Package ‘rddtools’

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Title Toolbox for Regression Discontinuity Design (‘RDD’)

Description Set of functions for Regression Discontinuity Design (‘RDD’), for data visualisation, estimation and testing.

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Imports KernSmooth, ggplot2, rdd, sandwich, lmtest, Formula, locpol, methods, rdrobust, rmarkdown

Depends AER, np

Suggests stats4, car, knitr, testthat

License GPL (>= 2)

URL https://qua.st/rddtools/

BugReports https://github.com/bquast/rddtools/issues

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as.lm

Convert a rdd object to lm

Description

Convert a rdd object to lm

Usage

as.lm(x)

Arguments

x An object to convert to lm

Value

An object of class lm

See Also

as.npreg which converts rdd_reg objects into npreg from package np.
Examples

```r
data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)
reg_para <- rdd_reg_lm(rdd_object=house_rdd)
reg_para_lm <- as.lm(reg_para)
reg_para_lm
plot(reg_para_lm, which=4)
```

---

### as.npregbw

Convert an `rdd_reg` object to a `npreg` object

**Description**

Convert an `rdd_object` to a non-parametric regression `npreg` from package `np`.

**Usage**

```r
as.npregbw(x, ...)
```

```r
as.npreg(x, ...)
```

**Arguments**

- `x` Object of class `rdd_reg` created by `rdd_reg_np` or `rdd_reg_lm`
- `...` Further arguments passed to the `npregbw` or `npreg` function.

**Details**

This function converts an `rdd_reg` object into an `npreg` object from package `np`. Note that the output won’t be the same, since `npreg` does not offer a triangular kernel, but a Gaussian or Epanechnikov one. Another reason why estimates might differ slightly is that `npreg` implements a multivariate kernel, while `rdd_reg` proceeds as if the kernel was univariate. A simple solution to make the multivariate kernel similar to the univariate one is to set the bandwidth for `x` and `Dx` to a large number, so that they converge towards a constant, and one obtains back the univariate kernel.

**Value**

An object of class `npreg` or `npregbw`.

**See Also**

- `as.lm` which converts `rdd_reg` objects into `lm`.
Examples

# Estimate usual rdd_reg:
data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)
reg_nonpara <- rdd_reg_np(rdd_object=house_rdd)

## Convert to npreg:
reg_nonpara_np <- as.npreg(reg_nonpara)
reg_nonpara_np
rdd_coef(reg_nonpara_np, allCo=TRUE, allInfo=TRUE)

## Compare with result obtained with a Gaussian kernel:
bw_lm <- dnorm(house_rdd$x, sd=rddtools:::getBW(reg_nonpara))
reg_nonpara_gaus <- rdd_reg_lm(rdd_object=house_rdd, w=bw_lm)
all.equal(rdd_coef(reg_nonpara_gaus),rdd_coef(reg_nonpara_np))

---

clusterInf

Post-inference for clustered data

Description

Correct standard-errors to account for clustered data, doing either a degrees of freedom correction or using a heteroskedasticity-cluster robust covariance matrix possibly on the range specified by bandwidth.

Usage

clusterInf(object, clusterVar, vcov. = NULL, type = c("df-adj", "HC"), ...)

Arguments

- **object**: Object of class lm, from which rdd_reg also inherits.
- **clusterVar**: The variable containing the cluster attributions.
- **vcov.**: Specific covariance function to pass to coeftest. See help of sandwich.
- **type**: The type of cluster correction to use: either the degrees of freedom, or a HC matrix.
- **...**: Further arguments passed to coeftest.

Value

The output of the coeftest function, which is itself of class coeftest.

References

covarTest_dis

See Also

vcovCluster, which implements the cluster-robust covariance matrix estimator used by clusterInf

Examples

data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)
reg_para <- rdd_reg_lm(rdd_object=house_rdd)

# here we just generate randomly a cluster variable:
nlet <- sort(c(outer(letters, letters, paste, sep='')))
clusRandom <- sample(nlet[1:60], size=nrow(house_rdd), replace=TRUE)

# now do post-inference:
clusterInf(reg_para, clusterVar=clusRandom)
clusterInf(reg_para, clusterVar=clusRandom, type='HC')

covarTest_dis

Testing for balanced covariates: equality of distribution

description

Tests equality of distribution with a Kolmogorov-Smirnov for each covariates, between the two full groups or around the discontinuity threshold

Usage

covarTest_dis(
  object,
  bw = NULL,
  exact = NULL,
  p.adjust = c("none", "holm", "BH", "BY", "hochberg", "hommel", "bonferroni")
)

## S3 method for class 'rdd_data'
covarTest_dis(
  object,
  bw = NULL,
  exact = FALSE,
  p.adjust = c("none", "holm", "BH", "BY", "hochberg", "hommel", "bonferroni")
)

## S3 method for class 'rdd_reg'
covarTest_dis(
  object,
  bw = NULL,
  exact = FALSE,
  p.adjust = c("none", "holm", "BH", "BY", "hochberg", "hommel", "bonferroni")
)
### covarTest_mean

**Testing for balanced covariates: equality of means with t-test**

Tests equality of means by a t-test for each covariate, between the two full groups or around the discontinuity threshold.

#### Arguments

- **object**
  - object of class rdd_data

- **bw**
  - a bandwidth

- **exact**
  - Argument of the `ks.test` function: NULL or a logical indicating whether an exact p-value should be computed.

- **p.adjust**
  - Whether to adjust the p-values for multiple testing. Uses the `p.adjust` function

#### Value

A data frame with, for each covariate, the K-S statistic and its p-value.

#### Author(s)

Matthieu Stigler <<Matthieu.Stigler@gmail.com>>

#### See Also

- [covarTest_mean](#) for the t-test of equality of means

#### Examples

```r
data(house)

## Add randomly generated covariates
set.seed(123)
n_Lee <- nrow(house)
Z <- data.frame(z1 = rnorm(n_Lee, sd=2),
    z2 = rnorm(n_Lee, mean = ifelse(house<0, 5, 8)),
    z3 = sample(letters, size = n_Lee, replace = TRUE))
house_rdd_Z <- rdd_data(y = house$y, x = house$x, covar = Z, cutpoint = 0)

## Kolmogorov-Smirnov test of equality in distribution:
covarTest_dis(house_rdd_Z, bw=0.3)

## Can also use function covarTest_dis() for a t-test for equality of means around cutoff:
covarTest_mean(house_rdd_Z, bw=0.3)

## covarTest_dis works also on regression outputs (bw will be taken from the model)
reg_nonpara <- rdd_reg_np(rdd_object=house_rdd_Z)
covarTest_dis(reg_nonpara)
```

---

**covarTest_mean**

Testing for balanced covariates: equality of means with t-test

**Description**

Tests equality of means by a t-test for each covariate, between the two full groups or around the discontinuity threshold.
covarTest_mean

Usage

covarTest_mean(
  object,
  bw = NULL,
  paired = FALSE,
  var.equal = FALSE,
  p.adjust = c("none", "holm", "BH", "BY", "hochberg", "hommel", "bonferroni")
)

## S3 method for class 'rdd_data'
covarTest_mean(
  object,
  bw = NULL,
  paired = FALSE,
  var.equal = FALSE,
  p.adjust = c("none", "holm", "BH", "BY", "hochberg", "hommel", "bonferroni")
)

## S3 method for class 'rdd_reg'
covarTest_mean(
  object,
  bw = NULL,
  paired = FALSE,
  var.equal = FALSE,
  p.adjust = c("none", "holm", "BH", "BY", "hochberg", "hommel", "bonferroni")
)

Arguments

- **object**: object of class rdd_data
- **bw**: a bandwidth
- **paired**: Argument of the `t.test` function: logical indicating whether you want paired t-tests.
- **var.equal**: Argument of the `t.test` function: logical variable indicating whether to treat the two variances as being equal
- **p.adjust**: Whether to adjust the p-values for multiple testing. Uses the `p.adjust` function

Value

A data frame with, for each covariate, the mean on each size, the difference, t-stat and ts p-value.

Author(s)

Matthieu Stigler <<Matthieu.Stigler@gmail.com>>

See Also

covarTest_dis for the Kolmogorov-Smirnov test of equality of distribution
Examples

data(house)

## Add randomly generated covariates
set.seed(123)
n_Lee <- nrow(house)
Z <- data.frame(z1 = rnorm(n_Lee, sd=2),
    z2 = rnorm(n_Lee, mean = ifelse(house<0, 5, 8)),
    z3 = sample(letters, size = n_Lee, replace = TRUE))
house_rdd_Z <- rdd_data(y = house$y, x = house$x, covar = Z, cutpoint = 0)

## test for equality of means around cutoff:
covarTest_mean(house_rdd_Z, bw=0.3)

## Can also use function covarTest_dis() for Kolmogorov-Smirnov test:
covarTest_dis(house_rdd_Z, bw=0.3)

## covarTest_mean works also on regression outputs (bw will be taken from the model)
reg_nonpara <- rdd_reg_np(rdd_object=house_rdd_Z)
covarTest_mean(reg_nonpara)

---

dens_test  

Run the McCracy test for manipulation of the forcing variable

Description

Calls the DCdensity test from package rdd on a rdd_object.

Usage

dens_test(rdd_object, bin = NULL, bw = NULL, plot = TRUE, ...)

Arguments

rdd_object object of class rdd_data
bin Argument of the DCdensity function, the binwidth
bw Argument of the DCdensity function, the bandwidth
plot Whether to return a plot. Logical, default ot TRUE.
... Further arguments passed to DCdensity.

Examples

data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)
dens_test(house_rdd)
**Generate Monte Carlo simulations of Imbens and Kalyanaraman**

**Description**
Generate the simulations reported in Imbens and Kalyanaraman (2012)

**Usage**

```r
gen_mc_ik(
  n = 200,
  version = 1,
  sd = 0.1295,
  output = c("data.frame", "rdd_data"),
  size
)
```

**Arguments**

- `n`: The size of sample to generate
- `version`: The MC version of Imbens and Kalyanaraman (between 1 and 4).
- `sd`: The standard deviation of the error term.
- `output`: Whether to return a data-frame, or already a rdd_data
- `size`: The size of the effect, this depends on the specific version, defaults are as in ik: 0.04, NULL, 0.1, 0.1

**Value**
An data frame with x and y variables.

**Examples**

```r
mc1_dat <- gen_mc_ik()
MC1_rdd <- rdd_data(y=mc1_dat$y, x=mc1_dat$x, cutpoint=0)

## Use np regression:
reg_nonpara <- rdd_reg_np(rdd_object=MC1_rdd)
reg_nonpara

# Represent the curves:
plotCu <- function(version=1, xlim=c(-0.1,0.1)){
  res <- gen_mc_ik(sd=0.0000001, n=1000, version=version)
  res <- res[order(res$x),]
  ylim <- range(subset(res, x>=min(xlim) & x<=max(xlim), 'y'))
  plot(res, type='l', xlab=xlim, ylim=ylim, main=paste('DGP', version))
  abline(v=0)
  xCut <- res[which(res$x==min(res$x[res$x>=0]))]+c(0,-1),]
}````
house

Dataset used in Lee (2008)

Description

Randomized experiments from non-random selection in U.S. House elections

Dataset described used in Imbens and Kalyanaraman (2012), and probably the same dataset used in Lee (2008).

Format

A data frame with 6558 observations and two variables:

- x Vote at election t-1
- y Vote at election t

Source

Guido Imbens webpage: https://scholar.harvard.edu/imbens/scholar_software/regression-discontinuity

References


Examples

data(house)
rdd_house <- rdd_data(x=x, y=y, data=house, cutpoint=0)
summary(rdd_house)
plot(rdd_house)
**Description**

Data from the Initiative Nationale du Development Humaine, collected as the part of the SNSF project "Development Aid and Social Dynamics"

**Format**

A data frame with two variables with 720 observations each

**Source**

Development Aid and social Dyanmics website: [https://qua.st/Development-Aid-Social-Dynamics/](https://qua.st/Development-Aid-Social-Dynamics/)

**References**

Arcand, Rieger, and Nguyen (2015) 'Development Aid and Social Dyanmics Data Set'

**Examples**

```r
# load the data
data(indh)

# construct rdd data frame
rdd_dat_indh <- rdd_data(y=choice_pg, x=poverty, data=indh, cutpoint=30)

# inspect data frame
summary(rdd_dat_indh)

# perform non-parametric regression
(reg_np_indh <- rdd_reg_np(rdd_dat_indh))
```

---

**Description**

Binned plot of the forcing and outcome variable
## Usage

```r
## S3 method for class 'rdd_data'
plot(
  x,
  h = NULL,
  nbins = NULL,
  xlim = range(object$x, na.rm = TRUE),
  cex = 0.7,
  nplot = 1,
  device = c("base", "ggplot"),
  ...
)
```

### Arguments

- **x**: Object of class `rdd_data`
- **h**: The binwidth parameter (note this differs from the bandwidth parameter!)
- **nbins**: Alternative to `h`, the total number of bins in the plot.
- **xlim**: The range of the x data
- **cex**: Size of the points, see `par`
- **nplot**: Number of plot to draw
- **device**: Type of device used. Currently not used.
- **...**: Further arguments passed to the `plot` function.

### Details

Produces a simple binned plot averaging values within each interval. The length of the intervals is specified with the argument `h`, specifying the whole binwidth (contrary to the usual bandwidth argument, that gives half of the length of the kernel window. When no bandwidth is given, the bandwidth of Ruppert et al is used, see `rdd_bw_rsw`.

### Value

A plot

### Author(s)

Matthieu Stigler < Matthieu.Stigler@gmail.com >

### Examples

```r
data(house)
house_rdd <- rdd(y=house$y, x=house$x, cutpoint=0)
plot(house_rdd)
```

```r
## Specify manually the bandwidth:
plot(house_rdd, h=0.2)
```
## Show three plots with different bandwidth:
```r
plot(house_rdd, h=c(0.2,0.3,0.4), nplot=3)
```

## Specify instead of the bandwidth, the final number of bins:
```r
plot(house_rdd, nbins=22)
```

## If the specified number of bins is odd, the larger number is given to side with largest range
```r
plot(house_rdd, nbins=21)
```

---

**plotBin**  
**Bin plotting**

### Description
Do a 'scatterplot bin smoothing’

### Usage
```r
plotBin(
  x,  
y,  
h = NULL,  
nbins = NULL,  
cutpoint = 0,  
plot = TRUE,  
type = c("value", "number"),  
xlim = range(x, na.rm = TRUE),  
cex = 0.9,  
main = NULL,  
xlab,  
ylab,  
...  
)
```

### Arguments
- **x**: Forcing variable
- **y**: Output
- **h**: the bandwidth (defaults to \(2\times\text{sd(\text{runvar})}\times\text{length(\text{runvar})}^{-0.5}\))
- **nbins**: number of Bins
- **cutpoint**: Cutpoint
- **plot**: Logical. Whether to plot or only returned silently
- **type**: Whether returns the y averages, or the x frequencies
- **xlim, cex, main, xlab, ylab**: Usual parameters passed to plot(), see `par`
- **...**: further arguments passed to plot.
Value

Returns silently values

References

McCrary, Justin.

---

**plotPlacebo**

*Draw a (density) plot of placebo tests*

### Description

Draw a plot of placebo tests, estimating the impact on fake cutpoints

### Usage

```r
plotPlacebo(object, device = c("ggplot", "base"), ...)
```

```r
## S3 method for class 'rdd_reg'
plotPlacebo(
  object,
  device = c("ggplot", "base"),
  from = 0.25,
  to = 0.75,
  by = 0.1,
  level = 0.95,
  same_bw = FALSE,
  vcov. = NULL,
  plot = TRUE,
  output = c("data", "ggplot"),
  ...
)
```

```r
plotPlaceboDens(object, device = c("ggplot", "base"), ...)
```

```r
## S3 method for class 'rdd_reg'
plotPlaceboDens(
  object,
  device = c("ggplot", "base"),
  from = 0.25,
  to = 0.75,
  by = 0.1,
  level = 0.95,
  same_bw = FALSE,
  vcov. = NULL,
  ...
)
```
computePlacebo(
  object,
  from = 0.25,
  to = 0.75,
  by = 0.1,
  level = 0.95,
  same_bw = FALSE,
  vcov. = NULL
)

Arguments

object the output of an RDD regression
device Whether to draw a base or a ggplot graph.
from Starting point of the fake cutpoints sequence. Refers ot the quantile of each side of the true cutpoint
to Ending point of the fake cutpoints sequence. Refers ot the quantile of each side of the true cutpoint
by Increments of the from-to sequence
level Level of the confidence interval shown
same_bw Whether to re-estimate the bandwidth at each point
vcov. Specific covariance function to pass to coeftest. See help of package sandwich.
plot Whether to actually plot the data.
output Whether to return (invisibly) the data frame containing the bandwidths and corresponding estimates, or the ggplot object
... Further arguments passed to specific methods.

Value

A data frame containing the cutpoints, their corresponding estimates and confidence intervals.

Author(s)

Matthieu Stigler <<Matthieu.Stigler@gmail.com>>

Examples

data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)
reg_nonpara <- rdd_reg_np(rdd_object=house_rdd)
plotPlacebo(reg_nonpara)

# Use with another vcov function; cluster case
reg_nonpara_lminf <- rdd_reg_np(rdd_object=house_rdd, inference='lm')
# need to be a function applied to updated object!
vc <- function(x) vcovCluster(x, clusterVar=model.frame(x)$x)
plotPlacebo(reg_nonpara_lminf, vcov. = vc)
Plot the sensitivity to the bandwidth

Description

Draw a plot showing the LATE estimates depending on multiple bandwidths.

Usage

```r
plotSensi(
  rdd_regobject,  # required
  from,  # required
  to,  # required
  by = 0.01,  # default 0.01
  level = 0.95,  # default 0.95
  output = c("data", "ggplot"),  # default "data"
  plot = TRUE,  # default TRUE
  ...  # additional arguments
)
```

## S3 method for class 'rdd_reg_np'
```r
plotSensi(
  rdd_regobject,  # required
  from,  # required
  to,  # required
  by = 0.05,  # default 0.05
  level = 0.95,  # default 0.95
  output = c("data", "ggplot"),  # default "data"
  plot = TRUE,  # default TRUE
  device = c("ggplot", "base"),  # default "ggplot"
  vcov. = NULL,  # default NULL
  ...  # additional arguments
)
```

## S3 method for class 'rdd_reg_lm'
```r
plotSensi(
  rdd_regobject,  # required
  from,  # required
  to,  # required
  by = 0.05,  # default 0.05
  level = 0.95,  # default 0.95
  output = c("data", "ggplot"),  # default "data"
  plot = TRUE,  # default TRUE
  order,  # default order
  type = c("colour", "facet"),  # default "colour"
  ...  # additional arguments
)
```
Arguments

- **rdd_regobject**: object of an RDD regression, from either `rdd_reg_lm` or `rdd_reg_np`
- **from**: First bandwidth point. Default value is `max(1e-3, bw-0.1)`
- **to**: Last bandwidth point. Default value is `bw+0.1`
- **by**: Increments in the from to sequence
- **level**: Level of the confidence interval
- **output**: Whether to return (invisibly) the data frame containing the bandwidths and corresponding estimates, or the ggplot object
- **plot**: Whether to actually plot the data.
- **device**: Whether to draw a base or a ggplot graph.
- **vcov.**: Specific covariance function to pass to `coeftest`. See help of package `sandwich`
- **order**: For parametric models (from `rdd_reg_lm`), the order of the polynomial.
- **type**: For parametric models (from `rdd_reg_lm`) whether different orders are represented as different colour or as different facets.
- **...**: Further arguments passed to specific methods

**Value**

A data frame containing the bandwidths and corresponding estimates and confidence intervals.

**Author(s)**

Mathieu Stigler <<Matthieu.Stigler@gmail.com>>

**Examples**

```r
data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)

#Non-parametric estimate
bw_ik <- rdd_bw_ik(house_rdd)
reg_nonpara <- rdd_reg_np(rdd_object=house_rdd, bw=bw_ik)
plotSensi(reg_nonpara)
plotSensi(reg_nonpara, device='base')

#Parametric estimate:
reg_para_ik <- rdd_reg_lm(rdd_object=house_rdd, order=4, bw=bw_ik)
plotSensi(reg_para_ik)
plotSensi(reg_para_ik, type='facet')
```

**Description**

Set of functions for Regression Discontinuity Design (RDD), for data visualisation, estimation and testing.
Description


Usage

```r
rdd_bw_cct_estim(
  rdd_object,
  method = c("mserd", "msetwo", "msesum", "msecomb1", "msecomb2", "cerrd", "certwo", "cersum", "cercomb1"),
  kernel = c("Triangular", "Uniform", "Epanechnikov"),
  ...)
```

Arguments

- `rdd_object` of class `rdd_data` created by `rdd_data`
- `method` The type of method used. See
- `kernel` The type of kernel used: either Triangular, Uniform or Epanechnikov.
- `...` further arguments passed to `rdbwselect`.

Value

See documentation of `rdbwselect`

Author(s)

Original code written by Calonico, Cattaneo, Farrell and Titiuni, see `rdbwselect`

References


See Also

- `rdd_bw_ik` Local RDD bandwidth selector using the plug-in method of Imbens and Kalyanaraman (2012)
Examples

```r
data(house)
rd<- rdd_data(x=house$x, y=house$y, cutpoint=0)
rdd_bw_cct_estim(rd)
```

Description


Usage

```r
rdd_bw_cct_plot(
  rdd_object,
  method = c("esmv", "es", "espr", "esmvpr", "qs", "qspr", "qsmv", "qsmvprier"),
  ...
)
```

Arguments

- `rdd_object` of class `rdd_data` created by `rdd_data`
- `method` The type of method used. See `rdplot`. Default is `esmv`, the variance mimicking evenly-spaced method.
- `...` further arguments passed to `rdplot`.

Value

See documentation of `rdplot`

Author(s)

Original code written by Calonico, Cattaneo, Farrell and Titiuni, see `rdplot`

References


See Also

`rdd_bw_ik` Local RDD bandwidth selector using the plug-in method of Imbens and Kalyanaraman (2012)
Examples

```r
data(house)
rd <- rdd_data(x=house$x, y=house$y, cutpoint=0)
rdd_bw_cct_plot(rd)
```

---

**rdd_bw_ik**  
*Imbens-Kalyanaraman Optimal Bandwidth Calculation*

**Description**

Imbens-Kalyanaraman optimal bandwidth for local linear regression in Regression discontinuity designs.

**Usage**

```r
rdd_bw_ik(rdd_object, kernel = c("Triangular", "Uniform", "Normal"))
```

**Arguments**

- `rdd_object`: of class `rdd_data` created by `rdd_data`
- `kernel`: The type of kernel used: either `triangular` or `uniform`.

**Value**

The optimal bandwidth

**Author(s)**

Matthieu Stigler <<Matthieu.Stigler@gmail.com>>

**References**


**See Also**

`rdd_bw_rsw` Global bandwidth selector of Ruppert, Sheather and Wand (1995)

**Examples**

```r
data(house)
rd <- rdd_data(x=house$x, y=house$y, cutpoint=0)
rdd_bw_ik(rd)
```
**rdd_bw_rsw**

*Global bandwidth selector of Ruppert, Sheather and Wand (1995)*

*from package KernSmooth*

---

**Description**

Uses the global bandwidth selector of Ruppert, Sheather and Wand (1995) either to the whole function, or to the functions below and above the cutpoint.

**Usage**

```r
rdd_bw_rsw(object, type = c("global", "sided"))
```

**Arguments**

- `object`: object of class `rdd_data` created by `rdd_data`
- `type`: Whether to choose a global bandwidth for the whole function (`global`) or for each side (`sided`)

**Value**

One (or two for `sided`) bandwidth value.

**References**

See `dpill`

**See Also**

- `rdd_bw_ik` Local RDD bandwidth selector using the plug-in method of Imbens and Kalyanaraman (2012)

**Examples**

```r
data(house)
rd<- rdd_data(x=house$x, y=house$y, cutpoint=0)
rdd_bw_rsw(rd)
```
**rdd_coef** | **RDD coefficient**

**Description**

Function to access the RDD coefficient in the various regressions.

**Usage**

```r
rdd_coef(object, allInfo = FALSE, allCo = FALSE, ...)
```

## Default S3 method:

```r
rdd_coef(object, allInfo = FALSE, allCo = FALSE, ...)
```

## S3 method for class 'rdd_reg_np'

```r
rdd_coef(object, allInfo = FALSE, allCo = FALSE, ...)
```

**Arguments**

- `object`: A RDD regression object
- `allInfo`: whether to return just the coefficients (allInfo=FALSE) or also the se/t stat/pval.
- `allCo`: Whether to give only the RDD coefficient (allCo=FALSE) or all coefficients
- `...`: Further arguments passed to/from specific methods

**Value**

Either a numeric value of the RDD coefficient estimate, or a data frame with the estimate, its standard value, t test and p-value and

---

**rdd_data** | **Construct rdd_data**

**Description**

Construct the base RDD object, containing x, y and the cutpoint, eventually covariates.

**Usage**

```r
rdd_data(y, x, covar, cutpoint, z, labels, data)
```
**Arguments**

- **y**: Output
- **x**: Forcing variable
- **covar**: Exogeneous variables
- **cutpoint**: Cutpoint
- **z**: Assignment variable for the fuzzy case. Should be 0/1 or TRUE/FALSE variable.
- **labels**: Additional labels to provide as list (with entries x, y, and eventually vector covar). Unused currently.
- **data**: A data-frame for the x and y variables. If this is provided, the column names can be entered directly for argument x and y

**Value**

Object of class `rdd_data`, inheriting from data.frame

**Author(s)**

Matthieu Stigler <<Matthieu.Stigler@gmail.com>>

**Examples**

```r
data(house)
rd<- rdd_data(x=house$x, y=house$y, cutpoint=0)
rd2 <- rdd_data(x=x, y=y, data=house, cutpoint=0)

# The print() function is the same as the print.data.frame:
rd

# The summary() and plot() function are specific to rdd_data
summary(rd)
plot(rd)

# for the fuzzy case, you need to specify the assignment variable z:
rd_dat_fakefuzzy <- rdd_data(x=house$x, y=house$y,
                             z=ifelse(house$x>0+rnorm(nrow(house), sd=0.05),1,0),
                             cutpoint=0)
summary(rd_dat_fakefuzzy)
```

---

**rdd_gen_reg**

*General polynomial estimator of the regression discontinuity*

**Description**

Compute RDD estimate allowing a locally kernel weighted version of any estimation function possibly on the range specified by bandwidth
Usage

```
rdd_gen_reg(
  rdd_object,
  fun = glm,
  covariates = NULL,
  order = 1,
  bw = NULL,
  slope = c("separate", "same"),
  covar.opt = list(strategy = c("include", "residual"), slope = c("same", "separate"),
                     bw = NULL),
  weights,
  ...
)
```

Arguments

- **rdd_object**: Object of class rdd_data created by `rdd_data`
- **fun**: The function to estimate the parameters
- **covariates**: Formula to include covariates
- **order**: Order of the polynomial regression.
- **bw**: A bandwidth to specify the subset on which the kernel weighted regression is estimated
- **slope**: Whether slopes should be different on left or right (separate), or the same.
- **covar.opt**: Options for the inclusion of covariates. Way to include covariates, either in the main regression (include) or as regressors of y in a first step (residual).
- **weights**: Optional weights to pass to the lm function. Note this cannot be entered together with `bw`
- **...**: Further arguments passed to `fun`. See the example.

Details

This function allows the user to use a custom estimating function, instead of the traditional `lm()`. It is assumed that the custom function has following behaviour:

1. A formula interface, together with a `data` argument
2. A `weight` argument
3. `coef(summary(x))` returning a data-frame containing a column Estimate

Note that for the last requirement, this can be accommodated by writing a specific `rdd_coef` function for the class of the object returned by `fun`.

Value

An object of class rdd_reg_lm and class lm, with specific print and plot methods
Examples

```r
## Step 0: prepare data
data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)

## Estimate a local probit:
house_rdd$y <- with(house_rdd, ifelse(y<quantile(y, 0.25), 0,1))
reg_bin_glm <- rdd_gen_reg(rdd_object=house_rdd, fun= glm, family=binomial(link='probit'))
print(reg_bin_glm)
summary(reg_bin_glm)
```

## rdd_pred

**RDD coefficient prediction**

**Description**

Function to predict the RDD coefficient in presence of covariate (without covariates, returns the same than rdd_coef)

**Usage**

```r
rdd_pred(
  object,
  covdata,
  se.fit = TRUE,
  vcov. = NULL,
  newdata,
  stat = c("identity", "sum", "mean"),
  weights
)
```

**Arguments**

- **object**: A RDD regression object
- **covdata**: New data.frame specifying the values of the covariates, can have multiple rows.
- **se.fit**: A switch indicating if standard errors are required.
- **vcov.**: Specific covariance function (see package sandwich ), by default uses the \texttt{vcov}
- **newdata**: Another data on which to evaluate the x/D variables. Useful in very few cases.
- **stat**: The statistic to use if there are multiple predictions, ‘identity’ just returns the single values, ‘mean’ averages them
- **weights**: Eventual weights for the averaging of the predicted values.
Details

The function rdd_pred does a simple prediction of the RDD effect

$$RDDeffect = \mu(x, z, D = 1) - \mu(x, z, D = 0)$$

When there are no covariates (and $z$ is irrelevant in the equation above), this amounts exactly to the usual RDD coefficient, shown in the outputs, or obtained with rdd_coef. If there were covariates, and if these covariates were estimated using the “include” strategy and with different coefficients left and right to the cutoff (i.e. had argument slope = “separate”), then the RDD effect is also dependent on the value of the covariate(s). rdd_pred allows to set the value of the covariate(s) at which to evaluate the RDD effect, by providing a data.frame with the values for the covariates. Note that the effect can be evaluated at multiple points, if you provide multiple rows of covdata.

In presence of covariate-specific RDD effect, one may wish to estimate an average effect. This can be done by setting the argument stat='mean'. Weights can additionally be added, with the argument weights, to obtain a weighted-average of the predictions. Note however that in most cases, this will be equivalent to provide covariates at their (weighted) mean value, which will be much faster also!

Standard errors, obtained setting the argument se.fit=TRUE, are computed using following formula:

$$x_i \Omega x_i'$$

where $\Omega$ is the estimated variance-covariance matrix ( by default $\sigma^2(X'X)^{-1}$ using vcov) and $x_i$ is the input data (a mix of covdata and input data). If one wishes individual predictions, standard errors are simply obtained as the square of that diagonal matrix, whereas for mean/sum, covariances are taken into account.

Value

Returns the predicted value(s), and, if se.fit=TRUE, their standard errors.

References

Froehlich (2007) Regression discontinuity design with covariates, IZA discussion paper 3024

Examples

# Load data, add (artificial) covariates:
data(house)
n_Lee <- nrow(house)
z1 <- runif(n_Lee)
house_rdd <- rdd_data(y=y, x=x, data=house, covar=z1, cutpoint=0)

# estimation without covariates: rdd_pred is the same than rdd_coef:
reg_para <- rdd_reg_lm(rdd_object=house_rdd)
rdd_pred(reg_para)
rdd_coef(reg_para, allInfo=TRUE)

# estimation with covariates:
reg_para_cov <- rdd_reg_lm(rdd_object=house_rdd,
### rdd_reg_lm

**Parametric polynomial estimator of the regression discontinuity**

**Description**

Compute a parametric polynomial regression of the ATE, possibly on the range specified by bandwidth

**Usage**

```r
rdd_reg_lm(
  rdd_object,
  covariates = NULL,
  order = 1,
  bw = NULL,
  slope = c("separate", "same"),
  covar.opt = list(strategy = c("include", "residual"), slope = c("same", "separate"),
                   bw = NULL),
  covar.strat = c("include", "residual"),
  weights
)
```

**Arguments**

- **rdd_object**: Object of class rdd_data created by `rdd_data`
- **covariates**: Formula to include covariates
- **order**: Order of the polynomial regression.
- **bw**: A bandwidth to specify the subset on which the parametric regression is estimated
- **slope**: Whether slopes should be different on left or right (separate), or the same.
- **covar.opt**: Options for the inclusion of covariates. Way to include covariates, either in the main regression (include) or as regressors of y in a first step (residual).
- **covar.strat**: DEPRECATED, use covar.opt instead.
- **weights**: Optional weights to pass to the lm function. Note this cannot be entered together with bw
Details

This function estimates the standard discontinuity regression:

\[ Y = \alpha + \tau D + \beta_1 (X - c) + \beta_2 D(X - c) + \epsilon \]

with \( \tau \) the main parameter of interest. Several versions of the regression can be estimated, either restricting the slopes to be the same, i.e. \( \beta_1 = \beta_2 \) (argument slope). The order of the polynomial in \( X - c \) can also be adjusted with argument order. Note that a value of zero can be used, which corresponds to the simple difference in means, that one would use if the samples were random. Covariates can also be added in the regression, according to the two strategies discussed in Lee and Lemieux (2010, sec 4.5), through argument covar.strat:

include  Covariates are simply added as supplementary regressors in the RD equation
residual  The dependent variable is first regressed on the covariates only, then the RDD equation is applied on the residuals from this first step

The regression can also be estimated in a neighborhood of the cutpoint with the argument bw. This make the parametric regression resemble the non-parametric local kernel rdd_reg_np. Similarly, weights can also be provided (but not simultaneously to bw).

The returned object is a classical lm object, augmented with a RDDslot, so usual methods can be applied. As is done in general in R, heteroskedasticity-robust inference can be done later on with the usual function from package sandwich. For the case of clustered observations a specific function clusterInf is provided.

Value

An object of class rdd_reg_lm and class lm, with specific print and plot methods

Examples

```r
## Step 0: prepare data
data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)

## Step 2: regression
# Simple polynomial of order 1:
reg_para <- rdd_reg_lm(rdd_object=house_rdd)
print(reg_para)
plot(reg_para)

# Simple polynomial of order 4:
reg_para4 <- rdd_reg_lm(rdd_object=house_rdd, order=4)
reg_para4
plot(reg_para4)

# Restrict sample to bandwidth area:
bw_ik <- rdd_bw_ik(house_rdd)
reg_para_ik <- rdd_reg_lm(rdd_object=house_rdd, bw=bw_ik, order=4)
reg_para_ik
plot(reg_para_ik)
```
**rdd_reg_np**

**Parametric polynomial estimator of the regression discontinuity**

**Description**

Compute a parametric polynomial regression of the ATE, possibly on the range specified by bandwidth.

**Usage**

```r
rdd_reg_np(
  rdd_object,  
  covariates = NULL,  
  bw = rdd_bw_ik(rdd_object),  
  slope = c("separate", "same"),  
  inference = c("np", "lm"),  
  covar.opt = list(slope = c("same", "separate"), bw = NULL)
)
```

**Arguments**

- **rdd_object**: Object of class rdd_data created by `rdd_data`
- **covariates**: TODO
- **bw**: A bandwidth to specify the subset on which the parametric regression is estimated.
- **slope**: Whether slopes should be different on left or right (separate), or the same.
- **inference**: Type of inference to conduct: non-parametric one (np) or standard (lm). See details.
- **covar.opt**: Options for the inclusion of covariates. Way to include covariates, either in the main regression (include) or as regressors of y in a first step (residual).

**Value**

An object of class `rdd_reg_np` and class `lm`, with specific print and plot methods.

**References**

TODO

**See Also**

- `rdd_bw_ik` Bandwidth selection using the plug-in bandwidth of Imbens and Kalyanaraman (2012)
Examples

```r
## Step 0: prepare data
data(house)
house_rdd <- rdd_data(y=house$y, x=house$x, cutpoint=0)

## Step 2: regression
# Simple polynomial of order 1:
reg_nonpara <- rdd_reg_np(rdd_object=house_rdd)
print(reg_nonpara)
plot(reg_nonpara)
```

---

### rot_bw

#### Bandwidth selector

**Description**

implements dpill

**Usage**

`rot_bw(object)`

**Arguments**

- `object` object of class rdd_data

**References**


**Examples**

```r
#No discontinuity
```

---

### STAR_MHE

Transformation of the STAR dataset as used in Angrist and Pischke (2008)

**Description**

Transformation of the STAR dataset as used in Table 8.2.1 of Angrist and Pischke (2008)
Format

A data frame containing 5743 observations and 6 variables. The first variable is from the original dataset, all other are created by Angrist and Pischke STAT code.

- **schidkn**: School ID in kindergarten (original variable, schoolidk in STAR)
- **pscore**: The propensity score (computed by A & P)
- **classid**: The id of the class (computed by A & P)
- **cs**: Class size (computed by A & P)
- **female, nwhite**: Various covariates (computed by A & P)

Details

This is a transformation of the dataset from the project STAR (Student/Teacher Achievement Ratio). The full dataset is described and available in package AER, STAR. The transformed data was obtained using the STATA script krueger.do, obtained from Joshua Angrist website (https://economics.mit.edu/faculty/angrist/data1/mhe/krueger), on the webstar.dta.

Source

Data obtained using the script krueger.do on data webstar.rda, found on J. Angrist website https://economics.mit.edu/faculty/angrist/data1/mhe/krueger, retrieved on 26 November 2012.

References


See Also

- STAR for the original dataset.

Examples

data(STAR_MHE)

# Compute the group means:
STAR_MHE_means <- aggregate(STAR_MHE[, c('classid', 'pscore', 'cs')],
by=list(STAR_MHE$classid), mean)

# Regression of means, with weighted average:
reg_krug_gls <- lm(pscore~cs, data=STAR_MHE_means, weights=cs)
coef(summary(reg_krug_gls))[2,2]
vcovCluster  

Cluster Heteroskedasticity-consistent estimation of the covariance matrix.

Description

Offer a cluster variant of the usual Heteroskedasticity-consistent

Usage

vcovCluster(object, clusterVar)

vcovCluster2(object, clusterVar1, clusterVar2)

Arguments

object Object of class lm, from which rdd_reg also inherits.
clusterVar The variable containing the cluster attributions.
clusterVar1, clusterVar2 The two cluster variables for the 2-cluster case.

Value

A matrix containing the covariance matrix estimate.

Author(s)

Mahmood Arai, see http://people.su.se/~ma/econometrics.html

References


See Also

clusterInf for a direct function, allowing also alternative cluster inference methods.
Examples

```r
data(STAR_MHE)
if(all(c(require(sandwich), require(lmtest)))){
  # Run simple regression:
  reg_krug <- lm(pscore~cs, data=STAR_MHE)
  # Row 1 of Table 8.2.1, inference with standard vcovHC:
  coeftest(reg_krug, vcov.=vcovHC(reg_krug, 'HC1'))[2,2]
  # Row 4 of Table 8.2.1, inference with cluster vcovHC:
  coeftest(reg_krug, vcov.=vcovCluster(reg_krug, clusterVar=STAR_MHE$classid))[2,2]
}
```

**waldci**

Confint allowing vcov

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Version of vcov allowing for confint</td>
</tr>
</tbody>
</table>

**Usage**

`waldci(x, parm=NULL, level=0.95, vcov=NULL, df=NULL, ...)`

**Arguments**

- `x` Object of class `lm` or else
- `parm` specification of which parameters are to be given confidence intervals, see `confint`
- `level` the confidence level required, see `confint()`
- `vcov.` Specific covariance function to pass to `coeftest`. See help of `sandwich`
- `df` Degrees of freedom
- `...` Further arguments
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