

# Package ‘chngpt’

August 7, 2018

**LazyLoad** yes

**LazyData** yes

**Version** 2018.7-25

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

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

**Depends** R (>= 3.2.0), MASS, boot

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

**Imports** survival, splines, kyotil

**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. 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) chngpt: threshold regression model estimation and inference, BMC Bioinformatics, in press, <DOI:10.1186/s12859-017-1863-x>.

**License** GPL (>= 2)

**NeedsCompilation** yes

**Author** Youyi Fong [cre],  
Zonglin He [aut]

**Repository** CRAN

**Date/Publication** 2018-08-07 15:20:03 UTC

## R topics documented:

chngpt . . . . .	2
chngpt.test . . . . .	2
chngptm . . . . .	5
coef.0.ls . . . . .	9
dat.mtct . . . . .	12
dat.mtct.2 . . . . .	12
hinge.test . . . . .	13

performance.unit.test . . . . .	14
sim.alphas . . . . .	15
sim.chngpt . . . . .	15
sim.hinge . . . . .	17
sim.my . . . . .	18
sim.pastor . . . . .	19

<b>Index</b>	<b>20</b>
--------------	-----------

---

chnppt	<i>chnppt Package</i>
--------	-----------------------

---

### Description

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

---

chnppt.test	<i>Change Point Tests</i>
-------------	---------------------------

---

### Description

Hypothesis testing for change point covariate in logistic regression and linear regression.

### 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.
chngppts	A grid of potential change points to maximize over. If not supplied, they will be set to a vector of length chngpt.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.
chngppts.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.
chngppt.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	
both	
main	
prec.weights	
p.val.method	
boot.B	
keep.fits	

### 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 formula.null=~z, formula.chngpt=~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, 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)

```

chngp<sub>tm</sub>*Estimate change point logistic model***Description**

Estimate change point logistic model

**Usage**

```

chngptm(formula.1, formula.2, family, data,
  type=c("step", "hinge", "segmented", "segmented2", "stegmented"),
  # segmented2 is the model studied in Cheng 2008
  weights=NULL, # this arg is kept here due to historical reasons
  est.method=c("default", "smoothapprox", "grid", "fastgrid"),
  var.type=c("none", "robust", "model", "smooth", "robusttruth", "bootstrap", "all"),
  aux.fit=NULL,
  lb.quantile=.1, ub.quantile=.9, grid.search.max=5000,
  test.inv.ci=TRUE, boot.test.inv.ci=FALSE,
  # test.inv.ci is passed to local functions, boot.test.inv.ci is global in this function
  ci.bootstrap.size=1000, alpha=0.05, save.boot=FALSE, m.out.of.n=FALSE,
  # grid.search.max is the maximum number of grid points used in grid search
  b.transition=Inf, # controls whether threshold model or smooth transition model
  tol=1e-4, maxit=1e2, chngpt.init=NULL, search.bound=10,
  keep.best.fit=TRUE, # best.fit is needed for making prediction and plotting
  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'
plot(x, which = NULL, xlim = NULL, lwd = 2, lcol = "red",
  add = FALSE, add.points = TRUE, add.ci = TRUE, breaks
  = 20, ...)
## S3 method for class 'chngptm'
summary(object, var.type=NULL, expo=FALSE, verbose=FALSE, ...)

lincomb(object, comb, alpha=0.05)

```

**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
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	types of threshold effects. segmented2 differs from segmented in parameterization.
b.transition	Numeric. Controls whether threshold model or smooth transition model. Default to Inf, which corresponds to threshold model
est.method	string. Better leave it at NULL. grid: grid search; smoothapprox: smooth approximation
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	integer.
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.
chngpt.init	numeric. Initial value for the change point.
weights	passed to glm
verbose	Boolean.
add.points	Boolean.
add.ci	Boolean.
add	Boolean.
breaks	integer.
keep.best.fit	Boolean.
y	outcome
x	chngptm fit object.
object	chngptm fit object.
...	arguments passed to glm or coxph

<code>m.out.of.n</code>	whether to perform m out of n 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>xlim</code>	xlim
<code>lwd</code>	lwd
<code>lcol</code>	line col
<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 expo is TRUE, coefficients summary will be shown on the scale of odds ratio instead of slopes

### 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.

### 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>	<code>hstest</code> . Max score test results
<code>iter</code>	integer. Number of iterations

### References

- Fong, Y. (2018) Fast bootstrap confidence intervals for continuous threshold linear regression. *Journal of Computational and Graphical Statistics*, in press.
- 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**

```

# threshold linear regression
dat.1=sim.chngpt("thresholded", "segmented", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4,
  family="gaussian")
# default search method is fastgrid
fit.1=chngptm(formula.1=y~z, formula.2=~x, family="gaussian", dat.1, type="segmented",
  est.method="fastgrid", var.type="bootstrap", ci.bootstrap.size=10)
summary(fit.1)
head(resid(fit.1))
plot(fit.1)
# with weights
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)

# threshold logistic regression
dat.2=sim.chngpt("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")

# threshold Cox regression, no variance estimates available
library(survival)
dat.3 <- data.frame(time=c(4,3,1,1,2,2,3), status=c(1,1,1,0,1,1,0), x=c(0,2,1,1,1,0,0),
  sex=c(0,0,0,0,1,1,1))
fit.3=chngptm(formula.1=Surv(time, status)~1, formula.2=~x, data=dat.3, family="coxph", type="step")
summary(fit.3)

# Poisson
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- as.integer(gl(3,1,9))
treatment <- gl(3,3)
print(d.AD <- data.frame(treatment, outcome, counts))
fit.4=chngptm(formula.1=counts ~ treatment, formula.2=~outcome, data=d.AD, family="poisson",
  type="segmented", var.type="bootstrap", verbose=1, ci.bootstrap.size=10)

```



```
summary(fit.4)

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

# an interaction model. est.method will be set to grid inside the function. fastgrid not
# available for models with interaction terms yet
fit=chngptm(formula.1=mpg~cyl + disp + hp, formula.2=~hp*drat, mtcars, type="segmented",
  family="gaussian", var.type="bootstrap", ci.bootstrap.size=100)
summary(fit)

## End(Not run)
```

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 3 \$ segmented :List of 32 ..\$ quadratic2b\_norm : Named num [1:5] 0 1 0 0 0 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ cubic2b\_lin : Named num [1:5] 0 1 7 0 0 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2\_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.9163 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b\_norm : Named num [1:5] -0.0943 0.3365 0.4005 0 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b1\_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.2231 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b2\_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.5108 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b3\_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.0513 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b4\_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.1054 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b5\_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.1625 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b6\_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0198 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b7\_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0392 4.5 .. ..- attr(\*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..\$ sigmoid2b8\_norm : Named num [1:5] -0.0943

```

0.3365 0.4005 0.0583 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
..$ sigmoid2b9_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.9163 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b10_norm : Named num [1:5] -0.0943
0.3365 0.4005 0 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$
sigmoid2b16_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0198 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b17_norm : Named num [1:5] -0.0943
0.3365 0.4005 0.0392 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$
sigmoid2b18_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0583 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b_norm : Named num [1:5] 0 0.336 0.4
0 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b1_norm :
Named num [1:5] 0 0.336 0.4 0.005 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-
chngpt)+" ... ..$ smooth2b2_norm : Named num [1:5] 0 0.336 0.4 0.01 4.8 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b3_norm : Named num [1:5] 0 0.336 0.4
0.02 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b4_norm
: Named num [1:5] 0 0.336 0.4 0.05 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-
chngpt)+" ... ..$ smooth2b5_norm : Named num [1:5] 0 0.336 0.4 0.1 4.8 .. ..- attr(*, "names")= chr
[1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2_gam : Named num [1:5] -1.3 0.336 0.4 -
0.916 2.2 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2_gam1
: Named num [1:5] -1 0.336 0.4 -0.916 1.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-
chngpt)+" ... ..$ sigmoid2_gam2 : Named num [1:5] -0.6 0.336 0.4 -0.916 1 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2a_gam : Named num [1:5] -0.5 0.336 0
-0.916 2.2 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ quadratic_gam
: Named num [1:5] -1.6355 0.3363 -0.0398 1.4869 2.8154 .. ..- attr(*, "names")= chr [1:5] "(Inter-
cept)" "z" "x" "(x-chngpt)+" ... ..$ exp_gam : Named num [1:5] -2.753 0.336 0.513 0.936 3.607 ..
..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ quadratic_norm_gaussian:
Named num [1:5] -3.735 0.336 0.898 1.845 4.7 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z"
"x" "(x-chngpt)+" ... ..$ quadratic_norm : Named num [1:5] -2.83 0.338 0.553 1.341 3.754 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ exp_norm : Named num [1:5]
-6.235 0.337 1.012 1.325 5.057 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+"
... $ hinge :List of 29 ..$ quadratic2b_norm : Named num [1:5] 0 1 0 0 0 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ cubic2b_lin : Named num [1:5] 0 1 7 0 0 ..
..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2_norm : Named
num [1:5] -0.0943 0.3365 0.4005 -0.9163 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z"
"x" "(x-chngpt)+" ... ..$ sigmoid2b_norm : Named num [1:5] -0.0943 0.3365 0.4005 0 4.5 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b1_norm : Named
num [1:5] -0.0943 0.3365 0.4005 -0.2231 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x"
"(x-chngpt)+" ... ..$ sigmoid2b2_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.5108 4.5 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b3_norm : Named
num [1:5] -0.0943 0.3365 0.4005 -0.0513 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x"
"(x-chngpt)+" ... ..$ sigmoid2b4_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.1054 4.5 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b5_norm : Named
num [1:5] -0.0943 0.3365 0.4005 -0.1625 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x"
"(x-chngpt)+" ... ..$ sigmoid2b6_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0198 4.5 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b7_norm : Named
num [1:5] -0.0943 0.3365 0.4005 0.0392 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x"
"(x-chngpt)+" ... ..$ sigmoid2b8_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0583 4.5 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b9_norm : Named
num [1:5] -0.0943 0.3365 0.4005 0.9163 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x"

```

```

"(x-chngpt)+" ... ..$ sigmoid2b10_norm : Named num [1:5] -0.0943 0.3365 0.4005 0 4.5 .. ..-
attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b16_norm : Named
num [1:5] -0.0943 0.3365 0.4005 0.0198 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x"
"(x-chngpt)+" ... ..$ sigmoid2b17_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0392 4.5
.. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b18_norm :
Named num [1:5] -0.0943 0.3365 0.4005 0.0583 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)"
"z" "x" "(x-chngpt)+" ... ..$ smooth2b_norm : Named num [1:5] 0 0.336 0.4 0 4.8 .. ..- attr(*,
"names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b1_norm : Named num [1:5]
0 0.336 0.4 0.005 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$
smooth2b2_norm : Named num [1:5] 0 0.336 0.4 0.01 4.8 .. ..- attr(*, "names")= chr [1:5] "(In-
tercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b3_norm : Named num [1:5] 0 0.336 0.4 0.02 4.8 ..
..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b4_norm : Named
num [1:5] 0 0.336 0.4 0.05 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+"
... ..$ smooth2b5_norm : Named num [1:5] 0 0.336 0.4 0.1 4.8 .. ..- attr(*, "names")= chr [1:5]
"(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2_gam : Named num [1:4] -0.5 0.336 -0.916 2.2 ..
..- attr(*, "names")= chr [1:4] "(Intercept)" "z" "(x-chngpt)+" "chngpt" ..$ sigmoid2_gam1 : Named
num [1:4] -0.2 0.336 -0.916 1.5 .. ..- attr(*, "names")= chr [1:4] "(Intercept)" "z" "(x-chngpt)+"
"chngpt" ..$ sigmoid2_gam2 : Named num [1:4] 0.2 0.336 -0.916 1 .. ..- attr(*, "names")= chr [1:4]
"(Intercept)" "z" "(x-chngpt)+" "chngpt" ..$ quadratic_gam : Named num [1:5] -1.695 0.336 1.464
2.871 NA .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "(x-chngpt)+" "chngpt" ... ..$ exp_gam
: Named num [1:5] -2.046 0.334 1.044 2.152 NA .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z"
"(x-chngpt)+" "chngpt" ... ..$ flatHyperbolic_norm: Named num [1:5] -4.173 0.334 3.239 4.437
NA .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "(x-chngpt)+" "chngpt" ... $ segmented2:List
of 23 ..$ quadratic2b_norm: Named num [1:5] 0 1 0 0 0 .. ..- attr(*, "names")= chr [1:5] "(Inter-
cept)" "z" "x" "(x-chngpt)+" ... ..$ cubic2b_lin : Named num [1:5] 0 1 7 0 0 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2_norm : Named num [1:5] -0.0943
0.3365 0.4005 -0.9163 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+"
... ..$ sigmoid2b_norm : Named num [1:5] -0.0943 0.3365 0.4005 0 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b1_norm : Named num [1:5] -0.0943
0.3365 0.4005 -0.2231 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
..$ sigmoid2b2_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.5108 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b3_norm : Named num [1:5] -0.0943
0.3365 0.4005 -0.0513 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
..$ sigmoid2b4_norm : Named num [1:5] -0.0943 0.3365 0.4005 -0.1054 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b5_norm : Named num [1:5] -0.0943
0.3365 0.4005 -0.1625 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
..$ sigmoid2b6_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0198 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b7_norm : Named num [1:5] -0.0943
0.3365 0.4005 0.0392 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
..$ sigmoid2b8_norm : Named num [1:5] -0.0943 0.3365 0.4005 0.0583 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b9_norm : Named num [1:5] -0.0943
0.3365 0.4005 0.9163 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
..$ sigmoid2b10_norm: Named num [1:5] -0.0943 0.3365 0.4005 0 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b16_norm: Named num [1:5] -0.0943
0.3365 0.4005 0.0198 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$
sigmoid2b17_norm: Named num [1:5] -0.0943 0.3365 0.4005 0.0392 4.5 .. ..- attr(*, "names")=
chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ sigmoid2b18_norm: Named num [1:5] -0.0943
0.3365 0.4005 0.0583 4.5 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$

```

```
smooth2b_norm : Named num [1:5] 0 0.336 0.4 0 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)"
"z" "x" "(x-chngpt)+" ... ..$ smooth2b1_norm : Named num [1:5] 0 0.336 0.4 0.005 4.8 .. ..- attr(*,
"names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b2_norm : Named num [1:5]
0 0.336 0.4 0.01 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$
smooth2b3_norm : Named num [1:5] 0 0.336 0.4 0.02 4.8 .. ..- attr(*, "names")= chr [1:5] "(In-
tercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b4_norm : Named num [1:5] 0 0.336 0.4 0.05 4.8 ..
..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ... ..$ smooth2b5_norm : Named
num [1:5] 0 0.336 0.4 0.1 4.8 .. ..- attr(*, "names")= chr [1:5] "(Intercept)" "z" "x" "(x-chngpt)+" ...
```

---

dat.mtct

*An Example Dataset*


---

### 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

*An Example Dataset*


---

### 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.

---

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

---

**Description**

Test a hinge model against a linear model.

**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

cov.interest

family

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

chngpts.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

**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, Fouda, 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
```

---

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.2  
 family  
 data  
 B  
 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"), threshold.type = c("NA", "step", "hinge",
  "segmented", "segmented2", "stegmented"), b.transition
  = Inf, family = c("binomial", "gaussian"), x.distr =
  c("norm", "norm3", "norm6", "imb", "lin", "mix",
  "gam", "zbinary", "gam1", "gam2", "fixnorm"), 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, n, seed,
  weighted = FALSE, heteroscedastic = FALSE, verbose =
  FALSE)
```

**Arguments**

threshold.type	string. Types of threshold effect to simulate, only applicable when label does not start with sigmoid.
family	string. Glm family.
n	
mu.z	
seed	
weighted	
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.	
verbose	Boolean
b.transition	
sd	
alpha.candidate	Candidate values of alpha, used in code to determine alpha values
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  
family  
thres  
X.ditr  
mu.X  
coef.X  
cov.X  
eps.sd  
seed  
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  $\text{logit}(\Pr(Y==1))=\alpha + \beta*(\text{transformed } x.\text{star})$ .

**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	<i>Simulate data according to one of the scenarios considered in Pastor-Barriuso et al 2003</i>
------------	---

---

**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

- \*Topic **\textasciitildekwd1**
  - performance.unit.test, 14
- \*Topic **\textasciitildekwd2**
  - performance.unit.test, 14
- \*Topic **distribution**
  - chngpt, 2
  
- antoch.test (chngpt.test), 2
  
- chngpt, 2
- chngpt.test, 2
- chngptm, 5
- coef.0.ls, 9
- coef.chngptm (chngptm), 5
  
- dat.mtct, 12
- dat.mtct.2, 12
  
- hinge.test, 13
  
- lincomb (chngptm), 5
  
- performance.unit.test, 14
- plot.chngpt.test (chngpt.test), 2
- plot.chngptm (chngptm), 5
- print.chngptm (chngptm), 5
  
- residuals.chngptm (chngptm), 5
  
- sim.alphas, 15
- sim.chngpt, 15
- sim.hinge, 17
- sim.my, 18
- sim.pastor, 19
- summary.chngptm (chngptm), 5
  
- vcov.chngptm (chngptm), 5