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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Author Douglas H Phanstiel <dphansti@stanford.edu>

Maintainer Douglas H Phanstiel <dphansti@stanford.edu>

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R topics documented:

`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 rang 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
`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 legned text
title.offset	offset of title from the key
title.font	font type of legend title
title.cex	font size of legned text

Examples

```
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,fl

labelgenome(chrom,chromstart,chromend,side=1,scipen=20,n=4,scale="Mb",edgeblankfraction=0.20,line=.18,chro

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

---

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

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 neccesary

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

```
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 chomosome label
chromcex	font size of the chomosome label

chromline	vertical offset of the chomosome 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
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)
```

---

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. Udeful 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 lable 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

```
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(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 strnad bed elements shold 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	umber 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

```
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_ChIPS
plotBed(beddata   = Sushi_ChIPSeq_severalfactors.bed,chrom = chrom,chromstart = chromstart,chromend =chromend
     rownumber  = Sushi_ChIPSeq_severalfactors.bed$row, type = "circles",color=Sushi_ChIPSeq_severalfactors.
     rowlabels=unique(Sushi_ChIPSeq_severalfactors.bed$name),rowlabelcol=unique(Sushi_ChIPSeq_severalfacto
```

```
Sushi_ChIPSeq_severalfactors.bed$color = heat.colors(max(Sushi_ChIPSeq_severalfactors.bed$row))[Sushi_ChIPS

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

colors = c("dodgerblue1","firebrick2","violet","yellow",
        "dodgerblue1","firebrick2","violet","yellow",
        "dodgerblue1","firebrick2","violet")
plotBed(beddata   = Sushi_ChIPSeq_severalfactors.bed,chrom = chrom,chromstart = chromstart,chromend =chromenc
      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

```
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 plpt (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 shold 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 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",li
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=c
```

---

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,
  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
```

```
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=20,n=3,scale="Mb",line=.18,chromline=.5,scaleline=0.5)
legend("topright",inset =0.01,legend=c("K562","HeLa","GM12878"),col=c(topo.colors(3)),pch=19,bty='n',text.f
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	postion 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=0.5
```

---

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 postions 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

Examples

```
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,fl

labelgenome(chrom,chromstart,chromend,side=1,scipen=20,n=4,scale="Mb",edgeblankfraction=0.20,line=.18,chro

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

---

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,ce
```

```
labelgenome(genome=Sushi_hg18_genome,side=1,scipen=20,n=4,scale="Mb",edgeblankfraction=0.20,line=.18,chroml
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 (SushiColors(list))

Examples

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

Sushi_5C.bedpe *Sushi_5C.bedpe*

Description

This data set list 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

Sanyal, A., Lajoie, B. R., Jain, G. & Dekker, J. The long-range interaction landscape of gene promoters. Nature 489, 109-113 (2012).

Sushi_ChIAPET_pol2.bedpe
Sushi_ChIAPET_pol2.bedpe

Description

This data set list 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

Li, G. et al. Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell 148, 84-98 (2012).

Sushi_ChIPExo_CTCF.bedgraph
Sushi_ChIPExo_CTCF.bedgraph

Description

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

Usage

```
Sushi_ChIPExo_CTCF.bedgrap
```

Format

bedgraph format

Source

Rhee, H. S. & Pugh, B. F. Comprehensive genome-wide protein-DNA interactions detected at single-nucleotide resolution. Cell 147, 1408-1419 (2011).

Sushi_ChIPSeq_CTCF.bedgraph
Sushi_ChIPSeq_CTCF.bedgraph

Description

This data set describes read depths across the genomce 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

Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Sushi_ChIPSeq_pol2.bed

Sushi_ChIPSeq_pol2.bed

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

Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Sushi_ChIPSeq_pol2.bedgraph

Sushi_ChIPSeq_pol2.bedgraph

Description

This data set describes read depths across the genomce 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

Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Sushi_ChIPSeq_severalfactors.bed *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

Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Sushi_DNaseI.bedgraph *Sushi_DNaseI.bedgraph*

Description

This data set describes read depths across the genomce 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

Neph, S. et al. An expansive human regulatory lexicon encoded in transcription factor footprints. Nature 489, 83-90 (2012).

Sushi_genes.bed *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 *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

Ehret, G. B. et al. Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature 478, 103-109 (2011).

Sushi_hg18_genome *Sushi_hg18_genome*

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

http://www.biomart.org/ and Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Sushi_HiC.matrix *Sushi_HiC.matrix*

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

Dixon, J. R. et al. Topological domains in mammalian genomes identified by analysis of chromatin interactions. Nature (2012). doi:10.1038/nature11082

Sushi_RNASeq_K562.bedgraph *Sushi_RNASeq_K562.bedgraph*

Description

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

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

Usage

```
Sushi_RNASeq_K562.bedgraph

Sushi_RNASeq_K562.bedgraph
```

Format

bedgraph format

Source

Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

Sushi_transcripts.bed *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

http://www.biomart.org/ and Consortium, T. E. P. An integrated encyclopedia of DNA elements in the human genome. Nature 489, 57-74 (2012).

zoombox *Adds a zoom box to a plot*

Description

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

Usage

```
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 exted 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 botoom of the plot

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,lineco

zoomsregion(zoomregion1,col=NA,zoomborder="black",lty=2,lwd=1,extend=c(0.01,0.09),wideextend=0.10,offsets=

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="
```

```
# plot chip-seq data
plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.30,flip=FALSE,co

# 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,sc

# 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
```

`zoomsregion` *Adds a zoom region to a plot*

Description

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

Usage

```
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 singe 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 cerntered on te 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,lineco

zoomsregion(zoomregion1,col=NA,zoomborder="black",lty=2,lwd=1,extend=c(0.01,0.09),wideextend=0.10,offsets=

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="

# plot chip-seq data
plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.30,flip=FALSE,c

# 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,s

# 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
```

Index