

Package ‘qqman’

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Title Q-Q and manhattan plots for GWAS data
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Author Stephen Turner <vustephen@gmail.com>
Maintainer Stephen Turner <vustephen@gmail.com>
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gwasResults	<i>Simulated GWAS results</i>
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Description

Simulated GWAS results as obtained from `plink --assoc`.

manhattan

*Creates a manhattan plot***Description**

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

Usage

```
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, ...)
```

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

Value

A manhattan plot.

Examples

```
manhattan(gwasResults)
```

qq	<i>Creates a Q-Q plot</i>
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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

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

qqman	<i>Create Q-Q and manhattan plots for GWAS data.</i>
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Description

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

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

Author(s)

Stephen Turner <<http://stephenturner.us>>

snpsOfInterest	<i>snpsOfInterest</i>
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snpsOfInterest

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