Package ‘Sushi’

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addlegend adds a legend to a Sushi plot

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

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

Arguments
range the range of values to be plotted. ie c(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
chromOffsets defines chromosome offsets for plotting multi chromosomal plot (e.g. plotManhattan)

defines chromosome offsets for plotting multi chromosomal plot (e.g. 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**
Converting 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**
Adding genome coordinates to the x-axis of a Sushi plot.

**Usage**
```
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
**labelplot**

adds a letter and a title to a plot

**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`

**Examples**

```r
data(Sushi_DNaseI.bedgraph)
# set the genomic regions

plotBedgraph(Sushi_DNaseI.bedgraph, chrom="chr1", chromstart=1650000, chromend=2350000, colorbycol=SushiColors(7),
labelgenome(chrom="chr1", 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)
```

---

- **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`
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)

Examples

par(mar=c(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")
maptolwd

maptolwd maps numeric vector to line widths

Description
maptolwd maps numeric vector to line widths

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

Arguments
- lwdby: numeric vector to map to line widths
- range: range of values to map

Examples
plot((1:10), lwd=maptolwd(lwdby=(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, binsmoothing = 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)
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')
**plotBed**

- **palettes** list of color palettes used for density plots. Each row can have a unique palette. If the 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))
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), rowlabelcex = 0.75, maxrows = 5000000000)

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(colors[1]),
```
plots data stored in bed file format

Usage

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 indication 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
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=.5,flip=FALSE,color="blue",linecolor="#E5001B",linecolor="blue")
plotBedgraph(Sushi_DNaseI.bedgraph,chrom,chromstart,chromend,transparency=.5,flip=FALSE,color="#E5001B",linecolor="#E5001B")

labelgenome(chrom,chromstart,chromend,side=1,scipen=20,n=3,line=.18,chromline=.5,scalleline=0.5,scalle="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("topleft",inset=0.025,legend=c("DnaseI","ChIP-seq (CTCF)"),fill=c(finalcolor1,finalcolor2),border=c("black"))

plotBedpe  plots data stored in bed file format

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,
lwby = 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 values 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

```r
data(Sushi_5C.bedpe)

chrom = "chr11"
chromstart = 1650000
chromend = 2350000
pbpe = plotBedpe(Sushi_5C.bedpe,chrom,chromstart,chromend,heights = Sushi_5C.bedpe$score,offset=0,flip=FALSE,lwd=1,plottype="ribbons",colorby=Sushi_5C.bedpe$samplenumber,colorbycol=topo.colors,border="black")
labelgenome(chrom,chromstart,chromend,side=1,scipen=3,scale="Mb",line=.18,chromline=.5,scaleline=.5)
legend("topright",inset=.01,legend=c("K562","HeLa","GM12878"),col=c(topo.colors(3)),pch=19,bty='n',text.font=axis(side=2,las=2,tcl=.2)

mtext("Z-score",side=2,line=1.75,cex=.75,font=2)
```
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)(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'
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","end")

...  values to be passed to plot

Examples

data(Sushi_genesis.bed)

  chrom   = "chr15"
  chromstart   = 72980000
  chromend     = 73020000
  chrom_biomart  = 15

plotGenes(Sushi_genesis.bed,chrom_biomart,chromstart,chromend,types=Sushi_genesis.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=0.5)

plotHic

plots HiC interaction matrix

Description

plots HiC interaction 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
  chrom            positions along a chromosome
  chromstart       chromosome of region to be plotted
  chromend         start position
  chromend         end position
  max_y            The maximum bin distance to plot
plotManhattan

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

Examples

data(Sushi_HiC.matrix)

chrom = "chr1"
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=2)

addlegend(phic[[1]],palette=phic[[2]],title="score",side="right",bottominset=0.4,topinset=0,xoffset=-.035,label="...

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)

crom1    = "chr11"
cromstart1 = 500000
cromend1   = 5050000

plotManhattan(bedfile=Sushi_GWAS.bed,pvalues=Sushi_GWAS.bed[,5],genome=Sushi_hg18_genome,col=topo.colors,cex=0
labelgenome(genome=Sushi_hg18_genome,side=1,scipen=20,n=4,scipen="Mb",edgeblankfraction=0.20,line=.18,chromline=18
axis(side=2,las=2,tcl=.2)
mtext("log10(P)",side=2,line=1.75,cex=.75,font=2)

sortChrom      sort chromosome files by chom name

Description

sort chromosome files by chom name

Usage

sortChrom(genome)

Arguments

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

SushiColors Generates a Sushi color palette

Description

Generates a Sushi color palette

Usage

SushiColors(palette = "fire")

Arguments

palette The name of the Sushi palette to return. For list of available palettes try (Sushi-
Colors(list))
**Examples**

```r
plot(1, xlab=' ', ylab=' ', xaxt='n', yaxt='n', 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)
```

---

**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**


---

**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**


---

**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**


---

**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**


---

**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**

Sushi_ChIPSeq_severalfactors.bed

**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**


Sushi_DNaseI.bedgraph

**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**

### Sushi_genes.bed

**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/

---

### Sushi_GWAS.bed

**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**


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**


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**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 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 through 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))
```

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**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 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 through 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))
```
The `zoomsregion` function adds a zoom region to a plot.

**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
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 width 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 value 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 necessary 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,scalene=0.5,scalene="Mb")
axis(side=2,las=2,tcl=.2)
mtext("Read Depth",side=2,line=1.75,cex=.75,font=2)

# plot dnase1 data
plotBedgraph(Sushi_DNase1.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.50,flip=FALSE,color="#E50808")

# plot chip-seq data
plotBedgraph(Sushi_ChIPseq_CTCF.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.30,flip=FALSE,color="#085080")

# 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=2)

# 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("#E50808")
finalcolor2 = rgb(col2[1],col2[2],col2[3],alpha=transparency * 255,max = 255)

# add legend
legend("topright",inset=0.025,legend=c("Dnase1","ChIP-seq (CTCF)"),fill=c(finalcolor1,finalcolor2),border=c("black"))
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