Package 'neftest'

July 18, 2021

Type Package

Title Goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions

Version 1.0.1

Author Author [aut],
Author [aut],
Author [aut],
Author [aut,cre],
Author [aut,cre]

Maintainer Xu Liu <liu.xu@sufe.edu.cn>

Description Provide test statistics for the goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions, and p-value of test statistic according to several specified distributions, which is based on the proposed method.

License GPL (>= 2)

Depends R (>= 3.2.0)

Imports SuppDists

LazyData true

NeedsCompilation yes

Repository CRAN

URL https://github.com/xliusufe/neftest

Encoding UTF-8

R topics documented:

`neftest-package` *Goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions*

Description

Provide test statistics for the goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions, and p-value of test statistic according to several specified distributions, which is based on the proposed method.

Details

Package:	neftest
Type:	Package
Version:	1.0.1
Date:	2021-07-18
License:	GPL (>= 2)

References

Authors (2021). Goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions. Manuscript.

`pvals` *The p-value of the test based on the test statistic Tnw*

Description

Compute the p-value of the test based on the test statistic T_{nw}.

Usage

```
pvals(x, distr="Poisson", bootstrap = FALSE, B = 1000, signif = 0.05,
                weight="normal", a = 1.0, max.iter = 100, tol = 1e-8)
```

Arguments

`x`	A length n vector of input data.
`distr`	The true distribution including Poisson distribution `distr = "Poisson"`, Gamma distribution `distr = "Gamma"` and Inverse Gaussian distribution `distr = "Inverse Gaussian"`. Default is `distr = "Poisson"`.
`bootstrap`	logical. Bootstrap method is used to compute the p-value if FALSE (default), and the maximum likelihood method otherwise.
`B`	Number of bootstrap samples. Default is 1000.

signif	The significance level of the test. Default is 0.05.
weight	The weight functions including normal distribution weight = "normal" and Laplace distribution weight = "laplace". Default is weight = "normal".
a	The parameter of the weight function. Default is 1.0. See details in the paper
max.iter	The maximum number of iterations in Newton method. Default is 100.
tol	The precision of the Newton method. Default is 1e-8.

Value

pval	The p-value of the test.

References

Authors (2021). Goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions. Manuscript.

Examples

```
# Poisson
n   <- 100
NS  <- 500
distr <- "Poisson"
pval  <- rep(NA, NS)
set.seed(100861)
for (i in 1:NS) {
  x       <- rpois(n,lambda = 1)
  pval[i] = pvals(x, distr, bootstrap = FALSE, B = 1000, signif = 0.05)
}
pvalue = mean(pval<0.05)


# Poisson
n   <- 100
NS  <- 500
B   <- 500
distr <- "Poisson"
pval  <- rep(NA, NS)
for(i in 1:NS){
  x       <- rpois(n,lambda = 1)
  pval[i] = pvals(x, distr, bootstrap = TRUE, B = B, signif = 0.05)
}
Pval = mean(pval<0.05)



# Gamma
n     <- 100
NS    <- 500
distr <- "Gamma"
pval  <- rep(NA, NS)
set.seed(100861)
for (i in 1:NS) {
  x       <- rgamma(n, shape = 1, rate = 1)
  pval[i] = pvals(x, distr, bootstrap = FALSE, B = 1000, signif = 0.05)
```

```
}
pvalue = mean(pval<0.05)


# Gamma
n     <- 100
NS    <- 500
B     <- 500
distr <- "Gamma"
pval  <- rep(NA, NS)
for(i in 1:NS){
  x       <- rgamma(n,lambda = 1)
  pval[i] = pvals(x, distr, bootstrap = TRUE, B = B, signif = 0.05)
}
Pval = mean(pval<0.05)



# Inverse Gaussian
n     <- 100
NS    <- 500
distr <- "Inverse Gaussian"
pval  <- rep(NA, NS)
set.seed(100861)
for (i in 1:NS) {
  x       <- rinvGauss(n, nu = 1, lambda = 1)
  pval[i] = pvals(x, distr, bootstrap = FALSE, B = 1000, signif = 0.05)
}
pvalue = mean(pval<0.05)



# Inverse Gaussian
n     <- 100
NS    <- 500
B     <- 500
distr <- "Inverse Gaussian"
pval  <- rep(NA, NS)
for(i in 1:NS){
  x       <- rinvGauss(n, nu = 1, lambda = 1)
  pval[i] = pvals(x, distr, bootstrap = TRUE, B = B, signif = 0.05)
}
Pval = mean(pval<0.05)
```

Tnw *The test statistic for testing if a distribution is a TBE($\gamma 0$)*

Description

Compute the test statistic T_{nw}.

Usage

```
Tnw(x, gamma0 = 1, weight = "normal", a = 1.0)
```

Arguments

x	A length n vector of input data.
gamma0	The power parameter in TBE(γ_0). Default is 1.
weight	The weight functions including normal distribution weight = "normal" and Laplace distribution weight = "laplace" . Default is weight = "normal".
a	The parameter of the weight function. Default is 1.0.

Value

Tn	The test statistic T_{nw}.

References

Authors (2021). Goodness of fit tests based on zero regression characterizations of Tweedie, Bar-Lev and Enis class of distributions. Manuscript.

Examples

```
# Poisson
n   <- 100
x   <- rpois(n,lambda = 1)
B   <- 1000
Tn  <- Tnw(x, gamma0 = 1, weight = "normal", a = 1.0)
Tb  = rep(NA, B)
lambdahat  = mean(x)
for(b in 1:B){
  xb  <- rpois(n, lambda = lambdahat)
  Tb[b] <- Tnw(xb, gamma0 = 1, weight = "normal", a = 1.0)
}
pval = mean(quantile(Tb, probs = 1-0.05) > Tn)

# Gamma
n   <- 100
x   <- rgamma(n, shape = 1, rate = 1)
Tn  <- Tnw(x, gamma0 = 1, weight = "normal", a = 1.0)

# Inverse Gaussian
n   <- 100
x   <- rinvGauss(n, nu = 1, lambda = 1)
B   <- 1000
Tn  <- Tnw(x, gamma0 = 1, weight = "normal", a = 1.0)
Tb  = rep(NA, B)
nuhat  = mean(x)
lambdahat = (mean(1/x)-nuhat^(-1))^(-1)
for(b in 1:B){
  xb  <- rinvGauss(n, nu = nuhat, lambda = lambdahat)
  Tb[b] <- Tnw(xb, gamma0 = 1, weight = "normal", a = 1.0)
}
pval = mean(quantile(Tb, probs = 1-0.05) > Tn)
```

Index