

Package ‘Dogoftest’

July 29, 2025

Title Distributed Online Goodness-of-Fit Tests for Distributed
Datasets

Date 2025-07-28

Version 0.3

Description Distributed Online Goodness-of-Fit Test can process the distributed datasets. The philosophy of the package is described in Guo G.(2024) <[doi:10.1016/j.apm.2024.115709](https://doi.org/10.1016/j.apm.2024.115709)>.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Imports stats

LazyData true

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

Author Guangbao Guo [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-4115-6218>>),
Di Chang [aut]

Maintainer Guangbao Guo <ggb11111111@163.com>

Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2025-07-29 04:50:02 UTC

Contents

AD2gof	2
ADgof	3
BSdata	4
CVM2gof	5
cvmgof	6
CVMgof2	7

goats	8
KS2gof	9
ksgof	10
KSgof2	11
Kuiper2gof	12
qCvMgof	13
simpleCvMgof	14
Snow	15
strength	15
Wgof	16
WhiteWine	17

Index	19
--------------	-----------

AD2gof	<i>Two-Sample Anderson-Darling Test (Bootstrap Version)</i>
--------	---

Description

Performs a two-sample Anderson-Darling (AD) goodness-of-fit test using bootstrap resampling to compare whether two samples come from the same distribution. This test is sensitive to differences in both location and shape between the two distributions.

Usage

```
AD2gof(  
  x,  
  y,  
  alternative = c("two.sided", "less", "greater"),  
  nboots = 2000,  
  keep.boots = FALSE  
)
```

Arguments

x	A numeric vector of data values from the first sample.
y	A numeric vector of data values from the second sample.
alternative	Character string specifying the alternative hypothesis. One of "two.sided" (default), "less", or "greater".
nboots	Integer. Number of bootstrap replicates to compute the null distribution (default: 2000).
keep.boots	Logical. If 'TRUE', returns the full vector of bootstrap statistics (default: 'FALSE').

Details

The test computes the Anderson-Darling statistic using the pooled empirical distribution functions (ECDFs) of the two samples. A bootstrap procedure resamples the group labels to approximate the null distribution and compute a p-value. If 'p.value = 0', it is adjusted to '1 / (2 * nboots)' for stability.

Value

A list of class `"hstest"` containing:

statistic The observed Anderson-Darling test statistic.

p.value The estimated bootstrap p-value.

alternative The alternative hypothesis used.

method A character string describing the test.

bootstraps (Optional) A numeric vector of bootstrap statistics if `'keep.boots = TRUE'`.

Examples

```
set.seed(123)
x <- rnorm(100, mean = 0, sd = 4)
y <- rnorm(100, mean = 2, sd = 4)
AD2gof(x, y)
```

ADgof

Anderson-Darling Goodness-of-Fit Test for a Specified Distribution

Description

Performs the Anderson-Darling (AD) goodness-of-fit test for a given univariate distribution. The function computes the AD statistic and returns an approximate p-value based on adjusted formulas.

Usage

```
ADgof(
  x,
  dist = c("norm", "exp", "unif", "lnorm", "weibull", "gamma", "t", "chisq"),
  ...,
  eps = 1e-15
)
```

Arguments

<code>x</code>	A numeric vector of sample observations.
<code>dist</code>	A character string specifying the null distribution. Options are "norm", "exp", "unif", "lnorm", "weibull", "gamma", "t", and "chisq".
<code>...</code>	Additional named parameters passed to the corresponding distribution functions (e.g., mean, sd, rate, df, etc.).
<code>eps</code>	A small positive constant to avoid $\log(0)$ during computation (default: $1e-15$).

Details

This implementation supports several common distributions. Parameters of the null distribution must be supplied via `. . .`. The p-value is calculated using the approximations suggested by Stephens (1986) and other refinements. For small samples or custom distributions, a bootstrap version may be preferred.

Value

A list of class "htest" with components:

statistic The value of the Anderson-Darling test statistic.

p.value The approximate p-value computed using adjustment formulas.

method A description of the test performed.

data.name The name of the input data.

Examples

```
set.seed(123)
x1 <- rnorm(500, mean = 5, sd = 2)
ADgof(x1, dist = "norm", mean = 5, sd = 2)

x2 <- rexp(400, rate = 1.5)
ADgof(x2, dist = "exp")
ADgof(x2, dist = "exp", rate = 1.5)

x3 <- runif(300, min = -2, max = 4)
ADgof(x3, dist = "unif", min = -2, max = 4)
```

BSdata

Data set

Description

psi21k, psi26k, and psi31k are from Birnbaum and Saunders (1969). The fatigue lifetimes of aluminum specimens exposed to a maximum stress of 21,000 psi, 26,000 psi, 31,000 psi, respectively.

bearings is from McCool (1974). The fatigue lifetimes (in hours) of ten bearings.

fatigue is from Brown and Miller (1978). The fatigue lifetimes of cylindrical specimens subjected to combined torsional and axial loads over constant-amplitude cycles until failure.

repair is from Hsieh (1990). This is a maintenance data set on active repair times (in hours) for an airborne communications transceiver.

Usage

```
data(BSdata)
```

References

Birnbaum, Z. W. and Saunders, S. C. (1969). A new family of life distributions. J. Appl. Probab. 6(2): 637-652.

McCool, J. I. (1974). Inferential techniques for Weibull populations. Aerospace Research Laboratories Report ARL T R74-0180, Wright-Patterson Air Force Base, Dayton, OH.

Rieck, J. R. and Nedelman, J. (1991). A Log-Linear Model for the Birnbaum-Saunders Distribution. Technometrics. 33, 51-60.

Brown, M. W. and Miller, K. J. (1978). Biaxial Fatigue Data. Report CEMR1/78. University of Sheffield, Dept. of Mechanical Engineering.

Hsieh, H. K. (1990). Estimating the Critical Time of Inverse Gaussian Hazard Rate. IEEE Transactions on Reliability, 39(10): 342-345.

Examples

```
# Attach data sets
data(BSdata)
```

CVM2gof

Two-Sample Cramér–von Mises Test (Bootstrap Version)

Description

Performs a nonparametric two-sample Cramér–von Mises test using a permutation-based bootstrap method to assess whether two samples come from the same distribution.

Usage

```
CVM2gof(
  x,
  y,
  alternative = c("two.sided", "less", "greater"),
  nboots = 2000,
  keep.boots = FALSE
)
```

Arguments

x	Numeric vector of observations from the first sample.
y	Numeric vector of observations from the second sample.
alternative	Character string specifying the alternative hypothesis. Must be one of "two.sided" (default), "less", or "greater".

nboots	Number of bootstrap replicates to approximate the null distribution (default: 2000).
keep.boots	Logical. If TRUE, the bootstrap statistics will be returned (default: FALSE).

Details

The test compares two empirical cumulative distribution functions (ECDFs). The bootstrap procedure permutes group labels to generate the null distribution. Tailored one-sided tests use one-sided squared differences of ECDFs.

Value

An object of class "htest" with elements:

statistic Observed Cramér–von Mises test statistic.

p.value Bootstrap-based p-value.

alternative The alternative hypothesis used.

method A description of the test.

bootstraps (Optional) Vector of bootstrap test statistics if keep.boots = TRUE.

Examples

```
set.seed(123)
x <- rnorm(100, mean = 0, sd = 4)
y <- rnorm(100, mean = 2, sd = 4)
CVM2gof(x, y)

# One-sided test
CVM2gof(x, y, alternative = "greater")

# Store bootstrap replicates
res <- CVM2gof(x, y, keep.boots = TRUE)
hist(res$bootstraps, main = "Bootstrap Distribution", xlab = "Test Statistic")
```

cvmgof

Perform the Cramer-von Mises Goodness-of-Fit Test for Normality

Description

Perform the Cramer-von Mises Goodness-of-Fit Test for Normality

Usage

```
cvmgof(x)
```

Arguments

`x` A numeric vector containing the sample data.

Value

`statistic` The value of the Cramer-von Mises test statistic.
`p.value` The p-value for the test.
`method` A character string describing the test.

Examples

```
# Example usage:
set.seed(123)
x <- rnorm(100) # Generate a sample from a normal distribution
result <- cvmgof(x)
print(result)

# Example with non-normal data:
y <- rexp(100) # Generate a sample from an exponential distribution
result <- cvmgof(y)
print(result)
```

CVMgof2

*One-Sample Cramér–von Mises Goodness-of-Fit Test***Description**

Performs the one-sample Cramér–von Mises goodness-of-fit (GoF) test to assess whether a sample comes from a specified distribution using asymptotic p-value approximations.

Usage

```
CVMgof2(
  x,
  dist = c("norm", "exp", "unif", "lnorm", "weibull", "gamma", "t", "chisq"),
  ...,
  eps = 1e-15
)
```

Arguments

`x` A numeric vector of observations.
`dist` A character string specifying the theoretical distribution. Must be one of "norm", "exp", "unif", "lnorm", "weibull", "gamma", "t", or "chisq".
`...` Distribution parameters passed to the corresponding p functions (e.g., mean, sd, rate, df, etc.).
`eps` A small value to truncate extreme p-values (default is 1e-15).

Details

The test uses the Cramér–von Mises statistic to assess how well the empirical distribution function (EDF) of the sample agrees with the cumulative distribution function (CDF) of the specified theoretical distribution. The p-value is computed using approximation formulas derived from the asymptotic distribution of the test statistic.

Value

An object of class "htest" with the following components:

statistic The computed Cramér–von Mises test statistic.

p.value The asymptotic p-value.

method A description of the test and distribution.

data.name The name of the data vector.

Examples

```
set.seed(123)
x1 <- rnorm(500, mean = 0, sd = 1)
CVMgof2(x1, dist = "norm", mean = 0, sd = 1)

x2 <- rexp(500, rate = 2)
CVMgof2(x2, dist = "exp", rate = 2)

x3 <- runif(200, min = -1, max = 3)
CVMgof2(x3, dist = "unif", min = -1, max = 3)
```

goats

Zoometric measurements of goats

Description

Zoometric measurements of 27 week old creole goats collected by Dorantes-Coronado (2013).

Usage

```
data(goats)
```

Format

A data frame with 52 rows and 7 columns containing measurements (in kilograms and centimeters) on the following variables.

```
body.weight
body.length
trunk.length
```

```
withers.height
thoracic.perimeter
hip.length
ear.length
```

Source

Dorantes-Coronado (2013).

References

Dorantes-Coronado, E.J. (2013). Estudio preliminar para el establecimiento de un programa de mejoramiento genetico de cabras en el Estado de Mexico. Ph.D. Thesis. Colegio de Postgraduados, Mexico.

Examples

```
data(goats)
plot(goats)
```

KS2gof

Two-Sample Kolmogorov–Smirnov Test with Bootstrap

Description

Performs a two-sample Kolmogorov–Smirnov (KS) test using a bootstrap method to assess whether two independent samples come from the same distribution.

Usage

```
KS2gof(
  x,
  y,
  alternative = c("two.sided", "less", "greater"),
  nboots = 5000,
  keep.boots = FALSE
)
```

Arguments

<code>x, y</code>	Numeric vectors of data values for the two independent samples.
<code>alternative</code>	Character string specifying the alternative hypothesis, must be one of "two.sided", "less", or "greater".
<code>nboots</code>	Number of bootstrap resamples used to approximate the null distribution (default: 5000).
<code>keep.boots</code>	Logical; if TRUE, return the vector of bootstrap statistics.

Details

This implementation performs a nonparametric KS test for equality of distributions by resampling under the null hypothesis. It supports one-sided and two-sided alternatives.

If `keep.boots = TRUE`, the function returns all bootstrap statistics, which can be used for further analysis (e.g., plotting).

If the p-value is zero due to no bootstrap statistic exceeding the observed value, it is adjusted to $1 / (2 * nboots)$ to avoid a zero p-value.

Value

An object of class "htest" with the following components:

statistic The observed KS statistic.

p.value The p-value based on the bootstrap distribution.

alternative The alternative hypothesis.

method Description of the test used.

Examples

```
set.seed(123)
x <- rnorm(100, mean = 0, sd = 4)
y <- rnorm(100, mean = 2, sd = 4)
KS2gof(x, y)
```

ksgof	<i>Perform the Lilliefors (Kolmogorov-Smirnov) Goodness-of-Fit Test for Normality</i>
-------	---

Description

Perform the Lilliefors (Kolmogorov-Smirnov) Goodness-of-Fit Test for Normality

Usage

```
ksgof(x)
```

Arguments

x A numeric vector containing the sample data.

Value

statistic The value of the Lilliefors (Kolmogorov-Smirnov) test statistic.

p.value The p-value for the test.

method A character string describing the test.

Examples

```
# Example usage:
set.seed(123)
x <- rnorm(100) # Generate a sample from a normal distribution
result <- ksgof(x)
print(result)

# Example with non-normal data:
y <- rexp(100) # Generate a sample from an exponential distribution
result <- ksgof(y)
print(result)
```

KSgof2

One-sample Kolmogorov-Smirnov goodness-of-fit test

Description

Performs the one-sample Kolmogorov-Smirnov test for a specified theoretical distribution.

Usage

```
KSgof2(
  x,
  dist = c("norm", "exp", "unif", "lnorm", "weibull", "gamma", "t", "chisq"),
  ...,
  eps = 1e-15
)
```

Arguments

x	Numeric vector of observations.
dist	Character string specifying the distribution to test against. One of "norm", "exp", "unif", "lnorm", "weibull", "gamma", "t", or "chisq".
...	Additional parameters passed to the distribution's cumulative distribution function (CDF). For example, mean and sd for the normal distribution.
eps	Numeric lower and upper bound for tail probabilities to avoid numerical issues (default: 1e-15).

Details

The test compares the empirical distribution function of x with the cumulative distribution function of a specified theoretical distribution using the Kolmogorov-Smirnov statistic. For large sample sizes, a p-value approximation based on the asymptotic distribution is used.

A correction is applied when sample size exceeds 100, adjusting the test statistic to approximate a fixed sample size. For very small or very large statistics, piecewise polynomial approximations are used to compute the p-value.

Value

An object of class "htest" containing the test statistic, p-value, method description, and data name.

Examples

```
set.seed(123)
x <- rnorm(1000, mean = 5, sd = 2)
KSgof2(x, dist = "norm", mean = 5, sd = 2)

y <- rexp(500, rate = 0.5)
KSgof2(y, dist = "exp", rate = 0.5)

u <- runif(300, min = 0, max = 10)
KSgof2(u, dist = "unif", min = 0, max = 10)
```

Kuiper2gof

Two-Sample Kuiper Test with Bootstrap

Description

Performs a two-sample Kuiper test using bootstrap resampling to test whether two independent samples come from the same distribution.

Usage

```
Kuiper2gof(
  x,
  y,
  alternative = c("two.sided", "less", "greater"),
  nboots = 2000,
  keep.boots = FALSE
)
```

Arguments

<code>x, y</code>	Numeric vectors of data values for the two samples.
<code>alternative</code>	Character string indicating the alternative hypothesis. Must be one of "two.sided", "less", or "greater".
<code>nboots</code>	Integer. Number of bootstrap resamples to compute the empirical null distribution (default: 2000).
<code>keep.boots</code>	Logical. If TRUE, returns all bootstrap test statistics.

Details

The Kuiper test is a nonparametric test similar to the Kolmogorov–Smirnov test, but sensitive to discrepancies in both location and shape between two distributions. This implementation uses bootstrap resampling to estimate the p-value.

The `two.sided` test uses the sum of maximum positive and negative ECDF differences. The `greater` and `less` options use one-sided variations.

If the observed test statistic exceeds all bootstrap values, the p-value is set to $1 / (2 * nboots)$ to avoid zero.

Value

An object of class "htest" containing:

statistic The observed Kuiper statistic.

p.value The p-value computed from the bootstrap distribution.

alternative The specified alternative hypothesis.

method A character string describing the test.

bootstraps (If requested) A numeric vector of bootstrap statistics.

Examples

```
set.seed(123)
x <- rnorm(100, 0, 4)
y <- rnorm(100, 2, 4)
Kuiper2gof(x, y)
```

qCvMgof

Calculate the Quantile of the Cramer-von Mises Goodness-of-Fit Statistic

Description

This function calculates the quantile of the Cramer-von Mises goodness-of-fit statistic using the ‘uniroot’ function to find the root of the given function.

Usage

```
qCvMgof(X, p)
```

Arguments

X A numeric vector containing the sample data.

p A numeric value representing the desired quantile probability.

Value

root The quantile value corresponding to the given probability.

Examples

```
# Example usage:
set.seed(123)
X <- rnorm(100) # Generate a sample from a normal distribution
p <- 0.95       # Desired quantile probability
result <- qCvMgof(X, p)
print(result)
```

simpleCvMgof

Perform a Simple Cramer-von Mises Goodness-of-Fit Test

Description

This function performs a simple Cramer-von Mises goodness-of-fit test to assess whether a given sample comes from a uniform distribution. The test statistic and p-value are calculated based on the sorted sample data.

Usage

```
simpleCvMgof(X)
```

Arguments

X A numeric vector containing the sample data.

Value

statistic The value of the Cramer-von Mises test statistic.
pvalue The p-value for the test.
statname The name of the test statistic.

Examples

```
# Example usage:
set.seed(123)
X <- runif(100) # Generate a sample from a uniform distribution
result <- simpleCvMgof(X)
print(result)

# Example with non-uniform data:
Y <- rnorm(100) # Generate a sample from a normal distribution
result <- simpleCvMgof(Y)
print(result)
```

Snow

*Snow Dataset***Description**

Snowfall dataset

Format

vector of values

Details

This file contains observations of the annual snowfall amounts in Buffalo, New York. 63 as observed from 1910/11 to 1972/73 as listed in *The autoregressive method: a method of approximating and estimating positive functions*. Carmichael, Jean-Pierre. DTIC Document. 1976

strength

*Compressive strength of maize seeds***Description**

Compressive strength and strain of maize seeds.

Usage`data("strength")`**Format**

A data frame with 90 observations on the following 2 variables.

`strain` a numeric vector giving the relative change in length under compression stress in millimeters.

`cstrength` a numeric vector giving the compressive strength in Newtons.

Details

These data correspond to maize seeds with floury endosperm and 8% of moisture.

Source

Mancera-Rico, A. (2014).

References

Mancera-Rico, A. (2014). Contenido de humedad y tipo de endospermo en la resistencia a compresión en semillas de maíz. Ph.D. Thesis. Colegio de Postgraduados, Mexico.

Examples

```
data(strength)
plot(strength)      # plot of "strain" versus "cstrength"
```

Wgof	<i>Watson goodness-of-fit test Performs the Watson test for goodness-of-fit to a specified distribution.</i>
------	--

Description

Watson goodness-of-fit test Performs the Watson test for goodness-of-fit to a specified distribution.

Usage

```
Wgof(x, dist = c("norm", "exp", "unif", "lnorm", "gamma"), ..., eps = 1e-15)
```

Arguments

x	Numeric vector of observations.
dist	Character string specifying the distribution to test against. One of "norm", "exp", "unif", "lnorm", or "gamma".
...	Additional parameters passed to the distribution's cumulative distribution function (CDF). For example, mean and sd for the normal distribution.
eps	Numeric tolerance for probability bounds to avoid extremes (default: 1e-15).

Details

The Watson test is a modification of the Cramér–von Mises test, adjusting for mean deviations. It measures the squared distance between the empirical distribution function of the data and the specified theoretical cumulative distribution function, with a correction for location.

Value

An object of class "htest" containing the test statistic, p-value, method description, data name, and any distribution parameters used.

Examples

```

set.seed(123)
x_norm <- rnorm(1000, mean = 5, sd = 2)
Wgof(x_norm, dist = "norm", mean = 5, sd = 2)

x_exp <- rexp(500, rate = 0.5)
Wgof(x_exp, dist = "exp", rate = 0.5)

x_unif <- runif(300, min = 0, max = 10)
Wgof(x_unif, dist = "unif", min = 0, max = 10)

x_lnorm <- rlnorm(200, meanlog = 0, sdlog = 1)
Wgof(x_lnorm, dist = "lnorm", meanlog = 0, sdlog = 1)

x_gamma <- rgamma(400, shape = 1, rate = 1)
Wgof(x_gamma, dist = "gamma", shape = 1, rate = 1)

```

WhiteWine

White wine quality dataset of the Portuguese "Vinho Verde" wine

Description

A white wine tasting preference data used in the study of Cortez, Cerdeira, Almeida, Matos, and Reis 2009. This white wine contains 4898 white vinho verde wine samples and 12 variables including the tasting preference score of white wine and its physicochemical characteristics.

Usage

```
data(WhiteWine)
```

Format

A data frame with 4898 rows, quality score, and 11 variables of physicochemical properties of wines.

- `quality` Tasting preference is a rating score provided by a minimum of three sensory with ordinal values from 0 (very bad) to 10 (excellent). The final sensory score is the median of these evaluations.
- `fixed.acidity` The fixed acidity is the physicochemical property in unit $\text{g}(\text{tartaric acid})/\text{dm}^3$.
- `volatile.acidity` The volatile acidity is in unit $\text{g}(\text{acetic acid})/\text{dm}^3$.
- `citric.acid` The citric acidity is in unit g/dm^3 .
- `residual.sugar` The residual sugar is in unit g/dm^3 .
- `chlorides` The chlorides is in unit $\text{g}(\text{sodium chloride})/\text{dm}^3$.
- `free.sulfur.dioxide` The free sulfur dioxide is in unit mg/dm^3 .
- `total.sulfur.dioxide` The total sulfur dioxide is in unit mg/dm^3 .

- density The density is in unit g/cm^3 .
- pH The wine's pH value.
- sulphates The sulphates is in unit $\text{g}(\text{potassium sulphates})/\text{dm}^3$.
- alcohol The alcohol is in unit \

References

Cortez, P., Cerdeira, A., Almeida, F., Matos, T., and Reis, J. (2009), "Modeling wine preferences by data mining from physicochemical properties," *Decision Support Systems*, 47, 547–553.
[doi:10.1016/j.dss.2009.05.016](https://doi.org/10.1016/j.dss.2009.05.016)

Examples

```
head(WhiteWine)
```

Index

* datasets

- BSdata, [4](#)
- goats, [8](#)
- Snow, [15](#)
- strength, [15](#)
- WhiteWine, [17](#)

AD2gof, [2](#)
ADgof, [3](#)

BSdata, [4](#)

CVM2gof, [5](#)
cvmgof, [6](#)
CVMgof2, [7](#)

goats, [8](#)

KS2gof, [9](#)
ksgof, [10](#)
KSgof2, [11](#)
Kuiper2gof, [12](#)

qCvMgof, [13](#)

simpleCvMgof, [14](#)
Snow, [15](#)
snow (Snow), [15](#)
strength, [15](#)

Wgof, [16](#)
WhiteWine, [17](#)