

Package ‘sac’

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Title Semiparametric Analysis of Change-Point

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Description Semiparametric empirical likelihood ratio
based tests of change-point with one-change or epidemic alternatives
with data-based model diagnostic are contained.

License GPL (>= 2)

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BootsChapt	<i>Bootstrap (Permutation) Test of Change-Point(s) with One-Change or Epidemic Alternative</i>
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Description

By resampling with(out) replacement from the original sample data, we can obtain bootstrap(permutation) versions of the test statistics. The p-values of the test(s) from the original data are approximated by the p-values of the bootstrap(permutation) version statistics.

Usage

```
BootsChapt(x, stat1, stat2 = NULL, B, replace = FALSE,
           alternative = c("one.change", "epidemic"), adj.Wn = FALSE,
           tol = 1.0e-7, maxit = 50, trace = FALSE, ... )
```

Arguments

x	a numeric vector or matrix containing the data, one row per observation;
stat1	test statistic S_n for "one-change" alternative or V_n for "epidemic" alternative, output of SemiparChangePoint .
stat2	test statistic W_n for "epidemic" alternative, output of SemiparChangePoint .
B	number of resamples
replace	a logical indicating whether bootstrap samples for bootstrap test of the change-point are selected with or without replacement, if <code>replace= FALSE</code> (default), corresponds to permutation test, otherwise, bootstrap test;
alternative	a character string specifying the alternative hypothesis, must be one of "one-change" (default) or "epidemic". You can specify just the initial letter.
adj.Wn	logical indicating if W_n should be adjusted or not for "epidemic" alternative.
tol	the desired accuracy (convergence tolerance), an argument of glm.control .
maxit	the maximum number of iterations, an argument of glm.control .
trace	logical indicating if output should be produced for each iteration, an argument of glm.control .
...	other arguments

Details

The procedure will fail when there is separation in the data in the sense of Albert & Anderson (1984, *Biometrika*) and Santner & Duffy (1986, *Biometrika*). In this case, the change-point(s) may be detected easily using nonparametric method based on cumsum. Now, this program does not check whether the data is separated.

Value

p.boots	bootstrap p-value of S_n for "one-change" alternative
p.boots.Vn	bootstrap p-value of V_n for "epidemic" alternative
p.boots.Wn	bootstrap p-value of W_n for "epidemic" alternative

Note

Default alternative is "one-change", even when `stat2` is not NULL. If `alternative = "epidemic"`, both `stat1` and `stat2` should be provided. Statistic W_n need be adjusted only for one dimensional observations and if no bootstrap test is conducted. However, if W_n is already adjusted, you have to assign `adj.Wn = TRUE` to calculate the p-value of W_n .

Author(s)

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References

- Guan, Z.(2001) Some Results About Empirical Likelihood Method, *Ph.D. Thesis, The University of Toledo*.
- Guan, Z.(2004) A semiparametric changepoint model, *Biometrika*, 91, 4, 849–862.
- Guan, Z. Semiparametric Tests for Change-points with Epidemic Alternatives.

See Also

[SemiparChangePoint](#), [schapt](#), [p.OneChange](#), [p.Epidemic.Vn](#), [p.Epidemic.Wn](#)

Examples

```
require(sac) #load the package

# one-change alternative
k<-10
n<-20
x<-rnorm(n,0,1)
x[(k+1):n]<-x[(k+1):n]+1.5
T<-SemiparChangePoint(x, alternative = "one.change")$Sn
BootsChapt(x, T, B = 5)
#Choose larger B to get better approximate p-value.
```

BootsModelTest	<i>Bootstrap Test of the Validity of the Semiparametric Change-Point Model</i>
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Description

Using bootstrap method to approximate the p-value of test of the model validity. Bootstrap samples are drawn from the semiparametric empirical distribution which are estimates of the underlying population distributions.

Usage

```
BootsModelTest(x, k, m, B, Alpha, Beta, tol = 1.0e-7, maxit=50, trace=FALSE)
```

Arguments

x	a numeric vector or matrix containing the data, one row per observation;
k	the estimated change-point, output of SemiparChangePoint
m	= n the sample size for "one-change" alternative, or the estimated second change-point for "epidemic" alternative, an output of SemiparChangePoint
B	number of resamples
Alpha	estimated parameter α , output of SemiparChangePoint
Beta	estimated parameter β , output of SemiparChangePoint
tol	the desired accuracy (convergence tolerance), an argument of glm.control .
maxit	the maximum number of iterations, an argument of glm.control .
trace	logical indicating if output should be produced for each iteration, an argument of glm.control .

Value

Delta	The test statistic of the model validity
Pvalue	The bootstrapped p-value

Author(s)

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References

Guan, Z.(2001) Some Results About Empirical Likelihood Method, *Ph.D. Thesis, The University of Toledo*.

Guan, Z.(2004) A semiparametric changepoint model, *Biometrika*, 91, 4, 849–862.

Guan, Z. Semiparametric Tests for Change-points with Epidemic Alternatives.

See Also

[SemiparChangePoint](#), [schapt](#)

Examples

```
## Nile data with one change-point: the annual flows drop in 1898.
## It is believed to be caused by the building of the first Aswan dam.
if(! "package:stats" %in% search()) library(stats)
data(Nile)
require(sac) #load the package
Nile.res<-SemiparChangePoint(Nile, alternative = "one.change")
BootsModelTest(Nile, Nile.res$k.hat, length(Nile), B=5, Nile.res$alpha.hat,
  Nile.res$beta.hat)
# Choose larger B to get better approximate p-value.
# It takes longer to do bootstrap model test for large B.
```

CriticalValues

Critical Values of Tests of Change-Point(s) with One-Change or Epidemic Alternative

Description

Return the approximate critical values of the test statistics given level α

Usage

```
Sn.alfa(alfa,n,d,model=c("parametric","semiparametric"),
  tol = .Machine$double.eps^0.25, maxiter = 1000)
CV.Epidemic.Vn(alfa, d, tol = 1e-10)
CV.Epidemic.Wn(alfa, tol = 1e-07)
```

Arguments

<code>alfa</code>	significance level
<code>n</code>	sample size
<code>model</code>	a character string specifying the model, must be one of "parametric" or "semiparametric" (default). You can specify just the initial letter
<code>d</code>	dimension of the data value
<code>tol</code>	the desired accuracy (convergence).
<code>maxiter</code>	the maximum number of iterations for uniroot.

Details

Function `Sn.alfa` returns the critical value of S_n for one-change alternative. The functions `CV.Epidemic.Vn` and `CV.Epidemic.Wn` calculate critical values for V_n and W_n .

Value

Critical values

Author(s)

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References

Csorgo, M. and Horvath, L. (1997), *Limit Theorems in Change-Point Analysis*, New York: John Wiley

See Also

[schapt](#)

Examples

```
require(sac) #load the package
alpha<-0.05
n<-20
d<-1
Sn.alfa(alpha, n, d, model="semiparametric")
CV.Epidemic.Vn(alpha, d)
CV.Epidemic.Wn(alpha)
```

cumsum.test	<i>Nonparametric Test for Change-Point with One-change or Epidemic Alternative</i>
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Description

Compute test statistic based on CUMSUM and change-point estimate

Usage

```
cumsum.test(x, alternative = c("one.change", "epidemic"))
```

Arguments

- x a numeric vector or matrix containing the data, one row per observation;
- alternative a character string specifying the alternative hypothesis, must be one of "one-change" (default) or "epidemic". You can specify just the initial letter.

Value

- Sn test statistic
- k.hat estimated change-point
- m.hat the second estimated change-point for epidemic alternative

Author(s)

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References

Csorgo, M. and Horvath, L. (1997), *Limit Theorems in Change-Point Analysis*, New York: John Wiley

See Also

[cumsum](#)

Examples

```
require(sac) #load the package
# one-change alternative
k<-10
n<-30
x<-rnorm(n,0,1)
x[(k+1):n]<-x[(k+1):n]+1.5
cumsum.test(x, alternative = "one.change")
# epidemic alternative
k<-10
m<-20
n<-30
x<-rnorm(n,0,1)
x[(k+1):m]<-x[(k+1):m]+1.5
cumsum.test(x, alternative = "epidemic")
```

plots

Visualized Model Diagnostic and Loglikelihood Plot

Description

Plot and compare the empirical likelihood and semiparametric empirical likelihood distribution functions, plot loglikelihood function.

Usage

```
Graf.Diagnostic(x, k, m, Alpha, Beta, Color, LTY, xlab = "x",
  ylab = "Estimated DF's", main = "Model Diagnostic",
  OneLegend = TRUE, lgnd1, lgnd2, arw1, arw2, ...)
Plot.ll(x, ll, col, xaxis.lab = NULL, xlab = "k", ylab = "Loglikelihood",
  main = "Plot of Loglikelihood",...)
```

Arguments

x	a numeric vector or matrix containing the data, one row per observation;
ll	loglikelihood function, output of SemiparChangePoint
col	color code or character string for the loglikelihood curve
xaxis.lab	a vector of character strings or numeric values to be placed at the tickpoints as labels of axis
k	the estimated change-point, output of SemiparChangePoint
m	= n, the sample size, for "one-change" alternative, or the estimated second change-point for "epidemic" alternative, an output of SemiparChangePoint
Alpha	estimated parameter α , output of SemiparChangePoint
Beta	estimated parameter β , output of SemiparChangePoint
Color	a vector of character strings or color codes for curves of estimated distribution functions $\hat{F}$, $\tilde{F}$, $\hat{G}$ and $\tilde{G}$
LTY	vector of lty's, $LTY=c(lty1, lty2, lty3, lty4)$, corresponds to the above color codes
xlab	character string for x-axis lable
ylab	character string for y-axis lable
main	character string for main title
OneLegend	a logical indicating whether plot one or two legend.
lgnd1	a numeric vector of two specify the position of the first legend box
lgnd2	a numeric vector of two specify the position of the second legend box, if OneLegend = FALSE
arw1	a numeric vector of four numbers indicating start and end positions of the first arrows point to curves
arw2	a numeric vector of four numbers indicating start and end positions of the second arrows point to curves
...	other arguments of function plot

Author(s)

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References

- Guan, Z.(2001) Some Results About Empirical Likelihood Method, *Ph.D. Thesis, The University of Toledo*;
- Guan, Z.(2004) A semiparametric change-point model, *Biometrika*, 91, 4, 849–862.
- Guan, Z. Semiparametric Tests for Changepoints with Epidemic Alternatives.

See Also

[schapt](#)

Examples

```
require(sac) #load the package
k<-30
n<-80
x<-rnorm(n,0,1)
x[(k+1):n]<-x[(k+1):n]+1.5
res<-SemiparChangePoint(x, alternative = "one.change")
Plot.ll(x, res$ll, col="blue")

## Nile data with one change-point: the annual flows drop in 1898 which corresponds
## to k=28. It is believed to be caused by the building of the first Aswan dam.
if(! "package:sac" %in% search()) library(sac)
  #if package sac has not been loaded, load it.
if(! "package:stats" %in% search()) library(stats)
data(Nile)
plot(Nile, type="p")
Nile.res<-SemiparChangePoint(Nile, alternative = "one.change")
Color<-c(1,2,3,4); LTY<-c(1,2,3,4)

## Plots of estimated distribution functions
Graf.Diagnostic(Nile, Nile.res$k.hat, length(Nile), Nile.res$alpha.hat,
  Nile.res$beta.hat, Color, LTY, xlab = "x", ylab = "Estimated DF's",
  main="Model Diagnostic for Nile Data", OneLegend = FALSE, lgnd1 =
  c(1100, 0.15), lgnd2 = c(600, .99), arw1=c(780, .93, 1010, .9),
  arw2 = c(1165, .15, 1015, .24))

## Plot of loglikelihood function
Plot.ll(Nile, Nile.res$ll, col = "blue")
Plot.ll(Nile, Nile.res$ll, col = "blue", xaxis.lab = seq(1871,1970, length = 100),
  xlab = "Year")
```

Pvalues

The p-values of Test Statistics Based on Asymptotic Distribution

Description

Calculate the approximate p-values of the test statistics T_n , V_n and W_n using limit null distributions.

Usage

```
p.OneChange(n, d, Sn)
p.Epidemic.Vn(Vn, d, tol = 1e-10)
p.Epidemic.Wn(Wn, tol = 1e-07)
```

Arguments

Sn	test statistic Sn of the one-change alternative
Vn	test statistic Vn of the epidemic alternative

Wn	test statistic Wn of the epidemic alternative
n	sample size
d	dimension of the data value
tol	the desired accuracy.

Value

p.value	p-value
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Author(s)

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References

Guan, Z.(2001) Some Results About Empirical Likelihood Method, *Ph.D. Thesis, The University of Toledo*.

Guan, Z.(2004) A semiparametric changepoint model, *Biometrika*, 91, 4, 849–862.

Guan, Z. Semiparametric Tests for Change-points with Epidemic Alternatives.

See Also

[schapt](#), [BootsChapt](#)

Examples

```
require(sac) #load the package
# one-change alternative
k<-10
n<-30
x<-rnorm(n,0,1)
x[(k+1):n]<-x[(k+1):n]+1.5
T<-SemiparChangePoint(x, alternative = "one.change")$Sn
p.OneChange(n, d=1, T)

# epidemic alternative
k<-5
m<-10
n<-20
x<-rnorm(n,0,1)
x[(k+1):m]<-x[(k+1):m]+1.5
res<-SemiparChangePoint(x, alternative = "e")
V<-res$Vn; W<-res$Wn
p.Epidemic.Vn(V, d=1)
p.Epidemic.Wn(W)
```

schapt

*Semiparametric Analysis of Changepoint***Description**

Semiparametric empirical likelihood ratio based test of changepoint with one-change or epidemic alternatives with data-based model diagnostic

Usage

```
schapt(x, n.boots = 0, replace = FALSE, alternative = c("one.change",
  "epidemic"), conf.level = 0.95, adj.Wn = FALSE, model.test = FALSE,
  n.model.boots = 0, tol=1.0e-7, maxit=50, trace=FALSE, ... )
```

Arguments

<code>x</code>	a numeric vector or matrix containing the data, one row per observation;
<code>n.boots</code>	number of bootstrap samples for bootstrap test of the change-point, if <code>n.boots = 0</code> , do not perform bootstrap test;
<code>replace</code>	a logical indicating whether bootstrap samples for bootstrap test of the change-point are selected with or without replacement, if <code>replace = FALSE</code> (default), corresponds to permutation test, otherwise, bootstrap test;
<code>alternative</code>	a character string specifying the alternative hypothesis, must be one of "one-change" (default) or "epidemic". You can specify just the initial letter. Epidemic alternative is also called square wave alternative in the literature.
<code>conf.level</code>	confidence level.
<code>adj.Wn</code>	logical indicating if <code>Wn</code> should be adjusted or not for "epidemic" alternative.
<code>model.test</code>	a logical indicating whether the test of model validity is performed.
<code>n.model.boots</code>	number of bootstrap samples for model test, if either <code>n.model.boots = 0</code> or <code>model.test = FALSE</code> , then model test will not be performed.
<code>tol</code>	the desired accuracy (convergence tolerance), an argument of glm.control .
<code>maxit</code>	the maximum number of iterations, an argument of glm.control .
<code>trace</code>	logical indicating if output should be produced for each iteration, an argument of glm.control .
<code>...</code>	other future arguments

Details

Model: $\log\{g(x)/f(x)\} = \exp\{\alpha + \beta'T(x)\}$, where $f(x)$ and $g(x)$ are the density (frequency) functions of the two hypothesized populations, and $T(x)$ can be chosen as $T(x) = x$ or $T(x) = (x, x^2)$. The procedure will fail when there is separation in the data in the sense of Albert & Anderson (1984, *Biometrika*) and Santner & Duffy (1986, *Biometrika*). In this case, the change-point(s) may be detected easily using nonparametric method based on cumsum. Currently, this function does not check whether the data are separated.

Value

data.name	dataset name
parameter	sample size n and degree(s) of freedom of the df of S_n for "one-change" alternative
alternative	the alternative hypothesis
statistic	a list contains S_n for "one-change" alternative, S_n , V_n and W_n for "epidemic" alternative; also contains Delta if model test is performed
estimate	a list contains change-point(s) and alpha and beta
p.value	a list contains p-value(s), $p(S_n)$, of S_n for "one-change" alternative, $p(V_n)$ and $p(W_n)$, of V_n and W_n , respectively, for "epidemic" alternative; also $p.boots(model)$ of Delta if model test is performed, if bootstrap test(s) of the change-point(s) are performed, then it also contains the corresponding p-values, $p.boots(S_n)$, $p.boots(V_n)$ and $p.boots(W_n)$ accordingly.

Note

Statistic W_n need be adjusted only for one dimensional observations and if no bootstrap test is conducted. If returned p-value is 0, this means that the p-value is less than $1.0e-7$.

Author(s)

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References

- Guan, Z. (2001). Some Results About Empirical Likelihood Method, *Ph.D. Thesis, The University of Toledo*.
- Guan, Z.(2004) A semiparametric change-point model, *Biometrika*, 91, 4, 849–862.
- Guan, Z. Semiparametric Tests for Change-points with Epidemic Alternatives.

See Also

[Graf.Diagnostic, Plot.11](#)

Examples

```
require(sac) #load the package
# one-change alternative
## Nile data with one change-point: the annual flows drop in 1898.
## It is believed to be caused by the building of the first Aswan dam.
if(! "package:sac" %in% search()) library(sac)
  #if package sac has not been loaded, load it.
if(! "package:stats" %in% search()) library(stats)
data(Nile)
plot(Nile, type="p")
schapt(Nile, alternative = "one.change")
```

SemiparChangePoint	<i>Semiparametric Test of Change-point(s) with One-change or Epidemic Alternative</i>
--------------------	---

Description

Calculate test statistics, loglikelihood function and estimate unknown parameters in the semiparametric model.

Usage

```
SemiparChangePoint(x, alternative = c("one.change", "epidemic"),
  adj.Wn = FALSE, tol = 1e-07, maxit = 50, trace = FALSE, ...)
```

Arguments

x	a numeric vector or matrix containing the data, one row per observation;
alternative	a character string specifying the alternative hypothesis, must be one of "one-change" (default) or "epidemic". You can specify just the initial letter.
tol	the desired accuracy (convergence tolerance), an argument of glm.control .
adj.Wn	logical indicating if Wn should be adjusted or not for "epidemic" alternative.
maxit	the maximum number of iterations, an argument of glm.control .
trace	logical indicating if output should be produced for each iteration, an argument of glm.control .
...	other future arguments

Details

Model: $\log\{g(x)/f(x)\} = \exp\{\alpha + \beta'T(x)\}$, where $f(x)$ and $g(x)$ are the density (frequency) functions of the two hypothesized populations, and $T(x)$ can be chosen as $T(x) = x$ or $T(x) = (x, x^2)$. The procedure will fail when there is separation in the data in the sense of Albert & Anderson (1984, *Biometrika*) and Santner & Duffy (1986, *Biometrika*). In this case, the change-point(s) may be detected easily using nonparametric method based on cumsum. Currently, this function does not check whether the data are separated.

Value

k.hat	change-point estimate
m.hat	second change-point estimate for "epidemic" alternative
ll	loglikelihood function
Sn	likelihood ratio test statistic for "one-change" alternative
Vn	test statistic based integral of weighted likelihood ratio for "epidemic" alternative

Wn	test statistic based supremum of weighted likelihood ratio for "epidemic" alternative
alpha.hat	estimate of α
beta.hat	estimate of β

Note

Statistic Wn need be adjusted only for one dimensional observations and if no bootstrap test is conducted.

Author(s)

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References

- Guan, Z.(2001) Some Results About Empirical Likelihood Method, *Ph.D. Thesis, The University of Toledo*.
- Guan, Z.(2004) A semiparametric change-point model, *Biometrika*, 91, 4, 849–862.
- Guan, Z. Semiparametric Tests for Change-points with Epidemic Alternatives.

See Also

[schapt](#), [p.OneChange](#), [p.Epidemic.Vn](#), [p.Epidemic.Wn](#)

Examples

```
require(sac) #load the package
# one-change alternative
k<-10
n<-30
x<-rnorm(n,0,1)
x[(k+1):n]<-x[(k+1):n]+1.5
SemiparChangePoint(x, alternative = "one.change")

# epidemic alternative
k<-5
m<-10
n<-20
x<-rnorm(n,0,1)
x[(k+1):m]<-x[(k+1):m]+1.5
SemiparChangePoint(x, alternative = "epidemic")
```

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