

# Package ‘BentoBox’

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**Title** Coordinate-based Genomic Visualization Package for R

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**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.

**Depends** R (>= 4.0)

**License** GPL (>= 2) | file LICENSE

**URL** <https://phanstiellab.github.io/bentobox>,  
<https://github.com/PhanstielLab/BentoBox>

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bb_annoGenomeLabel	<i>Annotate genomic coordinates along the x or y-axis of a BentoBox plot</i>
--------------------	--

---

**Description**

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

**Usage**

```
bb_annoGenomeLabel(
  plot,
  fontsize = 10,
  fontcolor = "black",
  linecolor = "black",
  margin = unit(1, "mm"),
  scale = "bp",
  commas = TRUE,
  sequence = TRUE,
  boxWidth = 0.5,
  axis = "x",
  at = NULL,
  tcl = 0.5,
  x,
  y,
  just = c("left", "top"),
  default.units = "inches",
  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: <ul style="list-style-type: none"> <li>• "bp": base pairs.</li> <li>• "Kb": kilobase pairs. 1 kilobase pair is equal to 1000 base pairs.</li> <li>• "Mb": megabase pairs. 1 megabase pair is equal to 1000000 base pairs.</li> </ul>
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: <ul style="list-style-type: none"> <li>• "x": Genome label will be plotted along the x-axis.</li> <li>• "y": Genome label will be plotted along the y-axis. This is typically used for a square Hi-C plot made with bb_plotHicSquare.</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters or digit specifications. See <a href="#">gpar</a> and <a href="#">formatC</a> .

**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
bb_pageCreate(width = 5, height = 2, default.units = "inches")

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

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

## Hide page guides
bb_pageGuideHide()
```

---

`bb_annoHeatmapLegend`    *Add a color scale legend for heatmap-style plots*

---

**Description**

Add a color scale legend for heatmap-style plots

**Usage**

```

bb_annoHeatmapLegend(
  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: <ul style="list-style-type: none"> <li>• "v": Vertical legend orientation.</li> <li>• "h": Horizontal legend orientation.</li> </ul>
fontsize	A numeric specifying text fontsize in points. Default value is fontsize = 8.
fontcolor	Character value specifying text fontcolor. Default value is fontcolor = "dark grey".
scientific	Logical value specifying if numeric color value labels should be encoded in scientific format. Default value is scientific = FALSE.
digits	Numeric specifying how many 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.

<code>just</code>	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 <code>just = c("left", "top")</code> .
<code>default.units</code>	A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is <code>default.units = "inches"</code> .
<code>params</code>	An optional <code>bb_params</code> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <code>gpar</code> .

## Value

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

## Examples

```
## Load Hi-C data
data("bb_imrHicData")

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

## Plot and place a square Hi-C plot
hicPlot <- bb_plotHicSquare(
  data = bb_imrHicData, resolution = 10000,
  xrange = 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"
)

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

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

## Hide page guides
bb_pageGuideHide()
```

---

<code>bb_annoHighlight</code>	<i>Annotates a highlight box around a specified genomic region of a BentoBox plot</i>
-------------------------------	---

---

## Description

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

## Usage

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

## Arguments

plot	Input 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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

## Value

Returns a `bb_highlight` object containing relevant genomic region, placement, and [grob](#) information.



**Examples**

```

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

## Plot and place a signal plot
data("bb_imrH3K27acData")
region <- bb_params(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  range = c(0, 45)
)
signalPlot <- bb_plotSignal(
  data = bb_imrH3K27acData, 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
bb_annoHighlight(
  plot = signalPlot,
  chrom = "chr21",
  chromstart = 29000000, chromend = 29125000,
  y = 0.25, height = 1, just = c("left", "top"),
  default.units = "inches"
)

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

## Plot genome label
bb_plotGenomeLabel(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  x = 0.5, y = 1.3, length = 6.5, default.units = "inches"
)

## Hide page guides
bb_pageGuideHide()

```

---

bb\_annoPixels

*Annotate pixels in a Hi-C plot*


---

**Description**

Annotate pixels in a Hi-C plot

**Usage**

```

bb_annoPixels(
  plot,

```

```

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

```

### Arguments

plot	Hi-C plot object from <code>bb_plotHicSquare</code> or <code>bb_plotHicTriangle</code> on which to annotate pixels.
data	A string specifying the BEDPE file path, a dataframe in BEDPE format specifying pixel positions, or a <a href="#">GInteractions</a> object specifying pixel positions.
type	Character value specifying type of annotation. Default value is <code>type = "box"</code> . Options are: <ul style="list-style-type: none"> <li>• <code>"box"</code>: Boxes are drawn around each pixel.</li> <li>• <code>"circle"</code>: Circles are drawn around each pixel.</li> <li>• <code>"arrow"</code>: Arrows are drawn pointing to each pixel.</li> </ul>
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 <code>half = "inherit"</code> . Options are: <ul style="list-style-type: none"> <li>• <code>"inherit"</code>: Pixels will be annotated on the half inherited by the input Hi-C plot.</li> <li>• <code>"both"</code>: Pixels will be annotated on both halves of the diagonal of a square Hi-C plot.</li> <li>• <code>"top"</code>: Pixels will be annotated on the upper diagonal half of a square Hi-C plot.</li> <li>• <code>"bottom"</code>: Pixels will be annotated on the bottom diagonal half of a square Hi-C plot.</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.
quiet	A logical indicating whether or not to print messages.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

### Value

Returns a `bb_pixel` object containing relevant genomic region, placement, and [grob](#) information.

### Examples

```

## Load Hi-C data and BEDPE data
data("bb_imrHicData")
data("bb_bedpeData")

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

```

```

## Plot and place a square Hi-C plot
hicPlot <- bb_plotHicSquare(
  data = bb_imrHicData, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  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 <- bb_annoPixels(
  plot = hicPlot, data = bb_bedpeData, type = "box",
  half = "both"
)

## Annotate loops on one side of Hi-C plot with arrows
## and the other side with circles
bb_pagePlotRemove(plot = pixels)
pixels1 <- bb_annoPixels(
  plot = hicPlot, data = bb_bedpeData,
  type = "arrow", half = "top", shift = 8
)
pixels2 <- bb_annoPixels(
  plot = hicPlot, data = bb_bedpeData,
  type = "circle", half = "bottom"
)

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

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

## Hide page guides
bb_pageGuideHide()

```

---

bb\_annoSegments

*Annotates a line segment within a BentoBox plot*


---

## Description

Annotates a line segment within a BentoBox plot

## Usage

```
bb_annoSegments(
```

```

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

```

### Arguments

<code>x0</code>	A numeric vector or unit object indicating the starting x-values of the line segments.
<code>y0</code>	A numeric vector or unit object indicating the starting y-values of the line segments.
<code>x1</code>	A numeric vector or unit object indicating the stopping x-values of the line segments.
<code>y1</code>	A numeric vector or unit object indicating the stopping y-values of the line segments.
<code>plot</code>	Input BentoBox plot to internally plot line segments relative to.
<code>default.units</code>	A string indicating the default units to use if <code>x0</code> , <code>y0</code> , <code>x1</code> , or <code>y1</code> are only given as numeric vectors. Default value is <code>default.units = "native"</code> .
<code>linecolor</code>	A character value specifying segment line color. Default value is <code>linecolor = "black"</code> .
<code>lwd</code>	A numeric specifying segment line width. Default value is <code>lwd = 1</code> .
<code>lty</code>	A numeric specifying segment line type. Default value is <code>lty = 1</code> .
<code>lineend</code>	A character value specifying line end style. Default value is <code>lineend = "butt"</code> . Options are: <ul style="list-style-type: none"> <li>• <code>"round"</code>: Segment ends are rounded.</li> <li>• <code>"butt"</code>: Segment ends end exactly where ended.</li> <li>• <code>"square"</code>: Segment ends are squared.</li> </ul>
<code>linejoin</code>	A character value specifying line join style. Default value is <code>linejoin = "mitre"</code> . Options are: <ul style="list-style-type: none"> <li>• <code>"round"</code>: Line joins are rounded.</li> <li>• <code>"mitre"</code>: Line joins are sharp corners.</li> <li>• <code>"bevel"</code>: Line joins are flattened corners.</li> </ul>
<code>arrow</code>	A list describing arrow heads to place at either end of the line segments, as produced by the <a href="#">arrow</a> function.
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

**Value**

Returns a `bb_segments` object containing relevant placement and [grob](#) information.

**See Also**

[grid.segments](#), [arrow](#)

**Examples**

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

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

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

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

## Plot y-axis label
bb_plotText(
  label = "-log10(p-value)", x = 0.15, y = 1, rot = 90,
  fontsize = 8, fontface = "bold", just = "center",
```

```

        default.units = "inches"
    )

    ## Hide page guides
    bb_pageGuideHide()

```

---

**bb\_annoText**
*Annotates text within a BentoBox plot*


---

## Description

Annotates text within a BentoBox plot

## Usage

```

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

```

## Arguments

<code>label</code>	Character or expression of text to be plotted.
<code>fontcolor</code>	A character value specifying text fontcolor. Default value is <code>fontcolor = "black"</code> .
<code>fontsize</code>	A numeric specifying text fontsize in points. Default value is <code>fontsize = 12</code> .
<code>rot</code>	A numeric specifying the angle to rotate the text. Default value is <code>rot = 0</code> .
<code>check.overlap</code>	A logical value to indicate whether to check for and omit overlapping text. Default value is <code>check.overlap = FALSE</code> .
<code>plot</code>	Input BentoBox plot to internally place text relative to.
<code>x</code>	A numeric vector or unit object specifying text x-location.
<code>y</code>	A numeric vector or unit object specifying text y-location.
<code>just</code>	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 <code>just = "center"</code> .
<code>default.units</code>	A string indicating the default units to use if x or y are only given as numerics or numeric vectors. Default value is <code>default.units = "native"</code> .
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

**Value**

Returns a `bb_text` object containing relevant placement and [grob](#) information.

**See Also**

[grid.text](#)

**Examples**

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

## Plot text relative to a BentoBox plot
data("bb_imrHicData")
hicPlot <- bb_plotHicSquare(
  data = bb_imrHicData, chrom = "chr21",
  chromstart = 28000000, chromend = 29500000,
  xrange = c(0, 70),
  x = 0.5, y = 0.5, width = 3, height = 3,
  just = c("left", "top"),
  default.units = "inches"
)
bb_annoGenomeLabel(
  plot = hicPlot, x = 0.5, y = 3.55, scale = "Mb",
  just = c("left", "top"), default.units = "inches"
)

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

## Hide page guides
bb_pageGuideHide()
```

---

bb\_annoXaxis

*Add an x-axis to a plot*


---

**Description**

Add an x-axis to a plot

**Usage**

```
bb_annoXaxis(
  plot,
  at = NULL,
  label = TRUE,
  main = TRUE,
  scipen = 999,
  axisLine = FALSE,
  params = NULL,
```

```
    ...  
  )
```

### Arguments

plot	Plot object to annotate with x-axis.
at	A numeric vector of x-value locations for tick marks.
label	A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the at argument.
main	A logical value indicating whether to draw the x-axis at the bottom of the plot. Default value is main = TRUE. Options are: <ul style="list-style-type: none"> <li>• TRUE: x-axis is drawn at the bottom of the plot.</li> <li>• FALSE: x-axis is drawn at the top of the plot.</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

### 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
bb_pageCreate(width = 7.5, height = 4.5, default.units = "inches")

## Plot gene transcripts
transcriptPlot <- bb_plotTranscripts(
  chrom = "chr1",
  chromstart = 1000000,
  chromend = 2000000,
  x = 0.5, y = 0,
  width = 6.5, height = 4,
  just = c("left", "top"),
  default.units = "inches"
)

## Add standard x-axis to transcript plot
bb_annoXaxis(
  plot = transcriptPlot,
  at = c(1000000, 1250000, 1500000, 1750000, 2000000),
  fontsize = 8
)
bb_plotText(
  label = "Basepairs", fontsize = 10, fontface = "bold",
```



```

      x = 3.75, y = 4.3, just = "top"
    )

## Hide page guides
bb_pageGuideHide()

```

---

bb\_annoYaxis

*Add a y-axis to a plot*


---

## Description

Add a y-axis to a plot

## Usage

```

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

```

## Arguments

plot	Plot object to annotate with y-axis.
at	A numeric vector of y-value locations for tick marks.
label	A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the at argument.
main	A logical value indicating whether to draw the y-axis at the left of the plot. Default value is main = TRUE. Options are: <ul style="list-style-type: none"> <li>• TRUE: y-axis is drawn at the left of the plot.</li> <li>• FALSE: y-axis is drawn at the right of the plot.</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

## Value

Returns a `bb_yaxis` object containing relevant [grob](#) information.

**Examples**

```
## Load Hi-C data
data("bb_imrHicData")

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

## Plot and place a square Hi-C plot
hicPlot <- bb_plotHicSquare(
  data = bb_imrHicData, resolution = 10000,
  zrange = c(0, 70),
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  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
bb_annoYaxis(
  plot = hicPlot, at = c(28000000, 29000000, 30300000),
  fontsize = 10
)

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

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

## Hide page guides
bb_pageGuideHide()
```

---

bb_annoZoomLines	<i>Annotates zoom lines for a specified genomic region of a BentoBox plot</i>
------------------	---

---

**Description**

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

**Usage**

```
bb_annoZoomLines(
  plot,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  y0,
  x1 = NULL,
```

```

    y1,
    extend = 0,
    default.units = "inches",
    linecolor = "grey",
    lty = 2,
    params = NULL,
    ...
)

```

### Arguments

plot	Input 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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

### Value

Returns a `bb_zoom` object containing relevant genomic region, placement, and [grob](#) information.

### Examples

```

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

## Plot and place a Manhattan plot
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
data("bb_gwasData")
manhattanPlot <- bb_plotManhattan(

```

```

    data = bb_gwasData, 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"
  )
  bb_annoYaxis(
    plot = manhattanPlot, at = c(0, 2, 4, 6, 8, 10, 12, 14),
    axisLine = TRUE, fontsize = 8
  )

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

  ## Annotate highlight region for zoom region
  bb_annoHighlight(
    plot = manhattanPlot, params = zoomRegion,
    y = 2, height = 2, just = c("left", "bottom"),
    default.units = "inches",
    fill = "red", alpha = 0.8
  )

  ## Plot Manhattan plot data and signal track under zoom lines
  manhattanPlotZoom <- bb_plotManhattan(
    data = bb_gwasData, fill = "grey",
    sigLine = FALSE,
    baseline = TRUE,
    params = zoomRegion, range = c(0, 14),
    x = 0.5, y = 2.6,
    width = 6.5, height = 1
  )
  data("bb_imrH3K27acData")
  signalPlot <- bb_plotSignal(
    data = bb_imrH3K27acData, 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
  bb_plotGenomeLabel(
    chrom = "chr21",
    chromstart = 28000000, chromend = 30300000,
    x = 0.5, y = 4.4, length = 6.5,

```

```

        default.units = "inches"
    )

    ## Hide page guides
    bb_pageGuideHide()

```

---

bb_assembly	<i>Make a bb_assembly object for alternate TxDb, OrgDb, and BSgenome genomic annotation packages</i>
-------------	--

---

## Description

Make a bb\_assembly object for alternate TxDb, OrgDb, and BSgenome genomic annotation packages

## Usage

```

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

```

## Arguments

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

## Value

Returns a bb\_assembly object containing all input parameters.

## See Also

[TxDb](#), [OrgDb-class](#), [BSgenome](#)

## Examples

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

---

bb\_bedData

*BentoBox example BED data*


---

## Description

A dataset listing aligned sequencing reads for CTCF in the IMR90 cell line as determined by ChIP-seq. Genomic coordinates fall within the region chr21:28000000-30300000 according to the hg19 genome build.

## Usage

```
data("bb_bedData")
```

## Format

a dataframe in BED format

**chrom** The name of the chromosome on which the genome feature exists.

**start** The starting position of the feature in the chromosome.

**end** The ending position of the feature in the chromosome.

**strand** An optional column defining the strand of the feature as either '+' or '-'.

## Source

Data from **Michael Snyder, Stanford** with accession number **ENCFF847VPR** was downloaded from the ENCODE portal <https://www.encodeproject.org/>.

## References

ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012 Sep 6;489(7414):57-74. doi: 10.1038/nature11247. PMID: 22955616; PMCID: PMC3439153.

Davis CA, Hitz BC, Sloan CA, Chan ET, Davidson JM, Gabdank I, Hilton JA, Jain K, Baymurov UK, Narayanan AK, Onate KC, Graham K, Miyasato SR, Dreszer TR, Strattan JS, Jolanki O, Tanaka FY, Cherry JM. The Encyclopedia of DNA elements (ENCODE): data portal update. *Nucleic Acids Res*. 2018 Jan 4;46(D1):D794-D801. doi: 10.1093/nar/gkx1081. PMID: 29126249; PMCID: PMC5753278.

---

bb_bedpeData	<i>BentoBox example BEDPE data</i>
--------------	------------------------------------

---

### Description

A dataset listing interaction data along genomic coordinates in the region chr21:28000000-30300000 according to the hg19 genome build. This data represents called DNA loops in the IMR90 cell line.

### Usage

```
data("bb_bedpeData")
```

### Format

a dataframe in BEDPE format

**chrom1** The name of the chromosome on which the first end of the feature exists.

**start1** The starting position of the first end of the feature on chrom1.

**end1** The ending position of the first end of the feature on chrom1.

**chrom2** The name of the chromosome on which the second end of the feature exists.

**start2** The starting position of the second end of the feature on chrom2.

**end2** The ending position of the second end of the feature on chrom2.

### References

Rao SS, Huntley MH, Durand NC, Stamenova EK, Bochkov ID, Robinson JT, Sanborn AL, Machol I, Omer AD, Lander ES, Aiden EL. A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. *Cell*. 2014 Dec 18;159(7):1665-80. doi: 10.1016/j.cell.2014.11.021. Epub 2014 Dec 11. Erratum in: *Cell*. 2015 Jul 30;162(3):687-8. PMID: 25497547; PMCID: PMC5635824. ([PubMed](#))

---

bb_CasesNYFL	<i>BentoBox example data for COVID-19 cases in New York and Florida</i>
--------------	---

---

### Description

A timeline dataset tracking positive COVID-19 cases in New York and Florida from 2020-01-29 to 2021-03-07.

### Usage

```
data("bb_CasesNYFL")
```

### Format

a dataframe with 3 columns

**date** The date of the case count.

**state** The state of the case count. Either "new york" or "florida".

**caseIncrease** The increase number of positive COVID-19 cases.

**Source**

Data was downloaded from The COVID Tracking Project <https://covidtracking.com/>.

---

bb_CasesUSA	<i>BentoBox example data for COVID-19 cases in the United States</i>
-------------	--

---

**Description**

A data frame of United States map data and COVID-19 cases as of 2021-03-07.

**Usage**

```
data("bb_CasesUSA")
```

**Format**

a dataframe with 7 columns

**state** The associated state in the United States.

**group** Numeric value describing a group for each state.

**long** Longitude value.

**lat** Latitude value.

**cases** The cumulative number of COVID-19 cases.

**population** Numeric value of total state population.

**cases\_100K** The cumulative number of COVID-19 cases, per 100000 individuals.

**Source**

COVID-19 case data was downloaded from The COVID Tracking Project <https://covidtracking.com/>. Data was turned into map data with [map\\_data](#).

---

bb_defaultPackages	<i>Display the default genomic annotation packages associated with a genome build</i>
--------------------	---

---

**Description**

Display the default genomic annotation packages associated with a genome build

**Usage**

```
bb_defaultPackages(Genome)
```

**Arguments**

Genome                      String indicating the name of the genome assembly.



**Value**

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

**Examples**

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

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

---

bb_genomes	<i>Display the included available default genome assemblies</i>
------------	---

---

**Description**

Display the included available default genome assemblies

**Usage**

```
bb_genomes()
```

**Value**

Returns the included available default genome assemblies

**Examples**

```
bb_genomes()
```

---

bb_gmCTCFData	<i>BentoBox example GM12878 CTCF signal data</i>
---------------	--

---

**Description**

A dataset listing read depths across the genome resulting from CTCF ChIP-seq in the GM12878 cell line. Genomic coordinates fall within the region chr21:28000000-30300000 according to the hg19 genome build.

**Usage**

```
data("bb_gmCTCFData")
```

**Format**

a dataframe in BED format with a "score" column

**chrom** The name of the chromosome on which the genome feature exists.

**start** The starting position of the feature in the chromosome.

**end** The ending position of the feature in the chromosome.

**score** Score value of read depth.

## Source

Data from **Michael Snyder, Stanford** with accession number **ENCFF312KXX** was downloaded from the ENCODE portal <https://www.encodeproject.org/>.

## References

ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012 Sep 6;489(7414):57-74. doi: 10.1038/nature11247. PMID: 22955616; PMCID: PMC3439153.

Davis CA, Hitz BC, Sloan CA, Chan ET, Davidson JM, Gabdank I, Hilton JA, Jain K, Baymuradov UK, Narayanan AK, Onate KC, Graham K, Miyasato SR, Dreszer TR, Strattan JS, Jolanki O, Tanaka FY, Cherry JM. The Encyclopedia of DNA elements (ENCODE): data portal update. *Nucleic Acids Res*. 2018 Jan 4;46(D1):D794-D801. doi: 10.1093/nar/gkx1081. PMID: 29126249; PMCID: PMC5753278.

---

bb\_gmH3K27acData

*BentoBox example GM12878 H3K27ac signal data*


---

## Description

A dataset listing read depths across the genome resulting from H3K27ac ChIP-seq in the GM12878 cell line. Genomic coordinates fall within the region chr21:28000000-30300000 according to the hg19 genome build.

## Usage

```
data("bb_gmH3K27acData")
```

## Format

a dataframe in BED format with a "score" column

**chrom** The name of the chromosome on which the genome feature exists.

**start** The starting position of the feature in the chromosome.

**end** The ending position of the feature in the chromosome.

**score** Score value of read depth.

## Source

Data with reference epigenome identifier **E116** was downloaded from the NIH Roadmap Epigenomics Project <http://www.roadmapepigenomics.org/>.

## References

Roadmap Epigenomics Consortium., Integrative analysis coordination., Kundaje, A. et al. Integrative analysis of 111 reference human epigenomes. *Nature* 518, 317–330 (2015). <https://doi.org/10.1038/nature14248>

---

bb\_gmHicData*BentoBox example GM12878 Hi-C data*

---

**Description**

A dataset containing interaction frequency matrix counts along genomic coordinates in the region chr21:28000000-30300000 according to the hg19 genome build. This data is from the GM12878 cell line.

**Usage**

```
data("bb_gmHicData")
```

**Format**

a 3-column data frame in sparse upper triangular format.

**References**

Rao SS, Huntley MH, Durand NC, Stamenova EK, Bochkov ID, Robinson JT, Sanborn AL, Machol I, Omer AD, Lander ES, Aiden EL. A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. *Cell*. 2014 Dec 18;159(7):1665-80. doi: 10.1016/j.cell.2014.11.021. Epub 2014 Dec 11. Erratum in: *Cell*. 2015 Jul 30;162(3):687-8. PMID: 25497547; PMCID: PMC5635824. ([PubMed](#))

---

bb\_gwasData*BentoBox example GWAS data*

---

**Description**

A dataset representing GWAS data from a GWAS study of insulin response with coordinates based on the hg19 genome build.

**Usage**

```
data("bb_gwasData")
```

**Format**

a dataframe with the following columns:

**chr** The name of the chromosome of the SNP.

**pos** The basepair position of the SNP.

**p** The p-value of the SNP.

**snp** The rsID of the SNP.

**LD** A simulated linkage disequilibrium score for the SNP.

**Source**

GWAS summary statistics were downloaded from LocusZoom <http://locuszoom.org/>.

## References

Prokopenko I, Poon W, Mägi R, Prasad B R, Salehi SA, Almgren P, Osmark P, Bouatia-Naji N, Wierup N, Fall T, Stančáková A, Barker A, Lagou V, Osmond C, Xie W, Lahti J, Jackson AU, Cheng YC, Liu J, O'Connell JR, Blomstedt PA, Fadista J, Alkayyali S, Dayeh T, Ahlqvist E, Taneera J, Lecoeur C, Kumar A, Hansson O, Hansson K, Voight BF, Kang HM, Levy-Marchal C, Vatin V, Palotie A, Syvänen AC, Mari A, Weedon MN, Loos RJ, Ong KK, Nilsson P, Isomaa B, Tuomi T, Wareham NJ, Stumvoll M, Widen E, Lakka TA, Langenberg C, Tönjes A, Rauramaa R, Kuusisto J, Frayling TM, Froguel P, Walker M, Eriksson JG, Ling C, Kovacs P, Ingelsson E, McCarthy MI, Shuldiner AR, Silver KD, Laakso M, Groop L, Lyssenko V. A central role for GRB10 in regulation of islet function in man. *PLoS Genet.* 2014 Apr 3;10(4):e1004235. doi: 10.1371/journal.pgen.1004235. PMID: 24699409; PMCID: PMC3974640.

---

bb\_imrCTCFData

*BentoBox example IMR90 CTCF signal data*


---

## Description

A dataset listing read depths across the genome resulting from CTCF ChIP-seq in the IMR90 cell line. Genomic coordinates fall within the region chr21:28000000-30300000 according to the hg19 genome build.

## Usage

```
data("bb_imrCTCFData")
```

## Format

a dataframe in BED format with a "score" column

**chrom** The name of the chromosome on which the genome feature exists.

**start** The starting position of the feature in the chromosome.

**end** The ending position of the feature in the chromosome.

**score** Score value of read depth.

## Source

Data from **Michael Snyder, Stanford** with accession number **ENCFF603PYX** was downloaded from the ENCODE portal <https://www.encodeproject.org/>.

## References

ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature.* 2012 Sep 6;489(7414):57-74. doi: 10.1038/nature11247. PMID: 22955616; PMCID: PMC3439153.

Davis CA, Hitz BC, Sloan CA, Chan ET, Davidson JM, Gabdank I, Hilton JA, Jain K, Baymurov UK, Narayanan AK, Onate KC, Graham K, Miyasato SR, Dreszer TR, Strattan JS, Jolanki O, Tanaka FY, Cherry JM. The Encyclopedia of DNA elements (ENCODE): data portal update. *Nucleic Acids Res.* 2018 Jan 4;46(D1):D794-D801. doi: 10.1093/nar/gkx1081. PMID: 29126249; PMCID: PMC5753278.

---

bb\_imrH3K27acData*BentoBox example IMR90 H3K27ac signal data*

---

### Description

A dataset listing read depths across the genome resulting from H3K27ac ChIP-seq in the IMR90 cell line. Genomic coordinates fall within the region chr21:28000000-30300000 according to the hg19 genome build.

### Usage

```
data("bb_imrH3K27acData")
```

### Format

a dataframe in BED format with a "score" column

**chrom** The name of the chromosome on which the genome feature exists.

**start** The starting position of the feature in the chromosome.

**end** The ending position of the feature in the chromosome.

**score** Score value of read depth.

### Source

Data with reference epigenome identifier **E017** was downloaded from the NIH Roadmap Epigenomics Project <http://www.roadmapepigenomics.org/>.

### References

Roadmap Epigenomics Consortium., Integrative analysis coordination., Kundaje, A. et al. Integrative analysis of 111 reference human epigenomes. Nature 518, 317–330 (2015). <https://doi.org/10.1038/nature14248>

---

bb\_imrHicData*BentoBox example IMR90 Hi-C data*

---

### Description

A dataset containing interaction frequency matrix counts along genomic coordinates in the region chr21:28000000-30300000 according to the hg19 genome build. This data is from the IMR90 cell line.

### Usage

```
data("bb_imrHicData")
```

### Format

a 3-column data frame in sparse upper triangular format.

## References

Rao SS, Huntley MH, Durand NC, Stamenova EK, Bochkov ID, Robinson JT, Sanborn AL, Machol I, Omer AD, Lander ES, Aiden EL. A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. *Cell*. 2014 Dec 18;159(7):1665-80. doi: 10.1016/j.cell.2014.11.021. Epub 2014 Dec 11. Erratum in: *Cell*. 2015 Jul 30;162(3):687-8. PMID: 25497547; PMCID: PMC5635824. ([PubMed](#))

---

bb\_pageCreate

---

*Create a page for a BentoBox layout*


---

## Description

Create a page for a BentoBox layout

## Usage

```
bb_pageCreate(
  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 <a href="#">bb_params</a> 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
bb_pageCreate(width = 6, height = 4.5, default.units = "inches")

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

---

bb_pageGuideHide	<i>Remove guides from a BentoBox page</i>
------------------	---

---

**Description**

Remove guides from a BentoBox page

**Usage**

```
bb_pageGuideHide()
```

**Value**

None.

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

```
## Hide page guides bb_pageGuideHide()
```

---

bb_pageGuideHorizontal	<i>Draw a horizontal guideline at a specified y-coordinate on a BentoBox page</i>
------------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

None.

**Examples**

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

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

---

<code>bb_pageGuideShow</code>	<i>Reshow guides drawn with</i>	<code>bb_pageCreate,</code>
	<i>bb_pageGuideHorizontal, and</i>	<code>bb_pageGuideVertical</code>

---

**Description**

Reshow guides drawn with `bb_pageCreate`, `bb_pageGuideHorizontal`, and `bb_pageGuideVertical`

**Usage**

```
bb_pageGuideShow()
```

**Value**

None.

**See Also**

[bb\\_pageCreate](#), [bb\\_pageGuideHorizontal](#), [bb\\_pageGuideVertical](#)



---

bb_pageGuideVertical	<i>Draw a vertical guideline at a specified x-coordinate on a BentoBox page</i>
----------------------	---

---

### Description

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

### Usage

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

### Arguments

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

### Value

None.

### Examples

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

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

---

bb_pagePlotPlace	<i>Place a BentoBox plot that has been previously created but not drawn</i>
------------------	---

---

### Description

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

**Usage**

```
bb_pagePlotPlace(
  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 <a href="#">bb_params</a> 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
data("bb_imrHicData")

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

```

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

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

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

## Hide page guides
bb_pageGuideHide()

```

---

bb_pagePlotRemove	<i>Remove BentoBox plots and annotations</i>
-------------------	--

---

## Description

Remove BentoBox plots and annotations

## Usage

```
bb_pagePlotRemove(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
data("bb_imrHicData")

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

## Plot and place a square Hi-C plot
hicPlot <- bb_plotHicSquare(
  data = bb_imrHicData, 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
bb_pagePlotRemove(plot = hicPlot)

```

---

bb\_params

*bb\_params: BentoBox parameters object*


---

## Description

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

## Usage

```
bb_params(assembly = "hg19", gene = NULL, geneBuffer = NULL, ...)
```

## Arguments

assembly	String defining the genome build. Default value is assembly = "hg19".
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.

## Details

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

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

## Examples

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

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

## Optionally add more parameters
p2 <- bb_params(fontsize = 10)

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

---

bb_plotBase	<i>Plot a base R plot in a BentoBox layout</i>
-------------	--

---

## Description

Plot a base R plot in a BentoBox layout

## Usage

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

## Arguments

plot	Plot formula of base R plotting functions.
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 base 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"`.

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

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

### Value

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

### Examples

```
## Define base R plot
p <- ~ plot(1:10) + abline(v = 2)

## Create BentoBox page
bb_pageCreate(width = 5, height = 4, default.units = "inches")

## Place base R plot in BentoBox page
bb_plotBase(
  plot = p,
  x = 0.5, y = 0.5, width = 4, height = 3,
  just = c("left", "top"), default.units = "inches"
)

## Add title
bb_plotText(
  label = "Base R Plot", fontsize = 14, fontface = "bold",
  x = 2.75, y = 0.5
)

## Remove BentoBox page guides
bb_pageGuideHide()
```

---

**bb\_plotCircle**
*Plot a circle within a BentoBox layout*


---

### Description

Plot a circle within a BentoBox layout

### Usage

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

```

    params = NULL,
    ...
)

```

### Arguments

<code>x</code>	A numeric vector or unit object specifying circle x-locations relative to center.
<code>y</code>	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.
<code>r</code>	A numeric vector or unit object specifying radii.
<code>default.units</code>	A string indicating the default units to use if <code>r</code> , <code>x</code> , or <code>y</code> are only given as numerics or numeric vectors. Default value is <code>default.units = "inches"</code> .
<code>linecolor</code>	A character value specifying circle line color. Default value is <code>linecolor = "black"</code> .
<code>lwd</code>	A numeric specifying circle line width. Default value is <code>lwd = 1</code> .
<code>lty</code>	A numeric specifying circle line type. Default value is <code>lty = 1</code> .
<code>fill</code>	A character value specifying circle fill color. Default value is <code>fill = NA</code> .
<code>alpha</code>	Numeric value specifying color transparency. Default value is <code>alpha = 1</code> .
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

### Value

Returns a `bb_circle` object containing relevant placement and [grob](#) information.

### See Also

[grid.circle](#)

### Examples

```

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

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

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

```

```
## Hide page guides
bb_pageGuideHide()
```

bb\_plotGenes

*Plot a gene track for a specified genomic region*

## Description

Plot a gene track for a specified genomic region

## Usage

```
bb_plotGenes(
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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 <code>fill = c("#669fd9", "#abcc8e")</code> .
geneOrder	An ordered character vector of gene names to prioritize when labeling genes.
geneHighlights	A two-column dataframe with the first column containing gene names as strings to highlight and the second column containing corresponding highlight colors.
geneBackground	If <code>geneHighlights</code> 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 <code>stroke = 0.1</code> .
bg	Character value indicating background color. Default value is <code>bg = NA</code> .
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 <code>just = c("left", "top")</code> .
default.units	A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is <code>default.units = "inches"</code> .
draw	A logical value indicating whether graphics output should be produced. Default value is <code>draw = TRUE</code> .
params	An optional <a href="#">bb_params</a> object containing relevant function parameters.

## Details

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

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

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

```
bb_plotGenes(chrom, chromstart = NULL, chromend = NULL)
```

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

**Value**

Returns a `bb_genes` object containing relevant genomic region, placement, and [grob](#) information.

**See Also**

[bb\\_assembly](#), [bb\\_genomes](#), [bb\\_defaultPackages](#)

**Examples**

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

## Load BEDPE data
data("bb_bedpeData")

## Set genomic coordinates
paramssmall <- bb_params(
  chrom = "chr8",
  chromstart = 0000000, chromend = 3000000,
  assembly = "hg19", width = 7
)
paramsbig <- bb_params(
  chrom = "chr8",
  chromstart = 0, chromend = 146364022,
  assembly = "hg19", width = 7
)
## Set colors
cols <- c("#41B6C4", "#225EA8")

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

## Plot genes big
genesPlot <- bb_plotGenes(
  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
bb_annoGenomeLabel(
  plot = genesPlot, x = 0.25, y = 1.0,
  scale = "Mb", just = c("left", "top")
)

## Plot genes small
genesPlot <- bb_plotGenes(
  params = paramssmall,
  geneHighlights = data.frame(
    "gene" = c("DLGAP2"),
    "color" = c("#225EA8")
  ),
  geneBackground = "grey",
```

```

    x = 0.25, y = 2.25, height = 0.75,
    just = c("left", "top"), default.units = "inches"
)

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

## Hide page guides
bb_pageGuideHide()

```

---

bb_plotGenomeLabel	<i>Plot genomic coordinates along the x or y-axis of a BentoBox plot</i>
--------------------	--

---

## Description

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

## Usage

```

bb_plotGenomeLabel(
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  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 <a href="#">bb_assembly</a> object.
fontsize	A numeric specifying text fontsize in points. Default value is <code>fontsize = 10</code> .
fontcolor	A character value indicating the color for text. Default value is <code>fontcolor = "black"</code> .
linecolor	A character value indicating the color of the genome label axis. Default value is <code>linecolor = "black"</code> .
margin	A numeric or unit vector specifying space between axis and coordinate labels. Default value is <code>margin = unit(1, "mm")</code> .
scale	A character value indicating the scale of the coordinates along the genome label. Default value is <code>scale = "bp"</code> . Options are: <ul style="list-style-type: none"> <li>• <code>"bp"</code>: base pairs.</li> <li>• <code>"Kb"</code>: kilobase pairs. 1 kilobase pair is equal to 1000 base pairs.</li> <li>• <code>"Mb"</code>: megabase pairs. 1 megabase pair is equal to 1000000 base pairs.</li> </ul>
commas	A logical value indicating whether to include commas in start and stop labels. Default value is <code>commas = TRUE</code> .
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 <code>boxWidth = 0.5</code> .
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 <code>axis = "x"</code> . Options are: <ul style="list-style-type: none"> <li>• <code>"x"</code>: Genome label will be plotted along the x-axis.</li> <li>• <code>"y"</code>: Genome label will be plotted along the y-axis. This is typically used for a square Hi-C plot made with <code>bb_plotHicSquare</code>.</li> </ul>
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 <code>tcl = 0.5</code> .
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: <code>"left"</code> , <code>"right"</code> , <code>"centre"</code> , <code>"center"</code> , <code>"bottom"</code> , and <code>"top"</code> . Default value is <code>just = c("left", "top")</code> .
default.units	A string indicating the default units to use if x, y, or length are only given as numerics. Default value is <code>default.units = "inches"</code> .
params	An optional <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters or digit specifications. See <a href="#">gpar</a> and <a href="#">formatC</a> .

**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
bb_pageCreate(width = 5, height = 3, default.units = "inches")

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

## Plot x-axis genome labels at different scales
bb_plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  scale = "Mb",
  x = 0.5, y = 1.25, length = 4, just = c("left", "top"),
  default.units = "inches"
)
bb_plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  scale = "Kb",
  x = 0.5, y = 1.5, length = 4, just = c("left", "top"),
  default.units = "inches"
)
bb_plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 2000000,
  assembly = "hg19",
  scale = "bp",
  x = 0.5, y = 1.75, length = 4, just = c("left", "top"),
  default.units = "inches"
)

## Plot a different genomic label region, zooming in enough
## to see base pairs
bb_plotGenomeLabel(
  chrom = "chr8",
  chromstart = 1000000, chromend = 1000050,
```

```

    assembly = "hg19",
    x = 0.25, y = 2.2, length = 4.5
  )
  bb_plotGenomeLabel(
    chrom = "chr8",
    chromstart = 1000000, chromend = 1000020,
    assembly = "hg19",
    x = 0, y = 2.6, length = 5
  )

## Hide page guides
bb_pageGuideHide()

```

bb\_plotGG

*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**

```

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

```

**Arguments**

plot	ggplot, gtable, or grob object.
x	A numeric or unit object specifying ggplot x-location.
y	A numeric, unit object, or character containing a "b" combined with a numeric value specifying ggplot y-location. The character value will place the ggplot y relative to the bottom of the most recently plotted 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 <a href="#">bb_params</a> 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
bb_pageCreate(width = 4, height = 4, default.units = "inches")

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

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

## Hide page guides
bb_pageGuideHide()
```

---

bb_plotHicRectangle	<i>Plot a triangular Hi-C interaction matrix in a rectangular format</i>
---------------------	--

---

**Description**

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

**Usage**

```
bb_plotHicRectangle(
  data,
  resolution = "auto",
  zrange = NULL,
  norm = "KR",
  matrix = "observed",
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  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: <ul style="list-style-type: none"> <li>• "observed": Observed counts.</li> <li>• "oe": Observed/expected counts.</li> <li>• "log2oe": Log2 transformed observed/expected counts.</li> </ul>
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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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 <a href="#">bb_params</a> object containing relevant function parameters.
quiet	A logical indicating whether or not to print messages.

## Details

This function is similar is [bb\\_plotHicTriangle](#) 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:

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

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

```
bb_plotHicRectangle(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

[bb\\_readHic](#), [bb\\_plotHicTriangle](#)

## Examples

```
## Load Hi-C data
data("bb_imrHicData")

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

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

```

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

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

## Hide page guides
bb_pageGuideHide()

```

---

bb\_plotHicSquare

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


---

## Description

Plot a Hi-C interaction matrix in a square format

## Usage

```

bb_plotHicSquare(
  data,
  resolution = "auto",
  zrange = NULL,
  norm = "KR",
  matrix = "observed",
  chrom,
  chromstart = NULL,
  chromend = NULL,
  altchrom = NULL,
  altchromstart = NULL,
  altchromend = NULL,
  assembly = "hg19",
  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: <ul style="list-style-type: none"> <li>• "observed": Observed counts.</li> <li>• "oe": Observed/expected counts.</li> <li>• "log2oe": Log2 transformed observed/expected counts.</li> </ul>
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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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". <ul style="list-style-type: none"> <li>• "both": Both diagonal halves.</li> <li>• "top": Half above the diagonal.</li> <li>• "bottom": Half below the diagonal.</li> </ul>
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.

<code>just</code>	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 <code>just = c("left", "top")</code> .
<code>default.units</code>	A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is <code>default.units = "inches"</code> .
<code>draw</code>	A logical value indicating whether graphics output should be produced. Default value is <code>draw = TRUE</code> .
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>quiet</code>	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:

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

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

```
bb_plotHicSquare(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

[bb\\_readHic](#)

### Examples

```
## Load Hi-C data
data("bb_imrHicData")

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

## Plot and place Hi-C plot
hicPlot <- bb_plotHicSquare(
  data = bb_imrHicData, 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"
)
```

```

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

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

## Hide page guides
bb_pageGuideHide()

```

---

bb_plotHicTriangle	<i>Plot a Hi-C interaction matrix in a triangular format</i>
--------------------	--

---

## Description

Plot a Hi-C interaction matrix in a triangular format

## Usage

```

bb_plotHicTriangle(
  data,
  resolution = "auto",
  zrange = NULL,
  norm = "KR",
  matrix = "observed",
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  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: <ul style="list-style-type: none"> <li>• "observed": Observed counts.</li> <li>• "oe": Observed/expected counts.</li> <li>• "log2oe": Log2 transformed observed/expected counts.</li> </ul>
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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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 <a href="#">bb_params</a> 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:

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

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

```
bb_plotHicTriangle(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

[bb\\_readHic](#)

## Examples

```
## Load Hi-C data
data("bb_imrHicData")

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

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

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

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

```
)

## Hide page guides
bb_pageGuideHide()
```

---

bb_plotIdeogram	<i>Plot a chromosome ideogram with or without cytobands</i>
-----------------	---

---

## Description

Plot a chromosome ideogram with or without cytobands

## Usage

```
bb_plotIdeogram(
  chrom,
  assembly = "hg19",
  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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
orientation	Character value indicating the orientation of the ideogram. Default value is orientation = "h". Options are: <ul style="list-style-type: none"> <li>• "v": Vertical ideogram orientation.</li> <li>• "h": Horizontal ideogram orientation.</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.

## Details

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

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

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

```
bb_plotIdeogram(chrom)
```

Giemsa stain band data from the UCSC Genome Browser is included with BentoBox.

## Value

Returns a `bb_ideogram` object containing relevant genomic region, placement, and [grob](#) information.

## Examples

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

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

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

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

## Hide page guides
bb_pageGuideHide()
```

bb\_plotLegend

*Plot a legend***Description**

Plot a legend

**Usage**

```
bb_plotLegend(
  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: <ul style="list-style-type: none"> <li>• "v": Vertical legend orientation.</li> <li>• "h": Horizontal legend orientation.</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

### Value

Returns a `bb_legend` object containing relevant placement and [grob](#) information.

### Examples

```
## Load BED data
data("bb_bedData")

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

## Plot a pileup plot, coloring elements by strand
pileupPlot <- bb_plotRanges(
  data = bb_bedData, chrom = "chr21",
  chromstart = 29072500, chromend = 29075000,
  fill = c("steel blue", "light salmon"),
  colorby = colorby("strand"),
  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 <- bb_plotLegend(
  legend = c("- strand", "+ strand"),
  fill = c("steel blue", "light salmon"),
  border = FALSE,
  x = 5, y = 0.5, width = 1.5, height = 0.7,
  just = c("left", "top"),
  default.units = "inches"
)

## Annotate genome label
bb_annoGenomeLabel(
  plot = pileupPlot, x = 0.5, y = 3.5,
```

```

    just = c("left", "top")
  )

  ## Hide page guides
  bb_pageGuideHide()

```

---

bb\_plotManhattan

*Plot a Manhattan plot*


---

## Description

Plot a Manhattan plot

## Usage

```

bb_plotManhattan(
  data,
  sigVal = 5e-08,
  chrom = NULL,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  fill = "black",
  pch = 19,
  cex = 0.25,
  leadSNP = NULL,
  scaleLD = 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 <a href="#">GRanges</a> object. Each of these data types must have the following columns:
------	---

	<ul style="list-style-type: none"> <li>• "chr": Chromosome names. This column must be a character.</li> <li>• "pos": Chromosomal position. This column must be an integer or numeric.</li> <li>• "p": p-value. This column must be numeric. p-values will be converted to <math>-\log(10)</math> space.</li> <li>• "snp"(optional): SNP name or rsid. This column should be a character.</li> </ul>
sigVal	A numeric specifying the significance level of p-values. Along with data p-values, this value will be converted to $-\log_{10}$ 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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
fill	Character value(s) as a single value, vector, or palette specifying fill colors of data points. If scaleLD is supplied, colors will be mapped to scaleLD values. If scaleLD is not supplied, color vectors and palettes will only be mapped to different chromosomes of a multi-chromosomal plot. Default value is fill = "black".
pch	A numeric value or numeric vector specifying point symbols. If scaleLD is supplied, point symbols will be mapped to scaleLD 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.
scaleLD	A character value specifying the data column name of linkage disequilibrium (LD) scores to apply fill and/or pch vectors or functions to. LD scores will be grouped into the following ranges: 0-0.2, 0.2-0.4, 0.4-0.6, 0.6-0.8, 0.8-1.
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 chromosome as a fraction of the width of the plot, if plotting multiple chromosomes. Default value is space = 0.01.
bg	Character value indicating background color. Default value is bg = NA.
baseline	Logical value indicating whether to include a baseline along the x-axis. Default value is baseline = FALSE.
baseline.color	Baseline color. Default value is baseline.color = "grey".

baseline.lwd	Baseline line width. Default value is <code>baseline.lwd = 1</code> .
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 <code>just = c("left", "top")</code> .
flip	Logical value indicating whether to reflect Manhattan plot over the x-axis. Default value is <code>flip = FALSE</code> .
default.units	A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is <code>default.units = "inches"</code> .
draw	A logical value indicating whether graphics output should be produced. Default value is <code>draw = TRUE</code> .
params	An optional <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

## Details

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

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

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

```
bb_plotManhattan(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
data("bb_gwasData")
```

```

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

## Plot all GWAS data
manhattanPlot <- bb_plotManhattan(
  data = bb_gwasData, 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
bb_annoGenomeLabel(
  plot = manhattanPlot, x = 0.5, y = 2, fontsize = 8,
  just = c("left", "top"),
  default.units = "inches"
)
bb_plotText(
  label = "Chromosome", fontsize = 8,
  x = 3.75, y = 2.20, just = "center", default.units = "inches"
)

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

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

## Plot GWAS data zooming in on chromosome 11
## highlighting a lead SNP, and coloring by LD score
leadSNP_p <- min(bb_gwasData[which(bb_gwasData$chr == "chr11"), ]$p)
leadSNP <- bb_gwasData[which(bb_gwasData$p == leadSNP_p), ]$snp
chr11_manhattanPlot <- bb_plotManhattan(
  data = bb_gwasData, chrom = "chr11",
  chromstart = 60000000,
  chromend = 130000000,
  fill = c(
    "#1f4297",
    "#37a7db", "green",
    "orange", "red"
  ),
  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
bb_plotLegend(
    legend = c(
        "LD Ref Var",
        expression(paste("0.4", ">", "r"^{
            paste("2")
        })),
        expression(paste("0.2", ">", "r"^{
            paste("2")
        })),
        "no LD data"
    ),
    fill = c("#7ecdbb", "#37a7db", "#1f4297", "grey"), cex = 0.75,
    pch = c(18, 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
bb_annoGenomeLabel(
    plot = chr11_manhattanPlot, x = 0.5, y = 4.01,
    fontsize = 8, scale = "Mb",
    just = c("left", "top"), default.units = "inches"
)

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

## Plot y-axis label
bb_plotText(
    label = "-log10(p-value)", x = 0.15, y = 3.25, rot = 90,
    fontsize = 8, fontface = "bold", just = "center",
    default.units = "inches"
)

## Hide page guides
bb_pageGuideHide()

```



## Description

Plot paired-end genomic range elements

## Usage

```
bb_plotPairs(
  data,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  fill = "#1f4297",
  colorby = NULL,
  linecolor = NA,
  bg = NA,
  boxHeight = unit(2, "mm"),
  spaceWidth = 0.02,
  spaceHeight = 0.3,
  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 <a href="#">GInteractions</a> 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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
fill	Character value(s) as a single value, vector, or palette specifying fill colors of BEDPE elements. Default value is fill = "#1f4297".
colorby	A " <a href="#">colorby</a> " object specifying information for scaling colors in data.
linecolor	A character value specifying the color of the lines outlining paired range elements. Default value is linecolor = NA.
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.
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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

## Details

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

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

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

```
bb_plotPairs(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
data("bb_bedpeData")

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

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

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

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

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

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

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

## Hide page guides
bb_pageGuideHide()
```

---

bb_plotPairsArches	<i>Plot paired-end genomic range data in an arch style</i>
--------------------	--

---

**Description**

Plot paired-end genomic range data in an arch style

**Usage**

```
bb_plotPairsArches(
  data,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  style = "2D",
  flip = FALSE,
  curvature = 5,
  archHeight = NULL,
  fill = "#1f4297",
  colorby = NULL,
  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 <a href="#">GInteractions</a> 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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
style	Character value describing the style of arches. Default value is style = "2D". Options are: <ul style="list-style-type: none"> <li>• "2D": Arches will be drawn in a 2-dimensional style.</li> <li>• "3D": Arches will be drawn in a 3-dimensional style.</li> </ul>
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



**Value**

Returns a `bb_arches` object containing relevant genomic region, placement, and [grob](#) information.

**Examples**

```
## Load paired ranges data in BEDPE format
data("bb_bedpeData")

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

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

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

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

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

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

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

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

## Hide page guides
```

```
bb_pageGuideHide()
```

---

bb_plotPolygon	<i>Plot a polygon within a BentoBox layout</i>
----------------	--

---

## Description

Plot a polygon within a BentoBox layout

## Usage

```
bb_plotPolygon(
  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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

**Value**

Returns a `bb_polygon` object containing relevant placement and [grob](#) information.

**See Also**

[grid.polygon](#)

**Examples**

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

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

bb_plotPolygon(
  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
bb_plotPolygon(
  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
bb_pageGuideHide()
```

---

**bb\_plotRanges**


---

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


---

**Description**

Plot genomic range elements in a pileup or collapsed format



**Usage**

```

bb_plotRanges(
  data,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  fill = "#7ecdbb",
  colorby = NULL,
  linecolor = NA,
  collapse = FALSE,
  boxHeight = unit(2, "mm"),
  spaceWidth = 0.02,
  spaceHeight = 0.3,
  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 <a href="#">GRanges</a> 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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
fill	Character value(s) as a single value, vector, or palette specifying fill colors of range elements. Default value is fill = "#7ecdbb".
colorby	A " <a href="#">colorby</a> " object specifying information for scaling colors in data.
linecolor	A character value specifying the color of the lines outlining range elements. Default value is linecolor = NA.
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.
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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

## Details

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

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

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

```
bb_plotRanges(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
data("bb_bedData")

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

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

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

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

## Hide page guides
bb_pageGuideHide()
```

---

bb\_plotRaster

---

*Plot a raster object within a BentoBox layout*


---

**Description**

Plot a raster object within a BentoBox layout

**Usage**

```
bb_plotRaster(
  image,
  x,
```

```

    y,
    width,
    height,
    just = "center",
    default.units = "inches",
    interpolate = TRUE,
    params = NULL,
    ...
  )

```

### Arguments

<code>image</code>	Any R object that can be coerced to a raster object.
<code>x</code>	A numeric vector or unit object specifying raster x-locations.
<code>y</code>	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.
<code>width</code>	A numeric vector or unit object specifying raster widths.
<code>height</code>	A numeric vector or unit object specifying raster heights.
<code>just</code>	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 <code>just = "center"</code> .
<code>default.units</code>	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 <code>default.units = "inches"</code> .
<code>interpolate</code>	A logical value indicating whether to linearly interpolate the image. Default value is <code>interpolate = TRUE</code> .
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

### 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
bb_pageCreate(width = 5, height = 6)

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

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

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

## Hide page guies
bb_pageGuideHide()

```

---

bb\_plotRect

*Plot a rectangle within a BentoBox layout*


---

## Description

Plot a rectangle within a BentoBox layout

## Usage

```

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

```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying rectangle x-locations.
<code>y</code>	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.
<code>width</code>	A numeric vector or unit object specifying rectangle widths.
<code>height</code>	A numeric vector or unit object specifying rectangle heights.
<code>just</code>	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 <code>just = "center"</code> .
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , and <code>height</code> are only given as numerics or numeric vectors. Default value is <code>default.units = "inches"</code> .
<code>linecolor</code>	A character value specifying rectangle line color. Default value is <code>linecolor = "black"</code> .
<code>lwd</code>	A numeric specifying rectangle line width. Default value is <code>lwd = 1</code> .
<code>lty</code>	A numeric specifying rectangle line type. Default value is <code>lty = 1</code> .
<code>fill</code>	A character value specifying rectangle fill color. Default value is <code>fill = NA</code> .
<code>alpha</code>	Numeric value specifying color transparency. Default value is <code>alpha = 1</code> .
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

**Value**

Returns a `bb_rect` object containing relevant placement and [grob](#) information.

**See Also**

[grid.rect](#)

**Examples**

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

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

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

```

)

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

## Hide page guides
bb_pageGuideHide()

```

bb\_plotSegments

*Draw a line segment within a BentoBox layout*

## Description

Draw a line segment within a BentoBox layout

## Usage

```

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

```

## Arguments

- |    |   |
|----|---|
| x0 | A numeric vector or unit object indicating the starting x-values of the line segments.  |
| y0 | A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying starting y-values of the line segments. The character vector will place starting y-values relative to the bottom of the most recently plotted 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.  |

<code>y1</code>	A numeric vector, unit object, or a character vector of <code>y</code> values containing a "b" combined with a numeric value specifying stopping <code>y</code> -values of the line segments. The character vector will place stopping <code>y</code> -values relative to the bottom of the most recently plotted BentoBox plot according to the units of the BentoBox page.
<code>default.units</code>	A string indicating the default units to use if <code>x0</code> , <code>y0</code> , <code>x1</code> , or <code>y1</code> are only given as numeric vectors. Default value is <code>default.units = "inches"</code> .
<code>linecolor</code>	A character value specifying segment line color. Default value is <code>linecolor = "black"</code> .
<code>lwd</code>	A numeric specifying segment line width. Default value is <code>lwd = 1</code> .
<code>lty</code>	A numeric specifying segment line type. Default value is <code>lty = 1</code> .
<code>lineend</code>	A character value specifying line end style. Default value is <code>lineend = "butt"</code> . Options are: <ul style="list-style-type: none"> <li>• "round": Segment ends are rounded.</li> <li>• "butt": Segment ends end exactly where ended.</li> <li>• "square": Segment ends are squared.</li> </ul>
<code>linejoin</code>	A character value specifying line join style. Default value is <code>linejoin = "mitre"</code> . Options are: <ul style="list-style-type: none"> <li>• "round": Line joins are rounded.</li> <li>• "mitre": Line joins are sharp corners.</li> <li>• "bevel": Line joins are flattened corners.</li> </ul>
<code>arrow</code>	A list describing arrow heads to place at either end of the line segments, as produced by the <a href="#">arrow</a> function.
<code>params</code>	An optional <a href="#">bb_params</a> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

**Value**

Returns a `bb_segments` object containing relevant placement and [grob](#) information.

**See Also**

[grid.segments](#), [arrow](#)

**Examples**

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

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

## Plot multiple line segments at different locations in different colors
bb_plotSegments(
  x0 = 0.5, y0 = c(1, 3, 5), x1 = 3.25, y1 = c(1, 3, 5),
```



```

        default.units = "inches",
        lwd = 2, linecolor = c("#7ecdbb", "#37a7db", "grey")
    )

    ## Plot a line segment with an arrowhead
    bb_plotSegments(
        x0 = 4.5, y0 = 0.5, x1 = 7, y1 = 3,
        default.units = "inches",
        arrow = arrow(type = "closed"), fill = "black"
    )

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

    ## Hide page guides
    bb_pageGuideHide()

```

---

bb\_plotSignal

---

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


---

## Description

Plot any kind of signal track data for a single chromosome

## Usage

```

bb_plotSignal(
  data,
  binSize = NA,
  binCap = TRUE,
  negData = FALSE,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  linecolor = "#37a7db",
  fill = NA,
  ymax = 1,
  range = NULL,
  scale = FALSE,
  bg = NA,
  baseline = TRUE,
  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 bigwig file path, a dataframe in BED format, or a <a href="#">GRanges</a> object with metadata column counts. 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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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.
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.

<code>just</code>	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 <code>just = c("left", "top")</code> .
<code>default.units</code>	A string indicating the default units to use if x, y, width, or height are only given as numerics. Default value is <code>default.units = "inches"</code> .
<code>draw</code>	A logical value indicating whether graphics output should be produced. Default value <code>draw = TRUE</code> .
<code>params</code>	An optional <code>bb_params</code> object containing relevant function parameters.
<code>...</code>	Additional grid graphical parameters. See <a href="#">gpar</a> .

## Details

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

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

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

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

## Value

Returns a `bb_signal` object containing relevant genomic region, placement, and [grob](#) information.

## Examples

```
## Load signal data
data("bb_imrH3K27acData")
data("bb_gmH3K27acData")

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

## Define region
region <- bb_params(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  range = c(0, 45)
)

## Plot and place signal plots
signal1 <- bb_plotSignal(
  data = bb_imrH3K27acData, params = region,
  x = 0.5, y = 0.25, width = 6.5, height = 0.65,
  just = c("left", "top"), default.units = "inches"
)
```

```

signal2 <- bb_plotSignal(
  data = bb_gmH3K27acData, 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
bb_plotGenomeLabel(
  chrom = "chr21",
  chromstart = 28000000, chromend = 30300000,
  x = 0.5, y = 1.68, length = 6.5,
  default.units = "inches"
)

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

## Hide page guides
bb_pageGuideHide()

```

---

bb\_plotText

*Plot text within a BentoBox layout*


---

## Description

Plot text within a BentoBox layout

## Usage

```

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

```

**Arguments**

label	Character or expression of text to be plotted.
fontcolor	A character value specifying text fontcolor. Default value is fontcolor = "black".
fontsize	A numeric specifying text fontsize in points. Default value is fontsize = 12.
rot	A numeric specifying the angle to rotate the text. Default value is rot = 0.
check.overlap	A logical value to indicate whether to check for and omit overlapping text. Default value is check.overlap = FALSE.
x	A numeric vector or unit object specifying text x-location.
y	A numeric vector, unit object, or a character vector of values containing a "b" combined with a numeric value specifying text y-locations. The character vector will place text y-locations relative to the bottom of the most recently plotted 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 <a href="#">bb_params</a> object containing relevant function parameters.
...	Additional grid graphical parameters. See <a href="#">gpar</a> .

**Value**

Returns a `bb_text` object containing relevant placement and [grob](#) information.

**See Also**

[grid.text](#)

**Examples**

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

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

## Plot text, adjusting color, rotation, and fontfamily
bb_plotText(
  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
bb_plotText(
  label = "R", x = c(0.5, 1, 1.5), y = 1.5, just = "center",
  default.units = "inches"
```

```

)

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

## Hide page guides
bb_pageGuideHide()

```

---

bb_plotTranscripts	<i>Plot gene transcripts in a pileup style for a single chromosome</i>
--------------------	--

---

## Description

Plot gene transcripts in a pileup style for a single chromosome

## Usage

```

bb_plotTranscripts(
  chrom,
  chromstart = NULL,
  chromend = NULL,
  assembly = "hg19",
  fill = c("#669fd9", "#abcc8e"),
  colorbyStrand = TRUE,
  strandSplit = FALSE,
  boxHeight = unit(2, "mm"),
  spaceWidth = 0.02,
  spaceHeight = 0.3,
  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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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.
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 = "transcript". Options are: <ul style="list-style-type: none"> <li>• NULL: No labels.</li> <li>• "transcript": Transcript name labels.</li> <li>• "gene": Gene name labels.</li> <li>• "both": Combined transcript and gene name labels with the format "gene name:transcript name".</li> </ul>
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 <a href="#">bb_params</a> object containing relevant function parameters.

## Details

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

```
bb_plotTranscripts(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:

```
bb_plotTranscripts(chrom, chromstart = NULL, chromend = NULL)
```

Genomic annotation information is acquired through [TxDb](#) and [OrgDb-class](#) packages, as determined through the assembly parameter.

## Value

Returns a `bb_transcripts` object containing relevant genomic region, placement, and [grob](#) information.

## See Also

[bb\\_assembly](#), [bb\\_genomes](#), [bb\\_defaultPackages](#)

## Examples

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

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

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

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

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



```
## Hide page guides
bb_pageGuideHide()
```

---

bb_readBigwig	<i>Read a bigWig file and return it as a data frame</i>
---------------	---

---

## Description

Read a bigWig file and return it as a data frame

## Usage

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

## Arguments

file	A character value specifying the path to the bigwig file.
chrom	Chromosome of data as a string, if data for a specific chromosome is desired.
chromstart	Integer start position on chromosome.
chromend	Integer end position on chromosome.
strand	A character value specifying strand. Default value is strand = "*". Options are: <ul style="list-style-type: none"> <li>"+": Plus strand.</li> <li>"-": Minus strand.</li> <li>*": Plus and minus strands.</li> </ul>
params	An optional <a href="#">bb_params</a> object containing relevant function parameters.

## Value

Returns a 6-column dataframe of bigwig information.

bb\_readHic

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

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

**Usage**

```
bb_readHic(
  file,
  chrom,
  chromstart = NULL,
  chromend = NULL,
  altchrom = NULL,
  altchromstart = NULL,
  altchromend = NULL,
  assembly = "hg19",
  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 <a href="#">bb_assembly</a> object. Default value is assembly = "hg19".
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: <ul style="list-style-type: none"> <li>• "BP": Base pairs.</li> <li>• "FRAG": Fragments.</li> </ul>
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: <ul style="list-style-type: none"> <li>• "observed": Observed counts.</li> <li>• "oe": Observed/expected counts.</li> <li>• "log2oe": Log2 transformed observed/expected counts.</li> </ul>
params	An optional <a href="#">bb_params</a> 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](#)

---

bb_VaccinesNYFL	<i>BentoBox example data for COVID-19 vaccinations in New York and Florida</i>
-----------------	--

---

### Description

A dataset describing groups of COVID-19 vaccinations in New York and Florida.

### Usage

```
data("bb_VaccinesNYFL")
```

### Format

a dataframe with 4 columns

**state** The state of the vaccinations. Either "new york" or "florida".

**vax\_group** Character value describing the 3 possibilities for vaccination status: "not", "partially", or "fully" vaccinated.

**value** Raw state population value in vaccination group.

**percent** State percentage in vaccination group.

### Source

State population data and state COVID-19 vaccination data were downloaded from the John Hopkins Centers for Civic Impact COVID-19 GitHub repository "<https://github.com/govex/COVID-19/>".

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.

**Author(s)**

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**See Also**

Useful links:

- <https://phanstiellab.github.io/bentobox>
- <https://github.com/PhanstiellLab/BentoBox>

c

*Combine multiple bb\_params objects into a vector***Description**

Combine multiple bb\_params objects into a vector

**Usage**

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

**Arguments**

... [bb\\_params](#) 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.)

---

colorby	<i>Handle BentoBox color scaling parameters</i>
---------	---

---

### Description

colorby should be used to create a set of parameters that specify color scaling for the functions `bb_plotPairs`, `bb_plotPairsArches`, and `bb_plotRanges`.

### Usage

```
colorby(column, range = NULL)
```

### Arguments

<code>column</code>	String specifying name of data column to scale colors by.
<code>range</code>	A numeric vector specifying the range of values to apply a color scale to.

### Value

Returns a "bb\_colorby" object.

---

cytoBand.Dmelanogaster.UCSC.dm6	<i>UCSC CytoBand information for the dm6 genome assembly</i>
---------------------------------	--

---

### Description

A dataset of Giemsa stain band information for every chromosome in the UCSC dm6 genome assembly.

### Usage

```
data("cytoBand.Dmelanogaster.UCSC.dm6")
```

### Format

dataframe with the following columns:

<b>seqnames</b>	chromosome of Giemsa stain band
<b>start</b>	start position of Giemsa stain band
<b>end</b>	end position of Giemsa stain band
<b>width</b>	width of Giemsa stain band
<b>strand</b>	strand of Giemsa stain band
<b>name</b>	name of Giemsa stain band
<b>gieStain</b>	Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

## References

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. *Nucleic Acids Res.* 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

cytoBand.Drerio.UCSC.danRer10

*UCSC CytoBand information for the danRer10 genome assembly*

---

## Description

A dataset of Giemsa stain band information for every chromosome in the UCSC danRer10 genome assembly.

## Usage

```
data("cytoBand.Drerio.UCSC.danRer10")
```

## Format

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

## References

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. *Nucleic Acids Res.* 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

`cytoBand.Hsapiens.UCSC.hg18`*UCSC CytoBand information for the hg18 genome assembly*

---

**Description**

A dataset of Giemsa stain band information for every chromosome in the UCSC hg18 genome assembly.

**Usage**

```
data("cytoBand.Hsapiens.UCSC.hg18")
```

**Format**

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

**References**

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. *Nucleic Acids Res.* 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

`cytoBand.Hsapiens.UCSC.hg19`*UCSC CytoBand information for the hg19 genome assembly*

---

**Description**

A dataset of Giemsa stain band information for every chromosome in the UCSC hg19 genome assembly.

**Usage**

```
data("cytoBand.Hsapiens.UCSC.hg19")
```

**Format**

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

**References**

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. *Nucleic Acids Res.* 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

cytoBand.Hsapiens.UCSC.hg38

*UCSC CytoBand information for the hg38 genome assembly*

---

**Description**

A dataset of Giemsa stain band information for every chromosome in the UCSC hg38 genome assembly.

**Usage**

```
data("cytoBand.Hsapiens.UCSC.hg38")
```

**Format**

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk



## References

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. Nucleic Acids Res. 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

cytoBand.Mmusculus.UCSC.mm10

*UCSC CytoBand information for the mm10 genome assembly*

---

## Description

A dataset of Giemsa stain band information for every chromosome in the UCSC mm10 genome assembly.

## Usage

```
data("cytoBand.Mmusculus.UCSC.mm10")
```

## Format

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

## References

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. Nucleic Acids Res. 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

`cytoBand.Mmusculus.UCSC.mm9`*UCSC CytoBand information for the mm9 genome assembly*

---

**Description**

A dataset of Giemsa stain band information for every chromosome in the UCSC mm9 genome assembly.

**Usage**

```
data("cytoBand.Mmusculus.UCSC.mm9")
```

**Format**

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

**References**

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. *Nucleic Acids Res.* 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

`cytoBand.Rnorvegicus.UCSC.rn5`*UCSC CytoBand information for the rn5 genome assembly*

---

**Description**

A dataset of Giemsa stain band information for every chromosome in the UCSC rn5 genome assembly.

**Usage**

```
data("cytoBand.Rnorvegicus.UCSC.rn5")
```

**Format**

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

**References**

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. Nucleic Acids Res. 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

---

cytoBand.Rnorvegicus.UCSC.rn6

*UCSC CytoBand information for the rn6 genome assembly*

---

**Description**

A dataset of Giemsa stain band information for every chromosome in the UCSC rn6 genome assembly.

**Usage**

```
data("cytoBand.Rnorvegicus.UCSC.rn6")
```

**Format**

dataframe with the following columns:

**seqnames** chromosome of Giemsa stain band

**start** start position of Giemsa stain band

**end** end position of Giemsa stain band

**width** width of Giemsa stain band

**strand** strand of Giemsa stain band

**name** name of Giemsa stain band

**gieStain** Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen, gvar, stalk

**References**

Navarro Gonzalez J, Zweig AS, Speir ML, Schmelter D, Rosenbloom KR, Raney BJ, Powell CC, Nassar LR, Maulding ND, Lee CM, Lee BT, Hinrichs AS, Fyfe AC, Fernandes JD, Diekhans M, Clawson H, Casper J, Benet-Pagès A, Barber GP, Haussler D, Kuhn RM, Haeussler M, Kent WJ. The UCSC Genome Browser database: 2021 update. *Nucleic Acids Res.* 2021 Jan 8;49(D1):D1046-D1057. doi: 10.1093/nar/gkaa1070. PMID: 33221922; PMCID: PMC7779060.

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