

Package ‘CMplot’

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Type Package

Title Circle Manhattan Plot

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Description Manhattan plot, a type of scatter plot, was widely used to display the association results. However, it is usually time-consuming and laborious for a non-specialist user to write scripts and adjust parameters of an elaborate plot. Moreover, the ever-growing traits measured have necessitated the integration of results from different Genome-wide association study researches. Circle Manhattan Plot is the first open R package that can lay out Genome-wide association study P-value results in both traditional rectangular patterns, QQ-plot and novel circular ones. United in only one bull's eye style plot, association results from multiple traits can be compared interactively, thereby to reveal both similarities and differences between signals.

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Description

Manhattan plot, a type of scatter plot, was widely used to display the association results. However, it is usually time-consuming and laborious for a non-specialist user to write scripts and adjust parameters of an elaborate plot. Moreover, the ever-growing traits measured have necessitated the integration of results from different Genome-wide association study researches. Circle Manhattan Plot is the first open R package that can lay out Genome-wide association study P-value results in QQ-plot, both traditional rectangular patterns and novel circular ones. United in only one bull's eye style plot, association results from multiple traits can be compared interactively, thereby to reveal both similarities and differences between signals.

Usage

```
CMplot(Pmap, col=c("#377EB8", "#4DAF4A", "#984EA3", "#FF7F00"),
       bin.size=1e6, bin.max=NULL, pch=19, band=1, cir.band=0.5, H=1.5,
       ylim=NULL, cex.axis=1, plot.type="b", multitracks=FALSE, cex=c(0.5,1,1),
       r=0.3, xlab="Chromosome", ylab=expression(-log[10](italic(p))), xaxs="i",
       yaxs="r", outward=FALSE, threshold = NULL, threshold.col="red",
       threshold.lwd=1, threshold.lty=2, amplify= TRUE, chr.labels=NULL,
       signal.cex = 1.5, signal.pch = 19, signal.col="red", signal.line=1,
       cir.chr=TRUE, cir.chr.h=1.5, chr.den.col=c("darkgreen", "yellow", "red")
       , cir.legend=TRUE, cir.legend.cex=0.6, cir.legend.col="black",
       LOG10=TRUE, box=FALSE, conf.int.col="grey", file.output=TRUE,
       file="jpg", dpi=300, memo="", verbose=TRUE)
```

Arguments

Pmap	a dataframe, at least four columns. The first column is the name of SNP, the second column is the chromosome of SNP, the third column is the position of SNP, and the remaining columns are the P-value of each trait(Note:each trait a column).
col	a vector or a matrix, if "col" equals to a vector, each circle use the same colors, it means that the same chromosome is drewed in the same color, the colors are not fixed, one, two, three or more colors can be used, if the length of the "col" is shorter than the length the chromosome, then colors will be applied circularly. if "col" equals to a matrix, the row is the number of circles(traits), the columns are the colors that users want to use for different circles, so each circle can be plotted in different number of colors, the missing value can be replaced by NA. For example: col=matrix(c("grey30","grey60",NA,"red","blue","green","orange",NA,NA),3,3,byrow=T).
bin.size	the size of bin for SNP_density plot.
bin.max	the max value of legend of SNP_density plot, the bin whose SNP number is bigger than 'bin.max' will be use the same color.
pch	a number, the type for the points, is the same with "pch" in <plot>.

band	a number, the space between chromosomes, the default is 1(if the band equals to 0, then there would be no space between chromosome).
cir.band	a number, the space between circles, the default is 1.
H	a number, the height for each circle, each circle represents a trait, the default is 1.
ylim	a vector, the range of Y-axis when plotting the two type of Manhattans, is the same with "ylim" in <plot>.
cex.axis	a number, controls the size of numbers of X-axis and the size of labels of circle plot.
plot.type	a character or vector, only "d", "c", "m", "q" or "b" can be used. if plot.type="d", SNP density will be plotted; if plot.type="c", only circle-Manhattan plot will be plotted; if plot.type="m",only Manhattan plot will be plotted; if plot.type="q",only Q-Q plot will be plotted;if plot.type="b", both circle-Manhattan, Manhattan and Q-Q plots will be plotted; if plot.type=c("m","q"), Both Manhattan and Q-Q plots will be plotted.
multitracks	a logical,if multitracks=FALSE, plotting multiple rectangular Manhattan plots on multiple tracks, if it is TRUE, all Manhattan plots will be plotted in only one track.
cex	a number or a vector, the size for the points, is the same with "size" in <plot>, and if it is a vector, the first number controls the size of points in circle plot(the default is 0.5), the second number controls the size of points in Manhattan plot(the default is 1), the third number controls the size of points in Q-Q plot(the default is 1)
r	a number, the radius for the circle(the inside radius), the default is 1.
xlab	a character, the labels for x axis.
ylab	a character, the labels for y axis.
xaxs	a character, The style of axis interval calculation to be used for the x-axis. Possible values are "r", "i", "e", "s", "d". The styles are generally controlled by the range of data or xlim, if given.
yaxs	a character, The style of axis interval calculation to be used for the y-axis. See xaxs above..
outward	logical, if outward=TRUE,then all points will be plotted from inside to outside.
threshold	a number or vector, the significant threshold. For example, Bonfferoni adjustment method: threshold=0.01/nrow(Pmap). More than one significant line can be added on the plots, if threshold=0 or NULL, then the threshold line will not be added.
threshold.col	a character or vector, the colour for the line of threshold levels.
threshold.lwd	a number or vector, the width for the line of threshold levels.
threshold.lty	a number or vector, the type for the line of threshold levels.
amplify	logical, CMplot can amplify the significant points, if amplify=T, then the points greater than the minimal significant level will be highlighted, the default: amplify=TRUE.
chr.labels	a vector, the labels for the chromosomes of circle-Manhattan plot.

signal.cex	a number, if amplify=TRUE, users can set the size of significant points.
signal.pch	a number, if amplify=TRUE, users can set the shape of significant points.
signal.col	a character, if amplify=TRUE, users can set the colour of significant points, if signal.col=NULL, then the colors of significant points will not be changed.
signal.line	a number, the width of the lines cross the circle
cir.chr	logical, a boundary represents chromosome, the default is TRUE.
cir.chr.h	a number, the width for the boundary, if cir.chr=FALSE, then this parameter will be useless.
chr.den.col	a character or vector or NULL, the colour for the SNP density. If the length of parameter 'chr.den.col' is bigger than 1, SNP density that counts the number of SNP within given size('bin.size') will be plotted around the circle. If chr.den.col=NULL, then the default colours are the same with the parameter "col" for circle.
cir.legend	logical, whether to add the legend of each circle.
cir.legend.cex	a number, the size of the number of legend.
cir.legend.col	a character, the color of the axis of legend.
LOG10	logical, whether to change the p-value into log10(p-value).
box	logical, this function draws a box around the current Manhattan plot.
conf.int.col	a character, the color of the confidence interval on QQ-plot.
file.output	a logical, users can choose whether to output the plot results.
file	a character, users can choose the different output formats of plot, so for, "jpg", "pdf", "tiff" can be selected by users.
dpi	a number, the picture element for .jpg and .tiff files. The default is 300.
memo	add a character to the output file name.
verbose	whether to print the reminder.

Details

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Note

1: In the data "Pmap", autosome and heterosome can both exist simultaneously, and heterosome can also be replaced by a number.

2: only when the amplify=TRUE, then the parameter signal.cex, signal.pch, signal.col will be efficacious.

3: In the circle Manhattan plot, traits will be plotted from inside to outside, it means that the first trait occupies the innermost circle.

Author(s)

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Examples

```
#plot rectangular Manhattan only one trait with 20000 markers:
data(pig60K)
CMplot(pig60K[sample(1:nrow(pig60K), 10000),c(1:4)],plot.type="m",
  threshold=c(0.01,0.05)/nrow(pig60K),threshold.col=c('red','orange'),
  multracks=FALSE, chr.den.col=NULL)

#####
#plot circular Manhattan for all traits with all markers: #
#####
#data(pig60K) #
#CMplot(pig60K,col=c("gray30","gray60"),r=0.5,plot.type="c",threshold=0.01, #
# signal.col=NULL,outward=TRUE) #
#####
```

cattle50K

Genotyped by Bovine50K chip

Description

This dataset gives the effects of all SNPs using rrBLUP algorithm for 3 traits, individuals were genotyped by Bovine50K chip.

Usage

```
data(cattle50K)
```

Format

A dataframe containing 3 traits' SNPs effects

pig60K

Genotyped by pig 60k chip

Description

This dataset gives the results of Genome-wide association study of 3 traits, individuals were genotyped by pig 60K chip.

Usage

```
data(pig60K)
```

Format

A dataframe containing 3 traits' Pvalue

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