Package 'manhplot'

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Type Package

Title The Manhattan++ Plot

Depends R (>= 3.4.0)

Version 1.1

Date 2019-11-25

Author Chris Grace <cgrace@well.ox.ac.uk>

Maintainer Chris Grace <cgrace@well.ox.ac.uk>

Description This plot integrates annotation into a manhattan plot. The plot is implemented as a heatmap, which is binned using -log10(p-value) and chromosome position. Annotation currently supported is minor allele frequency and gene function high impact variants.

License GPL (>= 2)

RoxygenNote 6.1.1

Imports reshape2, ggplot2, ggrepel, gridExtra

Suggests R.utils, testthat

URL https://github.com/cgrace1978/manhplot/

BugReports https://github.com/cgrace1978/manhplot/issues

NeedsCompilation no

Repository CRAN

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R topics documented:

manhplot-package *The Manhattan++ Plot*

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NeedsCompilation:	no
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Index of help topics:

Author(s)

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manhplusplot *Generate the manhattan++ plot*

Description

Generate the manhattan++ plot

Usage

```
manhplusplot(infile, outfile, configfile, snpfile, drawastiff = F,
  GWS = 5e-08, FDR = 0.001, MAF = 0.05, chrname = "chr",
  posname = "pos", pvalname = "pvalue", frqname = "maf",
  conseqname = "conseq", showgenes = F, showrsids = F,
  pos.split = 3e+06, pval.split = 0.125, max.pval = 20)
```

Arguments

infile	Input GWAS summary statistics
outfile	Output file prefix for the manhattan++ plot
configfile	Configuration file
snpfile	Table of SNPs to visualize
drawastiff	If TRUE draw a Tiff file, if FALSE draw a PDF file
GWS	Genome wise significance pvalue threshold (5E-8 by default)
FDR	False discovery Rate pvalue threshold (1E-3 by default)
MAF	Minor Allele Frequency threshold
chrname	Column name for chromosome in GWAS infile
posname	Column name for position in GWAS infile
pvalname	Column name for pvalue in GWAS infile
frqname	column name for allele frequency in GWAS infile
conseqname	column name for variant annotation consequence in GWAS infile
showgenes	If T shows known genes as bubbles on main manhattan plot, if F show positions of interest as bubbles
showrsids	If showgenes is T, then show the rsids, rather than genes
pos.split	The bin lengths for positions
pval.split	The bin lengths for pvalues
max.pval	The maximum pvalue to display

Details

For file formats see github page https://github.com/cgrace1978/manhplot

Author(s)

Chris Grace

Examples

```
library(manhplot)
## Load R.utils for gzip functionality
library(R.utils)

## unzip the data included with this package
gunzip(system.file("extdata","cad.add.160614_manhformat.txt.gz",package = "manhplot"))

infile<-system.file("extdata","cad.add.160614_manhformat.txt",package = "manhplot")
configfile<-system.file("extdata","config.txt", package = "manhplot")
snpfile<-system.file("extdata","56cad.add.160614.variants.txt", package = "manhplot")

manhplusplot(infile = infile,outfile = file.path(tempdir(), "default-plot"),
               configfile = configfile, snpfile = snpfile)

## zip the data
gzip(system.file("extdata","cad.add.160614_manhformat.txt",package = "manhplot"))
```

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