Package ‘qqman’

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Title Q-Q and Manhattan Plots for GWAS Data
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Description Create Q-Q and manhattan plots for GWAS data from PLINK results.
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Imports calibrate
Suggests knitr, rmarkdown
License GPL-3
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VignetteBuilder knitr
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Simulated GWAS results as obtained from plink --assoc.

Creates a manhattan plot from PLINK assoc output (or any data frame with chromosome, position, and p-value).

Usage

```r
manhattan(
x,
chr = "CHR",
bp = "BP",
p = "P",
snp = "SNP",
col = c("gray10", "gray60"),
chrlabs = NULL,
suggestiveline = -log10(1e-05),
genomewideline = -log10(5e-08),
highlight = NULL,
logp = TRUE,
annotatePval = NULL,
annotateTop = TRUE,
...
)
```

Arguments

- `x`: A data.frame with columns "BP," "CHR," "P," and optionally, "SNP."
- `chr`: A string denoting the column name for the chromosome. Defaults to PLINK’s "CHR." Said column must be numeric. If you have X, Y, or MT chromosomes, be sure to renumber these 23, 24, 25, etc.
- `bp`: A string denoting the column name for the chromosomal position. Defaults to PLINK’s "BP." Said column must be numeric.
- `p`: A string denoting the column name for the p-value. Defaults to PLINK’s "P." Said column must be numeric.
snp A string denoting the column name for the SNP name (rs number). Defaults to PLINK's "SNP." Said column should be a character.

col A character vector indicating which colors to alternate.

chrlabs A character vector equal to the number of chromosomes specifying the chromosome labels (e.g., c(1:22, "X", "Y", "MT").)

suggestiveline Where to draw a "suggestive" line. Default -log10(1e-5). Set to FALSE to disable.

genomewideline Where to draw a "genome-wide significant" line. Default -log10(5e-8). Set to FALSE to disable.

highlight A character vector of SNPs in your dataset to highlight. These SNPs should all be in your dataset.

logp If TRUE, the -log10 of the p-value is plotted. It isn’t very useful to plot raw p-values, but plotting the raw value could be useful for other genome-wide plots, for example, peak heights, bayes factors, test statistics, other "scores," etc.

annotatePval If set, SNPs below this p-value will be annotated on the plot. If logp is FALSE, SNPs above the specified value will be annotated.

annotateTop If TRUE, only annotates the top hit on each chromosome that is below the annotatePval threshold (or above if logp is FALSE).

... Arguments passed on to other plot/points functions

Value A manhattan plot.

Examples

manhattan(gwasResults)

qq Creates a Q-Q plot

Description

Creates a quantile-quantile plot from p-values from a GWAS study.

Usage

qq(pvector, ...)

Arguments

pvector A numeric vector of p-values.

... Other arguments passed to plot()
Value

A Q-Q plot.

Examples

```r
qq(gwasResults$P)
```

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**qqman**

*Create Q-Q and manhattan plots for GWAS data.*

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**Description**

A package for creating Q-Q and manhattan plots for GWAS data. See the package vignette for details:

```r
vignette("qqman")
```

**Author(s)**

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**snpsOfInterest**

*snpsOfInterest*

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**Description**

Example SNPs of interest from simulated `gwasResults` data.
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