

Package ‘MADtests’

February 3, 2026

Type Package
Title Hypothesis Tests and Confidence Intervals for Median Absolute Deviations
Version 0.1.1
Maintainer Luke A. Prendergast <luke.prendergast@latrobe.edu.au>
Description Conducts one- and two-sample hypothesis tests for median absolute deviations (mads) for robust inference of dispersion. Comparisons between two samples uses the ratio of mads. Confidence intervals are also computed.
Imports gld, stats
Encoding UTF-8
RoxygenNote 7.3.3
Suggests testthat (>= 3.0.0)
Config/testthat/edition 3
License MIT + file LICENSE
NeedsCompilation no
Author Luke A. Prendergast [cre, aut] (ORCID: <<https://orcid.org/0000-0002-9122-5429>>), Chandima Arachchige [aut]
Repository CRAN
Date/Publication 2026-02-03 12:40:26 UTC

Contents

madci	2
madtest	3
pop.mad	5
varmad	6
Index	8

madci

Test for a single the median absolute deviation (MAD)

Description

Calculates a confidence interval and test the null hypothesis for the median absolute deviation (MAD) for a single sample.

Usage

```
madci(
  x,
  constant = 1.4826,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  true.mad = 1,
  use.gld = FALSE,
  gld.est = "TM",
  ...
)
```

Arguments

<code>x</code>	a numeric vector of data values.
<code>constant</code>	a scale factor. Default choice ensures population mad is equal to sd for normal distributions.
<code>alternative</code>	a character string specifying the alternative hypothesis to be used. Needs to be one of "two.sided" (default), "greater" or "less".
<code>conf.level</code>	confidence level for the confidence interval. The default is 0.95 (for a 95% confidence interval).
<code>true.mad</code>	a number which is the nominated value for the population mad under the null hypothesis. Default is 1.
<code>use.gld</code>	a logical indicating whether the Generalised Lambda Distribution (GLD) should be used to estimate the density of the data. Default is FALSE in which case the function density is used.
<code>gld.est</code>	a character string indicating which gld estimator to use if use.gld = TRUE. See details below.
<code>...</code>	additional arguments, if desired, to be passed to function density for density estimation (see help file for density() for more details).

Details

This function calculates an approximate confidence interval and conducts a hypothesis test for a single mad. The approximate variance used in the construction of the confidence interval and the test statistic is calculated using the varmad() function (see Arachchige and Prendergast (2024) and

the help file for `varmad()` for further details). Note that the interval and test statistic are approximate and may be unreliable for small sample sizes. Arachchige and Prendergast (2024) showed that reliable results can be achieved for sample sizes of 50 or more when simulating data from various distributions. Additionally, the confidence interval is a Wald-type interval (estimate \pm crit*SE) and so it may be possible that the domain of the interval contains negative values. Since negative values are not possible for the mad, thought could be given to truncation (setting the lower bound to zero), although this may undermine interval coverage.

Value

Hypothesis test results comparing two mads from independent samples and associated confidence interval for the ratio of mads (a list with class "htest"). This list includes values

`statistic` the value of the Z-statistic.

`p.value` the p-value for the test.

`conf.int` a confidence interval for the MAD that is appropriate for the alternative hypothesis.

`estimate` the estimated MAD.

`null.value` the specified hypothesized value of the MAD under the null hypothesis.

`alternative` a character string describing the alternative hypothesis.

`data.name` a character string giving the names of the data.

References

Arachchige, C.N.P.G., & Prendergast, L.A. (2026) Confidence intervals for median absolute deviations. *Communications in Statistics-Simulation and Computation*, 55(1), 13-22.

Examples

```
# Create some data
set.seed(1234)
x <- rlnorm(100)

# Calculate the mad, 95% confidence interval and test the hypothesis
mad.est <- madci(x)
mad.est
```

madtest

Hypothesis Test to Compare Two Median Absolute Deviations (MADs)

Description

Performs hypothesis tests and calculates confidence intervals to compare MADs of two samples.

Usage

```
madtest(
  x,
  y,
  ratio = 1,
  conf.level = 0.95,
  use.squared = FALSE,
  use.gld = FALSE,
  gld.est = "TM",
  ...
)
```

Arguments

<code>x, y</code>	numeric vectors of data values.
<code>ratio</code>	a number representing the value of the ratio of the two MADs (or squared MADs) under the null hypothesis.
<code>conf.level</code>	confidence level for the confidence interval. The default is 0.95 (for a 95% confidence interval).
<code>use.squared</code>	a logical indicating whether the squared MADs should be used. Default is FALSE.
<code>use.gld</code>	a logical indicating whether the Generalised Lambda Distribution (GLD) should be used to estimate the density of the data. Default is FALSE in which case the function <code>density()</code> is used for kernel density estimation.
<code>gld.est</code>	a character string indicating which GLD estimator to use if <code>use.gld = TRUE</code> . See details below.
<code>...</code>	additional arguments, if desired, to be passed to function <code>density()</code> for density estimation (see help file for density() for more details).

Details

This function carries out hypothesis tests and calculates confidence intervals for comparing the MADs between two populations. Two independent samples are required, and the intervals are constructed for the ratio of mads (or squared mads as an analog to ratio of variances) as described in Arachchige and Prendergast (2024). The interval is first computed for the log of the ratio before being back-transformed to the ratio scale. The hypothesis test is carried out in a similar way, based on the log ratio and using asymptotic normality of the test statistic. The default for the ratio under the null hypothesis is one which tests against equality of mads.

Value

Hypothesis test results comparing two mads from independent samples and associated confidence interval for the ratio of mads (a list with class "htest"). This list includes values

`statistic` the value of the Z-statistic.

`p.value` the p-value for the test.

`conf.int` a confidence interval for the ratio of MADs (or squared MADs).

`estimate` the estimated ratio of MADs (or squared MADs).

`null.value` the specified hypothesized value of the ratio under the null hypothesis.

`alternative` a character string describing the alternative hypothesis. Note, for this test only two-sided alternatives are allowed.

`data.name` a character string giving the names of the data.

References

Arachchige, C.N.P.G., & Prendergast, L.A. (2026) Confidence intervals for median absolute deviations. *Communications in Statistics-Simulation and Computation*, 55(1), 13-22.

Examples

```
# Create some data
set.seed(1234)
x <- rlnorm(100)
y <- rlnorm(50, meanlog = 0.5)

# Calculate the mad, 95% confidence interval and test the hypothesis
mads.est <- madtest(x, y)
mads.est
```

pop.mad

Population Median Absolute Deviation (MAD)

Description

This function calculates the population Median Absolute Deviation (MAD) for a user-specified distribution.

Usage

```
pop.mad(qf, pf, upper, constant = 1.4826, ...)
```

Arguments

<code>qf</code>	the quantile function for the distribution.
<code>pf</code>	the distribution function for the distribution.
<code>upper</code>	an optional number specifying an upper limit for the MAD. This can be missing although the user may want to specify an upper limit if there are computation issues.
<code>constant</code>	a scale factor. Default choice ensures population MAD is equal to SD for the normal distribution.
<code>...</code>	additional parameter values for the distribution, otherwise default choices are used for the specific quantile and distribution functions.

Details

This function calculates the Median Absolute Deviation (MAD) for a distribution specified by the user. The user is required to input the quantile and distribution functions, as well as any parameters required for the nominated distribution. If the function is unable to find the MAD using function root, the user may specify another upper limit for the MAD to help with computation. If upper is missing, upper is chosen to be the maximum of the third quartile minus the median and the median minus the first quartile (the MAD cannot be greater than this upper limit). For more information in the MAD see, e.g., Hampel et al. (1986).

Value

A value representing the MAD for the distribution.

References

Hampel, F. R., Ronchetti, E. M., Rousseeuw, P. J. & Stahel, W. A. (1986). Robust statistics: The approach based on influence functions. New York, NY: John Wiley & Sons.

Examples

```
# Population MAD for the normal distribution
pop.mad(qnorm, pnorm, sd = 1.5)

# Note that due to the scaling constant used, the mad is equal to the SD for the normal distribution
```

varmad	<i>Approximate Variance of the Median Absolute Deviation (MAD) Estimator.</i>
--------	---

Description

This function calculates the approximate (large-sample) variance of the MAD estimator.

Usage

```
varmad(x, constant = 1.4826, use.gld = FALSE, gld.est = "TM", ...)
```

Arguments

x	a numeric vector of data values.
constant	a scale factor. Default choice ensures population mad is equal to the SD for normal distributions.
use.gld	a logical indicating whether to use the flexible Generalised Lambda Distribution (GLD) to estimate the density and distribution function.
gld.est	a character string indicating which estimator of the GLD parameters is to be used if use.gld=TRUE.
...	additional arguments, if desired, to be passed to function density for density estimation (see help file for density() for more details).

Details

This function calculates an approximate variance for the traditional Median of Absolute Deviations (MAD) estimator. The variance requires estimation of the probability density function and the distribution function which, by default, is carried out using the `density()` and `ecdf()` functions respectively. An alternative is to use the flexible four-parameter Generalised Lambda Distribution (GLD) to estimate these functions. This is done by using `use.gld = TRUE` and the default estimator is `gld.est = TM` for Titterington's Method (Titterington, 1985). Other estimators are available and further details can be found in the [gld::fit.fkml](#) documentation from the `gld` package (King et al., 2022). For further details on the approximate variance see Arachchige and Prendergast (2024).

Value

A number which is the estimated approximate variance of the `mad` estimator

References

- Arachchige, C.N.P.G., & Prendergast, L.A. (2026). Confidence intervals for median absolute deviations. *Communications in Statistics-Simulation and Computation*, 55(1), 13-22.
- King R, Dean B, Klinke S, & van Staden, P (2022). `gld`: Estimation and Use of the Generalised (Tukey) Lambda Distribution. R package version 2.6.6, <https://CRAN.R-project.org/package=gld>.
- Titterington, D. M. (1985), Comment on 'Estimating Parameters in Continuous Univariate Distributions', *Journal of the Royal Statistical Society, Series B*, 47, 115–116.

Examples

```
# Create some data
set.seed(1234)
x <- rlnorm(100)

# Calculate the mad and its variance
mad.est <- mad(x)
mad.est
v.est <- varmad(x)
v.est

# Calculate an approximate 95% confidence interval for the true mad
mad.est + c(-1, 1) * qnorm(0.975) * sqrt(v.est)
```

Index

`density()`, [4](#), [6](#)

`gld::fit.fkml`, [7](#)

`madci`, [2](#)

`madtest`, [3](#)

`pop.mad`, [5](#)

`varmad`, [6](#)