

# Package ‘chngpt’

May 8, 2026

**LazyLoad** yes

**LazyData** yes

**Version** 2024.11-15

**Title** Estimation and Hypothesis Testing for Threshold Regression

**Depends** R (>= 3.6)

**Suggests** R.rsp, RUnit, mvtnorm

**Imports** survival, splines, kyotil (>= 2020.10-12), boot, MASS,  
methods, lme4, parallel, RnpcBLASct1

**VignetteBuilder** R.rsp

**Description** Threshold regression models are also called two-phase regression, broken-stick regression, split-point regression, structural change models, and regression kink models, with and without interaction terms. Methods for both continuous and discontinuous threshold models are included, but the support for the former is much greater. This package is described in Fong, Huang, Gilbert and Permar (2017) <[DOI:10.1186/s12859-017-1863-x](https://doi.org/10.1186/s12859-017-1863-x)> and the package vignette.

**License** GPL (>= 2)

**NeedsCompilation** yes

**Author** Youyi Fong [cre],  
Qianqian Chen [aut],  
Shuangcheng Hua [aut],  
Hyunju Son [aut],  
Adam Elder [aut],  
Tao Yang [aut],  
Zonglin He [aut],  
Simone Giannerini [aut]

**Maintainer** Youyi Fong <youyifong@gmail.com>

**Repository** CRAN

**Date/Publication** 2024-11-12 20:40:02 UTC

## Contents

chngpt . . . . .	2
chngpt.test . . . . .	2
chngptm . . . . .	5
coef.0.ls . . . . .	12
convert.coef predictx threshold.func . . . . .	13
dat.mtct . . . . .	14
dat.mtct.2 . . . . .	14
double.hinge . . . . .	15
hinge.test . . . . .	16
lidar . . . . .	18
nutrition . . . . .	18
performance.unit.test . . . . .	19
sim.alphas . . . . .	19
sim.chngpt . . . . .	20
sim.hinge . . . . .	22
sim.my . . . . .	23
sim.pastor . . . . .	24
<b>Index</b>	<b>25</b>

---

chngpt

*chngpt Package*

---

### Description

Please see the Index link below for a list of available functions. The main testing function is `chngpt.test()`. The main estimation function is `chngptm()`.

---

chngpt.test

*Threshold Model Hypothesis Testing*

---

### Description

Hypothesis testing for threshold models. Only linear models and logistic models are supported at this point.

**Usage**

```
chnppt.test (formula.null, formula.chngpt, family=c("binomial","gaussian"), data,
  type=c("step","hinge","segmented","stegmented"),
  test.statistic=c("lr","score"), # support for score is gradually decreasing
  chngpts=NULL, lb.quantile=.1, ub.quantile=.9,
  chngpts.cnt=50, #this is set to 25 if int is weighted.two.sided or weighted.one.sided
  prec.weights=NULL,
  p.val.method=c("MC","param.boot"),
  mc.n=5e4, # 1e3 won't cut it, the p values estimated could be smaller than nominal
  boot.B=1e4,
  robust=FALSE,
  keep.fits=FALSE, verbose=FALSE
)
```

```
antoch.test (formula, data, chngpt.var, plot.=FALSE)
```

```
## S3 method for class 'chnppt.test'
plot(x, by.percentile=TRUE, both=FALSE, main=NULL, ...)
```

**Arguments**

- formula.null     formula for the null model.
- formula.chngpt     formula for the change point model. For example, suppose formula.null=y~z and we want to test whether  $I(x>cutff)$  is a significant predictor, formula.chngpt=~x. If instead we are interested in testing the null that neither  $I(x>cutff)$  nor  $z*I(x>cutff)$  is a significant predictor, formula.chngpt=~x\*z
- data             data frame.
- family            Currently only linear and logistic regression are supported.
- type             step: flat before and after change point; hinge: flat before and slope after change point; segmented: slope before and after change point
- test.statistic    method for testing main effects of some threshold model.
- chngpts           A grid of potential change points to maximize over. If not supplied, they will be set to a vector of length chngpts.cnt equally spaced between lb.quantile and ub.quantile.
- robust            Boolean.
- lb.quantile       number. The lower bound in the search for change point in the unit of quantile.
- ub.quantile       number. The upper bound in the search for change point in the unit of quantile.
- chngpts.cnt       integer. Number of potential change points to maximize over.
- mc.n              integer. Number of multivariate normal samples to generate in the Monte Carlo procedure to evaluate p-value.
- verbose           Boolean.
- chngpt.var        string. Name of the predictor to detect change point

plot.	Boolean. Whether to make a plot.
formula	formula.
x	An object of type chngpt.test.
...	arguments passed to or from methods
by.percentile	tbd
both	tbd
main	tbd
prec.weights	tbd
p.val.method	tbd
boot.B	tbd
keep.fits	tbd

### Details

The model under the alternative is the model under the null plus terms involving the threshold. For example, when the type is segmented and  $\text{formula.null}=\sim z$ ,  $\text{formula.chngpt}=\sim x$ , the model under the null is  $\sim z+x$  and the model under the alternative is  $\sim z+x+(x-e)_+$ .

If there are missing values in the chngpt formula, those rows will be removed from the whole dataset, including null model and chngpt model.

antoch.test is only implemented for main effect only and is based on Antoch et al. (2004). Also see Fong et al. (2014).

### Value

A list of class htest and chngpt.test

p.value	P-value
family	Family from input
method	Method from input

### References

- Fong, Y., Huang, Y., Gilbert, P., Permar S. (2017) chngpt: threshold regression model estimation and inference, *BMC Bioinformatics*, 18(1):454.
- Fong Y, Di C, and Permar S. (2015) Change-Point Testing in Logistic Regression Models with Interaction Term. *Statistics in Medicine*. 34:1483–1494
- Pastor-Barriuso, R. and Guallar, E. and Coresh, J. (2003) Transition models for change-point estimation in logistic regression. *Statistics in Medicine*. 22:13141
- Antoch, J. and Gregoire, G. and Jaruskova, D. (2004) Detection of structural changes in generalized linear models. *Statistics and probability letters*. 69:315

**Examples**

```

dat=sim.chngpt("thresholded", "step", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4,
  family="binomial")
test=chngpt.test(formula.null=y~z, formula.chngpt=~x, dat, type="step", family="binomial",
  mc.n=10)
test
plot(test)

```

```

dat=sim.chngpt("thresholded", "segmented", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4,
  family="binomial")
test=chngpt.test(formula.null=y~z, formula.chngpt=~x, dat, type="segmented", family="binomial",
  mc.n=10)
test
plot(test)

```

```

test = chngpt.test (formula.null=Volume~1, formula.chngpt=~Girth, family="gaussian", data=trees,
  type="segmented", mc.n=1e4, verbose=FALSE, chngpts.cnt=100, test.statistic="lr")
test
plot(test)

```

```

## Not run:
# not run because otherwise the examples take >5s and that is a problem for R CMD check

```

```

# has interaction
test = chngpt.test(formula.null=y~z, formula.chngpt=~x*z, dat, type="step", family="binomial")
test
plot(test)

```

```

## End(Not run)

```

---

chngptm

*Threshold Models Estimation*


---

**Description**

Estimate threshold generalized linear models, Cox proportional hazards models, and linear mixed models. Supports 14 types of two-phase (one threshold) models and 1 type of three-phase (two thresholds) model.

**Usage**

```

chngptm (formula.1, formula.2, family, data, type = c("hinge",
  "M01", "M02", "M03", "M04", "upperhinge", "M10",
  "M20", "M30", "M40", "M21", "M12", "M21c", "M12c",

```

```

"M22", "M22c", "M31", "M13", "M33c", "segmented",
"M11", "segmented2", "M111", "step", "stegmented"),
formula.strat = NULL, weights = NULL, offset = NULL,
REML = TRUE, re.choose.by.loglik = FALSE, est.method =
c("default", "fastgrid2", "fastgrid", "grid",
"smoothapprox"), var.type = c("default", "none",
"robust", "model", "bootstrap", "all"), aux.fit =
NULL, lb.quantile = 0.05, ub.quantile = 0.95,
grid.search.max = Inf, test.inv.ci = TRUE,
boot.test.inv.ci = FALSE, bootstrap.type =
c("nonparametric", "wild", "sieve", "wildsieve",
"awb"), m.out.of.n = 0, subsampling = 0, order.max =
10, ci.bootstrap.size = 1000, alpha = 0.05, save.boot
= TRUE, b.transition = Inf, tol = 1e-04, maxit = 100,
chngpt.init = NULL, search.bound = 10, keep.best.fit =
TRUE, ncpus = 1, verbose = FALSE, ...)

```

```

chngptm.xy(x, y, type=c("step","hinge","segmented","segmented2","stegmented"),
...)

```

```

## S3 method for class 'chngptm'
coef(object, ...)
## S3 method for class 'chngptm'
residuals(object, ...)
## S3 method for class 'chngptm'
vcov(object, var.type=NULL, ...)
## S3 method for class 'chngptm'
print(x, ...)
## S3 method for class 'chngptm'
predict(object, newdata = NULL,
type = c("link", "response", "terms"), ...)
## S3 method for class 'chngptm'
plot(x, which = NULL, xlim = NULL, ylim = NULL, lwd = 2,
lcol = "red", lty = 1, add = FALSE, add.points = TRUE,
add.ci = TRUE, breaks = 20, mark.chngpt = TRUE, xlab =
NULL, ylab = NULL, plot.individual.line = FALSE, main
= "", y.adj = NULL, auto.adj.y = FALSE, transform =
NULL, ...)
## S3 method for class 'chngptm'
summary(object, var.type = NULL, expo = FALSE,
show.slope.post.threshold = FALSE, verbose = FALSE,
boot.type = "perc", ...)
## S3 method for class 'chngptm'
logLik(object, ...)
## S3 method for class 'chngptm'
AIC(object, ...)

```

```
lincomb(object, comb, alpha = 0.05, boot.type = "perc")
```

### Arguments

formula.1	The part of formula that is free of terms involving thresholded variables
formula.2	The part of formula that is only composed of thresholded variables
formula.strat	stratification formula
family	string. coxph or any valid argument that can be passed to glm. But variance estimate is only available for binomial and gaussian (only model-based for latter)
data	data frame.
type	type
transform	transform
b.transition	Numeric. Controls whether threshold model or smooth transition model. Default to Inf, which corresponds to threshold model
est.method	default: estimation algorithm will be chosen optimally; fastgrid2: a super fast grid search algorithm, limited to linear regression; grid: plain grid search, works for almost all models; smoothapprox: approximates the likelihood function using a smooth function, only works for some models. fastgrid = fastgrid2, kept for backward compatibility
var.type	string. Different methods for estimating covariance matrix and constructing confidence intervals
aux.fit	a model fit object that is needed for model-robust estimation of covariance matrix
grid.search.max	The maximum number of grid points used in grid search. When doing fast grid search, grid.search.max is set to Inf internally because it does not take more time to examine all potential thresholds.
test.inv.ci	Boolean, whether or not to find test-inversion confidence interval for threshold
ci.bootstrap.size	integer, number of bootstrap
alpha	double, nominal type I error rate
save.boot	Boolean, whether to save bootstrap samples
lb.quantile	lower bound of the search range for change point estimate
ub.quantile	upper bound of the search range for change point estimate
tol	Numeric. Stopping criterion on the coefficient estimate.
maxit	integer. Maximum number of iterations in the outer loop of optimization.
chnppt.init	numeric. Initial value for the change point.
weights	passed to glm
verbose	Boolean.
add.points	Boolean.
add.ci	Boolean.

<code>add</code>	Boolean.
<code>breaks</code>	integer.
<code>ncpus</code>	Number of cores to use if the OS is not Windows.
<code>keep.best.fit</code>	Boolean.
<code>y</code>	outcome
<code>show.slope.post.threshold</code>	boolean
<code>x</code>	chngp fit object.
<code>newdata</code>	newdata
<code>object</code>	chngp fit object.
<code>...</code>	arguments passed to glm or coxph
<code>m.out.of.n</code>	sample size for m-out-of-n bootstrap, default 0 for not doing this type of bootstrap
<code>subsampling</code>	sample size for subsampling bootstrap, default 0 for not doing this type of bootstrap
<code>boot.test.inv.ci</code>	whether to get test inversion CI under bootstrap
<code>search.bound</code>	bounds for search for sloping parameters
<code>which</code>	an integer
<code>y.adj</code>	y.adj
<code>auto.adj.y</code>	auto.adj.y
<code>xlim</code>	xlim
<code>ylim</code>	ylim
<code>lwd</code>	lwd
<code>lcol</code>	line col
<code>mark.chngpt</code>	mark.chngpt
<code>xlab</code>	xlab
<code>ylab</code>	ylab
<code>offset</code>	offset
<code>lty</code>	lty
<code>boot.type</code>	lty
<code>bootstrap.type</code>	nonparametric: the default, classical Efron bootstrap, works for homoscedastic and heteroscedastic independent errors; sieve: works for homoscedastic autocorrelated errors; wild: works for heteroscedastic independent errors; wildsieve: works for heteroscedastic autocorrelated errors; awb: autoregressive wild bootstrap, also works for heteroscedastic autocorrelated errors, but performance may not be as good as wildsieve
<code>order.max</code>	order of autocorrelation for autocorrelated errors in sieve and wildsieve bootstrap

<code>comb</code>	a vector of combination coefficients that will be used to form an inner product with the estimated slope
<code>expo</code>	If family is binomial and <code>expo</code> is TRUE, coefficients summary will be shown on the scale of odds ratio instead of slopes
<code>REML</code>	mixed model fitting - should the estimates be chosen to optimize the REML criterion for a fixed threshold
<code>re.choose.by.loglik</code>	mixed model fitting - should the estimates be chosen to optimize likelihood (REML nor not) or goodness of fit
<code>plot.individual.line</code>	boolean
<code>main</code>	character string

### Details

Without `lb.quantile` and `ub.quantile`, finite sample performance of estimator drops considerably! When `est.method` is `smoothapprox`, Newton-Raphson is done with initial values chosen by change point hypothesis testing. The testing procedure may be less subjective to finite sample volatility.

If `var.method` is `bootstrap`, summary of fitted model contains p values for each estimated slope. These p values are approximate p-values, obtained assuming that the bootstrap distributions are normal.

When `var.method` is `bootstrap` and the OS is not Windows, the `boot` package we use under the hood takes advantage of ncpus cores through `parallel::mclapply`.

`lincomb` can be used to get the estimate and CI for a linear combination of slopes.

### Value

A an object of type `chngptm` with the following components

<code>converged</code>	Boolean
<code>coefficients</code>	vector. Estimated coefficients. The last element, named <code>".chngpt"</code> , is the estimated change point
<code>test</code>	htest. Max score test results
<code>iter</code>	integer. Number of iterations

### References

- Son, H, Fong, Y. (2020) Fast Grid Search and Bootstrap-based Inference for Continuous Two-phase Polynomial Regression Models, *Environmetrics*, in press.
- Elder, A., Fong, Y. (2020) Estimation and Inference for Upper Hinge Regression Models, *Environmental and Ecological Statistics*, 26(4):287-302.
- Fong, Y. (2019) Fast bootstrap confidence intervals for continuous threshold linear regression, *Journal of Computational and Graphical Statistics*, 28(2):466-470.

Fong, Y., Huang, Y., Gilbert, P., Permar S. (2017) chngpt: threshold regression model estimation and inference, BMC Bioinformatics, 18(1):454.

Fong, Y., Di, C., Huang, Y., Gilbert, P. (2017) Model-robust inference for continuous threshold regression models, Biometrics, 73(2):452-462.

Pastor-Barriuso, R. and Guallar, E. and Coresh, J. (2003) Transition models for change-point estimation in logistic regression. Statistics in Medicine. 22:13141

## Examples

```
# also see the vignette for examples

# threshold linear regression
# for actual use, set ci.bootstrap.size to default or higher
par(mfrow=c(2,2))
types=c("hinge", "segmented", "M02", "M03")
for (type in types) {
  fit=chngptm(formula.1=logratio~1, formula.2=~range, lidar, type=type, family="gaussian",
    var.type="bootstrap", ci.bootstrap.size=100)
  print(summary(fit))
  for (i in 1:3) plot(fit, which=i)
  out=predict(fit)
  plot(lidar$range, out, main=type)
}

# with weights
dat.1=sim.chngptm("thresholded", "segmented", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4,
  family="gaussian")
fit.1.a=chngptm(formula.1=y~z, formula.2=~x, family="gaussian", dat.1, type="segmented",
  est.method="fastgrid", var.type="bootstrap", weights=ifelse(dat.1$x<3.5,100,1)
  , ci.bootstrap.size=10)
summary(fit.1.a)
plot(fit.1.a)
# fit.1.a$vcov$boot.samples

## Not run:
# likelihood test, combination of slopes
dat=sim.chngptm("thresholded", "segmented", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4,
  family="gaussian")
fit=chngptm(y~z, ~x, family="gaussian", dat, type="segmented", ci.bootstrap.size=100)
fit.0=lm(y~1,dat)
# likelihood ratio test using lmtest::lrtest
library(lmtest)
lrtest(fit, fit.0)
# estimate the slope after threshold using lincomb function in the chngptm package
lincomb(fit, c(0,0,1,1))

## End(Not run)

# threshold logistic regression
dat.2=sim.chngptm("thresholded", "step", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4,
```

```

    family="binomial")

fit.2=chngptm(formula.1=y~z, formula.2=~x, family="binomial", dat.2, type="step", est.method="grid")
summary(fit.2)
# no variance estimates available for discontinuous threshold models such as step
# vcov(fit.2$best.fit) gives the variance estimates for the best model conditional on threshold est

# also supports cbind() formula on left hand side
set.seed(1)
dat.2$success=rbinom(nrow(dat.2), 10, 1/(1 + exp(-dat.2$eta)))
dat.2$failure=10-dat.2$success
fit.2a=chngptm(formula.1=cbind(success,failure)~z, formula.2=~x, family="binomial", dat.2,
  type="step")

# Poisson example
counts <- c(18,17,15,20,10,20,25,13,12,33,35)
x <- 1:length(counts)
print(d.AD <- data.frame(x, counts))
fit.4=chngptm(formula.1=counts ~ 1, formula.2=~x, data=d.AD, family="poisson",
  type="segmented", var.type="bootstrap", verbose=1, ci.bootstrap.size=1)
summary(fit.4)

fit.4a=chngptm(formula.1=counts ~ 1, formula.2=~x, data=d.AD, family="quasipoisson",
  type="segmented", var.type="bootstrap", verbose=1, ci.bootstrap.size=1)

## Not run:
# Not run because otherwise the examples take >5s and that is a problem for R CMD check

# coxph example
library(survival)
fit=chngptm(formula.1=Surv(time, status) ~ ph.ecog, formula.2=~age, data=lung, family="coxph",
  type="segmented", var.type="bootstrap", ci.bootstrap.size=10)
summary(fit)

# one interaction term (mtcars is part of R default installation)
# est.method will be grid as fastgrid not available for models with interaction terms yet
fit=chngptm(formula.1=mpg ~ hp, formula.2=~hp*drat, mtcars, type="segmented",
  family="gaussian", var.type="bootstrap", ci.bootstrap.size=10)
summary(fit)

# interaction, upperhinge model, bootstrap
fit=chngptm(formula.1=mpg ~ hp, formula.2=~hp*drat, mtcars, type="M10",
  family="gaussian", var.type="bootstrap", ci.bootstrap.size=10)
summary(fit)

# more than one interaction term
# subsampling bootstrap confidence interval for step model

```

```

fit=chngptm(formula.1=mpg~hp+wt, formula.2=~hp*drat+wt*drat, mtcars, type="step",
  family="gaussian", var.type="bootstrap", ci.bootstrap.size=10)
summary(fit)

# step model, subsampling bootstrap confidence intervals
fit=chngptm(formula.1=mpg~hp, formula.2=~drat, mtcars, type="step",
  family="gaussian", var.type="bootstrap", ci.bootstrap.size=10, verbose=TRUE)
summary(fit)

# higher order threshold models
dat=sim.chngpt(mean.model="thresholded", threshold.type="M22", n=500, seed=1,
  beta=c(32,2,10, 10), x.distr="norm", e.=6, b.transition=Inf, family="gaussian",
  alpha=0, sd=0, coef.z=0)
fit.0=chngptm(formula.1=y~z, formula.2=~x, dat, type="M22", family="gaussian",
  est.method="fastgrid2"); plot(fit.0)

dat=sim.chngpt(mean.model="thresholded", threshold.type="M22c", n=500, seed=1,
  beta=c(32,2,32, 10), x.distr="norm", e.=6, b.transition=Inf, family="gaussian",
  alpha=0, sd=0, coef.z=0)
fit.0=chngptm(formula.1=y~z, formula.2=~x, dat, type="M22c", family="gaussian",
  est.method="fastgrid2"); plot(fit.0)

# examples of aux.fit
fit.0=glm(yy~zz+ns(xx,df=3), data, family="binomial")
fit = chngptm (formula.1=yy~zz, formula.2=~xx, family="binomial", data, type="hinge",
  est.method="smoothapprox", var.type="all", verbose=verbose, aux.fit=fit.0,
  lb.quantile=0.1, ub.quantile=0.9, tol=1e-4, maxit=1e3)

## End(Not run)

# example of random intercept
dat=sim.twophase.ran.inte(threshold.type="segmented", n=50, seed=1)
fit = chngptm (formula.1=y~z+(1|id), formula.2=~x, family="gaussian", dat,
  type="segmented", est.method="grid", var.type="bootstrap", ci.bootstrap.size=1)
plot(fit)
out=predict(fit, re.form=NA)
plot(dat$x, out)
out.1=predict(fit, type="response", re.form=NULL)# includes re
plot(dat$x, out.1, type="p", xlab="x")

```

---

coef.0.ls

*Simulation Study Parameters***Description**

The true parameters used in the simulation studies.

**Usage**

```
data("coef.0.ls")
```

**Format**

The format is list of lists.

convert.coef predictx threshold.func

*Helper functions***Description**

Some helper functions. predictx returns confidence bands for predictions as functions of the change point variable. threshold.func returns thresholded covariates.

**Usage**

```
convert.coef(coef.0, threshold.type)
```

```
predictx(fit, boot.ci.type = c("perc", "basic", "symm"), alpha
= 0.05, xx = NULL, verbose = FALSE, return.boot =
FALSE, include.intercept = FALSE, get.simultaneous =
TRUE)
```

```
threshold.func(threshold.type, coef, xx, x.name, include.intercept=FALSE)
```

**Arguments**

```
include.intercept
                coef.0
coef.0          coef.0
threshold.type  threshold.type
get.simultaneous
                threshold.type
return.boot     threshold.type
fit            fit
```

boot.ci.type	boot.ci.type
alpha	alpha
verbose	verbose
coef	coef
xx	xx
x.name	x.name

---

dat.mtct	<i>An Example Dataset</i>
----------	---------------------------

---

### Description

A dataset from the immune correlates study of Maternal To Child Transmission of HIV-1

### Usage

```
data("dat.mtct")
```

### Format

A data frame with 236 observations on the following 3 variables.

y a numeric vector

birth a factor with levels C-section Vaginal

NAb\_SF162LS a numeric vector

### References

Permar, S. R., Fong, Y., Nathan Vandergrift, Genevieve G. Fouda, Peter Gilbert, Georgia D. Tomaras, Feng Gao and Barton F. Haynes et al. (2015) Maternal HIV-1 Envelope variable loop 3-specific IgG responses and reduced risk of perinatal transmission. *Journal of Clinical Investigation*, 125(7):2702:2706.

---

dat.mtct.2	<i>An Example Dataset</i>
------------	---------------------------

---

### Description

A dataset from the immune correlates study of Maternal To Child Transmission of HIV-1

### Usage

```
dat.mtct.2
```

**Format**

A data frame with 248 observations on the following 2 variables.

NAb\_score a numeric vector

V3\_BioV3B a numeric vector

**References**

Permar, S. R., Fong, Y., Nathan Vandergrift, Genevieve G. Fouda, Peter Gilbert, Georgia D. Tomaras, Feng Gao and Barton F. Haynes et al. (2015) Maternal HIV-1 Envelope variable loop 3-specific IgG responses and reduced risk of perinatal transmission. *Journal of Clinical Investigation*, 125(7):2702:2706.

---

double.hinge	<i>Fit Double Hinge Models</i>
--------------	--------------------------------

---

**Description**

Fit double hinge models.

**Usage**

```
double.hinge(x, y, lower.y = NULL, upper.y = NULL,
             var.type = c("none", "bootstrap"), ci.bootstrap.size =
             1000, alpha = 0.05, save.boot = TRUE, ncpus = 1,
             boot.ci.type=c("percentile", "symmetric"))
```

```
## S3 method for class 'double.hinge'
plot(x, which = NULL, xlim = NULL,
     lwd = 2, lcol = "red",
     lty = 1, add.points = TRUE, add.ci = TRUE, breaks =
     20, mark.chngpt = FALSE, xlab = NULL, ylab = NULL,
     ...)
```

```
## S3 method for class 'double.hinge'
fitted(object, ...)
```

```
## S3 method for class 'double.hinge'
residuals(object, ...)
```

**Arguments**

object	x
x	x
y	y
lower.y	lower.y
upper.y	upper.y
var.type	var.type

boot.ci.type	var.type
ci.bootstrap.size	ci.bootstrap.size
alpha	alpha
save.boot	save.boot
ncpus	ncpus
lcol	ncpus
lwd	ncpus
which	x
xlim	x
lty	x
add.points	x
add.ci	x
breaks	x
mark.chngpt	x
xlab	x
ylab	x
...	arguments passed along

### Details

If lower.y and upper.y are not supplied, min(y) is taken as the function value when x is less than or equal to the first threshold, and max(y) is taken as the function value when x is greater than or equal to the second threshold.

If the function is expected to be decreasing between the two thresholds, lower.y and upper.y should be supplied to ensure the correct fit.

mse is residual sum of squares

---

hinge.test	<i>A non-nested hypothesis testing problem for threshold regression models</i>
------------	--

---

### Description

Test a hinge effect against a linear effect

### Usage

```
hinge.test(formula, cov.interest, family = c("binomial", "gaussian"), data, thres = NA,
  lb.quantile = 0.1, ub.quantile = 0.9, chngpts.cnt = 10, method = c("FDB", "B", "DB"),
  boot.B = 10000, B2 = NA, verbose = FALSE)
```

**Arguments**

formula	formula
cov.interest	cov.interest
family	family
data	data
thres	If supplied, this will be the threshold value to use in the hinge model.
lb.quantile	lower bound of threshold candidates in quantile
ub.quantile	upper bound of threshold candidates in quantile
chngps.cnt	number of candidate thresholds
method	type of test. FDB: false double bootstrap, B: parametric bootstrap, DB: double bootstrap.
boot.B	number of parametric bootstrap replicates for B and FDB
B2	number of inner bootstrap replicates for DB
verbose	verbose

**Value**

A list of class htest

p.value	P-value
chngps	Vector of change points evaluated
TT	Standardized absolute score statistics
V.S.hat	Estimated variance-covariance matrix of the score statistics

**Author(s)**

Zonglin He

**References**

He, Fong, Fouada, Permar. A non-nested hypothesis testing problem for threshold regression model, under review

**Examples**

```
dat=sim.hinge(threshold.type = 'NA',family = 'binomial',thres='NA',X.ditr = 'norm',mu.X = c(0,0,0),
  coef.X = c(0,.5,.5,.4),cov.X = diag(3),eps.sd = 1,seed = 1,n=100)
test=hinge.test(Y~X1+X2, "x", family="binomial", data=dat,'method'='FDB',boot.B=10)
test
```

---

lidar	<i>Light Detection and Ranging Data</i>
-------	---

---

**Description**

LIDAR

**Usage**

```
data("lidar")
```

**Format**

A data frame with 221 observations on the following 2 variables.

range a numeric vector

logratio a numeric vector

**Source**

Holst, U., Hossjer, O., Bjorklund, C., Ragnarson, P. and Edner, H. (1996), Locally weighted least-squares kernel regression and statistical evaluation of LIDAR measurements, *Environmetrics*,7, 401-416. Wakefield (2013), *Bayesian and Frequentist Regression Methods*. Chapter 11 Spline and Kernel Methods.

---

nutrition	<i>Infant Nutrition Data</i>
-----------	------------------------------

---

**Description**

The infant nutrition dataset comprises data collected in a study on the nutrition of infants and preschool children in the north central region of the United States of America.

**Usage**

```
data("nutrition")
```

**Format**

A data frame with 72 observations on the following 2 variables.

woh weight/height ratio

age a numeric vector

**Source**

Eppright, E. S., Fox, H. M., Fryer, B. A., Lamkin, G. H., Vivian, V. M., Fuller, E. S. (1972). Nutrition of Infants and Preschool Children in the North Central Region of the United States of America. In World Review of Nutrition and Dietetics (Vol. 14, pp. 269-332). Karger Publishers.

---

performance.unit.test *Perform unit testing for performance evaluation.*

---

**Description**

This function performs unit testing for performance evaluation.

**Usage**

```
performance.unit.test(formula.1, formula.2, family, data, B, I)
```

**Arguments**

formula.1	formula.1
formula.2	formula.2
family	family
data	data
B	B
I	I

---

sim.alphas *Simulation Parameters*

---

**Description**

Simulation Parameters

**Usage**

```
data(sim.alphas)
```

**Format**

List of 6. Names: sigmoid2\_norm, sigmoid2\_norm3, sigmoid3\_norm, sigmoid3\_norm3, sigmoid4\_norm, sigmoid4\_norm3. Each element is a 5x4 matrix

sim.chngpt

*Simulation Function***Description**

Generate simulation datasets for change point Monte Carlo studies.

**Usage**

```
sim.chngpt (mean.model = c("thresholded", "thresholdedItxn",
  "quadratic", "quadratic2b", "cubic2b", "exp",
  "flatHyperbolic", "z2", "z2hinge", "z2segmented",
  "z2linear", "logistic"), threshold.type = c("NA",
  "M01", "M02", "M03", "M10", "M20", "M30", "M11",
  "M21", "M12", "M22", "M22c", "M31", "M13", "M33c",
  "hinge", "segmented", "upperhinge", "segmented2",
  "step", "stegmented"), b.transition = Inf, family =
  c("binomial", "gaussian"), x.distr = c("norm",
  "norm3", "norm6", "imb", "lin", "mix", "gam",
  "zbinary", "gam1", "gam2", "fixnorm", "unif"), e. =
  NULL, mu.x = 4.7, sd.x = NULL, sd = 0.3, mu.z = 0,
  alpha = NULL, alpha.candidate = NULL, coef.z =
  log(1.4), beta = NULL, beta.itxn = NULL,
  logistic.slope = 15, n, seed, weighted = FALSE,
  heteroscedastic = FALSE, ar = FALSE, verbose = FALSE)
```

```
sim.twophase.ran.inte(threshold.type, n, seed)
```

```
sim.threephase(n, seed, gamma = 1, e = 3, beta_e = 5, f = 7, beta_f = 2, coef.z = 1)
```

**Arguments**

threshold.type	string. Types of threshold effect to simulate, only applicable when label does not start with sigmoid.
family	string. Glm family.
n	n
mu.z	n
seed	seed
weighted	beta
beta	beta
coef.z	numeric. Coefficient for z.
beta.itxn	numeric. Coefficient for z.

alpha	numeric, intercept.
mu.x	numeric
sd.x	numeric
mean.model	numeric
x.distr	string. Possible values: norm (normal distribution), gam (gamma distribution). gam1 is a hack to allow e. be different
e.	e.
verbose	Boolean
b.transition	b.
sd	b.
ar	autocorrelation
alpha.candidate	Candidate values of alpha, used in code to determine alpha values
e	e
beta_e	beta_e
f	f
beta_f	beta_f
logistic.slope	beta_f
gamma	beta_f
heteroscedastic	Boolean.

### Details

mean.model, threshold.type and b.transition all affect mean models.

### Value

A data frame with following columns:

y	0/1 outcome
x	observed covariate that we are interested in
x.star	unobserved covariate that underlies x
z	additional covariate

In addition, columns starting with 'w' are covariates that we also adjust in the model; columns starting with 'x' are covariates derived from x.

**Examples**

```

seed=2
par(mfrow=c(2,2))
dat=sim.chngpt(mean.model="thresholded", threshold.type="hinge", family="gaussian", beta=0, n=200,
  seed=seed, alpha=-1, x.distr="norm", e.=4, heteroscedastic=FALSE)
plot(y~z, dat)
dat=sim.chngpt(mean.model="thresholded", threshold.type="hinge", family="gaussian", beta=0, n=200,
  seed=seed, alpha=-1, x.distr="norm", e.=4, heteroscedastic=TRUE)
plot(y~z, dat)
dat=sim.chngpt(mean.model="z2", threshold.type="hinge", family="gaussian", beta=1, n=200,
  seed=seed, alpha=1, x.distr="norm", e.=4, heteroscedastic=FALSE)
plot(y~z, dat)
dat=sim.chngpt(mean.model="z2", threshold.type="hinge", family="gaussian", beta=1, n=200,
  seed=seed, alpha=1, x.distr="norm", e.=4, heteroscedastic=TRUE)
plot(y~z, dat)

```

---

sim.hinge

*Simulation function*


---

**Description**

Simulate data for Monte Carlo study.

**Usage**

```

sim.hinge(threshold.type = c("NA", "hinge"), family = c("binomial", "gaussian"),
  thres = "NA", X.ditr = "norm", mu.X, coef.X, cov.X, eps.sd, seed, n)

```

**Arguments**

threshold.type	threshold.type
family	family
thres	thres
X.ditr	X.ditr
mu.X	mu.X
coef.X	coef.X
cov.X	cov.X
eps.sd	eps.sd
seed	seed
n	n

---

 sim.my

*Simulate data*


---

## Description

Simulate data

## Usage

```
sim.my(n, seed, label, alpha, beta, e. = NULL, b. = NULL, tr. = NULL)
```

## Arguments

n	Sample size
seed	Seed for random number generator
label	A character string which specifies the simulation scenario. sigmoid4, sigmoidgam4, elbow4
alpha	regression parameter
beta	regression parameter
e.	inflection point for the logistic transformation (the log scale)
b.	slope for the logistic transformation
tr.	threshold point

## Details

When the label starts with elbow, the transformation on x.star is elbow shaped. When the label starts with sigmoid, the transformation on x.star is sigmoid shaped. Data simulated from  $\text{logit}(\text{Pr}(Y==1)) = \alpha + \beta * (\text{transformed } x.\text{star})$ .

## Value

A data frame with columns: y, x.star, x.star.expit (if label starts with sigmoid), x.star.tr (if label starts with elbow), x.bin.med (x.star dichotomized at median), x.tri (x.star trichotomized at tertiles).

## Examples

```
alpha=-1; beta=log(0.2)
e.=5; b.=-30; t.=1
dat=sim.my(n=250, seed=1, label="sigmoid4", alpha, beta, e.=e., b.=b.)
```

---

`sim.pastor`*Simulate data according to one of the scenarios considered in Pastor-Barriuso et al 2003*

---

**Description**

Simulate data according to one of the scenarios considered in Pastor-Barriuso et al 2003

**Usage**

```
sim.pastor(seed)
```

**Arguments**

`seed` Seed for the random number generator.

**Value**

A data frame with columns: `y`, `x.star`, `x.star.expit`, and `x.bin.med` (`x.star` dichotomized at median).

**Examples**

```
dat=sim.pastor(seed=1)
```

# Index

## \* **distribution**

chgpt, 2

AIC.chngptm (chngptm), 5

antoch.test (chngpt.test), 2

chgpt, 2

chgpt.test, 2

chngptm, 5

coef.0.ls, 12

coef.chngptm (chngptm), 5

convert.coef (convert.coef predictx  
threshold.func), 13

convert.coef predictx threshold.func,  
13

dat.mtct, 14

dat.mtct.2, 14

double.hinge, 15

fitted.double.hinge (double.hinge), 15

hinge.test, 16

lidar, 18

lincomb (chngptm), 5

logLik.chngptm (chngptm), 5

nutrition, 18

performance.unit.test, 19

plot.chngpt.test (chngpt.test), 2

plot.chngptm (chngptm), 5

plot.double.hinge (double.hinge), 15

predict.chngptm (chngptm), 5

predictx (convert.coef predictx  
threshold.func), 13

print.chngptm (chngptm), 5

residuals.chngptm (chngptm), 5

residuals.double.hinge (double.hinge),  
15

sim.alphas, 19

sim.chngpt, 20

sim.hinge, 22

sim.my, 23

sim.pastor, 24

sim.threephase (sim.chngpt), 20

sim.twophase.ran.inte (sim.chngpt), 20

summary.chngptm (chngptm), 5

threshold.func (convert.coef predictx  
threshold.func), 13

vcov.chngptm (chngptm), 5