

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

Examples

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

## Plot and place a signal plot
library(BentoBoxData)
data("IMR90_ChIP_H3K27ac_signal")
region <- bbParams(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    assembly = "hg19",
    range = c(0, 45)
)
signalPlot <- bbPlotSignal(
    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
bbAnnoHighlight(
    plot = signalPlot,
    chrom = "chr21",
    chromstart = 29000000, chromend = 29125000,
    y = 0.25, height = 1, just = c("left", "top"),
    default.units = "inches"
)

## Plot text label
bbPlotText(
    label = "region of interest", fontsize = 8, fontcolor = "black",
    x = 3.5, y = 0.2, just = "bottom", default.units = "inches"
)

## Plot genome label
```

```
bbPlotGenomeLabel(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    assembly = "hg19",
    x = 0.5, y = 1.3, length = 6.5, default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

`bbAnnoPixels` *Annotate pixels in a Hi-C plot*

Description

Annotate pixels in a Hi-C plot

Usage

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

Arguments

`plot`	Hi-C plot object from `bbPlotHicSquare` or `bbPlotHicTriangle` 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. • `"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 ont 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 bbParams object containing relevant function parameters.
quiet	A logical indicating whether or not to print messages.
...	Additional grid graphical parameters. See gpar.

Value

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

Examples

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

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

## Plot and place a square Hi-C plot
hicPlot <- bbPlotHicSquare(
    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 <- bbAnnoPixels(
    plot = hicPlot, data = IMR90_DNAloops_pairs, type = "box",
    half = "both"
)

## Annotate loops on one side of Hi-C plot with arrows
## and the other side with circles
bbPagePlotRemove(plot = pixels)
pixels1 <- bbAnnoPixels(
    plot = hicPlot, data = IMR90_DNAloops_pairs,
    type = "arrow", half = "top", shift = 8
```

```
)
pixels2 <- bbAnnoPixels(
    plot = hicPlot, data = IMR90_DNAloops_pairs,
    type = "circle", half = "bottom"
)

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

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

## Hide page guides
bbPageGuideHide()
```

---

bbAnnoSegments *Annotates a line segment within a BentoBox plot*

Description

Annotates a line segment within a BentoBox plot

Usage

```
bbAnnoSegments(
    x0,
    y0,
    x1,
    y1,
    plot,
    default.units = "native",
    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 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 BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_segments object containing relevant placement and grob information.

See Also

grid.segments, arrow

Examples

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

## Plot a Manhattan plot
library(BentoBoxData)
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
data("hg19_insulin_GWAS")
manhattanPlot <- bbPlotManhattan(
    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
bbAnnoGenomeLabel(
    plot = manhattanPlot, x = 0.5, y = 2, fontsize = 8,
    just = c("left", "top"),
    default.units = "inches"
)
bbPlotText(
    label = "Chromosome", fontsize = 8,
    x = 3.75, y = 2.20, just = "center", default.units = "inches"
)

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

```
## Hide page guides
bbPageGuideHide()
```

---

bbAnnoText *Annotates text within a BentoBox plot*

Description

Annotates text within a BentoBox plot

Usage

```
bbAnnoText(
    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 BentoBox 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".
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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_text object containing relevant placement and grob information.

See Also

grid.text

Examples

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

## Plot text relative to a BentoBox plot
library(BentoBoxData)
data("IMR90_HiC_10kb")
hicPlot <- bbPlotHicSquare(
    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"
)
bbAnnoGenomeLabel(
    plot = hicPlot, x = 0.5, y = 3.55, scale = "Mb",
    just = c("left", "top"), default.units = "inches"
)

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

## Hide page guides
bbPageGuideHide()
```

---

bbAnnoXaxis *Add an x-axis to a plot*

Description

Add an x-axis to a plot

Usage

```
bbAnnoXaxis(
    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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_xaxis object containing relevant grob information.

Examples

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

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

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

```
    chromend = 2000000,
    assembly = "hg19",
    x = 0.5, y = 0,
    width = 6.5, height = 4,
    just = c("left", "top"),
    default.units = "inches"
)

## Add standard x-axis to transcript plot
bbAnnoXaxis(
    plot = transcriptPlot,
    at = c(1000000, 1250000, 1500000, 1750000, 2000000),
    fontsize = 8
)
bbPlotText(
    label = "Basepairs", fontsize = 10, fontface = "bold",
    x = 3.75, y = 4.3, just = "top"
)

## Hide page guides
bbPageGuideHide()
```

---

bbAnnoYaxis *Add a y-axis to a plot*

Description

Add a y-axis to a plot

Usage

```
bbAnnoYaxis(
    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.

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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_yaxis object containing relevant grob information.

Examples

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

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

## Plot and place a square Hi-C plot
hicPlot <- bbPlotHicSquare(
    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
bbAnnoYaxis(
    plot = hicPlot, at = c(28000000, 29000000, 30300000),
    fontsize = 10
)

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

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

```
## Hide page guides
bbPageGuideHide()
```

---

bbAnnoZoomLines *Annotates zoom lines for a specified genomic region of a BentoBox plot*

Description

Annotates zoom lines for a specified genomic region of a BentoBox plot

Usage

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

Arguments

plot	Input BentoBox 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.

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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

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

Examples

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

## Plot and place a Manhattan plot
library(BentoBoxData)
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
data("hg19_insulin_GWAS")
manhattanPlot <- bbPlotManhattan(
    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"
)
bbAnnoYaxis(
    plot = manhattanPlot, at = c(0, 2, 4, 6, 8, 10, 12, 14),
    axisLine = TRUE, fontsize = 8
)

## Annotate zoom lines for a region on chromsome 21
zoomRegion <- bbParams(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    assembly = "hg19"
)
bbAnnoZoomLines(
    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
bbAnnoHighlight(
    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
manhattanPlotZoom <- bbPlotManhattan(
    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
)
data("IMR90_ChIP_H3K27ac_signal")
signalPlot <- bbPlotSignal(
    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
bbPlotGenomeLabel(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    assembly = "hg19",
    x = 0.5, y = 4.4, length = 6.5,
    default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

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

Description

Make a `bbAssembly` object for alternate TxDb, OrgDb,and BSgenome genomic annotation packages

Usage

```
bbAssembly(
    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 bbAssembly object containing all input parameters.

See Also

TxDb, OrgDb-class, BSgenome

Examples

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

---

bbDefaultPackages *Display the default genomic annotation packages associated with a genome build*

Description

Display the default genomic annotation packages associated with a genome build

Usage

```
bbDefaultPackages(Genome)
```

Arguments

Genome	String indicating the name of the genome assembly.

Value

Returns a list of the default data packages for a genome build.

Examples

```
## View default genomic annotation packages associated with "hg19"
bbDefaultPackages(Genome = "hg19")

## View default genomic annotation packages associated with "mm9"
bbDefaultPackages(Genome = "mm9")
```

---

bbGenomes *Display the included available default genome assemblies*

Description

Display the included available default genome assemblies

Usage

```
bbGenomes()
```

Value

Returns the included available default genome assemblies

Examples

```
bbGenomes()
```

bbMapColors *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

```
bbMapColors(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 BentoBox 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

```
## Load paired ranges data in BEDPE format
library(BentoBoxData)
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 <- bbMapColors(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)
bbPageCreate(width = 7.5, height = 2.1, default.units = "inches",
            showGuides = FALSE, xgrid = 0, ygrid = 0)
params <- bbParams(
    chrom = "chr21",
    chromstart = 27900000, chromend = 30700000,
    assembly = "hg19",
    width = 7
)

archPlot <- bbPlotPairsArches(
    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"
)

bbAnnoGenomeLabel(plot = archPlot, x = 0.25, y = 1.78, scale = "Mb")
bbAnnoHeatmapLegend(
    plot = archPlot, fontcolor = "black",
    x = 7.0, y = 0.25,
    width = 0.10, height = 1, fontsize = 10
)
bbPlotText(
    label = "Kb", rot = 90, x = 6.9, y = 0.75,
    just = c("center", "center"),
    fontsize = 10
)
```

---

bbPageCreate *Create a page for a BentoBox layout*

Description

Create a page for a BentoBox layout

Usage

```
bbPageCreate(
    width = 8.5,
    height = 11,
    default.units = "inches",
    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".
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 showOutline = TRUE.
params	An optional bbParams object containing relevant function parameters.

Details

width and height must be specified in the same units.

Value

None.

Examples

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

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

---

bbPageGuideHide *Remove guides from a BentoBox page*

Description

Remove guides from a BentoBox page

Usage

```
bbPageGuideHide()
```

Value

None.

Examples

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

## Hide page guides
bbPageGuideHide()
```

`bbPageGuideHorizontal` *Draw a horizontal guideline at a specified y-coordinate on a BentoBox page*

Description

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

Usage

```
bbPageGuideHorizontal(
    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 bbParams object containing relevant function parameters.
`...`	Additional grid graphical parameters. See gpar.

Value

None.

Examples

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

## Add red horizontal guideline at y = 2.5 inches
bbPageGuideHorizontal(y = 2.5, linecolor = "red")
```

bbPageGuideShow *Reshow guides drawn with* bbPageCreate, bbPageGuideHorizontal, *and* bbPageGuideVertical

Description

Reshow guides drawn with bbPageCreate, bbPageGuideHorizontal, and bbPageGuideVertical

Usage

```
bbPageGuideShow()
```

Value

None.

See Also

bbPageCreate, bbPageGuideHorizontal, bbPageGuideVertical

Examples

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

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

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

## Plot and place Hi-C plot
hicPlot <- bbPlotHicSquare(
    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
bbPageGuideHide()

## Re-show page guides
bbPageGuideShow()

## Annotate genome label
```

```
bbAnnoGenomeLabel(
    plot = hicPlot, scale = "Mb", axis = "x",
    x = 0.5, y = 2.53, just = c("left", "top")
)
```

---

bbPageGuideVertical *Draw a vertical guideline at a specified x-coordinate on a BentoBox page*

Description

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

Usage

```
bbPageGuideVertical(
    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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

None.

Examples

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

## Add blue vertical guideline at x = 1.7 inches
bbPageGuideVertical(x = 1.7, linecolor = "blue")
```

bbPagePlotPlace *Place a BentoBox plot that has been previously created but not drawn*

Description

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

Usage

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

Arguments

plot	BentoBox plot object to be placed, defined by the output of a BentoBox 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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.

Value

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

Examples

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

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

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

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

## Annotate heatmap legend
bbAnnoHeatmapLegend(
    plot = hicPlot,
    x = 3.4, y = 0.25, width = 0.12, height = 1.2,
    just = c("left", "top"), default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

`bbPagePlotRemove` *Remove BentoBox plots and annotations*

Description

Remove BentoBox plots and annotations

Usage

```
bbPagePlotRemove(plot)
```

Arguments

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

Value

None.

Examples

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

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

## Plot and place a square Hi-C plot
hicPlot <- bbPlotHicSquare(
    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
bbPagePlotRemove(plot = hicPlot)
```

---

bbParams *bbParams: BentoBox parameters object*

Description

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

Usage

```
bbParams(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 BentoBox 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
- title
- TxDb
- type
- width
- x
- xgrid
- x0
- x1
- y
- ygrid
- ymax
- y0
- y1
- zrange

Details

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

bbParams also provides an alternative region definition mechanism. Given a gene name and genome assembly, bbParams 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 bbParams containing BentoBox function arguments.

Examples

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

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

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

## Combine parameters and pass them to a BentoBox function
bbPlotGenes(params = c(p1, p2))
```

---

bbPlotCircle *Plot a circle within a BentoBox layout*

Description

Plot a circle within a BentoBox layout

Usage

```
bbPlotCircle(
    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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_circle object containing relevant placement and grob information.

See Also

grid.circle

Examples

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

## Plot two circles, one at a time
bbPlotCircle(
    x = 0.6, y = 0.5, r = 0.1, fill = "black",
    default.units = "inches"
)
bbPlotCircle(
    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)))
bbPlotCircle(x = xVals, y = yVals, r = 0.05, default.units = "inches")

## Hide page guides
bbPageGuideHide()
```

bbPlotGenes *Plot a gene track for a specified genomic region*

Description

Plot a gene track for a specified genomic region

Usage

```
bbPlotGenes(
    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 bbAssembly 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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.

Details

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

```
bbPlotGenes(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 unnannotated gene track by ignoring plot placement parameters:

```
bbPlotGenes(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 bb_genes object containing relevant genomic region, placement, and grob information.

See Also

bbAssembly, bbGenomes, bbDefaultPackages

Examples

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

## Set genomic coordinates
paramssmall <- bbParams(
    chrom = "chr8",
    chromstart = 1, chromend = 3000000,
    assembly = "hg19", width = 7
)
paramsbig <- bbParams(
    chrom = "chr8",
    chromstart = 1, chromend = 146364022,
    assembly = "hg19", width = 7
)
## Set colors
cols <- c("#41B6C4", "#225EA8")

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

## Plot genes big
genesPlot <- bbPlotGenes(
    params = paramsbig, fill = cols,
    fontcolor = cols,
    x = 0.25, y = 0.25, height = 0.75,
    just = c("left", "top"),
    default.units = "inches"
)

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

## Plot genes small
genesPlot <- bbPlotGenes(
    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"
)

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

## Hide page guides
bbPageGuideHide()
```

---

bbPlotGenomeLabel *Plot genomic coordinates along the x or y-axis of a BentoBox plot*

Description

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

Usage

```
bbPlotGenomeLabel(
    chrom,
    chromstart = NULL,
    chromend = NULL,
    assembly = "hg38",
    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,
    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 bbAssembly 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.
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 `bbPlotHicSquare`.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters or digit specifications. See gpar and formatC.

Value

Returns a bb_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 BentoBox page
bbPageCreate(width = 5, height = 3, default.units = "inches")

## Plot and place gene track on a BentoBox page
genesPlot <- bbPlotGenes(
    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
bbPlotGenomeLabel(
    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"
)
bbPlotGenomeLabel(
    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"
)
bbPlotGenomeLabel(
    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
bbPlotGenomeLabel(
    chrom = "chr8",
    chromstart = 1000000, chromend = 1000050,
    assembly = "hg19",
    x = 0.25, y = 2.2, length = 4.5
)
bbPlotGenomeLabel(
    chrom = "chr8",
    chromstart = 1000000, chromend = 1000020,
    assembly = "hg19",
    x = 0, y = 2.6, length = 5
)

## Hide page guides
bbPageGuideHide()
```

---

bbPlotGG *Plot a ggplot2 plot, gtable, or grob object in a BentoBox layout*

Description

Plot a ggplot2 plot, gtable, or grob object in a BentoBox layout

Usage

```
bbPlotGG(
    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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.

Value

Returns a bb_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 BentoBox page
bbPageCreate(width = 4, height = 4, default.units = "inches")

## Place ggplot in BentoBox page
bbPlotGG(
    plot = p, x = 0.5, y = 0.5, width = 3, height = 3,
    just = c("left", "top"), default.units = "inches"
)

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

## Hide page guides
bbPageGuideHide()
```

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

Description

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

Usage

```
bbPlotHicRectangle(
    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",
    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 bbAssembly 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".
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
quiet	A logical indicating whether or not to print messages.

Details

This function is similar is bbPlotHicTriangle but will fill in additional pixels around the the triangular portion of the plot to make a rectangle.

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

```
bbPlotHicRectangle(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:

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

Value

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

See Also

bbReadHic, bbPlotHicTriangle

Examples

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

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

## Plot and place rectangle Hi-C plot
hicPlot <- bbPlotHicRectangle(
    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"
)

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

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

## Hide page guides
bbPageGuideHide()
```

bbPlotHicSquare *Plot a Hi-C interaction matrix in a square format*

Description

Plot a Hi-C interaction matrix in a square format

Usage

```
bbPlotHicSquare(
    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",
    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.
altchrom	Alternate chromosome for off-diagonal plotting or interchromosomal plotting, as a string.
altchromstart	Alternate chromosome integer start position for off-diagonal plotting or interchromosomal plotting.
altchromend	Alternate chromosome integer end position for off-diagonal plotting or interchromosomal plotting.
assembly	Default genome assembly as a string or a bbAssembly 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".
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.
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 BentoBox plot according to the units of the BentoBox 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 bbParams 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 BentoBox coordinate page by providing plot placement parameters:

```
bbPlotHicSquare(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:

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

Value

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

See Also

bbReadHic

Examples

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

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

## Plot and place Hi-C plot
hicPlot <- bbPlotHicSquare(
    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"
)
```

```
## Annotate heatmap legend
bbAnnoHeatmapLegend(
    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
bbAnnoGenomeLabel(
    plot = hicPlot, scale = "Mb", axis = "x",
    x = 0.5, y = 2.53, just = c("left", "top")
)
bbAnnoGenomeLabel(
    plot = hicPlot, scale = "Mb", axis = "y",
    x = 0.47, y = 0.5, just = c("right", "top")
)

## Hide page guides
bbPageGuideHide()
```

---

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

Description

Plot a Hi-C interaction matrix in a triangular format

Usage

```
bbPlotHicTriangle(
    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",
    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 bbAssembly 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"`.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
quiet	A logical indicating whether or not to print messages.

Details

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

```
bbPlotHicTriangle(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:

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

If height is $< 0.5 * sqrt(2)$, the top of the triangle will be cropped to the given height.

Value

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

See Also

bbReadHic

Examples

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

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

## Plot and place triangle Hi-C plot
hicPlot <- bbPlotHicTriangle(
    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
bbAnnoGenomeLabel(
    plot = hicPlot, scale = "Mb", x = 0.5, y = 2.03,
    just = c("left", "top")
)

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

## Hide page guides
bbPageGuideHide()
```

`bbPlotIdeogram` *Plot a chromosome ideogram with or without cytobands*

Description

Plot a chromosome ideogram with or without cytobands

Usage

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

Arguments

`chrom`	Chromosome to be plotted, as a string.
`assembly`	Default genome assembly as a string or a bbAssembly object. Default value is `assembly = "hg38"`.

data	Custom cytoband data, as a dataframe with the following columns: "seqnames", "start", "end", "width", "strand", "name", "gieStain".
orientation	Character value indicating the orientation of the ideogram. Default value is orientation = "h". Options are: • "v": Vertical ideogram orientation. • "h": Horizontal ideogram orientation.
showBands	Logical value indicating whether to draw colored cytobands within ideogram. Default value is showBands = TRUE.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.

Details

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

```
bbPlotIdeogram(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:

```
bbPlotIdeogram(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 bb_ideogram object containing relevant genomic region, placement, and grob information.

See Also

AnnotationHub

Examples

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

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

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

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

## Hide page guides
bbPageGuideHide()
```

---

bbPlotLegend *Plot a legend*

Description

Plot a legend

Usage

```
bbPlotLegend(
    legend,
    fill = NULL,
    pch = NULL,
    lty = NULL,
    orientation = "v",
    title = NULL,
    fontsize = 10,
    border = TRUE,
    bg = NA,
```

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

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 BentoBox plot according to the units of the BentoBox 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"`.
draw	A logical value indicating whether graphics output should be produced. Default value is `draw = TRUE`.
params	An optional bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_legend object containing relevant placement and grob information.

Examples

```
## Load BED data
library(BentoBoxData)
data("IMR90_ChIP_CTCF_reads")

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

## Plot a pileup plot, coloring elements by strand
pileupPlot <- bbPlotRanges(
    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 <- bbPlotLegend(
    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
bbAnnoGenomeLabel(
    plot = pileupPlot, x = 0.5, y = 3.5,
    just = c("left", "top")
)

## Hide page guides
bbPageGuideHide()
```

---

bbPlotManhattan *Plot a Manhattan plot*

Description

Plot a Manhattan plot

Usage

```
bbPlotManhattan(
    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,
    ymax = 1,
    range = NULL,
    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. This column must be numeric. p-values will be converted to -log(10) space. • `"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 to -log1=(10) space. 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 bbAssembly 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. If scaleLD is supplied, sigCol will be ignored.
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 p-values to plot (c(min, max)).
space	A numeric value indicating the space between each chromsome 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.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Details

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

```
bbPlotManhattan(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:

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

Value

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

Examples

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

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

## Plot all GWAS data
manhattanPlot <- bbPlotManhattan(
```

```
    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
bbAnnoGenomeLabel(
    plot = manhattanPlot, x = 0.5, y = 2, fontsize = 8,
    just = c("left", "top"),
    default.units = "inches"
)
bbPlotText(
    label = "Chromosome", fontsize = 8,
    x = 3.75, y = 2.20, just = "center", default.units = "inches"
)

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

## Plot y-axis label
bbPlotText(
    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(
                                        hg19_insulin_GWAS$LD,
                                        c(0, 0.2, 0.4, 0.6, 0.8, 1))))
hg19_insulin_GWAS$LDgrp <- addNA(hg19_insulin_GWAS$LDgrp)
leadSNP_p <- min(hg19_insulin_GWAS[
    which(hg19_insulin_GWAS$chrom == "chr11"), ]$p)
leadSNP <- hg19_insulin_GWAS[which(hg19_insulin_GWAS$p == leadSNP_p), ]$snp
chr11_manhattanPlot <- bbPlotManhattan(
    data = hg19_insulin_GWAS, chrom = "chr11",
    chromstart = 60000000,
    chromend = 130000000,
    assembly = "hg19",
    fill = colorby("LDgrp",
    palette = colorRampPalette(c(
        "#1f4297",
```

```
        "#37a7db", "green",
        "orange", "red", "grey"
    ))),
    sigLine = TRUE, col = "grey",
    lty = 2, range = c(0, 16),
    leadSNP = list(
        snp = leadSNP,
        pch = 18,
        cex = 0.75,
        fill = "#7ecdbb",
        fontsize = 8
    ),
    scaleLD = "LD",
    x = 0.5, y = 2.5, width = 6.5,
    height = 1.5,
    just = c("left", "top"),
    default.units = "inches"
)

## Plot legend for LD scores
bbPlotLegend(
    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
bbAnnoGenomeLabel(
    plot = chr11_manhattanPlot, x = 0.5, y = 4.01,
    fontsize = 8, scale = "Mb",
    just = c("left", "top"), default.units = "inches"
)

## Annotate y-axis
bbAnnoYaxis(
    plot = chr11_manhattanPlot,
    at = c(0, 2, 4, 6, 8, 10, 12, 14, 16),
    axisLine = TRUE, fontsize = 8
)

## Plot y-axis label
bbPlotText(
    label = "-log10(p-value)", x = 0.15, y = 3.25, rot = 90,
```

```
    fontsize = 8, fontface = "bold", just = "center",
    default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

---

bbPlotPairs *Plot paired-end genomic range elements*

Description

Plot paired-end genomic range elements

Usage

```
bbPlotPairs(
    data,
    chrom,
    chromstart = NULL,
    chromend = NULL,
    assembly = "hg38",
    fill = "#1f4297",
    linecolor = NA,
    bg = NA,
    boxHeight = unit(2, "mm"),
    spaceWidth = 0.02,
    spaceHeight = 0.3,
    limitLabel = TRUE,
    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 bbAssembly 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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Details

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

```
bbPlotPairs(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:

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

Value

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

Examples

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

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

## Create a page
bbPageCreate(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 <- bbPlotPairs(
    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
```

```
bbAnnoGenomeLabel(plot = bedpePlot, x = 0.25, y = 1.78, scale = "Mb")

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

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

## Hide page guides
bbPageGuideHide()
```

---

bbPlotPairsArches *Plot paired-end genomic range data in an arch style*

Description

Plot paired-end genomic range data in an arch style

Usage

```
bbPlotPairsArches(
    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,
    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 bbAssembly 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 or numeric vector 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`.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Details

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

```
bbPlotPairsArches(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:

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

Value

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

Examples

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

## Set the coordinates
params <- bbParams(
    chrom = "chr21",
    chromstart = 27900000, chromend = 30700000,
    assembly = "hg19",
```

```
    width = 7
)

## Create a page
bbPageCreate(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
heights <- IMR90_DNAloops_pairs$length / max(IMR90_DNAloops_pairs$length)

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

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


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

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


## Hide page guides
bbPageGuideHide()
```

---

bbPlotPolygon *Plot a polygon within a BentoBox layout*

Description

Plot a polygon within a BentoBox layout

Usage

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

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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_polygon object containing relevant placement and grob information.

See Also

grid.polygon

Examples

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

## Plot complex polygons one at a time
bbPlotPolygon(
    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
)

bbPlotPolygon(
    x = c(4.65, 4.75, 6.05, 5.05, 4.4),
    y = c(3.1, 3.5, 4, 1.45, 1.2),
    fill = "#9d28b0", linecolor = NA
)

## Plot multiple triangles with different id's and colors
bbPlotPolygon(
    x = c(
        0.45, 6.05, 3, 3, 6.05, 5.25, 4.4, 5.05, 4.95,
        1.3, 2.6, 1, 4.4, 4.95, 5, 4.95, 5, 6.25
    ),
    y = c(
        2.85, 4, 5.55, 5.55, 4, 5.55, 1.2, 1.45, 1.1,
        2.8, 2.5, 2.1, 1.2, 1.1, 0.45, 1.1, 0.45, 1.1
    ),
    id = c(1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4, 5, 5, 5, 6, 6, 6),
    fill = c(
        "#ce93d9", "#bb6ac9", "#4a168e",
        "#7b1fa0", "#bb6ac9", "#ce93d9"
    ),
    linecolor = NA
)

## Hide page guides
bbPageGuideHide()
```

---

bbPlotRanges *Plot genomic range elements in a pileup or collapsed format*

Description

Plot genomic range elements in a pileup or collapsed format

Usage

```
bbPlotRanges(
    data,
    chrom,
    chromstart = NULL,
    chromend = NULL,
    assembly = "hg38",
    fill = "#7ecdbb",
    linecolor = NA,
    collapse = FALSE,
    boxHeight = unit(2, "mm"),
    spaceWidth = 0.02,
    spaceHeight = 0.3,
    limitLabel = TRUE,
    strandSplit = FALSE,
    bg = NA,
    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`	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 bbAssembly 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.

.

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 = 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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Details

A ranges plot can be placed on a BentoBox coordinate page by providing plot placement parameters:

```
bbPlotRanges(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:

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

Value

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

Examples

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

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

## Plot and place a pileup ranges plot
pileupPlot <- bbPlotRanges(
    data = IMR90_ChIP_CTCF_reads, chrom = "chr21",
    chromstart = 29073000, chromend = 29074000,
    assembly = "hg19",
    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
bbAnnoGenomeLabel(
    plot = pileupPlot, x = 0.5, y = 4.5,
    just = c("left", "top")
)

## Add text labels
bbPlotText(
    label = "+ strand", fontcolor = "#37a7db", fontsize = 12,
    x = 0.5, y = 1.25, just = "left"
)
```

```
bbPlotText(
    label = "- strand", fontcolor = "#7ecdbb", fontsize = 12,
    x = 0.5, y = 3.5, just = "left"
)

## Hide page guides
bbPageGuideHide()
```

`bbPlotRaster` *Plot a raster object within a BentoBox layout*

Description

Plot a raster object within a BentoBox layout

Usage

```
bbPlotRaster(
    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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_raster object containing relevant placement and grob information.

See Also

grid.raster

Examples

```
library(png)

## Load images
edamaman <- readPNG(system.file("images",
    "bento-edamaman.png",
    package = "BentoBox"
))
logotype <- readPNG(system.file("images",
    "bento-logotype-singleline-black.png",
    package = "BentoBox"
))
rlogo <- readPNG(system.file("images", "Rlogo.png", package = "BentoBox"))

## Create page
bbPageCreate(width = 5, height = 6)

## Plot various images
bbPlotRaster(
    image = logotype,
    x = 2.5, y = 0.25, width = 3.25, height = 0.5, just = "top"
)

bbPlotRaster(
    image = edamaman,
    x = 2.5, y = 5.5, width = 2, height = 4, just = "bottom"
)

bbPlotRaster(
    image = rlogo,
    x = 2.5, y = 1, width = 0.5, height = 0.45,
    just = c("right", "top")
)

## Hide page guies
bbPageGuideHide()
```

bbPlotRect *Plot a rectangle within a BentoBox layout*

Description

Plot a rectangle within a BentoBox layout

Usage

```
bbPlotRect(
    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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
`...`	Additional grid graphical parameters. See gpar.

Value

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

See Also

grid.rect

Examples

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

## Plot one rectangle with no fill
bbPlotRect(
    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
bbPlotRect(
    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
bbPlotRect(
    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
bbPageGuideHide()
```

bbPlotSegments *Draw a line segment within a BentoBox layout*

Description

Draw a line segment within a BentoBox layout

Usage

```
bbPlotSegments(
    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 BentoBox plot according to the units of the BentoBox 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 v alues 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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
`...`	Additional grid graphical parameters. See gpar.

Value

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

See Also

grid.segments, arrow

Examples

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

## Plot one line segment
bbPlotSegments(
    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
bbPlotSegments(
    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
bbPlotSegments(
    x0 = 4.5, y0 = 0.5, x1 = 7, y1 = 3,
```

```
    default.units = "inches",
    arrow = arrow(type = "closed"), fill = "black"
)

## Plot lines with round lineends
bbPlotSegments(
    x0 = c(4, 7), y0 = 3.5, x1 = 5.5, y1 = 4.5,
    default.units = "inches",
    lwd = 5, lineend = "round"
)

## Hide page guides
bbPageGuideHide()
```

---

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

Description

Plot any kind of signal track data for a single chromosome

Usage

```
bbPlotSignal(
    data,
    binSize = NA,
    binCap = TRUE,
    negData = FALSE,
    chrom,
    chromstart = NULL,
    chromend = NULL,
    assembly = "hg38",
    linecolor = "#37a7db",
    fill = NA,
    ymax = 1,
    range = NULL,
    scale = FALSE,
    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,
    ...
)
```

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.
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 data has both positive and negative scores and the y-axis 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 bbAssembly 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.
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.
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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Details

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

```
bbPlotSignal(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:

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

Value

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

Examples

```
## Load signal data
library(BentoBoxData)
data("IMR90_ChIP_H3K27ac_signal")
data("GM12878_ChIP_H3K27ac_signal")

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

## Define region
```

```
region <- bbParams(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    assembly = "hg19",
    range = c(0, 45)
)

## Plot and place signal plots
signal1 <- bbPlotSignal(
    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 <- bbPlotSignal(
    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
bbPlotGenomeLabel(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    assembly = "hg19",
    x = 0.5, y = 1.68, length = 6.5,
    default.units = "inches"
)

## Add text labels
bbPlotText(
    label = "IMR90", fonsize = 10, fontcolor = "#37a7db",
    x = 0.5, y = 0.25, just = c("left", "top"),
    default.units = "inches"
)
bbPlotText(
    label = "GM12878", fonsize = 10, fontcolor = "#7ecdbb",
    x = 0.5, y = 1, just = c("left", "top"),
    default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

`bbPlotText` *Plot text within a BentoBox layout*

Description

Plot text within a BentoBox layout

Usage

```
bbPlotText(
    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 BentoBox plot according to the units of the BentoBox 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 bbParams object containing relevant function parameters.
...	Additional grid graphical parameters. See gpar.

Value

Returns a bb_text object containing relevant placement and grob information.

See Also

grid.text

Examples

```
## Create a BentoBox page
bbPageCreate(width = 4, height = 2, default.units = "inches")

## Plot text, adjusting fontsize and fontface
bbPlotText(
    label = "BentoBox", fontsize = 14, fontface = "bold",
    x = 1, y = 1, just = "center", default.units = "inches"
)

## Plot text, adjusting color, rotation, and fontfamily
bbPlotText(
    label = "coordinate-based", fontcolor = "#225EA8", rot = 90,
    fontfamily = "HersheyScript", x = 2, y = 1, just = "center",
    default.units = "inches"
)

## Plot a text label in multiple places at once
bbPlotText(
    label = "R", x = c(0.5, 1, 1.5), y = 1.5, just = "center",
    default.units = "inches"
)

## Plot a vector of text labels
bbPlotText(
    label = c("bb", "Bento", "Box"), x = 3, y = c(0.5, 1, 1.75),
    just = "center", default.units = "inches"
)

## Hide page guides
bbPageGuideHide()
```

---

bbPlotTranscripts *Plot gene transcripts in a pileup style for a single chromosome*

Description

Plot gene transcripts in a pileup style for a single chromosome

Usage

```
bbPlotTranscripts(
    chrom,
    chromstart = NULL,
    chromend = NULL,
    assembly = "hg38",
    fill = c("#669fd9", "#abcc8e"),
    colorbyStrand = TRUE,
    strandSplit = FALSE,
```

```
    boxHeight = unit(2, "mm"),
    spaceWidth = 0.02,
    spaceHeight = 0.3,
    limitLabel = TRUE,
    fontsize = 8,
    labels = "transcript",
    stroke = 0.1,
    bg = NA,
    x = NULL,
    y = 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 bbAssembly 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 limitLabel = TRUE.
fontsize	A numeric specifying text fontsize in points. Default value is fontsize = 8.
labels	A character value describing the format of transcript text labels. Default value is labels = "trancript". 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 stroke = 0.1.
bg	Character value indicating background color. Default value is bg = 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 BentoBox plot according to the units of the BentoBox 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 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 bbParams object containing relevant function parameters.

Details

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

```
bbPlotTranscripts(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 transcripts plot by ignoring plot placement parameters:

```
bbPlotTranscripts(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 bb_transcripts object containing relevant genomic region, placement, and grob information.

See Also

bbAssembly, bbGenomes, bbDefaultPackages

Examples

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

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

## Plot and place transcripts
bbPlotTranscripts(
    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
bbPlotGenomeLabel(
    chrom = "chr8", chromstart = 1000000, chromend = 2000000,
    assembly = "hg19",
    x = 0.5, y = 3.03, length = 6.5, default.units = "inches"
)

## Plot a legend
bbPlotLegend(
    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
bbPageGuideHide()
```

---

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

Description

Read a bigWig file and return it as a data frame

Usage

```
bbReadBigwig(
    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 strand = "*". Options are: • "+": Plus strand. • "-": Minus strand. • "*": Plus and minus strands.
params	An optional bbParams object containing relevant function parameters.

Details

This function does not work on Windows.

Value

Returns a 6-column dataframe of bigwig information.

See Also

import.bw

Examples

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

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

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

bbReadHic *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

```
bbReadHic(
    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.
`chromend`	Integer end position on chromosome.
`altchrom`	Alternate chromosome for interchromosomal data, as a string.
`altchromstart`	Alternate chromosome integer start position for interchromosomal data.
`altchromend`	Alternate chromosome integer end position for interchromosomal data.
`assembly`	Default genome assembly as a string or a bbAssembly 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 bbParams 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, altchrom, counts.

See Also

straw

Examples

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

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

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

BentoBox *BentoBox: Coordinate-based Genomic Visualization Package for R*

Description

BentoBox is a coordinate-based genomic visualization package for R. It grants users the ability to programmatically produce complex, multi-paneled figures. Tailored for genomics, BentoBox 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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See Also

Useful links:

- https://phanstiellab.github.io/BentoBox
- https://github.com/PhanstielLab/BentoBox

---

c *Combine multiple bbParams objects into a vector*

Description

Combine multiple bbParams objects into a vector

Usage

```
c(..., recursive = FALSE)
```

Arguments

...	bbParams 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 <- bbParams(chrom = "chr1", assembly = "hg19")

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

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

---

colorby *Handle BentoBox color scaling parameters*

Description

colorby should be used to create a set of parameters that specify color scaling for the functions bbPlotPairs, bbPlotPairsArches, and bbPlotRanges.

Usage

```
colorby(column, 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.
scalePerRegion	A logical value indicating whether to adjust NULL range of numerical 'colorby' values to subset of data in a plotted genomic regoin. Default value is scalePerRegion = FALSE.

Value

Returns a "bb_colorby" object.

Examples

```
## Load paired ranges data in BEDPE format
library(BentoBoxData)
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 <- bbPlotPairs(
```

```
    data = IMR90_DNAloops_pairs,
    chrom = "chr21",
    chromstart = 27900000, chromend = 30700000,
    assembly = "hg19",
    fill = colorby("length", palette =
                colorRampPalette(c("dodgerblue2", "firebrick2"))),
    lwd = 2, spaceHeight = .7,
)
```

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