

Package ‘fastqq’

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Type Package

Title Faster Generation of Quantile Quantile Plots with Large Samples

Version 0.1.5

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Description New and faster implementations for quantile quantile plots.
The package also includes a function to prune data for quantile quantile plots. This can drastically reduce the running time for large samples, for 100 million samples, you can expect a factor 80X speedup.

URL <https://github.com/gumeo/fastqq>

BugReports <https://github.com/gumeo/fastqq/issues>

License GPL (>= 3)

Encoding UTF-8

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Imports Rcpp

LinkingTo Rcpp

Suggests testthat (>= 3.0.0)

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Contents

drop_dense	2
qq	2
qqchisq1	3
qqlog	4
qqnorm	4
qqplot	5

Index**7**

drop_dense	<i>Internal function to prune quantiles of non-important values for visualization.</i>
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Description

This function is not exposed, since we want to hard-code the parameters for simplicity of usage.

Usage

```
drop_dense(x, y, N_hard = 10000)
```

Arguments

x	A numeric vector of sample/theoretical points.
y	A numeric vector of theoretical/sample points.
N_hard	Desired upper bound on the number of points to plot.

Value

data.frame with o and e pruned as columns.

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

Creates a quantile-quantile plot from p-values from an association study, e.g. a genome wide association study (GWAS). We compare the data quantile with a theoretical quantile from a uniform distribution. This code is mostly adapted from the qqman package, but improved for speed. A graph with a hundred million points should only take a few seconds to generate.

Usage

```
qq(pvector, zero_action = NULL, ...)
```

Arguments

pvector	A numeric vector of p-values.
zero_action	A numeric value to substitute for p-values of exactly zero before plotting. If NULL (default), zero p-values are treated like any other invalid value and silently excluded. If a numeric value is provided (e.g. 1e-300), all zero p-values are replaced with that value and a warning is emitted stating how many were replaced.
...	Other arguments passed to plot()

Value

No return value, called for plotting side effects.

Examples

```
qq(stats::runif(1e6))

# Handle p-values of zero by substituting a small finite value
pvec <- c(stats::runif(1e4), 0, 0)
qq(pvec, zero_action = 1e-300)
```

qqchisq1	<i>Creates a Q-Q plot from chi-squared statistics</i>
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Description

Accepts χ^2 test statistics as input and converts them to $-\log_{10}(p)$ values assuming 1 degree of freedom. The conversion uses log-space computation via `pchisq(..., log.p = TRUE)`, which avoids floating-point underflow for very large test statistics and is numerically precise well beyond `.Machine$double.xmin`. Produces the same style of plot as `qq` and `qqlog`.

Usage

```
qqchisq1(chisq_vector, ...)
```

Arguments

<code>chisq_vector</code>	A numeric vector of χ^2 statistics (non-negative). Negative, infinite, NA, and NaN values are excluded.
<code>...</code>	Other arguments passed to <code>plot()</code>

Value

No return value, called for plotting side effects.

Examples

```
chisq_vals <- stats::rchisq(1e5, df = 1)
qqchisq1(chisq_vals)
```

qqlog	<i>Creates a Q-Q plot from pre-computed $-\log_{10}(p)$-values</i>
-------	---

Description

Accepts $-\log_{10}(p)$ values directly as input. This is useful when the caller has already transformed their p-values, or when higher numerical precision is required before passing values to the plotting layer. Produces the same style of plot and uses the same fast pruning algorithm as `qq`.

Usage

```
qqlog(log10_pvector, ...)
```

Arguments

`log10_pvector` A numeric vector of $-\log_{10}(p)$ values. Values must be positive and finite; non-positive, infinite, NA, and NaN values are excluded (consistent with `qq` excluding p-values ≥ 1 or ≤ 0).

`...` Other arguments passed to `plot()`

Value

No return value, called for plotting side effects.

Examples

```
pvec <- stats::runif(1e5)
qqlog(-log10(pvec))
```

qqnorm	<i>Creates a Q-Q plot for comparing with normal quantiles</i>
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Description

Faster alternative to `stats::qqnorm()`. For more than $1e5$ points we remove excess points, that would not be visible in the plot, since the points are so close. Otherwise this should work exactly the same, and the code is mostly adapted from `stats::qqnorm()`. This code produces more lightweight plots for excessive amounts of data.

Usage

```
qqnorm(  
  y,  
  ylim,  
  main = "Normal Q-Q Plot",  
  xlab = "Theoretical Quantiles",  
  ylab = "Sample Quantiles",  
  plot.it = TRUE,  
  datax = FALSE,  
  ...  
)
```

Arguments

y	sample, to compare to normal quantiles.
ylim	graphical limits.
main	Plot title.
xlab	X label.
ylab	Y label.
plot.it	Should the plot be created.
datax	logical. Should data values be on x-axis?
...	Other arguments passed to plot()

Value

data.frame with sorted sample and normal quantiles, NA values are excluded.

Examples

```
qqnorm(stats::rnorm(1e6))
```

qqplot

Creates a Q-Q plot

Description

Faster alternative to stats::qqplot(). For more than 1e5 points we remove excess points, that would not be visible in the plot, since the points are so close.

Usage

```
qqplot(  
  x,  
  y,  
  plot.it = TRUE,  
  xlab = deparse1(substitute(x)),  
  ylab = deparse1(substitute(y)),  
  ...  
)
```

Arguments

x	First sample for qqplot.
y	Second sample for qqplot.
plot.it	Should the plot be created.
xlab	x label for plot.
ylab	y label for plot.
...	Other arguments passed to plot()

Value

list with sorted samples, interpolated to be same size.

Examples

```
qqplot(stats::runif(1e6), stats::runif(1e6))
```

Index

* qqplot

qq, 2
qqchisq1, 3
qqlog, 4
qqnorm, 4
qqplot, 5

* qq

qq, 2
qqchisq1, 3
qqlog, 4
qqnorm, 4
qqplot, 5

* visualization

qq, 2
qqchisq1, 3
qqlog, 4
qqnorm, 4
qqplot, 5

drop_dense, 2

qq, 2, 3, 4
qqchisq1, 3
qqlog, 3, 4
qqnorm, 4
qqplot, 5