Package ‘Sushi’

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Type Package

Title Tools for visualizing genomics data

Description Flexible, quantitative, and integrative genomic visualizations for publication-quality multi-panel figures

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NeedsCompilation no

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addlegend

This function adds a legend to Sushi plots that have a colorby function (e.g. plotHic, plotGenes, and plotBedpe)

Usage

\[
\text{addlegend}(\text{range}, \text{title} = \text{""}, \text{labels.digits} = 1, \text{palette} = \text{topo.colors},
\text{side} = \text{"right"}, \text{labelside} = \text{"left"}, \text{xoffset} = 0.1, \text{width} = 0.05,
\text{bottominset} = 0.025, \text{topinset} = 0.025, \text{tick.num} = 5,
\text{tick.length} = 0.01, \text{txt.font} = 1, \text{txt.cex} = 0.75, \text{title.offset} = 0.05,
\text{title.font} = 2, \text{title.cex} = 1)
\]

Arguments

- **range**: the range of values to be plotted. i.e \((\text{min, max})\)
- **title**: title of values to be mapped
- **labels.digits**: Number of digits after the decimal point to include in labels
- **palette**: color palette to use
- **side**: side of plot to place legend ("right", "left")
- **labelside**: side of legend to place legend title
- **xoffset**: fraction of plot to offset the legend
- **width**: width as a fraction of the plot width
- **bottominset**: inset from the bottom of the blot as a fraction of the plot width
- **topinset**: inset from the top of the blot as a fraction of the plot width
- **tick.num**: desired number of tickmarks
- **tick.length**: length of tick marks
- **txt.font**: font type of legend text
- **txt.cex**: font size of legend text
**chromOffsets**

- **title.offset**: offset of title from the key
- **title.font**: font type of legend title
- **title.cex**: font size of legend text

**Examples**

```r
data(Sushi_HiC.matrix)

chrom = "chr11"
chromstart = 500000
chromend = 5050000

phic = plotHic(Sushi_HiC.matrix, chrom, chromstart, chromend, max_y = 20, zrange = c(0, 28), palette = topo.colors, flip = FALSE)

labelgenome(chrom, chromstart, chromend, side = 1, scipen = 20, n = 4, scale = "Mb", edgeblankfraction = 0.20, line = .18, chromline = .5, scaleline = 0.5)

addlegend(phic[[1]], palette = phic[[2]], title = "score", side = "right", bottominset = 0.4, topinset = 0, xoffset = -.035, labelside = "left", width = 0.025, title.offset = 0.035)
```

---

**Description**

defines chromosome offsets for plotting multi chromosomal plot (eg `plotManhattan`)

**Usage**

`chromOffsets(genome, space = 0.01)`

**Arguments**

- **genome**: A genome object to be used (2 columns: column 1 = chromosome name, column 2 = length of chromosome)
- **space**: the space in between each chromosome as a fraction of the width of the plot

---

**convertstrandinfo**

Converts strand info to 1 / -1

**Description**

Converts strand info to 1 / -1

**Usage**

`convertstrandinfo(strandvector)`

**Arguments**

- **strandvector**: vector of strand information to convert from +/- to 1/-1 if necessary
labelgenome

_Adds genome coordinates to the x-axis of a Sushi plot_

**Description**

Adds genome coordinates to the x-axis of a Sushi plot.

**Usage**

```r
labelgenome(chrom, chromstart, chromend, genome = NULL, space = 0.01, scale = "bp", side = 1, scipen = 20, n = 5, chromfont = 2, chromadjust = 0.015, chromcex = 1, chromline = 0.5, scalefont = 2, scaleadjust = 0.985, scalecex = 1, scaleline = 0.5, line = 0.18, edgeblankfraction = 0.1, ...)
```

**Arguments**

- `chrom`: chromosome to plot
- `chromstart`: start position
- `chromend`: end position
- `genome`: a genome object (2 columns: column 1 = chromosome name, column 2 = length of chromosome). Only for multi chromosomal plots
- `space`: the space in between each chromosome as a fraction of the width of the plot. Only for multi chromosomal plots
- `scale`: Scale of the plot ("bp", 'Kb', 'Mb')
- `side`: Side of the scale to add the plot to. Only tested for sides 1 and 3.
- `scipen`: higher values decrease the likelihood of using scientific for the position labels.
- `n`: Desired number of ticks
- `chromfont`: font type of chromosome label
- `chromadjust`: position, as a fraction of the width of the plot, of the chromosome label
- `chromcex`: font size of the chromosome label
- `chromline`: vertical offset of the chromosome label
- `scalefont`: font type of scale label
- `scaleadjust`: position, as a fraction of the width of the plot, of the scale label
- `scalecex`: font size of the scale label
- `scaleline`: vertical offset of the scale label
- `line`: vertical offset of position labels
- `edgeblankfraction`: percent of the edges to leave black for chromosome and scale labels
- `...`: values to be passed to `axis`
Examples

data(Sushi_DNaseI.bedgraph)
# set the genomic regions

plotBedgraph(Sushi_DNaseI.bedgraph, chrom="chr11", chromstart=1650000, chromend=2350000, colorbycol=SushiColors(7))
labelgenome(chrom="chr11", chromstart=1650000, chromend=2350000, side=1,n=4, scale="Mb")
axis(side=2, las=2, tcl=.2)
mtext("Read Depth", side=2, line=1.75, cex=.75, font=2)

Description

This function adds a letter and a title (both are optional) to the top of a plot. Useful for generating paper figures.

Usage

`labelplot(letter = NULL, title = NULL, letteradj = -0.05, titleadj = 0,
letterfont = 2, titlefont = 2, lettercex = 1.2, titlecex = 1,
letterline = 0.5, titleline = 0.5, lettercol = "black",
titlecol = "black")`

Arguments

- `letter`: A string, typically a letter or number (eg 'A', 'A)', '1', etc) to label the plot with
- `title`: A string for a plot title
- `letteradj`: adj of letter. See `par`
- `titleadj`: adj of title. See `par`
- `letterfont`: font of letter. See `par`
- `titlefont`: font of title. See `par`
- `lettercex`: cex of letter. See `par`
- `titlecex`: cex of title. See `par`
- `letterline`: line of letter. See `par`
- `titleline`: line of title. See `par`
- `lettercol`: color of letter. See `par`
- `titlecol`: color of title. See `par`

Examples

```r
par(mar=c(3,3,3,3))
plot((1:10),col=maptocolors(vec=(1:10), colorRampPalette(c("blue","red"))),pch=19,cex=4)
labelplot("A"," sample plot",lettercex=2,titlecex=2,titlecol="blue")
```
maptocolors  

maps numeric vector to color palette

Description
maps numeric vector to color palette

Usage
maptocolors(vec, col, num = 100, range = NULL)

Arguments
vec  numeric vector to map to color
col  color palette to which to be mapped
num  number of bins of colors
range range of values to map

Examples
plot((1:10),col=maptocolors(vec=(1:10),colorRampPalette(c("blue","red"))),pch=19,cex=4)

maptolwd  

maps numeric vector to line widths

Description
maps numeric vector to line widths

Usage
maptolwd(lwby, range = c(1, 5))

Arguments
lwby  numeric vector to map to line widths
range range of values to map

Examples
plot((1:10),lwd=maptolwd(lwby=(1:10)))
opaque  

makes colors transparent (or opaque)

**Description**

makes colors transparent (or opaque)

**Usage**

opaque(color = SushiColors(7)(7), transparency = 0.5)

**Arguments**

color  color or colors to make opaque
transparency  value between 0 and 1 indicating desired opaqueness

**Examples**

plot((1:10),col="red",pch=19)
points((10:1),col=opaque("red",transparency=0.3),pch=19)

plotBed  

plots data stored in bed file format

**Description**

plots data stored in bed file format

**Usage**

plotBed(beddata, chrom, chromstart, chromend, type = "region",
colorby = NULL, colorbycol = NULL, colorbyrange = NULL,
rownumber = NULL, row = "auto", height = 0.4, plotbg = "white",
wiggle = 0.02, splitstrand = FALSE, numbins = 200, binsmothing = 10,
palettes = topo.colors, rowlabels = NULL, rowlabelcol = "dodgerblue2",
rowlabelfont = 2, rowlabelcex = 1, maxrows = 1e+06,
color = "dodgerblue4", xaxt = "none", yaxt = "none", xlab = "",
ylab = "", xaxs = "i", yaxs = "i", bty = "n", border = NA, ...)

**Arguments**

beddata  genomic data to be plotted (in bed format)
chrom  chromosome of region to be plotted
chromstart  start position
chromend  end position
type  type of plot ("region","circles","density")
colorby  vector to scale colors by
colorbycol  palette to apply color scale to (only valid when colorby is not NULL)
plotBed

- **colorbyrange**: the range of values to apply the color scale to. Values outside that range will be set to the limits of the range.
- **rownumber**: vector giving the row numbers of each bed element to be plotted.
- **row**: How row number should be determined. Appropriate values are 'auto' or 'supplied'
- **height**: Value, typically between 0 and 1, that sets the height of each bed element
- **plotbg**: The background color of the plot
- **wiggle**: the fraction of the plot to leave blank on either side of each element to avoid overcrowding.
- **splitstrand**: TRUE/FALSE indicating whether reverse strand bed elements should be plotted below the x axis. (only valid when row is set to 'auto')
- **numbins**: The number of bins to divide the region into when type is set to density (only valid when type is set to 'density')
- **binsmoothing**: number of bins to sum together when type is set to density (only valid when type is set to 'density')
- **palettes**: list of color palettes used for density plots. Each row can have a unique palette. Number of palettes is less than the number of rows then only the first palette is used (only valid when type is set to 'density')
- **rowlabels**: labels for the y-axis
- **rowlabelcol**: color of the y-axis labels
- **rowlabelfont**: font of the y-axis labels
- **rowlabelcex**: font size of the y-axis labels
- **maxrows**: The maximum number of rows to plot on the y-axis
- **color**: single color or vector of colors to use to plot the points or regions (not valid when type is set to 'density')
- **xaxt**: A character which specifies the x axis type. See `par`
- **yaxt**: A character which specifies the y axis type. See `par`
- **xlab**: Label for the x-axis
- **ylab**: Label for the y-axis
- **xaxs**: Must be set to 'i' for appropriate integration into Sushi plots. See `par`
- **yaxs**: Must be set to 'i' for appropriate integration into Sushi plots. See `par`
- **bty**: A character string which determined the type of box which is drawn about plots. See `par`
- **border**: border color drawn around each bed element or density bin. Set to 'n' for none.
- **...**: values to be passed to other functions

**Examples**

```r
data(Sushi_ChIPSeq_severalfactors.bed)
chrom = "chr15"
chromstart = 72800000
chromend = 73100000
Sushi_ChIPSeq_severalfactors.bed$color = heat.colors(max(Sushi_ChIPSeq_severalfactors.bed$row))[Sushi_ChIPSeq_severalfactors.bed$row]
plotBed(beddata = Sushi_ChIPSeq_severalfactors.bed, chrom = chrom, chromstart = chromstart, chromend = chromend, 
rownumber = Sushi_ChIPSeq_severalfactors.bed$row, type = "circles", color = Sushi_ChIPSeq_severalfactors.bed$color, rowlabels=unique(Sushi_ChIPSeq_severalfactors.bed$name), rowlabelcol=unique(Sushi_ChIPSeq_severalfactors.bed$name),
```
Sushi_ChIPSeq_severalfactors.bed$color = heat.colors(max(Sushi_ChIPSeq_severalfactors.bed$row))[Sushi_ChIPSeq_severalfactors.bed$row]

plotBed(beddata = Sushi_ChIPSeq_severalfactors.bed, chrom = chrom, chromstart = chromstart, chromend = chromend, rownumber = Sushi_ChIPSeq_severalfactors.bed$row, type = "region", color = Sushi_ChIPSeq_severalfactors.bed$row, rowlabels = unique(Sushi_ChIPSeq_severalfactors.bed$name), rowlabelcol = unique(Sushi_ChIPSeq_severalfactors.bed$name), rowlabelcex = 0.75)

colors = c("dodgerblue1", "firebrick2", "violet", "yellow", "dodgerblue1", "firebrick2", "violet", "yellow", "dodgerblue1", "firebrick2", "violet")

plotBed(beddata = Sushi_ChIPSeq_severalfactors.bed, chrom = chrom, chromstart = chromstart, chromend = chromend, rownumber = Sushi_ChIPSeq_severalfactors.bed$row, type = "density", row = "supplied", rowlabels = unique(Sushi_ChIPSeq_severalfactors.bed$name), rowlabelcol = colors, rowlabelcex = 0.75, palettes = list(
  colorRampPalette(c("black", colors[1]))),
  colorRampPalette(c("black", colors[2])),
  colorRampPalette(c("black", colors[3])),
  colorRampPalette(c("black", colors[4])),
  colorRampPalette(c("black", colors[5])),
  colorRampPalette(c("black", colors[6])),
  colorRampPalette(c("black", colors[7])),
  colorRampPalette(c("black", colors[8])),
  colorRampPalette(c("black", colors[9])),
  colorRampPalette(c("black", colors[10])),
  colorRampPalette(c("black", colors[11]))))

---

plotBedgraph

**plots data stored in bed file format**

### Description

plots data stored in bed file format

### Usage

```r
plotBedgraph(signal, chrom, chromstart, chromend, range = NULL, color = SushiColors(2)(2)[1], lwd = 1, linecolor = NA, addscale = FALSE, overlay = FALSE, rescaleoverlay = FALSE, transparency = 1, flip = FALSE, xaxt = "none", yaxt = "none", xlab = "", ylab = "", xaxs = "i", yaxs = "i", bty = "n", ymax = 1.04, colorbycol = NULL, ...)
```

### Arguments

- **signal**: signal track data to be plotted (in bedgraph format)
- **chrom**: chromosome of region to be plotted
- **chromstart**: start position
- **chromend**: end position
- **range**: y-range to plot (c(min, max))
- **color**: color of signal track
- **lwd**: color of line outlining signal track. (only valid if linecol is not NA)
linecolor: color of line outlining signal track. Use NA for no outline
addscale: TRUE/FALSE whether to add a y-axis
overlay: TRUE / FALSE whether this data should be plotted on top of an existing plot
rescaleoverlay: TRUE/FALSE whether the new plot should be rescaled based on the maximum value to match the existing plot (only valid when overlay is set to ‘TRUE’) 
transparency: Value between 0 and 1 indicating the degree of transparency of the plot
flip: TRUE/FALSE whether the plot should be flipped over the x-axis
xaxt: A character which specifies the x axis type. See par
yaxt: A character which specifies the y axis type. See par
xlab: Label for the x-axis
ylab: Label for the y-axis
xaxs: Must be set to ‘i’ for appropriate integration into Sushi plots. See par
yaxs: Must be set to ‘i’ for appropriate integration into Sushi plots. See par plottype
bty: A character string which determined the type of box which is drawn about plots. See par
ymax: fraction of max y value to set as height of plot.
colorbycol: palette to use to shade the signal track plot. Only applicable when overlay is set to FALSE.
... values to be passed to plot

Examples

data(Sushi_ChIPSeq_CTCF.bedgraph)
data(Sushi_DNaseI.bedgraph)

chrom = "chr11"
chromstart = 1955000
chromend = 1965000

plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph, chrom, chromstart, chromend, transparency=.50, flip=FALSE, color="blue")
plotBedgraph(Sushi_DNaseI.bedgraph, chrom, chromstart, chromend, transparency=.50, flip=FALSE, color="#E5001B", lty=1)
labelgenome(chrom, chromstart, chromend, side=1, scipen=20, n=3, line=.18, chromline=.5, scaleline=0.5, scale="Mb")

transparency = 0.5
col1 = col2rgb("blue")
finalcolor1 = rgb(col1[1], col1[2], col1[3], alpha=transparency * 255, maxColorValue = 255)
col2 = col2rgb("#E5001B")
finalcolor2 = rgb(col2[1], col2[2], col2[3], alpha=transparency * 255, maxColorValue = 255)

legend("topright", inset=0.025, legend=c("DnaseI", "ChIP-seq (CTCF)"), fill=c(finalcolor1, finalcolor2), border=col1[4])

Description

plots data stored in bed file format
Usage

plotBedpe(bedpedata, chrom, chromstart, chromend, heights, color = "black", colorby = NULL, colorbycol = NULL, colorbyrange = NULL, border = NULL, lwdby = NULL, lwdrange = c(1, 5), offset = 0, flip = FALSE, lwd = 1, xaxt = "n", yaxt = "n", bty = "n", plottype = "loops", maxrows = 10000, height = 0.3, ymax = 1.04, ...)

Arguments

bedpedata | bed paired end data to be plotted
chrom | chromosome of region to be plotted
chromstart | start position
chromend | end position
heights | single value or vector specifying the height of the arches to be plotted (only valid when plottype is set to "loops")
color | single value or vector specifying colors of bedpe elements
colorby | vector to scale colors by
colorbycol | palette to apply color scale to (only valid when colorby is not NULL)
colorbyrange | the range of values to apply the color scale to. Values outside that range will be set to the limits of the range.
lwdby | vector to scale line widths by
lwdrange | the range of values to apply the line width scale to. Values outside that range will be set to the limits of the range.
offset | offset of bedpe elements from the x-axis
flip | TRUE/FALSE whether the plot should be flipped over the x-axis
lwd | linewidth for bedpe elements (only valid when colorby is not NULL)
xaxt | A character which specifies the x axis type. See par
yaxt | A character which specifies the y axis type. See par
bty | A character string which determined the type of box which is drawn about plots. See par
plottype | type of plot (acceptable values are 'loops', 'ribbons', or 'lines')
maxrows | The maximum number of rows to plot on the y-axis
height | the height of the boxes at either end of a bedpe element if plottype is set to 'lines'. Typical vaues range form 0 to 1. (only valid when plottype is set to 'lines')
ymax | fraction of max y value to set as height of plot. Only applies when plottype is set to 'loops' or 'ribbons'
... | values to be passed to plot

Examples

data(Sushi_5C.bedpe)

chrom = "chr11"
chromstart = 1650000
chromend = 2350000
plotGenes

plots gene structure or transcript structures

description

plots gene structure or transcript structures

usage

plotGenes(geneinfo = NULL, chrom = NULL, chromstart = NULL, chromend = NULL, col = SushiColors(2)[1], bheight = 0.3, lheight = 0.3, bentline = TRUE, packrow = TRUE, maxrows = 10000, colorby = NULL, colorbyrange = NULL, colorbycol = colorRampPalette(c("blue", "red")), types = "exon", plotgenetype = "box", arrowlength = 0.005, wigglefactor = 0.05, labeltext = TRUE, labeloffset = 0.4, fontsize = 0.7, fonttype = 2, labelat = "middle", ...)

arguments

geneinfo gene info stored in a bed-like format. If NULL it will look up genes in the region using biomart (with biomart="ensembl" and dataset="hsapiens_gene_ensembl"). See also useMart
chrom chromosome of region to be plotted
chromstart start position
chromend end position
col single value or vector specifying colors of gene structures
bheight the height of the boxes drawn for exons
lheight the height of the bent line is bent is set to TRUE
bentline TRUE/FALSE indicating whether lines between exons should be bent
packrow TRUE / FALSE indicating whether genes should be packed or whether each gene should be plotted on its own row
maxrows The maximum number of rows to plot on the y-axis
colorby vector to scale colors by
colorbyrange the range of values to apply the color scale to. Values outside that range will be set to the limits of the range.
colorbycol palette to apply color scale to (only valid when colorby is not NULL)
types single value or vector specifying types of elements (acceptable values are "exon", "utr")
plotgenetype String specifying whether the genes should resemble a "box" or a "arrow"
plotHic

arrowlength  value (between 0 and 1) specifying the length of the tail of each arrow as a fraction of the total plot width (only valid when plotgenetype is set to "arrow")

wigglefactor  the fraction of the plot to leave blank on either side of each element to avoid overcrowding.

labeltext  TRUE/FALSE indicating whether genes should be labeled

labeloffset  value (between 0 and 1) specifying the vertical offset of gene labels

fontsize  font size of gene labels

fonttype  font type of gene labels

labelat  position along gene to place labels (acceptable values are "middle", "start", and "end")

...  values to be passed to plot

Examples

data(Sushi_genes.bed)

chrom = "chr15"
chromstart = 72998000
chromend = 73020000
chrom_biomart = 15

plotGenes(Sushi_genes.bed, chrom_biomart, chromstart, chromend, types=Sushi_genes.bed$type,
maxrows=1, height=0.5, plotgenetype="arrow", bentline=FALSE, col="blue",
labeloffset=1, fontsize=1.2)

labelgenome( chrom, chromstart, chromend, side=1, scipen=20, n=3, scale="Mb", line=.18, chromline=.5, scaleline=.5)

plotHic  plots HiC interactio matrix

Description
plots HiC interactio matrix

Usage
plotHic(hicdata, chrom, chromstart, chromend, max_y = 30, zrange = NULL,
palette = SushiColors(7), flip = FALSE)

Arguments
hicdata  interaction matrix representing HiC data. Row and column names should be positions along a chromosome

chrom  chromosome of region to be plotted

chromstart  start position

chromend  end position

max_y  The maximum bin distance to plot

zrange  The range of interaction scores to plot (more extreme value will be set to the max or min)

palette  color palette to use for representing interaction scores

flip  TRUE/FALSE whether plot should be flipped over the x-axis
plotManhattan

plots a Manhattan plot

Description
plots a Manhattan plot

Usage
plotManhattan(bedfile, chrom = NULL, chromstart = NULL, chromend = NULL, pvalues, genome = NULL, col = SushiColors(5), space = 0.01, ymax = 1.04, ...)

Arguments
bedfile: bedfile for Manhattan plot
chrom: chromosome of region to be plotted
chromstart: start position
chromend: end position
pvalues: pvalues to be used for plotting (will be converted to \(-\log(10)\) space)
genome: A genome object (2 columns: column 1 = chromosome name, column 2 = length of chromosome). Required if plotting multiple chromosomes at once.
col: single colors, vector of colors, or color palette for coloring points
space: the space in between each chromosome as a fraction of the width of the plot
ymax: fraction of max y value to set as height of plot.
...: Arguments to be passed to methods such as plot

Examples
data(Sushi_GWAS.bed)
data(Sushi_hg18_genome)

chrom1 = "chr11"
chromstart1 = 500000
chromend1 = 5050000

plotManhattan(bedfile=Sushi_GWAS.bed,pvalues=Sushi_GWAS.bed[,5],genome=Sushi_hg18_genome,col=topo.colors, ...)
sortChrom

**Description**

sort chromosome files by chom name

**Usage**

```r
sortChrom(genome)
```

**Arguments**

- `genome` A genome object to be used (2 columns: column 1 = chromosome name, column 2 = length of chromosome)

**Examples**

```r
plot(1, xlab="\"Var\"", ylab="\"Var\"", xlim=c(0,8), ylim=c(2,8), type="n", bg="grey")
for (i in (2:7))
{
  points(x=(1:i), y=rep(i,i), bg=SushiColors(i)(i), cex=3, pch=21)
}
axis(side=2, at=(2:7), labels=(2:7), las=2)
axis(side=1, at=(1:7), labels=(1:7))
mtext("SushiColors", side=3, font=2, line=1, cex=1.5)
mtext("colors", side=1, font=2, line=2)
mtext("palette", side=2, font=2, line=2)
```

SushiColors

**Description**

Generates a Sushi color palette

**Usage**

```r
SushiColors(palette = "fire")
```

**Arguments**

- `palette` The name of the Sushi palette to return. For list of available palettes try (SushiColors(list))

**Examples**

```r
plot(1, xlab="\"Var\"", ylab="\"Var\"", xlim=c(0,8), ylim=c(2,8), type="n", bg="grey")
for (i in (2:7))
{
  points(x=(1:i), y=rep(i,i), bg=SushiColors(i)(i), cex=3, pch=21)
}
axis(side=2, at=(2:7), labels=(2:7), las=2)
axis(side=1, at=(1:7), labels=(1:7))
mtext("SushiColors", side=3, font=2, line=1, cex=1.5)
mtext("colors", side=1, font=2, line=2)
mtext("palette", side=2, font=2, line=2)
```
**Sushi_5C.bedpe**

**Description**
This data set lists the genomic locations of 5C interactions in multiple cell lines with coordinates based on the NCBI36/hg18 genome build.

**Usage**
Sushi_5C.bedpe

**Format**
bedpe format

**Source**

**Sushi_ChIAPET_pol2.bedpe**

**Description**
This data set lists the genomic locations of Pol2 ChIA PET interactions in K562 cells with coordinates based on the NCBI36/hg18 genome build.

**Usage**
Sushi_ChIAPET_pol2.bedpe

**Format**
bedpe format

**Source**
**Sushi_ChIPExo_CTCF.bedgraph**

---

**Description**

This data set describes read depths across the genome resulting from a CTCF ChIP Exo experiment in K562 cells with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

Sushi_ChIPExo_CTCF.bedgraph

**Format**

bedgraph format

**Source**


---

**Sushi_ChIPSeq_CTCF.bedgraph**

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**Description**

This data set describes read depths across the genome resulting from a CTCF ChIP seq experiment in K562 cells with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

Sushi_ChIPSeq_CTCF.bedgraph

**Format**

bedgraph format

**Source**

**Description**

This data set describes aligned sequencing reads for Pol2 in K562 cells as determined by ChIP-seq with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

*Sushi_ChIPSeq_pol2.bed*

**Format**

bed format

**Source**


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**Description**

This data set describes read depths across the genome resulting from a Pol2 ChIP seq experiment in K562 cells with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

*Sushi_ChIPSeq_pol2.bedgraph*

**Format**

bedgraph format

**Source**

**Description**

This data set describes binding sites for multiple factors in K562 cells as determined by ChIP-seq with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

Sushi_ChIPSeq_severalfactors.bed

**Format**

bed format

**Source**


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**Description**

This data set describes read depths across the genome resulting from a DNaseI hypersensitivity experiment in K562 cells with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

Sushi_DNaseI.bedgraph

**Format**

bedgraph format

**Source**

**Description**

Bed data representing human genes with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

Sushi_genes.bed

**Format**

bed format

**Source**

http://www.biomart.org/

**Description**

Bed data representing results from a GWAS study of blood pressure and cardiovascular disease risk with coordinates based on the NCBI36 / hg18 genome build.

**Usage**

Sushi_GWAS.bed

**Format**

bed format

**Source**

Description
This data set describes the length of human chromosomes according to the NCBI36 / hg18 genome build.

Usage
Sushi_hg18_genome

Format
two columns (column 1 = chromosome name, column 2 = length of chromosome)

Source

Description
Bed data representing results from a GWAS study of blood pressure and cardiovascular disease risk with coordinates based on the NCBI36 / hg18 genome build.

Usage
Sushi_HiC.matrix

Format
matrix

Source
**Sushi_RNASeq_K562.bedgraph**

**Description**
Bedgraph data representing RNA-seq data from K562 with coordinates based on the NCBI36 / hg18 genome build.

**Usage**
Sushi_RNASeq_K562.bedgraph

**Format**
bedgraph format

**Source**

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**Sushi_transcripts.bed**

**Description**
Bed data representing human transcripts and their expression in K562 cells with coordinates based on the NCBI36 / hg18 genome build.

**Usage**
Sushi_transcripts.bed

**Format**
bed format

**Source**
**zoombox**

Adds a zoom box to a plot

**Description**

This function is used on the second plot of a zoom in.

**Usage**

```r
zoombox(zoomregion = NULL, lty = 2, lwd = 1, col = "black",
         topextend = 2, passthrough = FALSE)
```

**Arguments**

- **zoomregion**: Region of another zoom on this plot. Only required if this plot has another zoomregion on it.
- **lty**: line type for box. See `par`
- **lwd**: line width. See `par`
- **col**: Color for zoombox line
- **topextend**: How far to extend the lines above the current plot (as a fraction of the plot height)
- **passthrough**: TRUE / FALSE whether or not to pass the zoom though this plot. If set to FALSE no horizontal line is drawn on the bottom of the plot

**Examples**

```r
data(Sushi_DNaseI.bedgraph)
data(Sushi_ChIPSeq_CTCF.bedgraph)

# make a layout for all of the plots
layout(matrix(c(1,1,
               2,2),2, 2, byrow = TRUE))
par(mgp=c(3, .3, 0))
par(mar=c(3,4,2,1))
chrom = "chr11"
chromstart = 1650000
chromend = 2350000
zoomregion1 = c(1955000,1965000)
plotBedgraph(Sushi_DNaseI.bedgraph,chrom,chromstart,chromend,transparency=1.0,color="#5900E5",lwd=1,linecol="#5900E5")
zoomsregion(zoomregion1,col=NA,zoomborder="black",lty=2,lwd=1,extend=c(0.01,0.09),wideextend=0.10,offsets=c(0,0))
labelgenome(chrom,chromstart,chromend,side=1,scipen=20,n=4,line=.18,chromline=.5,scaleline=0.5,scale="Mb")
axis(side=2,las=2,tcl=.2)
mtext("Read Depth",side=2,line=1.75,cex=.75,font=2)

# plot dnaseI data
plotBedgraph(Sushi_DNaseI.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.50,flip=FALSE,color="#E5001B")
```
# plot chip-seq data
plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph, chrom, zoomregion1[1], zoomregion1[2], transparency=.30, flip=FALSE, color="blue", linecol="blue", overlay=TRUE, rescaleoverlay=TRUE)

# add zoombox
zoombox(zoomregion = NULL, lwd = 1, col="black")

axis(side=2, las=2, tcl=.2)
mtext("Read Depth", side=2, line=1.75, cex=.75, font=2)

# add the genome labels
labelgenome(chrom, zoomregion1[1], zoomregion1[2], side=1, scipen=20, n=3, line=.18, chromline=.5, scaleline=0.5, scale="Mb")

# set the legend colors
transparency = 0.5
col1 = col2rgb("blue")
finalcolor1 = rgb(col1[1], col1[2], col1[3], alpha=transparency * 255, max = 255)
col2 = col2rgb("#E5001B")
finalcolor2 = rgb(col2[1], col2[2], col2[3], alpha=transparency * 255, max = 255)

# add legend
legend("topright", inset=0.025, legend=c("DnaseI","ChIP-seq (CTCF)"), fill=c(finalcolor1, finalcolor2), border=c("blue", "#E5001B"), text.font=2, cex=0.75)

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### zoomsregion

**Description**

This function is used on the first plot of a zoom in

**Usage**

```r
zoomsregion(region, chrom = NULL, genome = NULL, space = 0.01, padding = 0.005, col = NA, zoomborder = "black", lty = 2, lwd = 1, extend = 0, wideextend = 0.1, offsets = c(0, 0), highlight = FALSE)
```

**Arguments**

- **region**: chromosome start and stop to zoom in on
- **chrom**: chromosome of region to be plotted
- **genome**: A genome object (2 columns: column 1 = chromosome name, column 2 = length of chromosome). Set to NULL if adding zoom to a plot with only a single chromosome.
- **space**: the space in between each chromosome as a fraction of the width of the plot. Only used when adding a zoomsregion to a plot with multiple chromosomes (e.g. a Manhattan plot)
- **padding**: The minimum size of a zoom region (as a fraction of the plot width). If the specified zoom region is too small it will zoom on a region twice this wide centered on the specified zoom region.
- **col**: Color of the zoom region
- **zoomborder**: Color of the border of the zoom region
- **lty**: line type of zoom region border. See `plot`
lwd
  line type of zoom region border. See plot
extend
  single value or vector of 2 values specifying how far the zoom region extend
  above and below the plot region (as a fraction of the plot height). Note this valu
  only applies to the narrow portion of the zoom region.
wideextend
  Value specifying how below the plot region (as a fraction of the plot height) the
  wide portion of the zoom window starts. Only applicable if highlight is set to
  FALSE.
offsets
  vector of 2 values specifying offsets to the left and right side of the wide portion
  of the zoom window. It may be neccesary to adjust these by trial and error for
  more complicated layouts. Only applicable if highlight is set to FALSE.
highlight
  TRUE/FALSE indicating if you are adding a highlight region as opposed to a
  zoom in. Highlight regions simply draw a box around the region of interest

Examples

data(Sushi_DNaseI.bedgraph)
data(Sushi_ChIPSeq_CTCF.bedgraph)

# make a layout for all of the plots
layout(matrix(c(1,1,
                2,2)
       ,2, 2, byrow = TRUE))
par(mgp=c(3, .3, 0))
par(mar=c(3,4,2,1))
chrom = "chr11"
chromstart = 1650000
chromend = 2350000
zoomregion1 = c(1955000,1965000)

plotBedgraph(Sushi_DNaseI.bedgraph,chrom,chromstart,chromend,transparency=1.0,color="#5900E5",lwd=1,linecol="#5900E5")
zoomsregion(zoomregion1,col=NA,zoomborder="black",lty=2,lwd=1,extend=c(0.01,0.09),wideextend=0.10,offsets=c(0,0))
labelgenome(chrom,chromstart,chromend,side=1,scipen=20,n=4,line=.18,chromline=.5,scaleline=0.5,scale="Mb")

axis(side=2,las=2,tcl=.2)
mtext("Read Depth",side=2,line=1.75,cex=.75,font=2)

# plot dnaseI data
plotBedgraph(Sushi_DNaseI.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.50,flip=FALSE,color="#E5001B",linecol="#E5001B")

# plot chip-seq data
plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.30,flip=FALSE,color="blue",linecol="blue",overlay=TRUE,rescaleoverlay=TRUE)

# add zoombox
zoombox(zoomregion = NULL,lwd = 1,col="black")

axis(side=2,las=2,tcl=.2)
mtext("Read Depth",side=2,line=1.75,cex=.75,font=2)

# add the genome labels
labelgenome(chrom,zoomregion1[1],zoomregion1[2],side=1,scipen=20,n=3,line=.18,chromline=.5,scaleline=0.5,scipen=20)

# set the legend colors
transparency = 0.5
col1 = col2rgb("blue")
finalcolor1 = rgb(col1[1],col1[2],col1[3],alpha=transparency * 255,max = 255)
col2 = col2rgb("#E5001B")
finalcolor2 = rgb(col2[1],col2[2],col2[3],alpha=transparency * 255,max = 255)

# add legend
legend("topright",inset=0.025,legend=c("DnaseI","ChIP-seq (CTCF)"),fill=c(finalcolor1,finalcolor2),border=c("blue","#E5001B"),text.font=2,cex=0.75)
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