

Package ‘chngpt’

March 29, 2018

LazyLoad yes

LazyData yes

Version 2018.3-29

Title Estimation and Hypothesis Testing for Threshold Regression

Author Youyi Fong

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

Repository CRAN

Date/Publication 2018-03-29 20:05:42 UTC

R topics documented:

chngpt	2
chngpt.test	2
chngptm	5
coef.0.ls	8
dat.mtct	11
dat.mtct.2	12
performance.unit.test	12
sim.alphas	13

sim.chngpt	13
sim.my	15
sim.pastor	16

Index	17
--------------	-----------

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"),
  main.method=c("lr", "score"),
  robust = FALSE,
  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
  single.weight=1,
  mc.n=5e4,
  prob.weights=NULL,
  compute.p.value=TRUE,
  verbose=FALSE,
  use.fastgrid=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. The outcome needs to be a 0/1 variable.
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
main.method	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.
use.fastgrid	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.
single.weight	numeric. Only used when interaction.method="weighted.single.arg".
prob.weights	numeric. Not yet fully supported.
compute.p.value	Boolean. Computing p values takes a lot of time. Sometimes we just want the maximal statistic and change point associated with it.
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	
both	
main	

Details

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

The test results, e.g. p-value, should not change if the same function is called twice, because internally seed to random number generator is set to 1 before MC and set back to the R state afterwards

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

References

Fong, Y., Huang, Y., Gilbert, P. (2017) chngpt: threshold regression model estimation and hypothesis testing, BMC Bioinformatics, in press.

Fong Y, Di C, and Permar S. (2014) Change-Point Testing in Logistic Regression Models with Interaction Term. Statistics in Medicine.

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)

test=chnppt.test(formula.null=y~z, formula.chngpt=~x, dat, type="step", family="binomial")
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)
```

```
#antoch.test(y~1, dat, "x.star")

## Not run:

test=chngptm.test(formula.null=mpg~cyl + disp + hp, formula.chngptm=~hp*drat, family="gaussian",
  data=mtcars, type="segmented")

## End(Not run)
```

chngp_{tm}
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"),
  est.method=c("default", "smoothapprox", "grid", "fastgrid"), useC=TRUE,
  var.type=c("none", "robust", "model", "smooth", "robusttruth", "bootstrap", "all"),
  aux.fit=NULL, test.inv.ci=TRUE, boot.test.inv.ci=FALSE,
  lb.quantile=.1, ub.quantile=.9, grid.search.max=5000,
  ci.bootstrap.size=1000, alpha=0.05, save.boot=FALSE, m.out.of.n=FALSE,
  b.transition=Inf,
  tol=1e-4, maxit=1e2, chngpt.init=NULL, search.bound=10,
  weights=NULL, verbose=FALSE, ...)
```

```
## S3 method for class 'chngptm'
coef(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="darkgray", add=FALSE,
  add.points=TRUE, add.ci=TRUE, breaks=20, ...)
```

```
## S3 method for class 'chngptm'
summary(object, var.type=NULL, 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.
chngp _t .init	numeric. Initial value for the change point.
weights	passed to glm
verbose	Boolean.
useC	Boolean.
add.points	Boolean.
add.ci	Boolean.
add	Boolean.
breaks	integer.
x	chngp _{tm} fit object.

object	chngrtm fit object.
...	arguments passed to glm or coxph
m.out.of.n	whether to perform m out of n bootstrap
boot.test.inv.ci	whether to get test inversion CI under bootstrap
search.bound	bounds for search for sloping parameters
which	an integer
xlim	xlim
lwd	lwd
lcol	line col
comb	a vector of combination coefficients that will be used to form an inner product with the estimated slope

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.

Value

A an object of type chngrtm with the following components

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

References

Fong, Y., Huang, Y., Gilbert, P. (2017) chngrt: threshold regression model estimation and hypothesis testing, BMC Bioinformatics, 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

```
dat=sim.chngrt("thresholded", "step", n=200, seed=1, beta=1, alpha=-1, x.distr="norm", e.=4)

fit.1=chngrt(formula.1=y~z, formula.2=~x, family="binomial", dat, type="step", est.method="grid")
print(fit.1)
summary(fit.1)
```

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

# a survival example
library(survival)
test1 <- 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=chngptm(formula.1=Surv(time, status)~1, formula.2=~x, data=test1, family="coxph", type="step")

# an interaction example, not working yet
fit=chngptm(formula.1=mpg~cyl + disp + hp, formula.2=~hp*drat, mtcars, type="segmented",
            family="gaussian", est.method="grid", var.type="bootstrap", ci.bootstrap.size=10)
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] "(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 [1:4] -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] "(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] "(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.

`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"),
  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","fixnorm3","fixnorm6"),
  e.=NULL, mu.x=4.7, sd.x=NULL, sd=0.3,
  alpha=NULL, alpha.candidate=NULL, coef.z=log(1.4), beta=NULL, beta.itxn=NULL,
  n, seed,
  weighted=FALSE, # sampling weights
  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	
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

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.

 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, 12

*Topic **\textasciitildekwd2**
performance.unit.test, 12

*Topic **distribution**
chgpt, 2

antoch.test (chgpt.test), 2

chgpt, 2
chgpt.test, 2
chgptm, 5
coef.0.ls, 8
coef.chgptm (chgptm), 5

dat.mtct, 11
dat.mtct.2, 12

lincomb (chgptm), 5

performance.unit.test, 12
plot.chgpt.test (chgpt.test), 2
plot.chgptm (chgptm), 5
print.chgptm (chgptm), 5

sim.alphas, 13
sim.chgpt, 13
sim.my, 15
sim.pastor, 16
summary.chgptm (chgptm), 5

vcov.chgptm (chgptm), 5