Package ‘rddapp’

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rddapp-package .......................................................... 3
attr_check ................................................................. 4
bw_ik09 ................................................................. 4
bw_ik12 ................................................................. 5
CARE ................................................................. 6
dc_test ................................................................. 7
mfrd_est ................................................................. 9
mrd_est ................................................................. 12
mrd_impute ........................................................... 16
mrd_power ............................................................ 20
mrd_sens_bw .......................................................... 23
mrd_sens_cutoff ....................................................... 24
plot.mfrd ............................................................. 25
plot.rd ............................................................... 26
predict.rd ............................................................ 27
print.mfrd ............................................................. 28
print.rd ............................................................... 29
rd_est ................................................................. 29
rd_impute ............................................................ 32
rd_power ............................................................. 35
rd_sens_bw .......................................................... 37
rd_sens_cutoff ......................................................... 38
rd_type ............................................................. 39
sens_plot ............................................................ 40
shiny_run ............................................................ 41
summary.mfrd ........................................................ 42
summary.mrd ........................................................ 43
summary.mrdi ......................................................... 44
summary.mrdp ........................................................ 45
summary.rd ........................................................ 45
summary.rdp ........................................................ 46
treat_assign .......................................................... 47
var_center ............................................................ 47
wt_kern ............................................................... 48
wt_kern_bivariate ..................................................... 49

Index 51
Description

rddapp: A package for regression discontinuity designs (RDDs).

Details

The rddapp package provides a set of functions for the analysis of the regression-discontinuity design (RDD). The three main parts are: estimation of effects of interest, power analysis, and assumption checks.

Estimation

A variety of designs can be estimated in various ways. The single-assignment RDD (both sharp and fuzzy) can be analyzed using both a parametric (global) or non-parametric (local) approach. The multiple-assignment RDD (both sharp and fuzzy) can be analyzed using both parametric and non-parametric estimation. The analysis choices are further to use estimate effects based on univariate scaling, the centering approach, or the frontier approach. The frontier approach can currently only be estimated using parametric regression with bootstrapped standard errors.

Power analysis

Statistical power can be estimated for both the single- and multiple-assignment RDD, (both sharp and fuzzy), including all parametric and non-parametric estimators mentioned in the estimation section. All power analyses are based on a simulation approach, which means that the user has to provide all necessary parameters for a data-generating model.

Assumption checks

An important part of any RDD are checks of underlying assumptions. The package provides users with the option to estimate McCriry’s sorting test (to identify violations of assignment rules), checks of discontinuities of other baseline covariates, along with sensitivity checks of the chosen bandwidth parameter for non-parametric models, and so-called placebo tests, that examine the treatment effect at other cut-points along the assignment variable.

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attr_check

Attrition Checks

Description

attr_check reports missing data on treatment variable, assignment variable, and outcome. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp:::attr_check().

Usage

attr_check(x1, y, t, x2 = NULL)

Arguments

x1 A numeric object containing the assignment variable.

y A numeric object containing the outcome variable, with the same dimensionality as x1.

t A numeric object containing the treatment variable (coded as 0 for untreated and 1 for treated), with the same dimensionality as x1 and y.

x2 A numeric object containing the secondary assignment variable.

Value

attr_check returns a list containing the amount and percentage of missing data for all variables and subgroups, by treatment.

bw_ik09

Imbens-Kalyanaraman 2009 Optimal Bandwidth Calculation

Description

bw_ik09 calculates the Imbens-Kalyanaraman (2009) optimal bandwidth for local linear regression in regression discontinuity designs. It is based on the IKbandwidth function in the "rdd" package. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp:::bw_ik09().

Usage

bw_ik09(X, Y, cutpoint = NULL, verbose = FALSE, kernel = "triangular")
Arguments

X A numeric vector containing the running variable.
Y A numeric vector containing the outcome variable.
cutpoint A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.
verbose A logical value indicating whether to print more information to the terminal. The default is FALSE.
kernel A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

Value

ik_bw09 returns a numeric value specifying the optimal bandwidth.

References


Description

bwIk12 calculates the Imbens-Kalyanaraman (2012) optimal bandwidth for local linear regression in regression discontinuity designs. It is based on a function in the "rddtools" package. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp:::bwIk12().

Usage

bwIk12(X, Y, cutpoint = NULL, verbose = FALSE, kernel = "triangular")

Arguments

X A numeric vector containing the running variable.
Y A numeric vector containing the outcome variable.
cutpoint A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.
verbose A logical value indicating whether to print more information to the terminal. The default is FALSE.
kernel

A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

Value

ik_bw12 returns a numeric value specifying the optimal bandwidth.

References


Description

A dataset containing a subset of children from the CARE trial on early childhood intervention. The randomized controlled trial was subsetted to mimic a regression-discontinuity design in which treatment was assigned only to mothers whose IQ was smaller than 85.

Usage

CARE

Format

A data frame with 81 rows and 5 variables:

SUBJECT Unique ID variable
DC_TRT Day Care (Preschool) Treatment Group, 1 = Treatment, 0 = Control
APGAR5 APGAR ("Appearance, Pulse, Grimace, Activity, and Respiration") score at 5 minutes after birth
MOMWAIS0 Biological mother’s WAIS (Wechsler Adult Intelligence Scale) full-scale score at subject’s birth
SBIQ48 Subject’s Stanford Binet IQ score at 48 months

Source

http://www.icpsr.umich.edu/icpsrweb/ICPSR/studies/4091
dc_test

Examples

```r
data("CARE")
head(CARE)
```

dc_test  McCrary Sorting Test

Description

dc_test implements the McCrary (2008) sorting test to identify violations of assignment rules. It is based on the DCdensity function in the 'rdd' package.

Usage

```r
dc_test(
  runvar,
  cutpoint,
  bin = NULL,
  bw = NULL,
  verbose = TRUE,
  plot = TRUE,
  ext.out = FALSE,
  htest = FALSE,
  level = 0.95,
  digits = max(3, getOption("digits") - 3),
  timeout = 30
)
```

Arguments

- **runvar**: A numeric vector containing the running variable.
- **cutpoint**: A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.
- **bin**: A numeric value containing the binwidth. The default is `2*sd(runvar)*length(runvar)^(1/2)`.
- **bw**: A numeric value containing bandwidth to use. If no bandwidth is supplied, the default uses bandwidth selection calculation from McCrary (2008).
- **verbose**: A logical value indicating whether to print diagnostic information to the terminal. The default is TRUE.
- **plot**: A logical value indicating whether to plot the histogram and density estimations. The default is TRUE. The user may wrap this function in additional graphical options to modify the plot.
- **ext.out**: A logical value indicating whether to return extended output. The default is FALSE. When FALSE dc_test will return only the p-value of the test, but will print more information. When TRUE, dc_test will return and print the additional information documented below.
dc_test

htest A logical value indicating whether to return an "htest" object compatible with base R's hypothesis test output. The default is FALSE.

level A numerical value between 0 and 1 specifying the confidence level for confidence intervals. The default is 0.95.

digits A non-negative integer specifying the number of digits to display in all output. The default is max(3,getOption("digits") - 3).

timeout A non-negative numerical value specifying the maximum number of seconds that expressions in the function are allowed to run. The default is 30. Specify Inf to run all expressions to completion.

Value

If ext.out is FALSE, dc_test returns a numeric value specifying the p-value of the McCrary (2008) sorting test. Additional output is enabled when ext.out is TRUE. In this case, dc_test returns a list with the following elements:

theta The estimated log difference in heights of the density curve at the cutpoint.
se The standard error of theta.
z The z statistic of the test.
p The p-value of the test. A p-value below the significance threshold indicates that the user can reject the null hypothesis of no sorting.

binsize The calculated size of bins for the test.
bw The calculated bandwidth for the test.
cutpoint The cutpoint used.
data A dataframe for the binning of the histogram. Columns are cellmp (the midpoints of each cell) and cellval (the normalized height of each cell).

References


Examples

set.seed(12345)
# No discontinuity
x <- runif(1000, -1, 1)
dc_test(x, 0)

# Discontinuity
x <- runif(1000, -1, 1)
x <- x + 2 * (runif(1000, -1, 1) > 0 & x < 0)
dc_test(x, 0)
Description

*mfrd_est* implements the frontier approach for multivariate regression discontinuity estimation in Wong, Steiner and Cook (2013). It is based on the MFRDD code in Stata from Wong, Steiner, and Cook (2013).

Usage

```r
mfrd_est(
  y,
  x1,
  x2,
  c1,
  c2,
  t.design = NULL,
  local = 0.15,
  front.bw = NA,
  m = 10,
  k = 5,
  kernel = "triangular",
  ngrid = 250,
  margin = 0.03,
  boot = NULL,
  cluster = NULL,
  stop.on.error = TRUE
)
```

Arguments

- **y** A numeric object containing outcome variable.
- **x1** A numeric object containing the first assignment variable.
- **x2** A numeric object containing the second assignment variable.
- **c1** A numeric value containing the cutpoint at which assignment to the treatment is determined for `x1`.
- **c2** A numeric value containing the cutpoint at which assignment to the treatment is determined for `x2`.
- **t.design** A character vector of length 2 specifying the treatment option according to design. The first entry is for `x1` and the second entry is for `x2`. Options are "g" (treatment is assigned if `x1` is greater than its cutoff), "geq" (treatment is assigned if `x1` is greater than or equal to its cutoff), "l" (treatment is assigned if `x1` is less than its cutoff), and "leq" (treatment is assigned if `x1` is less than or equal to its cutoff). The same options are available for `x2`. 

local  A non-negative numeric value specifying the range of neighboring points around the cutoff on the standardized scale, for each assignment variable. The default is 0.15.

front.bw  A non-negative numeric vector of length 3 specifying the bandwidths at which to estimate the RD for each of three effects models (complete model, heterogeneous treatment model, and treatment only model) detailed in Wong, Steiner, and Cook (2013). If NA, front.bw will be determined by cross-validation. The default is NA.

m  A non-negative integer specifying the number of uniformly-at-random samples to draw as search candidates for front.bw, if front.bw is NA. The default is 10.

k  A non-negative integer specifying the number of folds for cross-validation to determine front.bw, if front.bw is NA. The default is 5.

kernel  A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

ngrid  A non-negative integer specifying the number of non-zero grid points on each assignment variable, which is also the number of zero grid points on each assignment variable. The default is 250. The value used in Wong, Steiner and Cook (2013) is 2500, which may cause long computational time.

margin  A non-negative numeric value specifying the range of grid points beyond the minimum and maximum of sample points on each assignment variable. This grid is used to impute potential outcomes along the frontier, as in Wong, Steiner, and Cook (2013). The default is 0.03.

boot  An optional non-negative integer specifying the number of bootstrap samples to obtain standard error of estimates.

cluster  An optional vector of length n specifying clusters within which the errors are assumed to be correlated. This will result in reporting cluster robust SEs. It is suggested that data with a discrete running variable be clustered by each unique value of the running variable (Lee and Card, 2008).

stop.on.error  A logical value indicating whether to remove bootstraps which cause error in the integrate function. If TRUE, bootstraps which cause error are removed and resampled until the specified number of bootstrap samples are acquired. If FALSE, bootstraps which cause error are not removed. The default is TRUE.

Value

mfrd_est returns an object of class "mfrd". The functions summary and plot are used to obtain and print a summary and plot of the estimated regression discontinuity. The object of class mfrd is a list containing the following components:

w  Numeric vector specifying the weight of frontier 1 and frontier 2, respectively.

est  Numeric matrix of the estimate of the discontinuity in the outcome under a complete model (no prefix), heterogeneous treatment (ht) effects model, and treatment (t) only model, for the parametric case and for each corresponding bandwidth. Estimates with suffix "ev1" and "ev2" correspond to expected values for each frontier, under a given model. Estimates with suffix "ate" correspond to average treatment effects across both frontiers, under a given model.
mfrd_est

**d**
Numeric matrix of the effect size (Cohen’s d) for estimate.

**se**
Numeric matrix of the standard error for each corresponding bandwidth, if applicable.

**m_s**
A list containing estimates for the complete model, under parametric and non-parametric (optimal, half, and double bandwidth) cases. A list of coefficient estimates, residuals, effects, weights (in the non-parametric case), lm output (rank of the fitted linear model, fitted values, assignments for the design matrix, qr for linear fit, residual degrees of freedom, levels of the x value, function call, and terms), and output data frame are returned for each model.

**m_h**
A list containing estimates for the heterogeneous treatments model, under parametric and non-parametric (optimal, half, and double bandwidth) cases. A list of coefficient estimates, residuals, effects, weights (in the non-parametric case), lm output (rank of the fitted linear model, fitted values, assignments for the design matrix, qr for linear fit, residual degrees of freedom, levels of the x value, function call, and terms), and output data frame are returned for each model.

**m_t**
A list containing estimates for the treatment only model, under parametric and non-parametric (optimal, half, and double bandwidth) cases. A list of coefficient estimates, residuals, effects, weights (in the non-parametric case), lm output (rank of the fitted linear model, fitted values, assignments for the design matrix, qr for linear fit, residual degrees of freedom, levels of the x value, function call, and terms), and output data frame are returned for each model.

**dat_h**
A list containing four data frames, one for each case: parametric or non-parametric (optimal, half, and double bandwidth). Each data frame contains functions and densities for each frontier and treatment model.

**dat**
A data frame containing the outcome (y) and each input (x1, x2) for each observation. The data frame also contains indicators of being within the local boundary of the cutpoint for x1 and x2 (x1res, x2res), scaled (zx1, zx2) and centered x1 and x2 values (zcx1, zcx2), and treatment indicators for overall treatment (tr) based on treatment assignment from x1 (tr1), x2 (tr2), and both assignment variables (trb).

**obs**
List of the number of observations used in each model.

**impute**
A logical value indicating whether multiple imputation is used or not.

**call**
The matched call.

**front.bw**
Numeric vector of each bandwidth used to estimate the density at the frontier for the three effects models (complete model, heterogeneous treatment model, and treatment only model) detailed in Wong, Steiner, and Cook (2013).

**References**


Examples

```r
set.seed(12345)
x1 <- runif(1000, -1, 1)
x2 <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * (x1 >= 0) + 3 * cov + 10 * (x2 >= 0) + rnorm(1000)
mfrd_est(y = y, x1 = x1, x2 = x2, c1 = 0, c2 = 0, t.design = c("geq", "geq"))
```

Description

`mrd_est` estimates treatment effects in a multivariate regression discontinuity design (MRDD) with two assignment variables, including the frontier average treatment effect (`tau_MRD`) and frontier-specific effects (`tau_R` and `tau_M`) simultaneously.

Usage

```r
mrd_est(
  formula,
  data,
  subset = NULL,
  cutpoint = NULL,
  bw = NULL,
  front.bw = NA,
  m = 10,
  k = 5,
  kernel = "triangular",
  se.type = "HC1",
  cluster = NULL,
  verbose = FALSE,
  less = FALSE,
  est.cov = FALSE,
  est.itt = FALSE,
  local = 0.15,
  ngrid = 250,
  margin = 0.03,
  boot = NULL,
  method = c("center", "univ", "front"),
  t.design = NULL,
  stop.on.error = TRUE
)
```
Arguments

**formula**
The formula of the MRDD; a symbolic description of the model to be fitted. This is supplied in the format of \( y \sim x_1 + x_2 \) for a simple sharp MRDD or \( y \sim x_1 + x_2 | c_1 + c_2 \) for a sharp MRDD with two covariates. A fuzzy MRDD may be specified as \( y \sim x_1 + x_2 + z \) where \( x_1 \) is the first running variable, \( x_2 \) is the second running variable, and \( z \) is the endogenous treatment variable. Covariates are then included in the same manner as in a sharp MRDD.

**data**
An optional data frame containing the variables in the model. If not found in data, the variables are taken from `environment(formula)`.

**subset**
An optional vector specifying a subset of observations to be used in the fitting process.

**cutpoint**
A numeric vector of length 2 containing the cutpoints at which assignment to the treatment is determined. The default is \( c(0, 0) \).

**bw**
A vector specifying the bandwidths at which to estimate the RD for non-parametric models. Possible values are "IK09", "IK12", or a user-specified non-negative numeric vector containing the bandwidths at which to estimate the RD. The default is "IK12". If `bw` is "IK12", the bandwidth is calculated using the Imbens-Kalyanaraman 2012 method. If `bw` is "IK09", the bandwidth is calculated using the Imbens-Kalyanaraman 2009 method. Then, the RD is estimated with that bandwidth, half that bandwidth, and twice that bandwidth. If only a single value is passed into the function, the RD will similarly be estimated at that bandwidth, half that bandwidth, and twice that bandwidth.

**front.bw**
A non-negative numeric vector of length 3 specifying the bandwidths at which to estimate the RD for each of three effects models (complete model, heterogeneous treatment model, and treatment only model) detailed in Wong, Steiner, and Cook (2013). If NA, `front.bw` will be determined by cross-validation. The default is NA.

**m**
A non-negative integer specifying the number of uniformly-at-random samples to draw as search candidates for `front.bw`, if `front.bw` is NA. The default is 10.

**k**
A non-negative integer specifying the number of folds for cross-validation to determine `front.bw`, if `front.bw` is NA. The default is 5.

**kernel**
A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

**se.type**
This specifies the robust standard error calculation method to use, from the "sandwich" package. Options are, as in `vcovHC`, "HC3", "const", "HC", "HC0", "HC1", "HC2", "HC4", "HC4m", "HC5". The default is "HC1". This option is overridden by `cluster`.

**cluster**
An optional vector of length n specifying clusters within which the errors are assumed to be correlated. This will result in reporting cluster robust SEs. This option overrides anything specified in `se.type`. It is suggested that data with a discrete running variable be clustered by each unique value of the running variable (Lee and Card, 2008).

**verbose**
A logical value indicating whether to print additional information to the terminal, including results of instrumental variable regression, and outputs from background regression models. The default is FALSE.
logical. If TRUE, return the estimates of parametric linear and optimal bandwidth non-parametric models only. If FALSE return the estimates of linear, quadratic, and cubic parametric models and optimal, half and double bandwidths in non-parametric models. The default is FALSE.

est_cov
Logical. If TRUE, the estimates of covariates will be included. If FALSE, the estimates of covariates will not be included. The default is FALSE. This option is not applicable if method is "front".

est.itr
Logical. If TRUE, the estimates of intent-to-treat (ITT) will be returned. If FALSE, the estimates of ITT will not be returned. The default is FALSE. This option is not applicable if method is "front".

local
A non-negative numeric value specifying the range of neighboring points around the cutoff on the standardized scale, for each assignment variable. The default is 0.15.

ngrid
A non-negative integer specifying the number of non-zero grid points on each assignment variable, which is also the number of zero grid points on each assignment variable. The default is 250. The value used in Wong, Steiner and Cook (2013) is 2500, which may cause long computational time.

margin
A non-negative numeric value specifying the range of grid points beyond the minimum and maximum of sample points on each assignment variable. The default is 0.03.

boot
An optional non-negative integer specifying the number of bootstrap samples to obtain standard error of estimates. This argument is not optional if method is "front".

method
A string specifying the method to estimate the RD effect. Options are "center", "univ", "front", based on the centering, univariate, and frontier approaches (respectively) from Wong, Steiner, and Cook (2013).

t.design
A character vector of length 2 specifying the treatment option according to design. The first entry is for x1 and the second entry is for x2. Options are "g" (treatment is assigned if x1 is greater than its cutoff), "geq" (treatment is assigned if x1 is greater than or equal to its cutoff), "l" (treatment is assigned if x1 is less than its cutoff), and "leq" (treatment is assigned if x1 is less than or equal to its cutoff). The same options are available for x2.

stop.on.error
A logical value indicating whether to remove bootstraps which cause error in the integrate function. If TRUE, bootstraps which cause error are removed and resampled until the specified number of bootstrap samples are acquired. If FALSE, bootstraps which cause error are not removed. The default is TRUE.

Value

mrd_est returns an object of class "mrd". The function summary is used to obtain and print a summary of the estimated regression discontinuity. The object of class mrd is a list containing the following components for each estimated treatment effect, tau_MRD or tau_R and tau_M:

type
A string denoting either "sharp" or "fuzzy" RDD.

call
The matched call.
est
Numeric vector of the estimate of the discontinuity in the outcome under a sharp MRDD or the Wald estimator in the fuzzy MRDD, for each corresponding bandwidth, if applicable.

se
Numeric vector of the standard error for each corresponding bandwidth, if applicable.

ci
The matrix of the 95 for each corresponding bandwidth, if applicable.

bw
Numeric vector of each bandwidth used in estimation.

z
Numeric vector of the z statistic for each corresponding bandwidth, if applicable.

p
Numeric vector of the p-value for each corresponding bandwidth, if applicable.

obs
Vector of the number of observations within the corresponding bandwidth, if applicable.

cov
The names of covariates.

model
For a sharp design, a list of the \texttt{lm} objects is returned. For a fuzzy design, a list of lists is returned, each with two elements: \texttt{firststage}, the first stage \texttt{lm} object, and \texttt{iv}, the \texttt{ivreg} object. A model is returned for each parametric and non-parametric case and corresponding bandwidth.

frame
Returns the model frame used in fitting.

na.action
The observations removed from fitting due to missingness.

impute
A logical value indicating whether multiple imputation is used or not.

d
Numeric vector of the effect size (Cohen’s d) for each estimate.

References


Examples

set.seed(12345)
x1 <- runif(1000, -1, 1)
x2 <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * (x1 >= 0) + 3 * cov + 10 * (x2 >= 0) + rnorm(1000)
# centering
mrd_est(y ~ x1 + x2 | cov, method = "center", t.design = c("geq", "geq"))
# univariate
mrd_est(y ~ x1 + x2 | cov, method = "univ", t.design = c("geq", "geq"))
# frontier
mrd_est(y ~ x1 + x2 | cov, method = "front", t.design = c("geq", "geq"))

mrd_impute

Multiple Imputation of Multivariate Regression Discontinuity Estimation

Description

mrd_impute estimates treatment effects in a multivariate regression discontinuity design (MRDD) with imputed missing values.

Usage

mrd_impute(
  formula,
  data,
  subset = NULL,
  cutpoint = NULL,
  bw = NULL,
  front.bw = NA,
  m = 10,
  k = 5,
  kernel = "triangular",
  se.type = "HC1",
  cluster = NULL,
  impute = NULL,
  verbose = FALSE,
  less = FALSE,
  est.cov = FALSE,
  est.itt = FALSE,
  local = 0.15,
  ngrid = 250,
  margin = 0.03,
  boot = NULL,
  method = c("center", "univ", "front"),
  t.design = NULL,
  stop.on.error = TRUE
)
Arguments

**formula**
The formula of the MRDD; a symbolic description of the model to be fitted. This is supplied in the format of $y \sim x_1 + x_2$ for a simple sharp MRDD or $y \sim x_1 + x_2 | c_1 + c_2$ for a sharp MRDD with two covariates. A fuzzy MRDD may be specified as $y \sim x_1 + x_2 + z$ where $x_1$ is the first running variable, $x_2$ is the second running variable, and $z$ is the endogenous treatment variable. Covariates are then included in the same manner as in a sharp MRDD.

**data**
An optional data frame containing the variables in the model. If not found in data, the variables are taken from `environment(formula)`.

**subset**
An optional vector specifying a subset of observations to be used in the fitting process.

**cutpoint**
A numeric vector of length 2 containing the cutpoints at which assignment to the treatment is determined. The default is $c(0, 0)$.

**bw**
A vector specifying the bandwidths at which to estimate the RD. Possible values are "IK09", "IK12", and a user-specified non-negative numeric vector specifying the bandwidths at which to estimate the RD. The default is "IK12". If `bw` is "IK12", the bandwidth is calculated using the Imbens-Kalyanaraman 2012 method. If `bw` is "IK09", the bandwidth is calculated using the Imbens-Kalyanaraman 2009 method. Then the RD is estimated with that bandwidth, half that bandwidth, and twice that bandwidth. If only a single value is passed into the function, the RD will similarly be estimated at that bandwidth, half that bandwidth, and twice that bandwidth.

**front.bw**
A non-negative numeric vector of length 3 specifying the bandwidths at which to estimate the RD for each of three effects models (complete model, heterogeneous treatment model, and treatment only model) detailed in Wong, Steiner, and Cook (2013). If NA, `front.bw` will be determined by cross-validation. The default is NA.

**m**
A non-negative integer specifying the number of uniformly-at-random samples to draw as search candidates for `front.bw`, if `front.bw` is NA. The default is 10.

**k**
A non-negative integer specifying the number of folds for cross-validation to determine `front.bw`, if `front.bw` is NA. The default is 5.

**kernel**
A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

**se.type**
This specifies the robust standard error calculation method to use, from the "sandwich" package. Options are, as in `vcovHC`, "HC3", "const", "HC", "HC0", "HC1", "HC2", "HC4", "HC4m", "HC5". The default is "HC1". This option is overridden by `cluster`.

**cluster**
An optional vector of length n specifying clusters within which the errors are assumed to be correlated. This will result in reporting cluster robust SEs. This option overrides anything specified in `se.type`. It is suggested that data with a discrete running variable be clustered by each unique value of the running variable (Lee and Card, 2008).

**impute**
An optional vector of length n containing a grouping variable that specifies the imputed variables with missing values.
verbatim A logical value indicating whether to print additional information to the terminal. The default is FALSE.

less Logical. If TRUE, return the estimates of parametric linear and optimal bandwidth non-parametric models only. If FALSE return the estimates of linear, quadratic, and cubic parametric models and optimal, half and double bandwidths in non-parametric models. The default is FALSE.

est.cov Logical. If TRUE, the estimates of covariates will be included. If FALSE, the estimates of covariates will not be included. The default is FALSE. This option is not applicable if method is "front".

est.itt Logical. If TRUE, the estimates of intent-to-treat (ITT) will be returned. If FALSE, the estimates of ITT will not be returned. The default is FALSE. This option is not applicable if method is "front".

local A non-negative numeric value specifying the range of neighboring points around the cutoff on the standardized scale, for each assignment variable. The default is 0.15.

ngrid A non-negative integer specifying the number of non-zero grid points on each assignment variable, which is also the number of zero grid points on each assignment variable. The default is 250. The value used in Wong, Steiner and Cook (2013) is 2500, which may cause long computational time.

margin A non-negative numeric value specifying the range of grid points beyond the minimum and maximum of sample points on each assignment variable. The default is 0.03.

boot An optional non-negative integer specifying the number of bootstrap samples to obtain standard error of estimates. This argument is not optional if method is "front".

method A string specifying the method to estimate the RD effect. Options are "center", "univ", "front", based on the centering, univariate, and frontier approaches (respectively) from Wong, Steiner, and Cook (2013).

t.design A character vector of length 2 specifying the treatment option according to design. The first entry is for x1 and the second entry is for x2. Options are "g" (treatment is assigned if x1 is greater than its cutoff), "geq" (treatment is assigned if x1 is greater than or equal to its cutoff), "l" (treatment is assigned if x1 is less than its cutoff), and "leq" (treatment is assigned if x1 is less than or equal to its cutoff). The same options are available for x2.

stop.on.error A logical value indicating whether to remove bootstraps which cause error in the integrate function. If TRUE, bootstraps which cause error are removed and resampled until the specified number of bootstrap samples are acquired. If FALSE, bootstraps which cause error are not removed. The default is TRUE.

Value

mrd_impute returns an object of class "mrd" or "mrdi" for "front" method. The function summary is used to obtain and print a summary of the estimated regression discontinuity. The object of class mrd is a list containing the following components for each estimated treatment effect, tau_MRD or tau_R and tau_M:

18 mrd_impute

verbatim
call  The matched call.
type  A string denoting either "sharp" or "fuzzy" RDD.
cov   The names of covariates.
bw    Numeric vector of each bandwidth used in estimation.
obsv  Vector of the number of observations within the corresponding bandwidth.
model For a sharp design, a list of the lm objects is returned. For a fuzzy design, a list of lists is returned, each with two elements: firststage, the first stage lm object, and iv, the ivreg object. A model is returned for each parametric and non-parametric case and corresponding bandwidth.
frame Returns the model frame used in fitting.
na.action The observations removed from fitting due to missingness.
est   Numeric vector of the estimate of the discontinuity in the outcome under a sharp MRDD or the Wald estimator in the fuzzy MRDD, for each corresponding bandwidth.
d    Numeric vector of the effect size (Cohen’s d) for each estimate.
se    Numeric vector of the standard error for each corresponding bandwidth.
z     Numeric vector of the z statistic for each corresponding bandwidth.
p     Numeric vector of the p-value for each corresponding bandwidth.
ci    The matrix of the 95 for each corresponding bandwidth.
impute A logical value indicating whether multiple imputation is used or not.

References


Examples

```r
set.seed(12345)
x1 <- runif(300, -1, 1)
x2 <- runif(300, -1, 1)
cov <- rnorm(300)
y <- 3 + 2 * (x1 >= 0) + 3 * cov + 10 * (x2 >= 0) + rnorm(300)
imp <- rep(1:3, each = 100)
```
mrd_power

Power Analysis of Multivariate Regression Discontinuity

Description

mrd_power computes the empirical probability that a resulting parameter estimate of the MRD is significant, i.e. the empirical power (1 - beta).

Usage

mrd_power(
  num.rep = 100,
  sample.size = 100,
  x1.dist = "normal",
  x1.para = c(0, 1),
  x2.dist = "normal",
  x2.para = c(0, 1),
  x1.cut = 0,
  x2.cut = 0,
  x1.fuzzy = c(0, 0),
  x2.fuzzy = c(0, 0),
  x1.design = NULL,
  x2.design = NULL,
  coeff = c(0.1, 0.5, 0.5, 1, rep(0.1, 9)),
  eta.sq = 0.5,
  alpha.list = c(0.001, 0.01, 0.05)
)

Arguments

num.rep A non-negative integer specifying the number of repetitions used to calculate the empirical power. The default is 100.

data.size A non-negative integer specifying the number of observations in each sample. The default is 100.
x1.dist A string specifying the distribution of the first assignment variable, x1. Options are "normal" and "uniform". The default is the "normal" distribution.
x1.para  A numeric vector of length 2 specifying parameters of the distribution of the first assignment variable, x1. If x1.dist is "normal", then x1.para includes the mean and standard deviation of the normal distribution. If x1.dist is "uniform", then x1.para includes the upper and lower boundaries of the uniform distribution. The default is c(0, 1).

x2.dist  A string specifying the distribution of the second assignment variable, x2. Options are "normal" and "uniform". The default is the "normal" distribution.

x2.para  A numeric vector of length 2 specifying parameters of the distribution of the second assignment variable, x2. If x2.dist is "normal", then x2.para includes the mean and standard deviation of the normal distribution. If x2.dist is "uniform", then x2.para includes the upper and lower boundaries of the uniform distribution. The default is c(0, 1).

x1.cut  A numeric value containing the cutpoint at which assignment to the treatment is determined for the first assignment variable, x1. The default is 0.

x2.cut  A numeric value containing the cutpoint at which assignment to the treatment is determined for the second assignment variable, x2. The default is 0.

x1.fuzzy  A numeric vector of length 2 specifying the probabilities to be assigned to the control condition, in terms of the first assignment variable, x1, for individuals in the treatment based on the cutoff, and to treatment for individuals in the control condition based on the cutoff. For a sharp design, both entries are 0. For a fuzzy design, the first entry is the probability to be assigned to control for individuals above the cutpoint, and the second entry is the probability to be assigned to treatment for individuals below the cutpoint. The default is c(0, 0), indicating a sharp design.

x2.fuzzy  A numeric vector of length 2 specifying the probabilities to be assigned to the control, in terms of the second assignment variable, x2, for individuals in the treatment based on the cutoff, and to treatment for individuals in the control based on the cutoff. For a sharp design, both entries are 0. For a fuzzy design, the first entry is the probability to be assigned to control for individuals above the cutpoint, and the second entry is the probability to be assigned to treatment for individuals below the cutpoint. The default is c(0, 0), indicating a sharp design.

x1.design  A string specifying the treatment option according to design for x1. Options are "g" (treatment is assigned if x1 is greater than its cutoff), "geq" (treatment is assigned if x1 is greater than or equal to its cutoff), "l" (treatment is assigned if x1 is less than its cutoff), and "leq" (treatment is assigned if x1 is less than or equal to its cutoff).

x2.design  A string specifying the treatment option according to design for x2. Options are "g" (treatment is assigned if x2 is greater than its cutoff), "geq" (treatment is assigned if x2 is greater than or equal to its cutoff), "l" (treatment is assigned if x2 is less than its cutoff), and "leq" (treatment is assigned if x2 is less than or equal to its cutoff).

coeff  A numeric vector specifying coefficients of variables in the linear model to generate data. Coefficients are in the following order:

- The 1st entry is the intercept.
• The 2nd entry is the slope of treatment 1, i.e. treatment effect 1.
• The 3rd entry is the slope of treatment 2, i.e. treatment effect 2.
• The 4th entry is the slope of treatment, i.e. treatment effect.
• The 5th entry is the slope of assignment 1.
• The 6th entry is the slope of assignment 2.
• The 7th entry is the slope of interaction between assignment 1 and assignment 2.
• The 8th entry is the slope of interaction between treatment 1 and assignment 1.
• The 9th entry is the slope of interaction between treatment 2 and assignment 1.
• The 10th entry is the slope of interaction between treatment 1 and assignment 2.
• The 11th entry is the slope of interaction between treatment 2 and assignment 2.
• The 12th entry is the slope of interaction between treatment 1, assignment 1 and assignment 2.
• The 13th entry is the slope of interaction between treatment 2, assignment 1 and assignment 2.

The default is c(0.1, 0.5, 0.5, 1, rep(0.1, 9)).

eta.sq A numeric value specifying the expected partial eta-squared of the linear model with respect to the treatment itself. It is used to control the variance of noise in the linear model. The default is 0.50.

alpha.list A numeric vector containing significance levels (between 0 and 1) used to calculate the empirical alpha. The default is c(0.001, 0.01, anad 0.05).

Value

mrd_power returns an object of class "mrdp" containing the number of successful iterations, mean, variance, and power (with alpha of 0.001, 0.01, and 0.05) for six estimators. The function summary is used to obtain and print a summary of the power analysis. The six estimators are as follows:

• The 1st estimator, Linear, provides results of the linear regression estimator of combined RD using the centering approach.
• The 2nd estimator, Opt, provides results of the local linear regression estimator of combined RD using the centering approach, with the optimal bandwidth in the Imbens and Kalyanaraman (2012) paper.
• The 3rd estimator, Linear, provides results of the linear regression estimator of separate RD in terms of x1 using the univariate approach.
• The 4th estimator, Opt, provides results of the local linear regression estimator of separate RD in terms of x1 using the univariate approach, with the optimal bandwidth in the Imbens and Kalyanaraman (2012) paper.
• The 5th estimator, Linear, provides results of the linear regression estimator of separate RD in terms of x2 using the univariate approach.
• The 6th estimator, Opt, provides results of the local linear regression estimator of separate RD in terms of x2 using the univariate approach, with the optimal bandwidth in the Imbens and Kalyanaraman (2012) paper.
### References


### Examples

```r
## Not run:
summary(mrd_power(x1.design = "l", x2.design = "l"))
summary(mrd_power(x1.dist = "uniform", x1.cut = 0.5,
                   x1.design = "l", x2.design = "l"))
summary(mrd_power(x1.fuzzy = c(0.1, 0.1), x1.design = "l", x2.design = "l"))
## End(Not run)
```

### Description

`mrd_sens_bw` refits the supplied model with varying bandwidths. All other aspects of the model are held constant.

### Usage

```r
mrd_sens_bw(object, approach = c("center", "univ1", "univ2"), bws)
```

### Arguments

- **object**: An object returned by `mrd_est` or `mrd_impute`.
- **approach**: A string of the approaches to be refitted, choosing from `c("center", "univ1", "univ2")`. 
- **bws**: A positive numeric vector of the bandwidths for refitting an `mrd` object.

### Value

`mrd_sens_bw` returns a dataframe containing the estimate `est` and standard error `se` for each supplied bandwidth and for the Imbens-Kalyanaraman (2012) optimal bandwidth, `bw`, and for each supplied approach, `model`. Approaches are either user specified ("usr") or based on the optimal bandwidth ("origin").

### References

Examples

```r
set.seed(12345)
x1 <- runif(10000, -1, 1)
x2 <- rnorm(10000, 10, 2)
cov <- rnorm(10000)
y <- 3 + 2 * x1 + 1 * x2 + 3 * cov + 10 * (x1 >= 0) + 5 * (x2 >= 10) + rnorm(10000)
# front.bw argument was supplied to speed up the example
# users should choose appropriate values for front.bw
mrd <- mrd_est(y ~ x1 + x2 | cov,
               cutpoint = c(0, 10), t.design = c("geq", "geq"), front.bw=c(1,1,1))
mrd_sens_bw(mrd, approach = "univ1", bws = seq(0.1, 1, length.out = 3))
```

---

### mrd_sens_cutoff

#### Cutoff Sensitivity Simulation for Multivariate Regression Discontinuity

**Description**

`mrd_sens_cutoff` refits the supplied model with varying cutoff(s). All other aspects of the model, such as the automatically calculated bandwidth, are held constant.

**Usage**

```r
mrd_sens_cutoff(object, cutoffs)
```

**Arguments**

- `object`: An object returned by `mrd_est` or `mrd_impute`.
- `cutoffs`: A two-column numeric matrix of paired cutoff values to be used for refitting an `mrd` object. The first column corresponds to cutoffs for `x1` and the second column corresponds to cutoffs for `x2`.

**Value**

`mrd_sens_cutoff` returns a dataframe containing the estimate `est` and standard error `se` for each pair of cutoffs (`A1` and `A2`) and for each model. `A1` contains varying cutoffs for assignment 1 and `A2` contains varying cutoffs for assignment 2. The `model` column contains the approach (either centering, univariate 1, or univariate 2) for determining the cutoff and the parametric model (linear, quadratic, or cubic) or non-parametric bandwidth setting (Imbens-Kalyanaraman 2012 optimal, half, or double) used for estimation.

**References**

Examples

```r
set.seed(12345)
x1 <- runif(5000, -1, 1)
x2 <- rnorm(5000, 10, 2)
cov <- rnorm(5000)
y <- 3 + 2 * x1 + 1 * x2 + 3 * cov + 10 * (x1 >= 0) + 5 * (x2 >= 10) + rnorm(5000)
# front.bw argument was supplied to speed up the example
# users should choose appropriate values for front.bw
mrd <- mrd_est(y ~ x1 + x2 | cov,
               cutpoint = c(0, 10), t.design = c("geq", "geq"), front.bw = c(1,1,1))
mrd_sens_cutoff(mrd, expand.grid(A1 = seq(-.5, .5, length.out = 3), A2 = 10)
```

plot.mfrd

Plot the Multivariate Frontier Regression Discontinuity

Description

plot.mfrd plots a 3D illustration of the bivariate frontier regression discontinuity design (RDD).

Usage

```r
## S3 method for class 'mfrd'
plot(
x, model = c("m_s", "m_h", "m_t"),
methodname = c("Param", "bw", "Half-bw", "Double-bw"),
gran = 10,
raw_data = TRUE,
color_surface = FALSE,
...)
```

Arguments

- **x**: An mfrd object returned by mfrd_est or contained in the object returned by mrd_est.
- **model**: A string containing the model specification. Options include one of c("m_s", "m_h", "m_t"), which denote the complete model, heterogeneous treatment model, and treatment only model, respectively.
- **methodname**: A string containing the method specification. Options include one of c("Param", "bw", "Half-bw", "Double-bw").
- **gran**: A non-negative integer specifying the granularity of the surface grid (i.e. the desired number of predicted points before and after the cutoff, along each assignment variable). The default is 10.
- **raw_data**: A logical value indicating whether the raw data points are plotted. The default is TRUE.
color_surface  A logical value indicating whether the treated surface is colored. The default is FALSE.
...  Additional graphic arguments passed to persp.

Examples

set.seed(12345)
x1 <- runif(1000, -1, 1)
x2 <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * (x1 >= 0) + 3 * cov + 10 * (x2 >= 0) + rnorm(1000)
model <- mrd_est(y ~ x1 + x2, cutpoint = c(0, 0), t.design = c("geq", "geq"))
plot(model$front$tau_MRD, "m_s", "Param")
predict.rd

A character vector specifying models to be shown as fitted lines. Options are c("linear", "quadratic", "cubic", "optimal", "half", "double").

fit_ci

A string specifying whether and how to plot prediction confidence intervals around the fitted lines. Options are c("area", "dot", "hide").

fit_ci_level

A numeric value between 0 and 1 specifying the confidence level of prediction CIs. The default is 0.95.

bin_n

An integer specifying the number of bins for binned data points. If bin_n is 0, raw data points are plotted. If bin_n is < 0, data points are suppressed. The default is 20.

bin_level

A numeric value between 0 and 1 specifying the confidence level for CIs around binned data points. The default is 0.95.

bin_size

A string specifying how to plot the number of observations in each bin, by "size" or "shape".

quant_bin

A logical value indicating whether the data are binned by quantiles. The default is TRUE.

xlim

An optional numeric vector containing the x-axis limits.

ylim

An optional numeric vector containing the y-axis limits.

include_rugs

A logical value indicating whether to include the 1d plot for both axes. The default is FALSE.

...

Additional graphic arguments passed to plot.

References


Examples

set.seed(12345)
dat <- data.frame(x = runif(1000, -1, 1), cov = rnorm(1000))
dat$tr <- as.integer(dat$x >= 0)
dat$y <- 3 + 2 * dat$x + 3 * dat$cov + 10 * (dat$x >= 0) + rnorm(1000)
rd <- rd_est(y ~ x + tr | cov, data = dat, cutpoint = 0, t.design = "geq")
plot(rd)

predict.rd

Predict the Regression Discontinuity

Description

predict.rd makes predictions of means and standard deviations of RDs at different cutoffs.

Usage

## S3 method for class 'rd'
predict(object, gran = 50, ...)
Arguments

object
An rd object, typically the result of rd_est.

gran
A non-negative integer specifying the granularity of the data points (i.e. the desired number of predicted points). The default is 50.

... Additional arguments passed to predict.

Examples

```r
set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x >= 0) + rnorm(1000)
tr <- as.integer(x >= 0)
rd <- rd_est(y ~ x + tr | cov, cutpoint = 0, t.design = "geq")
predict(rd)
```

Description

print.mfrd prints a very basic summary of the multivariate frontier regression discontinuity. It is based on the print.RD function in the "rdd" package.

Usage

```r
## S3 method for class 'mfrd'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

x
An mfrd object, typically the result of mfrd_est.

digits
A non-negative integer specifying the number of digits to print. The default is max(3, getOption("digits") - 3).

... Additional arguments passed to print.

References

print.rd

*Print the Regression Discontinuity*

**Description**

print.rd prints a basic summary of the regression discontinuity. print.rd is based on the print.RD function in the "rdd" package.

**Usage**

```r
## S3 method for class 'rd'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

- `x` An rd object, typically the result of rd_est.
- `digits` A non-negative integer specifying the number of digits to print. The default is `max(3, getOption("digits") - 3)`.
- `...` Additional arguments passed to print.

**References**


---

rd_est

*Regression Discontinuity Estimation*

**Description**

rd_est estimates both sharp and fuzzy RDDs using parametric and non-parametric (local linear) models. It is based on the RDestimate function in the "rdd" package. Sharp RDDs (both parametric and non-parametric) are estimated using lm in the stats package. Fuzzy RDDs (both parametric and non-parametric) are estimated using two-stage least-squares ivreg in the AER package. For non-parametric models, Imbens-Kalyanaraman optimal bandwidths can be used.

**Usage**

```r
rd_est(
  formula,
  data,
  subset = NULL,
  cutpoint = NULL,
  bw = NULL,
  kernel = "triangular",
)```
Arguments

**formula**  
The formula of the RDD; a symbolic description of the model to be fitted. This is supplied in the format of \( y \sim x \) for a simple sharp RDD or \( y \sim x | c1 + c2 \) for a sharp RDD with two covariates. A fuzzy RDD may be specified as \( y \sim x + z \) where \( x \) is the running variable, and \( z \) is the endogenous treatment variable. Covariates are included in the same manner as in a sharp RDD.

**data**  
An optional data frame containing the variables in the model. If not found in data, the variables are taken from `environment(formula)`.

**subset**  
An optional vector specifying a subset of observations to be used in the fitting process.

**cutpoint**  
A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.

**bw**  
A vector specifying the bandwidths at which to estimate the RD. Possible values are "IK09", "IK12", and a user-specified non-negative numeric vector specifying the bandwidths at which to estimate the RD. The default is "IK12". If `bw` is "IK12", the bandwidth is calculated using the Imbens-Kalyanaraman 2012 method. If `bw` is "IK09", the bandwidth is calculated using the Imbens-Kalyanaraman 2009 method. Then the RD is estimated with that bandwidth, half that bandwidth, and twice that bandwidth. If only a single value is passed into the function, the RD will similarly be estimated at that bandwidth, half that bandwidth, and twice that bandwidth.

**kernel**  
A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

**se.type**  
This specifies the robust standard error calculation method to use, from the "sandwich" package. Options are, as in `vcovHC`, "HC3", "const", "HC", "HC0", "HC1", "HC2", "HC4", "HC4m", "HC5". The default is "HC1". This option is overridden by `cluster`.

**cluster**  
An optional vector of length n specifying clusters within which the errors are assumed to be correlated. This will result in reporting cluster robust SEs. This option overrides anything specified in `se.type`. It is suggested that data with a discrete running variable be clustered by each unique value of the running variable (Lee and Card, 2008).

**verbose**  
A logical value indicating whether to print additional information to the terminal. The default is FALSE.
logical. If TRUE, return the estimates of linear and optimal. If FALSE return the estimates of linear, quadratic, cubic, optimal, half and double. The default is FALSE.

est.cov Logical. If TRUE, the estimates of covariates will be included. If FALSE, the estimates of covariates will not be included. The default is FALSE. This option is not applicable if method is "front".

est.itt Logical. If TRUE, the estimates of ITT will be returned. The default is FALSE.

t.design A string specifying the treatment option according to design. Options are "g" (treatment is assigned if x is greater than its cutoff), "geq" (treatment is assigned if x is greater than or equal to its cutoff), "l" (treatment is assigned if x is less than its cutoff), and "leq" (treatment is assigned if x is less than or equal to its cutoff).

Value

rd_est returns an object of class "rd". The functions summary and plot are used to obtain and print a summary and plot of the estimated regression discontinuity. The object of class rd is a list containing the following components:

type A string denoting either "sharp" or "fuzzy" RDD.
est Numeric vector of the estimate of the discontinuity in the outcome under a sharp RDD or the Wald estimator in the fuzzy RDD, for each corresponding bandwidth.
se Numeric vector of the standard error for each corresponding bandwidth.
z Numeric vector of the z statistic for each corresponding bandwidth.
p Numeric vector of the p-value for each corresponding bandwidth.
ci The matrix of the 95 for each corresponding bandwidth.
d Numeric vector of the effect size (Cohen’s d) for each estimate.
cov The names of covariates.
bw Numeric vector of each bandwidth used in estimation.
obs Vector of the number of observations within the corresponding bandwidth.
call The matched call.
na.action The number of observations removed from fitting due to missingness.
impute A logical value indicating whether multiple imputation is used or not.
model For a sharp design, a list of the lm objects is returned. For a fuzzy design, a list of lists is returned, each with two elements: firststage, the first stage lm object, and iv, the ivreg object. A model is returned for each corresponding bandwidth.
frame Returns the dataframe used in fitting the model.
References


Examples

```r
set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x >= 0) + rnorm(1000)
rd_est(y ~ x, t.design = "geq")
# Efficiency gains can be made by including covariates (review SEs in "summary" output).
rd_est(y ~ x | cov, t.design = "geq")
```

---

**rd_impute**

Multiple Imputation of Regression Discontinuity Estimation

**Description**

`rd_impute` estimates treatment effects in an RDD with imputed missing values.

**Usage**

```r
rd_impute(formula, data, subset = NULL, cutpoint = NULL, bw = NULL, kernel = "triangular", se.type = "HC1")
```
Arguments

**formula**  
The formula of the RDD; a symbolic description of the model to be fitted. This is supplied in the format of \( y \sim x \) for a simple sharp RDD or \( y \sim x | c1 + c2 \) for a sharp RDD with two covariates. A fuzzy RDD may be specified as \( y \sim x + z \) where \( x \) is the running variable, and \( z \) is the endogenous treatment variable. Covariates are included in the same manner as in a sharp RDD.

**data**  
An optional data frame containing the variables in the model. If not found in data, the variables are taken from `environment(formula)`.

**subset**  
An optional vector specifying a subset of observations to be used in the fitting process.

**cutpoint**  
A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.

**bw**  
A vector specifying the bandwidths at which to estimate the RD. Possible values are "IK09", "IK12", and a user-specified non-negative numeric vector specifying the bandwidths at which to estimate the RD. The default is "IK12". If bw is "IK12", the bandwidth is calculated using the Imbens-Kalyanaraman 2012 method. If bw is "IK09", the bandwidth is calculated using the Imbens-Kalyanaraman 2009 method. Then the RD is estimated with that bandwidth, half that bandwidth, and twice that bandwidth. If only a single value is passed into the function, the RD will similarly be estimated at that bandwidth, half that bandwidth, and twice that bandwidth.

**kernel**  
A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

**se.type**  
This specifies the robust standard error calculation method to use, from the "sandwich" package. Options are, as in `vcovHC`, "HC3", "const", "HC", "HC0", "HC1", "HC2", "HC4", "HC4m", "HC5". This option is overridden by `cluster`.

**cluster**  
An optional vector specifying clusters within which the errors are assumed to be correlated. This will result in reporting cluster robust SEs. This option overrides anything specified in `se.type`. It is suggested that data with a discrete running variable be clustered by each unique value of the running variable (Lee and Card, 2008).

**impute**  
An optional vector of length n, indexing whole imputations.

**verbose**  
A logical value indicating whether to print additional information to the terminal. The default is FALSE.
less Logical. If TRUE, return the estimates of linear and optimal. If FALSE return the estimates of linear, quadratic, cubic, optimal, half and double. The default is FALSE.
est.cov Logical. If TRUE, the estimates of covariates will be included. If FALSE, the estimates of covariates will not be included. The default is FALSE. This option is not applicable if method is "front".
est.itt Logical. If TRUE, the estimates of ITT will be returned. If FALSE, the estimates of ITT will not be returned. The default is FALSE. This option is not applicable if method is "front".
t.design A string specifying the treatment option according to design. Options are "g" (treatment is assigned if x is greater than its cutoff), "geq" (treatment is assigned if x is greater than or equal to its cutoff), "l" (treatment is assigned if x is less than its cutoff), and "leq" (treatment is assigned if x is less than or equal to its cutoff).

Value

rd_impute returns an object of class "rd". The functions summary and plot are used to obtain and print a summary and plot of the estimated regression discontinuity. The object of class rd is a list containing the following components:
call The matched call.
impute A logical value indicating whether multiple imputation is used or not.
type A string denoting either "sharp" or "fuzzy" RDD.
cov The names of covariates.
bw Numeric vector of each bandwidth used in estimation.
obs Vector of the number of observations within the corresponding bandwidth.
model For a sharp design, a list of the lm objects is returned. For a fuzzy design, a list of lists is returned, each with two elements: firststage, the first stage lm object, and iv, the ivreg object. A model is returned for each parametric and non-parametric case and corresponding bandwidth.
frame Returns the model frame used in fitting.
na.action The observations removed from fitting due to missingness.
est Numeric vector of the estimate of the discontinuity in the outcome under a sharp RDD or the Wald estimator in the fuzzy RDD, for each corresponding bandwidth.
d Numeric vector of the effect size (Cohen’s d) for each estimate.
se Numeric vector of the standard error for each corresponding bandwidth.
z Numeric vector of the z statistic for each corresponding bandwidth.
p Numeric vector of the p-value for each corresponding bandwidth.
ci The matrix of the 95 for each corresponding bandwidth.
References


Examples

```r
set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x < 0) + rnorm(1000)
group <- rep(1:10, each = 100)
rd_impute(y ~ x, impute = group, t.design = "l")
# Efficiency gains can be made by including covariates (review SEs in "summary" output).
rd_impute(y ~ x | cov, impute = group, t.design = "l")
```

---

**rd_power**

*Power Analysis of Regression Discontinuity*

Description

`rd_power` computes the empirical probability that a resulting parameter estimate of the MRD is significant, i.e. the empirical power (1 - beta).

Usage

```r
rd_power(
  num.rep = 100,
  sample.size = 100,
  x.dist = "normal",
  x.para = c(0, 1),
  x.cut = 0,
  x.fuzzy = c(0, 0),
  x.design = NULL,
  coeff = c(0.3, 1, 0.2, 0.3),
  eta.sq = 0.5,
  alpha.list = c(0.001, 0.01, 0.05)
)
```
Arguments

num.rep  A non-negative integer specifying the number of repetitions used to calculate the empirical power. The default is 100.

sample.size  A non-negative integer specifying the number of observations in each sample. The default is 100.

x.dist  A string specifying the distribution of the assignment variable, x. Options are "normal" and "uniform". The default is the "normal" distribution.

x.para  A numeric vector of length 2 specifying parameters of the distribution of the first assignment variable, x1. If x.dist is "normal", then x.para includes the mean and standard deviation of the normal distribution. If x.dist is "uniform", then x.para includes the upper and lower boundaries of the uniform distribution. The default is c(0,1).

x.cut  A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.

x.fuzzy  A numeric vector of length 2 specifying the probabilities to be assigned to the control, in terms of the assignment variable, x, for individuals in the treatment based on the cutoff, and to treatment for individuals in the control based on the cutoff. For a sharp design, both entries are 0. For a fuzzy design, the first entry is the probability to be assigned to control for individuals above the cutpoint, and the second entry is the probability to be assigned to treatment for individuals below the cutpoint. The default is c(0,0), indicating a sharp design.

x.design  A string specifying the treatment option according to design. Options are "g" (treatment is assigned if x is greater than its cutoff), "geq" (treatment is assigned if x is greater than or equal to its cutoff), "l" (treatment is assigned if x is less than its cutoff), and "leq" (treatment is assigned if x is less than or equal to its cutoff).

coeff  A numeric vector specifying coefficients of variables in the linear model to generate data. Coefficients are in the following order:
• The 1st entry is the intercept.
• The 2nd entry is the slope of treatment, i.e. treatment effect.
• The 3rd entry is the slope of assignment.
• The 4th entry is the slope of interaction between treatment and assignment.
The default is c(0.3, 1, 0.2, 0.3).

eta.sq  A numeric value specifying the expected partial eta-squared of the linear model with respect to the treatment itself. It is used to control the variance of noise in the linear model. The default is 0.50.

alpha.list  A numeric vector containing significance levels (between 0 and 1) used to calculate the empirical alpha. The default is c(0.001, 0.01, 0.05).

Value

rd_power returns an object of class "rdp", including containing the mean, variance, and power (with alpha of 0.001, 0.01, and 0.05) for two estimators. The function summary is used to obtain and print a summary of the power analysis. The two estimators are:
• The 1st estimator, Linear, provides results of the linear regression estimator.
• The 2nd estimator, Opt, provides results of the local linear regression estimator of RD, with the optimal bandwidth in the Imbens and Kalyanaraman (2012) paper.

References

Examples
```r
## Not run:
summary(rd_power(x.design = "l"))
summary(rd_power(x.dist = "uniform", x.cut = 0.5, x.design = "l"))
summary(rd_power(x.fuzzy = c(0.1, 0.1), x.design = "l"))
## End(Not run)
```

---

**rd_sens_bw**

*Bandwidth Sensitivity Simulation for Regression Discontinuity*

**Description**
rd_sens_bw refits the supplied model with varying bandwidths. All other aspects of the model are held constant.

**Usage**
```r
rd_sens_bw(object, bws)
```

**Arguments**
- **object**: An object returned by rd_est or rd_impute.
- **bws**: A positive numeric vector of the bandwidths for refitting an rd object.

**Value**
rd_sens_bw returns a dataframe containing the estimate est and standard error se for each supplied bandwidth and for the Imbens-Kalyanaraman (2012) optimal bandwidth, bw, and for each supplied approach, model. Approaches are either user specified ("usr") or based on the optimal bandwidth ("origin").

**References**
Examples

```r
set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x >= 0) + rnorm(1000)
rd <- rd_est(y ~ x | cov, t.design = "geq")
rd_sens_bw(rd, bws = seq(.1, 1, length.out = 5))
```

---

**Description**

`rd_sens_cutoff` refits the supplied model with varying cutoff(s). All other aspects of the model, such as the automatically calculated bandwidth, are held constant.

**Usage**

```r
rd_sens_cutoff(object, cutoffs)
```

**Arguments**

- `object`: An object returned by `rd_est` or `rd_impute`.
- `cutoffs`: A numeric vector of cutoff values to be used for refitting an rd object.

**Value**

`rd_sens_cutoff` returns a dataframe containing the estimate `est` and standard error `se` for each cutoff value (`A1`). Column `A1` contains varying cutoffs on the assignment variable. The model column contains the parametric model (linear, quadratic, or cubic) or non-parametric bandwidth setting (Imbens-Kalyanaraman 2012 optimal, half, or double) used for estimation.

**References**


**Examples**

```r
set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x >= 0) + rnorm(1000)
rd <- rd_est(y ~ x | cov, t.design = "geq")
rd_sens_cutoff(rd, seq(-.5, .5, length.out = 10))
```
**rd_type**

*Determine Type of Regression Discontinuity Design*

**Description**

`rd_type` cross-tabulates observations based on (1) a binary treatment and (2) one or two assignments and their cutoff values. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp::rd_type().

**Usage**

```r
rd_type(
  data,
  treat,
  assign_1,
  cutoff_1,
  operator_1 = NULL,
  assign_2 = NULL,
  cutoff_2 = NULL,
  operator_2 = NULL
)
```

**Arguments**

- `data`: A `data.frame`, with each row representing an observation.
- `treat`: A string specifying the name of the numeric treatment variable (treated = positive values).
- `assign_1`: A string specifying the variable name of the primary assignment.
- `cutoff_1`: A numeric value containing the cutpoint at which assignment to the treatment is determined, for the primary assignment.
- `operator_1`: The operator specifying the treatment option according to design for the primary assignment. Options are "g" (treatment is assigned if x1 is greater than its cutoff), "geq" (treatment is assigned if x1 is greater than or equal to its cutoff), "l" (treatment is assigned if x1 is less than its cutoff), and "leq" (treatment is assigned if x1 is less than or equal to its cutoff).
- `assign_2`: An optional string specifying the variable name of the secondary assignment.
- `cutoff_2`: An optional numeric value containing the cutpoint at which assignment to the treatment is determined, for the secondary assignment.
- `operator_2`: The operator specifying the treatment option according to design for the secondary assignment. Options are "g" (treatment is assigned if x2 is greater than its cutoff), "geq" (treatment is assigned if x2 is greater than or equal to its cutoff), "l" (treatment is assigned if x2 is less than its cutoff), and "leq" (treatment is assigned if x2 is less than or equal to its cutoff).
sens_plot

Value

do_type returns a list of two elements:

crosstab     The cross-table as a data.frame. Columns in the dataframe include treatment rules, number of observations in the control condition, number of observations in the treatment condition, and the probability of an observation being in treatment or control.

type         A string specifying the type of design used, either "SHARP" or "FUZZY".

Examples

set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x >= 0) + rnorm(1000)
df <- data.frame(cbind(y, x, t = x>=0))
rdapp::rd_type(df, 't', 'x', 0, 'geq')

sens_plot     Plot the Simulated Estimates for Sensitivity Analyses

Description

sens_plot plots the sensitivity analysis for cutpoints or bandwidths.

Usage

sens_plot(
  sim_results,
  level = 0.95,
  x = c("A1", "A2", "bw"),
  plot_models = unique(sim_results$model),
  yrange = NULL
)

Arguments

sim_results     A data.frame returned by rd_sens_cutoff, rd_sens_bw, mrd_sens_cutoff, or mrd_sens_bw.
level           A numeric value between 0 and 1 specifying the confidence level for CIs (assuming a normal sampling distribution). The default is 0.95.

x               A string of the column name of the varying parameter in sim_results. This will be used as the x-axis in the plot. Possible values are c("A1", "A2", "bw"), which are column names in sim_results. A1 specifies that the varying cutoffs are for assignment 1 and A2 specifies assignment 2. bw indicates that the varying parameter is bandwidth.
plot_models A character vector specifying the models to be plotted (i.e. models estimated with different approaches). Possible values are unique(sim_results$model).

yrange An optional numeric vector specifying the range of the y-axis.

Examples

```r
set.seed(12345)
x <- runif(1000, -1, 1)
cov <- rnorm(1000)
y <- 3 + 2 * x + 3 * cov + 10 * (x >= 0) + rnorm(1000)
m <- rd_est(y ~ x | cov, t.design = "geq")
sim_cutoff <- rd_sens_cutoff(m, seq(-.5, .5, length.out = 10))
sens_plot(sim_cutoff, x = "A1", plot_models = c("linear", "optimal"))
sim_bw <- rd_sens_bw(m, seq(.1, 1, length.out = 10))
sens_plot(sim_bw, x = "bw")
```

Description

shiny_run launches the R Shiny application for "rddapp".

Usage

```r
shiny_run(app_name = "shinyrdd")
```

Arguments

app_name A string specifying the name of the R Shiny app. The default is "shinyrdd".

Examples

```r
## Not run:
shiny_run()
shiny_run("shinyrdd")
## End(Not run)
```
Summary

**summary.mfrd** is a summary method for class "mfrd". It is based on the summary.RD function in the "rdd" package.

**Usage**

```r
## S3 method for class 'mfrd'
summary(object, level = 0.95, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

- `object` An object of class "mfrd", usually a result of a call to mfrd_est.
- `level` A numeric value between 0 and 1 specifying the confidence level for confidence intervals. The default is 0.95.
- `digits` A non-negative integer specifying the number of digits to display. The default is `max(3, getOption("digits") - 3)`.
- `...` Additional arguments passed to summary.

**Value**

summary.mfrd returns a list containing the following components:

- `coefficients` A matrix containing estimates and confidence intervals (if applicable) for the complete model.
- `ht_coefficients` A matrix containing estimates and confidence intervals (if applicable) for the heterogeneous treatment model.
- `t_coefficients` A matrix containing estimates and confidence intervals (if applicable) for the treatment only model.

**References**

**summary.mrd**

*Summarize the Multivariate Regression Discontinuity*

**Description**

`summary.mrd` is a summary method for class "mrd". It is based on `summary.RD` function in the "rdd" package.

**Usage**

```r
## S3 method for class 'mrd'
summary(object, level = 0.95, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

- `object`: An object of class "mrd", usually a result of a call to `mrd_est`.
- `level`: A numeric value between 0 and 1 specifying the confidence level for confidence intervals. The default is 0.95.
- `digits`: A non-negative integer specifying the number of digits to display. The default is `max(3, getOption("digits") - 3)`.
- `...`: Additional arguments passed to `summary`.

**Value**

`summary.mrd` returns a list which has the following components depending on methods implemented in the "mrd" object:

- `center_coefficients`: A matrix containing bandwidths, number of observations, estimates, SEs, confidence intervals, z-values and p-values for each estimated bandwidth and/or parametric model.
- `univR_coefficients`: A matrix containing bandwidths, number of observations, estimates, SEs, confidence intervals, z-values and p-values for each estimated bandwidth and/or parametric model.
- `univM_coefficients`: A matrix containing bandwidths, number of observations, estimates, SEs, confidence intervals, z-values and p-values for each estimated bandwidth and/or parametric model.
- `front_coefficients`: A matrix containing estimates and confidence intervals (if applicable) for the complete model.
- `front_ht_coefficients`: A matrix containing estimates and confidence intervals (if applicable) for the heterogeneous treatment model.
front_t_coefficients
A matrix containing estimates and confidence intervals (if applicable) for the treatment only model.

References

summary.mrdi

Description
summary.mrdi is a summary method for class "mrdi". It is based on summary.RD function in the "rdd" package.

Usage
## S3 method for class 'mrdi'
summary(object, level = 0.95, digits = max(3, getOption("digits") - 3), ...)

Arguments
object An object of class "mrdi", usually a result of a call to mrd_impute with "front" method.
level A numeric value between 0 and 1 specifying the confidence level for confidence intervals. The default is 0.95.
digits A non-negative integer specifying the number of digits to display. The default is max(3, getOption("digits") - 3).
... Additional arguments passed to summary.

Value
summary.mrdi returns a list which has the following components:

coefficients A matrix containing estimates and confidence intervals (if applicable) for the complete model.
ht_coefficients A matrix containing estimates and confidence intervals (if applicable) for the heterogeneous treatment model.
t_coefficients A matrix containing estimates and confidence intervals (if applicable) for the treatment only model.

References
**summary.mrdp**

*Summarize the Power Analysis of Regression Discontinuity*

**Description**

`summary.mrdp` is a summary method for class "mrdp". It is based on `summary.RD` function in the "rdd" package.

**Usage**

```r
## S3 method for class 'mrdp'
summary(object, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

- `object`: An object of class "mrdp", usually a result of a call to `mrd_power`.
- `digits`: A non-negative integer specifying the number of digits to display. The default is `max(3, getOption("digits") - 3)`.
- `...`: Additional arguments passed to `summary`.

**Value**

`summary.mrdp` returns a list which has the following components:

- `coefficients`: A matrix containing the mean, variance, and empirical alpha of each estimator.

**References**


---

**summary.rd**

*Summarize the Regression Discontinuity*

**Description**

`summary.rd` is a summary method for class "rd". It is based on `summary.RD` function in the "rdd" package.

**Usage**

```r
## S3 method for class 'rd'
summary(object, level = 0.95, digits = max(3, getOption("digits") - 3), ...)
```
Arguments

object 
An object of class "rd", usually a result of a call to rd_est.

level  
A numeric value between 0 and 1 specifying the confidence level for confidence 
intervals. The default is 0.95.

digits  
A non-negative integer specifying the number of digits to display. The default 
is max(3, getOption("digits") - 3).

...  
Additional arguments passed to summary..

Value

summary.rdp returns a list which has the following components:

coefficients  
A matrix containing bandwidths, number of observations, estimates, SEs, con-
fidence intervals, z-values and p-values for each estimated bandwidth.

References

project.org/package=rdd

summarize.rdp  |  Summarize the Power Analysis of Regression Discontinuity

Description

summary.rdp is a summary method for class "rdp". It is based on summary.RD function in the "rdd" 
package.

Usage

## S3 method for class 'rdp'
summary(object, digits = max(3, getOption("digits") - 3), ...)

Arguments

object  
An object of class "rdp", usually a result of a call to rd_power.

digits  
A non-negative integer specifying the number of digits to display. The default 
is max(3, getOption("digits") - 3).

...  
Additional arguments passed to summary.

Value

summary.rdp returns a list which has the following components:

coefficients  
A matrix containing the mean, variance, and empirical alpha of each estimator.
References

---

treat_assign

Treatment Assignment for Regression Discontinuity

Description
treat_assign computes the treatment variable, t, based on the cutoff of assignment variable, x. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp:::treat_assign().

Usage
treat_assign(x, cut = 0, t.design = "l")

Arguments
- x: A numeric vector containing the assignment variable, x.
- cut: A numeric value containing the cutpoint at which assignment to the treatment is determined. The default is 0.
- t.design: A string specifying the treatment option according to design. Options are "g" (treatment is assigned if x is greater than its cutoff), "geq" (treatment is assigned if x is greater than or equal to its cutoff), "l" (treatment is assigned if x is less than its cutoff), and "leq" (treatment is assigned if x is less than or equal to its cutoff). The default is "l".

Value
treat_assign returns the treatment variable as a vector according to the design, where 1 means the treated group and 0 means the control group.

---

var_center

Assignment Centering for Multivariate Frontier Regression Discontinuity

Description
var_center computes the univariate assignment variable, x based on the cutoffs of two assignment variables: x1 and x2. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp:::var_center().
Usage

```r
var_center(x, cut = c(0, 0), t.design = NULL, t.plot = FALSE)
```

Arguments

- `x`: Data frame or matrix of two assignment variables, where the first column is `x1` and the second column is `x2`.
- `cut`: A numeric vector of length 2 containing the cutpoints at which assignment to the treatment is determined. The default is `c(0, 0)`.
- `t.design`: A character vector of length 2 specifying the treatment option according to design. The first entry is for `x1` and the second entry is for `x2`. Options are "g" (treatment is assigned if `x1` is greater than its cutoff), "geq" (treatment is assigned if `x1` is greater than or equal to its cutoff), "l" (treatment is assigned if `x1` is less than its cutoff), and "leq" (treatment is assigned if `x1` is less than or equal to its cutoff). The same options are available for `x2`.
- `t.plot`: A logical value indicating whether to calculate the univariate treatment variable, `t`, and make a plot. The default is `FALSE`.

Value

`var_center` returns the univariate assignment variable as a vector according to the design.

---

```r
wt_kern(X, center, bw, kernel = "triangular")
```

Arguments

- `X`: A numeric vector containing the input `X` values. This variable represents the axis along which kernel weighting should be performed.
- `center`: A numeric value specifying the point from which distances should be calculated.
- `bw`: A numeric value specifying the bandwidth.
- `kernel`: A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

Description

`wt_kern` calculates the appropriate kernel weights for a vector. This is useful when, for instance, one wishes to perform local regression. It is based on the `kernelwts` function in the "rdd" package. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in `rddapp:::wt_kern()`.
wt_kern_bivariate

Value

wt_kern returns a vector of weights with length equal to that of the X input (one weight per element of X).

References


wt_kern_bivariate Bivariate Kernel Weight Calculation

Description

wt_kern_bivariate calculates the appropriate weights for two variables for Multivariate Frontier Regression Discontinuity Estimation with nonparametric implementation. Kernel weights are calculated based on the L1 distance of the two variables from the frontiers. This is an internal function and is typically not directly invoked by the user. It can be accessed using the triple colon, as in rddapp::wt_kern_bivariate().

Usage

wt_kern_bivariate(
  x1,
  x2,
  center1,  # A numeric value specifying the point from which distances should be calculated for the second vector, x2.
  center2,  # A numeric value specifying the point from which distances should be calculated for the first vector, x1.
  bw,
  kernel = "triangular",  # The input x1 values for the first vector. This variable represents the axis along which kernel weighting should be performed; the first assignment variable in an MRDD.
  t.design = NULL
)

Arguments

X1  

The input x1 values for the first vector. This variable represents the axis along which kernel weighting should be performed; the first assignment variable in an MRDD.

X2  

The input x2 values for the second vector. X2 has the same length as X1. This variable represents the axis along which kernel weighting should be performed; the second assignment variable in an MRDD.

center1  

A numeric value specifying the point from which distances should be calculated for the first vector, X1.

center2  

A numeric value specifying the point from which distances should be calculated for the second vector, X2.
bw  A numeric vector specifying the bandwidths for each of three effects models (complete model, heterogeneous treatment model, and treatment only model) detailed in Wong, Steiner, and Cook (2013).

kernel  A string indicating which kernel to use. Options are "triangular" (default and recommended), "rectangular", "epanechnikov", "quartic", "triweight", "tricube", and "cosine".

t.design  A character vector of length 2 specifying the treatment option according to design. The first entry is for $x_1$ and the second entry is for $x_2$. Options are "g" (treatment is assigned if $x_1$ is greater than its cutoff), "geq" (treatment is assigned if $x_1$ is greater than or equal to its cutoff), "l" (treatment is assigned if $x_1$ is less than its cutoff), and "leq" (treatment is assigned if $x_1$ is less than or equal to its cutoff). The same options are available for $x_2$.

Value

wt_bivariate_kern returns a matrix of weights and distances with length equal to that of the $X_1$ and $X_2$ input. The first and second weights and distances are calculated with respect to all frontiers of different treatments. The third weight and distance are calculated with respect to the overall frontier of treatment versus non-treatment.
Index

* datasets
  CARE, 6
  attr_check, 4
  bw_ik09, 4
  bw_ik12, 5
  CARE, 6
  class, 10, 14, 18, 22, 31, 34, 36
  dc_test, 7
  mfrd_est, 9, 28, 42
  mrd_est, 12, 43
  mrd_impute, 16, 44
  mrd_power, 20, 45
  mrd_sens_bw, 23
  mrd_sens_cutoff, 24
  plot.mfrd, 25
  plot.rd, 26
  predict.rd, 26, 27
  print.mfrd, 28
  print.rd, 29
  rd_est, 26, 28, 29, 29, 46
  rd_impute, 32
  rd_power, 35, 46
  rd_sens_bw, 37
  rd_sens_cutoff, 38
  rd_type, 39
  rddapp (rddapp-package), 3
  rddapp-package, 3
  sens_plot, 40
  shiny_run, 41
  summary.mfrd, 42
  summary.mrd, 43
  summary.mrdi, 44
  summary.mrdp, 45