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.
as.npregbw

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

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 Epanechinkov 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

```r
# 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

```r
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.
- ...

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"))

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 currently not used
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

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

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,
covarTest_mean

```r
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
- `...` currently not used

**Value**

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

**Author(s)**

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

**See Also**

covarTest_dis for the Kolmogorov-Smirnov test of equality of distribution

**Examples**

data(house)

```r
## 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)

---

gen_mc_ik

*Generate Monte Carlo simulations of Imbens and Kalyanaraman*

### Description

Generate the simulations reported in Imbens and Kalyanaraman (2012)

### Usage

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

n The size of sampel to generate
version The MC version of Imbens and Kalnayaraman (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

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$x),]
  ylim <- range(subset(res, x>=min(xlim) & x<=max(xlim), 'y'))
  plot(res, type='l', xlim=xlim, ylim=ylim, main=paste('DGP', version))
  abline(v=0)
  xCut <- res[which(res$x==min(res$x[0]))]+c(0,-1),]
  points(xCut, col=2)
}
layout(matrix(1:4, 2, byrow=TRUE))
plotCu(version=1)
plotCu(version=2)
plotCu(version=3)
plotCu(version=4)
layout(matrix(1))

house

Dataset used in Lee (2008)

Description

Randomized experiments from non-random selection in U.S. House elections
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: http://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)

indh

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: http://qua.st/Development-Aid-Social-Dynamics

References

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

# 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) )
plot(reg_np_indh)

---

plot.rdd_data  

Description

Binned plot of the forcing and outcome variable

Usage

## S3 method for class 'rdd_data'
plot(x, h, 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

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

## Specify manually the bandwidth:
plot(house_rdd, h=0.2)

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

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

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

plotBin  

### Bin plotting

Description

Do a 'scatterplot bin smoothing'

Usage

plotBin(x, y, h = 0.05, 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*sd(runvar)*length(runvar)^(-.5))
nbins number of Bins
cutpoint Cutpoint
plot   Logical. Whether to plot or only returned silently
**plotPlacebo**

- **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"), ...)
```

```
## 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"), ...)
```

```
## 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, ...)
```

```r
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 to the quantile of each side of the true cutpoint
to

Ending point of the fake cutpoints sequence. Refers to 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)

---

plotSensi

Plot the sensitivity to the bandwidth

Description

Draw a plot showing the LATE estimates depending on multiple bandwidths

Usage

plotSensi(rdd_regobject, from, to, by = 0.01, level = 0.95,
    output = c("data", "ggplot"), plot = TRUE, ...)

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

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

Arguments

rdd_regobject object of a 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 <<Mathieu.Stigler@gmail.com>>

Examples

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')
## rdd_bw_ik

### Description
Regression Discontinuity Design

### 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**

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

```r
default S3 method:
rdd_coef(object, allInfo = FALSE, allCo = FALSE, ...)
```

**S3 method for class 'rdd_reg_np'**

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**

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.
- **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

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)

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. A `coef(summary(x))` returning a data-frame containing a column `Estimate`

Note that for the last requirement, this can be accomodated 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

References

TODO

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)
```
**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 `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

\[
\text{RDD effect} = \mu(x, z, D = 1) - \mu(x, z, D = 0)
\]

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”), than 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**

```r
# 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,
 covariates='z1',
 covar.opt=list(slope='separate'))

# should obtain same result as with RDesign
rdd_pred(reg_para_cov, covdata=data.frame(z1=0))

# evaluate at mean of z1 (as comes from uniform)
rdd_pred(reg_para_cov, covdata=data.frame(z1=0.5))
```

### 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
ddd_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 Rdds1ot, 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).
rot_bw

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
```r
rot_bw(object)
```

Arguments
```r
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)

### Usage

`STAR_MHE`

### 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 kindergarden (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 [http://economics.mit.edu/faculty/angrist/data1/mhe/krueger](http://economics.mit.edu/faculty/angrist/data1/mhe/krueger), on the webstar.dta.

### Source


### References


### See Also

`STAR` for the original dataset.
vcovCluster

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

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

Description

Version of vcov allowing for confint

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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