

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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R topics documented:

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| | |
|-----------|--------------------------------------|
| addlegend | <i>adds a legend to a Sushi plot</i> |
|-----------|--------------------------------------|

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 legend text |
| title.offset | offset of title from the key |
| title.font | font type of legend title |
| title.cex | font size of legend 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, flip=F)
```

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

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

| | |
|--------------|------------------------------------------------------------------------------------------|
| chromOffsets | <i>defines chromosome offsets for plotting multi chromosomal plot (eg plotManhattan)</i> |
|--------------|------------------------------------------------------------------------------------------|

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 | <i>Converts strand info to 1 / -1</i> |
|-------------------|---------------------------------------|

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 | <i>Adds genome coordinates to the x-axis of a Sushi plot</i> |
|-------------|--------------------------------------------------------------|

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 chromosome label |
| chromcex | font size of the chromosome label |
| chromline | vertical offset of the chromosome label |
| scafont | font type of scale label |
| scaadjust | position, as a fraction of the width of the plot, of the scale label |
| scaecex | font size of the scale label |
| scaeline | 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)
```

| | |
|-----------|--------------------------------------------|
| labelplot | <i>adds a letter and a title to a plot</i> |
|-----------|--------------------------------------------|

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 | <i>maps numeric vector to line widths</i> |
|----------|-------------------------------------------|

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 | <i>makes colors transparent (or opaque)</i> |
|--------|---------------------------------------------|

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 | 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_several.factors.bed)
chrom      = "chr15"
chromstart = 72800000
chromend   = 73100000
Sushi_ChIPSeq_several.factors.bed$color = heat.colors(max(Sushi_ChIPSeq_several.factors.bed$row))[Sushi_ChIPSeq_several.factors.bed$row]
plotBed(beddata = Sushi_ChIPSeq_several.factors.bed, chrom = chrom, chromstart = chromstart, chromend = chromend,
        rownumber = Sushi_ChIPSeq_several.factors.bed$row, type = "circles", color=Sushi_ChIPSeq_several.factors.bed$color,
        rowlabels=unique(Sushi_ChIPSeq_several.factors.bed$name), rowlabelcol=unique(Sushi_ChIPSeq_several.factors.bed$color))

Sushi_ChIPSeq_several.factors.bed$color = heat.colors(max(Sushi_ChIPSeq_several.factors.bed$row))[Sushi_ChIPSeq_several.factors.bed$row]

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

colors = c("dodgerblue1", "firebrick2", "violet", "yellow",
           "dodgerblue1", "firebrick2", "violet", "yellow",
           "dodgerblue1", "firebrick2", "violet")
plotBed(beddata = Sushi_ChIPSeq_several.factors.bed, chrom = chrom, chromstart = chromstart, chromend = chromend,
        rownumber = Sushi_ChIPSeq_several.factors.bed$row, type = "density", row="supplied",
        rowlabels=unique(Sushi_ChIPSeq_several.factors.bed$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 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 plotype |
| 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",li
plotBedgraph(Sushi_DNaseI.bedgraph,chrom,chromstart,chromend,transparency=.50,flip=FALSE,color="#E5001B",linec
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("b

```

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, lwdby = NULL,
lwdrange = c(1, 5), offset = 0, flip = FALSE, lwd = 1, yaxt = "n",
yaxt = "n", bty = "n", plotype = "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 |
| plottype | type of plot (acceptable values are 'loops' and 'lines') |
| maxrows | The maximum number of rows to plot on the y-axis |
| ymax | fraction of max y value to set as height of plot. Only applies when plottype is set to 'loops' |
| 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') |
| bty | A character string which determined the type of box which is drawn about plots. See par |
| ... | 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$score,offset=0,flip=FALSE,bty="n",
lwd=1,plottype="loops",colorby=Sushi_5C.bedpe$samplenummer,colorbycol=topo.colors)
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.font=2)
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 |
| 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. |
| 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 |
| 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. |

| | |
|-------------|---------------------------------------------------------------------------------------|
| maxrows | The maximum number of rows to plot on the y-axis |
| 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 <code>plot</code> |

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, flip=F)
```

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

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

| | |
|---------------|-------------------------------|
| plotManhattan | <i>plots a Manhattan plot</i> |
|---------------|-------------------------------|

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,cex=0
labelgenome(genome=Sushi_hg18_genome,side=1,scipen=20,n=4,scale="Mb",edgeblankfraction=0.20,line=.18,chromline
axis(side=2,las=2,tcl=.2)
mtext("log10(P)",side=2,line=1.75,cex=.75,font=2)

```

| | |
|-----------|-------------------------------------------|
| sortChrom | <i>sort chromosome files by chom name</i> |
|-----------|-------------------------------------------|

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 | <i>Generates a Sushi color palette</i> |
|-------------|----------------------------------------|

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 genome 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 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

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 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

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 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

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 | <i>Sushi_hg18_genome</i> |
|-------------------|--------------------------|

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 | <i>Sushi_HiC.matrix</i> |
|------------------|-------------------------|

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 | <i>Adds a zoom box to a plot</i> |
|---------|----------------------------------|

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 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

```
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="#
zoomsregion(zoomregion1,col=NA,zoomborder="black",lty=2,lwd=1,extend=c(0.01,0.09),wideextend=0.10,offsets=c(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="#E501B")

# plot chip-seq data
plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.30,flip=FALSE,color="#E501B")

# 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("black","black"))

```

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 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 extends 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. |
| widextend | 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,lincol="#
zoomsregion(zoomregion1,col=NA,zoomborder="black",lty=2,lwd=1,extend=c(0.01,0.09),widextend=0.10,offsets=c(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="#E501B")

# plot chip-seq data
plotBedgraph(Sushi_ChIPSeq_CTCF.bedgraph,chrom,zoomregion1[1],zoomregion1[2],transparency=.30,flip=FALSE,color="#E501B")

# 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=1)

# 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("#E501B")
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("black","black"))
```

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