

# Package ‘qqman’

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**Title** Q-Q and manhattan plots for GWAS data

**Version** 0.1.1

**Author** Stephen Turner <vustephen@gmail.com>

**Maintainer** Stephen Turner <vustephen@gmail.com>

**Description** Q-Q and manhattan plots for GWAS data

**Depends** R (>= 3.0.0)

**Suggests** knitr

**License** GPL-3

**LazyData** true

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

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|             |                               |
|-------------|-------------------------------|
| gwasResults | <i>Simulated GWAS results</i> |
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### Description

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

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| manhattan | <i>Creates a manhattan plot</i> |
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### 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"), ymax = NULL,
  suggestiveline = -log10(1e-05), genomewideline = -log10(5e-08),
  highlight = NULL, ...)
```

### 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.  |
| ymax           | The upper limit to the y-axis. Set automatically based on the most significant SNP unless set here specifically.  |
| suggestiveline | Where to draw a "suggestive" line. Default $-\log_{10}(1e-5)$ . Set to FALSE to disable.  |
| genomewideline | Where to draw a "genome-wide significant" line. Default $-\log_{10}(5e-8)$ . Set to FALSE to disable.   |
| highlight      | A character vector of SNPs in your dataset to highlight. These SNPs should all be in your dataset.  |
| ...            | Arguments passed on to other plot/points functions  |

**Value**

A manhattan plot.

**Examples**

```
manhattan(gwasResults)
```

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|----|---------------------------|
| 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)
```

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| 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>>

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snpsOfInterest

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**Description**

snpsOfInterest

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