Package ‘qte’

October 13, 2022

Title  Quantile Treatment Effects
Version  1.3.1
Description  Provides several methods for computing the Quantile Treatment Effect (QTE) and Quantile Treatment Effect on the Treated (QTT). The main cases covered are (i) Treatment is randomly assigned, (ii) Treatment is as good as randomly assigned after conditioning on some covariates (also called conditional independence or selection on observables) using the methods developed in Firpo (2007) <doi:10.1111/j.1468-0262.2007.00738.x>, (iii) Identification is based on a Difference in Differences assumption (several varieties are available in the package e.g. Athey and Imbens (2006) <doi:10.1111/j.1468-0262.2006.00668.x> Callaway and Li (2019) <doi:10.3982/QE935>, Callaway, Li, and Oka (2018) <doi:10.1016/j.jeconom.2018.06.008>.

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R topics documented:

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Description

bounds estimates bounds for the Quantile Treatment Effect on the Treated (QTET) using the method of Fan and Yu (2012).

Usage

```
bounds(
  formula,
  xformla = NULL,
  t,
  tmin1,
  tname,
```
bounds

data,  
idname,  
probs = seq(0.05, 0.95, 0.05)
)

Arguments

formula The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated

xformula A optional one sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the x parameter.

t The 3rd time period in the sample. Treated individuals should be treated in this time period and untreated individuals should not be treated. The code attempts to enforce this condition, but it is good try to handle this outside the panel.qtet method.

tmin1 The 2nd time period in the sample. This should be a pre-treatment period for all individuals in the sample.

tname The name of the column containing the time periods

data A data.frame containing all the variables used

idname The individual (cross-sectional unit) id name

probs A vector of values between 0 and 1 to compute the QTET at

Value

A BoundsObj object

References


Examples

## load the data
data(lalonde)

## Run the bounds method with no covariates
b1 <- bounds(re ~ treat, t=1978, tmin1=1975, data=lalonde.psid.panel,  
idname="id", tname="year")
summary(b1)
The ci.qte method implements estimates the Quantile Treatment Effect (QTE) under a Conditional Independence Assumption (sometimes this is called Selection on Observables) developed in Firpo (2007). This method using propensity score re-weighting and minimizes a check function to compute the QTET. Standard errors (if requested) are computed using the bootstrap.

**Usage**

```r
ci.qte(
  formla,  
  xformla = NULL, 
  x = NULL,  
  data,  
  w = NULL,  
  probs = seq(0.05, 0.95, 0.05),  
  se = TRUE,  
  iters = 100,  
  alp = 0.05,  
  method = "logit",  
  retEachIter = FALSE,  
  printIter = FALSE,  
  pl = FALSE,  
  cores = 2)
```

**Arguments**

- `formla` The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated
- `xformla` A optional one sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the x paramater.
- `x` Vector of covariates. Default is no covariates
- `data` A data.frame containing all the variables used
- `w` an additional vector of sampling weights
- `probs` A vector of values between 0 and 1 to compute the QTET at
- `se` Boolean whether or not to compute standard errors
- `iters` The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE
- `alp` The significance level used for constructing bootstrap confidence intervals
ci.qtet

<table>
<thead>
<tr>
<th>method</th>
<th>Method to compute propensity score. Default is logit; other option is probit.</th>
</tr>
</thead>
<tbody>
<tr>
<td>retEachIter</td>
<td>Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.</td>
</tr>
<tr>
<td>printIter</td>
<td>For debugging only; should leave at default FALSE unless you want to see a lot of output</td>
</tr>
<tr>
<td>pl</td>
<td>boolean for whether or not to compute bootstrap error in parallel. Note that computing standard errors in parallel is a new feature and may not work at all on Windows.</td>
</tr>
<tr>
<td>cores</td>
<td>the number of cores to use if bootstrap standard errors are computed in parallel</td>
</tr>
</tbody>
</table>

### Value

QTE object

### References


### Examples

```r
## Load the data
data(lalonde)

##Estimate the QTET of participating in the job training program;
##This is the no covariate case. Note: Because individuals that participate
##in the job training program are likely to be much different than
##individuals that do not (e.g. less experience and less education), this
##method is likely to perform poorly at estimating the true QTET
q1 <- ci.qte(re78 ~ treat, x=NULL, data=lalonde.psid, se=FALSE, probs=seq(0.05,0.95,0.05))
summary(q1)

##This estimation controls for all the available background characteristics.
q2 <- ci.qte(re78 ~ treat,
            xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
data=lalonde.psid, se=FALSE, probs=seq(0.05, 0.95, 0.05))
summary(q2)
```

### Description

The ci.qtet method implements estimates the Quantile Treatment Effect on the Treated (QTET) under a Conditional Independence Assumption (sometimes this is called Selection on Observables) developed in Firpo (2007). This method using propensity score re-weighting and minimizes a check function to compute the QTET. Standard errors (if requested) are computed using the bootstrap.
Usage

ci.qtet(
  formula,  # The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated
  xformula = NULL,  # A optional one sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the x paramater.
  w = NULL,  # an additional vector of sampling weights
  data,  # A data.frame containing all the variables used
  probs = seq(0.05, 0.95, 0.05),  # A vector of values between 0 and 1 to compute the QTET at
  se = TRUE,  # Boolean whether or not to compute standard errors
  iters = 100,  # The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE
  alp = 0.05,  # The significance level used for constructing bootstrap confidence intervals
  method = "logit",  # Method to compute propensity score. Default is logit; other option is probit.
  retEachIter = FALSE,  # Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.
  indsample = TRUE,  # Binary variable for whether to treat the samples as independent or dependent. This affects bootstrap standard errors. In the job training example, the samples are independent because they are two samples collected independently and then merged. If the data is from the same source, usually should set this option to be FALSE.
  printIter = FALSE,  # For debugging only; should leave at default FALSE unless you want to see a lot of output
  pl = FALSE,  # Whether or not to compute standard errors in parallel
  cores = 2  # Number of cores to use if computing in parallel
)

Arguments

formula The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated

xformula A optional one sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the x paramater.

w an additional vector of sampling weights

data A data.frame containing all the variables used

probs A vector of values between 0 and 1 to compute the QTET at

se Boolean whether or not to compute standard errors

iters The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE

alp The significance level used for constructing bootstrap confidence intervals

method Method to compute propensity score. Default is logit; other option is probit.

retEachIter Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.

indsample Binary variable for whether to treat the samples as independent or dependent. This affects bootstrap standard errors. In the job training example, the samples are independent because they are two samples collected independently and then merged. If the data is from the same source, usually should set this option to be FALSE.

printIter For debugging only; should leave at default FALSE unless you want to see a lot of output

pl Whether or not to compute standard errors in parallel

cores Number of cores to use if computing in parallel
**Value**

QTE object

**References**


**Examples**

```r
## Load the data
data(lalonde)

## Estimate the QTET of participating in the job training program;
## This is the no covariate case. Note: Because individuals that participate
## in the job training program are likely to be much different than
## individuals that do not (e.g. less experience and less education), this
## method is likely to perform poorly at estimating the true QTET
q1 <- ci.qtet(re78 ~ treat, x=NULL, data=lalonde.psid, se=FALSE,
              probs=seq(0.05,0.95,0.05))
summary(q1)

## This estimation controls for all the available background characteristics.
q2 <- ci.qtet(re78 ~ treat,
             xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
             data=lalonde.psid, se=FALSE, probs=seq(0.05, 0.95, 0.05))
summary(q2)
```

---

**CiC**

**Change in Changes**

**Description**

CiC computes the Quantile Treatment Effect on the Treated (QTET) using the method of Athey and Imbens (2006). CiC is a Difference in Differences type method. It requires having two periods of data that can be either repeated cross sections or panel data.

The method can accommodate conditioning on covariates though it does so in a restrictive way: It specifies a linear model for outcomes conditional on group-time dummies and covariates. Then, after residualizing (see details in Athey and Imbens (2006)), it computes the Change in Changes model based on these quasi-residuals.

**Usage**

```r
CiC(
   formula,
   xformla = NULL,
   t,
   ...)
```
```r
min1, tname, data, 
panel = FALSE, 
se = TRUE, 
idname = NULL, 
alp = 0.05, 
probs = seq(0.05, 0.95, 0.05), 
iters = 100, 
pl = FALSE, 
cores = 2, 
retEachIter = FALSE
)

Arguments

formla The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated

xformla A optional one sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the x paramater.

t The 3rd time period in the sample. Treated individuals should be treated in this time period and untreated individuals should not be treated. The code attempts to enforce this condition, but it is good try to handle this outside the panel.qtet method.

tmin1 The 2nd time period in the sample. This should be a pre-treatment period for all individuals in the sample.

tname The name of the column containing the time periods

data A data.frame containing all the variables used

panel Binary variable indicating whether or not the dataset is panel. This is used for computing bootstrap standard errors correctly.

se Boolean whether or not to compute standard errors

idname The individual (cross-sectional unit) id name

alp The significance level used for constructing bootstrap confidence intervals

probs A vector of values between 0 and 1 to compute the QTET at

iters The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE

pl Whether or not to compute standard errors in parallel

cores Number of cores to use if computing in parallel

retEachIter Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.
compute.panel.qtet

Value

QTE Object

References


Examples

```r
## load the data
data(lalonde)
## Run the Change in Changes model conditioning on age, education,
## black, hispanic, married, and nodegree
cl <- CiC(re ~ treat, t=1978, tmin1=1975, tname="year",
xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
data=lalonde.psid.panel, idname="id", se=FALSE,
probs=seq(0.05, 0.95, 0.05))
summary(cl)
```

Description

compute.panel.qtet uses third period of data, combined with Distributional Difference in Differences assumption (Fan and Yu, 2012) to point identify QTET.

Usage

`compute.panel.qtet(qp)`

Arguments

- `qp` QTEparams object containing the parameters passed to ciqte

Value

QTE object
computeDiffSE

Description
Takes two sets of initial estimates and bootstrap estimations (they need to have the same number of iterations) and determines whether or not the estimates are statistically different from each other. It can be used to compare any sets of estimates, but it is particularly used here to compare estimates from observational methods with observations from the experimental data (which also have standard errors because, even though the estimates are cleanly identified, they are still estimated).

Usage
```r
computeDiffSE(est1, bootIters1, est2, bootIters2, alp = 0.05)
```

Arguments
- `est1`: A QTE object containing the first set of estimates
- `bootIters1`: A List of QTE objects that have been bootstrapped
- `est2`: A QTE object containing a second set of estimates
- `bootIters2`: A List of QTE objects that have been bootstrapped using the second method
- `alp`: The significance level used for constructing bootstrap confidence intervals

ddid2

Description
`ddid2` computes the Quantile Treatment Effect on the Treated (QTET) using the method of Callaway, Li, and Oka (2015).

Usage
```r
ddid2(
  formula,
  xformula = NULL,
  t,
  tmin1,
  tname,
  data,
  panel = TRUE,
  dropalwaystreated = TRUE,
  idname = NULL,
  probs = seq(0.05, 0.95, 0.05),
)```
ddid2

```r
iters = 100,
alp = 0.05,
method = "logit",
se = TRUE,
retEachIter = FALSE,
seedvec = NULL,
pl = FALSE,
cores = NULL
)
```

**Arguments**

- `formula` The formula `y ~ d` where `y` is the outcome and `d` is the treatment indicator (`d` should be binary)
- `xformula` A optional one sided formula for additional covariates that will be adjusted for. E.g `~ age + education`. Additional covariates can also be passed by name using the `x` parameter.
- `t` The 3rd time period in the sample (this is the name of the column)
- `tmin1` The 2nd time period in the sample (this is the name of the column)
- `tname` The name of the column containing the time periods
- `data` The name of the data.frame that contains the data
- `panel` Boolean indicating whether the data is panel or repeated cross sections
- `dropalwaysTreated` How to handle always treated observations in panel data case (not currently used)
- `idname` The individual (cross-sectional unit) id name
- `probs` A vector of values between 0 and 1 to compute the QTET at
- `iters` The number of iterations to compute bootstrap standard errors. This is only used if `se=TRUE`
- `alp` The significance level used for constructing bootstrap confidence intervals
- `method` The method for estimating the propensity score when covariates are included
- `se` Boolean whether or not to compute standard errors
- `retEachIter` Boolean whether or not to return list of results from each iteration of the bootstrap procedure
- `seedvec` Optional value to set random seed; can possibly be used in conjunction with bootstrapping standard errors.
- `pl` boolean for whether or not to compute bootstrap error in parallel. Note that computing standard errors in parallel is a new feature and may not work at all on Windows.
- `cores` the number of cores to use if bootstrap standard errors are computed in parallel

**Value**

QTE object
References

Examples
```r
##load the data
data(lalonde)

## Run the ddid2 method on the observational data with no covariates
d1 <- ddid2(re ~ treat, t=1978, tmin1=1975, tname="year",
data=lalonde.psid.panel, idname="id", se=FALSE,
probs=seq(0.05, 0.95, 0.05))
summary(d1)

## Run the ddid2 method on the observational data with covariates
d2 <- ddid2(re ~ treat, t=1978, tmin1=1975, tname="year",
data=lalonde.psid.panel, idname="id", se=FALSE,
xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
probs=seq(0.05, 0.95, 0.05))
summary(d2)
```

diffQ

diffQ
diffQ

Description
takes a single set of quantiles:
(not qtes as in diffquantiles) and returns the difference between particular ones

Usage
diffQ(qvec, tauvec, hightau, lowtau)

Arguments
qvec vector of quantiles
tauvec vector of tau (should be same length as qvec)
hightau upper quantile
lowtau lower quantile

Value
scalar difference between quantiles
**Description**

A distribution regression object

**Usage**

```r
DR(yvals, drlist)
```

**Arguments**

- `yvals`: A vector of values that `y` can take
- `drlist`: A list where for each value of `y`, a distribution regression

---

**ggqte**

**Description**

Makes somewhat nicer plots of quantile treatment effects by using ggplot

**Usage**

```r
ggqte(
    qteobj,
    main = "",
    ylab = "QTE",
    ylim = NULL,
    ybreaks = NULL,
    xbreaks = c(0.1, 0.3, 0.5, 0.7, 0.9),
    setype = "pointwise"
)
```

**Arguments**

- `qteobj`: a QTE object
- `main`: optional title
- `ylab`: optional y axis label
- `ylim`: optional limits of y axis
- `ybreaks`: optional breaks in y axis
- `xbreaks`: optional breaks in x axis
options are "pointwise", "uniform" or both; pointwise confidence intervals cover the QTE at each particular point with a fixed probability, uniform confidence bands cover the entire curve with a fixed probability. Uniform confidence bands will tend to be wider. The option "both" will plot both types of confidence intervals.

**Value**

a ggplot object

---

### lalonde

**Lalonde (1986)'s NSW Dataset**

**Description**

lalonde contains data from the National Supported Work Demonstration. This program randomly assigned applicants to the job training program (or out of the job training program). The dataset is discussed in Lalonde (1986). The experimental part of the dataset is combined with an observational dataset from the Panel Study of Income Dynamics (PSID). Lalonde (1986) and many subsequent papers (e.g. Heckman and Hotz (1989), Dehejia and Wahba (1999), Smith and Todd (2005), and Firpo (2007) have used this combination to study the effectiveness of various ‘observational’ methods (e.g. regression, Heckman selection, Difference in Differences, and propensity score matching) of estimating the Average Treatment Effect (ATE) of participating in the job training program. The idea is that the results from the observational method can be compared to results that can be easily obtained from the experimental portion of the dataset.

To be clear, the observational data combines the observations that are treated from the experimental portion of the data with untreated observations from the PSID.

**Usage**

```r
data(lalonde)
```

**Format**

Four data.frames: (i) lalonde.exp contains a cross sectional version of the experimental data, (ii) lalonde.psid contains a cross sectional version of the observational data, (iii) lalonde.exp.panel contains a panel version of the experimental data, and (iv) lalonde.psid.panel contains a panel version of the observational data. Note: the cross sectional and panel versions of each dataset are identical up to their shape; in demonstrating each of the methods, it is sometimes convenient to have one form of the data or the other.

**References**

LaLonde, Robert. “Evaluating the Econometric Evaluations of Training Programs with Experimental Data.” The American Economics Review, pp. 604-620, 1986. @source The dataset comes from Lalonde (1986) and has been studied in much subsequent work. The qte package uses a version from the causalsens package (https://CRAN.R-project.org/package=causalsens)
<table>
<thead>
<tr>
<th>Dataset</th>
<th>Description</th>
</tr>
</thead>
</table>
| lalonde.exp | Lalonde’s Experimental Dataset  
The cross sectional version of the experimental part of the lalonde dataset. It is loaded with all the datasets with the command data(lalonde) |
| lalonde.exp.panel | Lalonde’s Panel Experimental Dataset  
The panel version of the experimental part of the lalonde dataset. It is loaded with all the datasets with the command data(lalonde) |
| lalonde.psid | Lalonde’s Observational Dataset  
The cross sectional version of the observational part of the lalonde dataset. It is loaded with all the datasets with the command data(lalonde) |
| lalonde.psid.panel | Lalonde’s Experimental Dataset  
The panel version of the observational part of the lalonde dataset. It is loaded with all the datasets with the command data(lalonde) |
MDiD

Mean Difference in Differences

Description

MDiD is a Difference in Differences type method for computing the QTET.

The method can accommodate conditioning on covariates though it does so in a restrictive way: It specifies a linear model for outcomes conditional on group-time dummies and covariates. Then, after residualizing (see details in Athey and Imbens (2006)), it computes the Change in Changes model based on these quasi-residuals.

Usage

MDiD(
  formula,
  xformla = NULL,
  t,
  tmin1,
  tname,
  data,
  panel = FALSE,
  se = TRUE,
  idname = NULL,
  alp = 0.05,
  probs = seq(0.05, 0.95, 0.05),
  iters = 100,
  retEachIter = FALSE
)

Arguments

formula The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated

xformla A optional one sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the x paramater.

t The 3rd time period in the sample. Treated individuals should be treated in this time period and untreated individuals should not be treated. The code attempts to enforce this condition, but it is good try to handle this outside the panel.qtet method.

tmin1 The 2nd time period in the sample. This should be a pre-treatment period for all individuals in the sample.

tname The name of the column containing the time periods

data A data.frame containing all the variables used
### panel.checks

**panel**
Binary variable indicating whether or not the dataset is panel. This is used for computing bootstrap standard errors correctly.

**se**
Boolean whether or not to compute standard errors

**idname**
The individual (cross-sectional unit) id name

**alp**
The significance level used for constructing bootstrap confidence intervals

**probs**
A vector of values between 0 and 1 to compute the QTET at

**iters**
The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE

**retEachIter**
Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.

### Value

A QTE object

### References


### Examples

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

## Run the Mean Difference in Differences method conditioning on age, education, black, hispanic, married, and nodegree
md1 <- MDiD(re ~ treat, t=1978, tmin1=1975, tname="year", xformla=~age + I(age^2) + education + black + hispanic + married + nodegree, data=lalonde.psid.panel, idname="id", se=FALSE, probs=seq(0.05, 0.95, 0.05))
summary(md1)
```

---

### panel.checks

**Description**

Does some checking that data setup is valid for using methods in qte package

**Usage**

`panel.checks(qp)`
Arguments

qp
QTEparams object containing the parameters passed to ciqte

Description

panel.qtet computes the Quantile Treatment Effect on the Treated (QTET) using the method of Callaway and Li (2015). This method should be used when the researcher wants to invoke a Difference in Differences assumption to identify the QTET. Relative to the other Difference in Differences methods available in the qte package, this method’s assumptions are more intuitively similar to the identifying assumptions used in identifying the Average Treatment Effect on the Treated (ATT).

Additionally, this method can accommodate covariates in a more flexible way than the other Difference in Differences methods available. In order to accommodate covariates, the user should specify a vector x of covariate names. The user also may specify a method for estimating the propensity score. The default is logit.

panel.qtet can only be used in some situations, however. The method requires three periods of panel data where individuals are not treated until the last period. The data should be formatted as a panel; the names of columns containing time periods and ids for each cross sectional unit need to be passed to the method.

Usage

panel.qtet(
  formula,  
  xformla = NULL,  
  t,  
  tmin1,  
  tmin2,  
  tname,  
  data,  
  idname,  
  probs = seq(0.05, 0.95, 0.05),  
  iters = 100,  
  alp = 0.05,  
  method = c("qr", "pscore"),  
  se = TRUE,  
  retEachIter = FALSE,  
  pl = FALSE,  
  cores = NULL  
)
Arguments

formula
The formula \( y \sim d \) where \( y \) is the outcome and \( d \) is the treatment indicator (\( d \) should be binary), \( d \) should be equal to one in all time periods for individuals that are eventually treated.

xformula
A optional one sided formula for additional covariates that will be adjusted for. E.g \( \sim \text{age} + \text{education} \). Additional covariates can also be passed by name using the x paramater.

t
The 3rd time period in the sample. Treated individuals should be treated in this time period and untreated individuals should not be treated. The code attempts to enforce this condition, but it is good try to handle this outside the panel.qtet method.

tmin1
The 2nd time period in the sample. This should be a pre-treatment period for all individuals in the sample.

tmin2
The 1st time period in the sample. This should be a pre-treatment period for all individuals in the sample.

tname
The name of the column containing the time periods

data
A data.frame containing all the variables used

idname
The individual (cross-sectional unit) id name

probs
A vector of values between 0 and 1 to compute the QTET at

iters
The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE

alp
The significance level used for constructing bootstrap confidence intervals

method
The method for including covariates, should either be "QR" for quantile regression or "pscore" for propensity score

se
Boolean whether or not to compute standard errors

retEachIter
Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.

pl
Whether or not to compute standard errors in parallel

cores
Number of cores to use if computing in parallel

Value

QTE object

References

### Examples

```r
# Load the data
data(lalonde)

## Run the panel.qtet method on the experimental data with no covariates
pq1 <- panel.qtet(re ~ treat, t=1978, tmin1=1975, tmin2=1974, tname="year",
data=lalonde.exp.panel, idname="id", se=FALSE,
probs=seq(0.05, 0.95, 0.05))
summary(pq1)

## Run the panel.qtet method on the observational data with no covariates
pq2 <- panel.qtet(re ~ treat, t=1978, tmin1=1975, tmin2=1974, tname="year",
data=lalonde.psid.panel, idname="id", se=FALSE,
probs=seq(0.05, 0.95, 0.05))
summary(pq2)

## Run the panel.qtet method on the observational data conditioning on age, education, black, hispanic, married, and nodegree.
## The propensity score will be estimated using the default logit method.
pq3 <- panel.qtet(re ~ treat, t=1978, tmin1=1975, tmin2=1974, tname="year",
xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
data=lalonde.psid.panel, idname="id", se=FALSE, method="pscore",
probs=seq(0.05, 0.95, 0.05))
summary(pq3)
pq4 <- panel.qtet(re ~ treat, t=1978, tmin1=1975, tmin2=1974, tname="year",
xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
data=lalonde.psid.panel, idname="id", se=FALSE, method="qr",
probs=seq(0.05, 0.95, 0.05))
summary(pq4)
```

---

### panelize.data

**Description**

get data in correct format for using panel methods in qte package

**Usage**

```r
panelize.data(data, idname, tname, t, tmin1, tmin2 = NULL)
```

**Arguments**

- `data`: A data.frame containing all the variables used
- `idname`: The individual (cross-sectional unit) id name
- `tname`: The name of the column containing the time periods
The 3rd time period in the sample. Treated individuals should be treated in this time period and untreated individuals should not be treated. The code attempts to enforce this condition, but it is good try to handle this outside the panel.qte method.

tmin1
The 2nd time period in the sample. This should be a pre-treatment period for all individuals in the sample.

tmin2
The 1st time period in the sample. This should be a pre-treatment period for all individuals in the sample.

Value
data.frame

plot.BoundsObj

### S3 method for class 'BoundsObj'

```r
plot(
x,
plotate = FALSE,
plot0 = FALSE,
qtecol = "black",
atecol = "black",
col0 = "black",
ylim = NULL,
uselegend = FALSE,
legloc = "topright",
...
)
```

Arguments

- **x**: A BoundsObj Object
- **plotate**: Boolean whether or not to plot the ATE
- **plot0**: Boolean whether to plot a line at 0
- **qtecol**: Color for qte plot. Default "black"
- **atecol**: Color for ate plot. Default "black"
- **col0**: Color for 0 plot. Default "black"
ylim

The ylim for the plot; if not passed, it will be automatically set based on the values that the QTE takes.

uselegend

Boolean whether or not to print a legend.

legloc

String location for the legend. Default "topright".

... Other parameters to be passed to plot (e.g lwd).

Description

Plots a QTE Object.

Usage

```r
## S3 method for class 'QTE'
plot(
x, plotate = FALSE, plot0 = FALSE, qtecol = "black", atecol = "black", col0 = "black", xlab = "tau", ylab = "QTE", legend = NULL, onetreated = FALSE, ylim = NULL, uselegend = FALSE, legendcol = NULL, legloc = "topright", ...
)
```

Arguments

- **x**: a QTE Object
- **plotate**: Boolean whether or not to plot the ATE
- **plot0**: Boolean whether to plot a line at 0
- **qtecol**: Color for qte plot. Default "black"
- **atecol**: Color for ate plot. Default "black"
- **col0**: Color for 0 plot. Default "black"
- **xlab**: Custom label for x-axis. Default "tau"
- **ylab**: Custom label for y-axis. Default "QTE"
print.summary.BoundsObj

Print a summary.BoundsObj

Description
Prints a Summary QTE Object

Usage
## S3 method for class 'summary.BoundsObj'
print(x, ...)

Arguments
x A summary.BoundsObj
...
Other objects to pass (not used)

print.summary.QTE

Print

Description
Prints a Summary QTE Object

Usage
## S3 method for class 'summary.QTE'
print(x, ...)

Arguments
x A summary.QTE object
...
Other params (required as generic function, but not used)
QDiD

Quantile Difference in Differences

Description

QDiD is a Difference in Differences type method for computing the QTET.

The method can accommodate conditioning on covariates though it does so in a restrictive way: It specifies a linear model for outcomes conditional on group-time dummies and covariates. Then, after residualizing (see details in Athey and Imbens (2006)), it computes the Change in Changes model based on these quasi-residuals.

Usage

```r
QDiD(
  formula,
  xformula = NULL,
  t,
  tmin1,
  tname,
  data,
  panel = FALSE,
  se = TRUE,
  idname = NULL,
  alp = 0.05,
  probs = seq(0.05, 0.95, 0.05),
  iters = 100,
  retEachIter = FALSE,
  pl = FALSE,
  cores = NULL
)
```

Arguments

- **formula**: The formula y ~ d where y is the outcome and d is the treatment indicator (d should be binary), d should be equal to one in all time periods for individuals that are eventually treated.
- **xformula**: An optional one-sided formula for additional covariates that will be adjusted for. E.g ~ age + education. Additional covariates can also be passed by name using the `x` parameter.
- **t**: The 3rd time period in the sample. Treated individuals should be treated in this time period and untreated individuals should not be treated. The code attempts to enforce this condition, but it is good to try to handle this outside the `panel.qtet` method.
- **tmin1**: The 2nd time period in the sample. This should be a pre-treatment period for all individuals in the sample.
QDiD

tname  The name of the column containing the time periods
data  A data.frame containing all the variables used
panel  Binary variable indicating whether or not the dataset is panel. This is used for computing bootstrap standard errors correctly.
se  Boolean whether or not to compute standard errors
idname  The individual (cross-sectional unit) id name
alp  The significance level used for constructing bootstrap confidence intervals
probs  A vector of values between 0 and 1 to compute the QTET at
iters  The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE
reEachIter  Boolean whether or not to return list of results from each iteration of the bootstrap procedure (default is FALSE). This is potentially useful for debugging but can cause errors due to running out of memory.
pl  Whether or not to compute standard errors in parallel
cores  Number of cores to use if computing in parallel

Value

QTE Object

References


Examples

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

## Run the Quantile Difference in Differences method conditioning on age, education, black, hispanic, married, and nodegree
qd1 <- QDiD(re ~ treat, t=1978, tmin=1975, tname="year",
            xformla=~age + I(age^2) + education + black + hispanic + married + nodegree,
            data=lalonde.psid.panel, idname="id", se=FALSE,
            probs=seq(0.05, 0.95, 0.05))
summary(qd1)
```
qte: A package for computing quantile treatment effects

Description

Main class of objects. A QTE object is returned by all of the methods that compute the QTE or QTET.

Usage

```r
QTE(
  qte,
  ate = NULL,
  qte.se = NULL,
  qte.lower = NULL,
  qte.upper = NULL,
  ate.se = NULL,
  ate.lower = NULL,
  ate.upper = NULL,
  c = NULL,
  pscore.reg = NULL,
  probs,
  type = "On the Treated",
  F.treated.t = NULL,
  F.un treated.t = NULL,
  F.treated.t.cf = NULL,
  F.treated.tmin1 = NULL,
  F.treated.tmin2 = NULL,
  F.treated.change.tmin1 = NULL,
  F.un treated.change.t = NULL,
  F.un treated.change.tmin1 = NULL,
  F.un treated.tmin1 = NULL,
  F.un treated.tmin2 = NULL,
  condQ.treated.t = NULL,
  condQ.treated.t.cf = NULL,
  eachIterList = NULL,
  inffunct = NULL,
  inffuncu = NULL
)
```

Arguments

- **qte**: The Quantile Treatment Effect at each value of `probs`
- **ate**: The Average Treatment Effect (or Average Treatment Effect on the Treated)
- **qte.se**: A vector of standard errors for each `qte`
qte.lower A vector of lower confidence intervals for each qte (it is based on the bootstrap confidence interval – not the se – so it may not be symmetric about the qte
qte.upper A vector of upper confidence intervals for each qte (it is based on the bootstrap confidence interval – not the se – so it may not be symmetric about the qte
ate.se The standard error for the ATE
ate.lower Lower confidence interval for the ATE (it is based on the bootstrap confidence interval – not the se – so it may not be symmetric about the ATE
ate.upper Upper confidence interval for the ATE (it is based on the bootstrap confidence interval – not the se – so it may not be symmetric about the ATE
c The critical value from a KS-type statistic used for creating uniform confidence bands
pscore.reg The results of propensity score regression, if specified
probs The values for which the qte is computed
type Takes the values "On the Treated" or "Population" to indicate whether the estimated QTE is for the treated group or for the entire population
F.treated.t Distribution of treated outcomes for the treated group at period t
F.untreated.t Distribution of untreated potential outcomes for the untreated group at period t
F.treated.t.cf Counterfactual distribution of untreated potential outcomes for the treated group at period t
F.treated.tmin1 Distribution of treated outcomes for the treated group at period tmin1
F.treated.tmin2 Distribution of treated outcomes for the treated group at period tmin2
F.treated.change.tmin1 Distribution of the change in outcomes for the treated group between periods tmin1 and tmin2
F.untreated.change.t Distribution of the change in outcomes for the untreated group between periods t and tmin1
F.untreated.change.tmin1 Distribution of the change in outcomes for the untreated group between periods tmin1 and tmin2
F.untreated.tmin1 Distribution of outcomes for the untreated group in period tmin1
F.untreated.tmin2 Distribution of outcomes for the untreated group in period tmin2
condQ.treated.t Conditional quantiles for the treated group in period t
condQ.treated.t.cf Counterfactual conditional quantiles for the treated group in period t
eachIterList An optional list of the outcome of each bootstrap iteration
inffunct The influence function for the treated group; used for inference when there are multiple periods and in the case with panel data. It is needed for computing covariance terms in the variance-covariance matrix.
inffuncu The influence function for the untreated group
QTEparams

Description

QTEparams is an object that contains all the parameters passed to QTE methods.

Usage

QTEparams(
  formula,
  xformula = NULL,
  t = NULL,
  tmin1 = NULL,
  tmin2 = NULL,
  tname = NULL,
  data,
  panel = FALSE,
  w = NULL,
  idname = NULL,
  probs,
  alp = NULL,
  method = NULL,
  plot = NULL,
  se = NULL,
  iters = NULL,
  retEachIter = NULL,
  bootstrapiter = NULL,
  seedvec = NULL,
  pl = NULL,
  cores = NULL
)

Arguments

formula Should be some y on treatment variable
xformula a formula for the other covariates such as ~ x1 + x2
t The last period (not always used)
tmin1 The last pre-treatment period (not always used)
tmin2 The 2nd to last pre-treatment period (not always used)
tname The name of the column containing time periods (not always used)
data The name of the data frame
panel Whether or not the data is panel
w Additional (usually sampling) weights
qtes2mat

**Description**

Turn multiple qtes into a matrix for printing

**Usage**

```r
qtes2mat(qteList, sset = NULL, se = TRUE, rnd = 3)
```

**Arguments**

- `qteList`: a list of qte objects
- `sset`: subset of qtes to keep
- `se`: whether or not to include standard errors in the resulting matrix
- `rnd`: how many digits to round to

**Value**

matrix
### qteToTexreg

**diffQ**

**Description**

*takes a single set of quantiles:*

(not qtes as in diffquantiles) and returns the difference between particular ones

**Usage**

```r
qteToTexreg(qteobj, tau = NULL, reportAte = T)
```

**Arguments**

- **qteobj**  
  A QTE object
- **tau**  
  Optional vector of taus to texreg results for
- **reportAte**  
  Whether or not texreg the ATE (or ATT) as well

---

### setupData

**setupData**

**Description**

*setupData sets up the data to use in each compute method in the QTE package*

**Usage**

```r
setupData(qteParams)
```

**Arguments**

- **qteParams**  
  object holding the function parameters

**Value**

*qteData object holding data to be used in QTE functions*
**Description**

`spatt` computes the Average Treatment Effect on the Treated (ATT) using the method of Abadie (2005)

**Usage**

```r
spatt(formla, xformla = NULL, t, tmin1, tname, data, w = NULL, panel = FALSE, idname = NULL, iters = 100, alp = 0.05, method = "logit", plot = FALSE, se = TRUE, retEachIter = FALSE, seedvec = NULL, pl = FALSE, cores = 2)
```

**Arguments**

- `formla` The formula `y ~ d` where `y` is the outcome and `d` is the treatment indicator (`d` should be binary)
- `xformla` A optional one sided formula for additional covariates that will be adjusted for. E.g `~ age + education`. Additional covariates can also be passed by name using the `x` parameter.
- `t` The 3rd time period in the sample (this is the name of the column)
- `tmin1` The 2nd time period in the sample (this is the name of the column)
- `tname` The name of the column containing the time periods
- `data` The name of the data.frame that contains the data
- `w` an additional vector of sampling weights
- `panel` Boolean indicating whether the data is panel or repeated cross sections
- `idname` The individual (cross-sectional unit) id name
**summary.BoundsObj**

### Description

summary.BoundsObj is an object for holding bounds results

### Value

QTE object

### References

Abadie (2005)

### Examples

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

# Run the panel.qtet method on the experimental data with no covariates
att1 <- spatt(re ~ treat, t=1978, tmin1=1975, tname="year",
               x=NULL, data=lalonde.psid.panel, idname="id", se=FALSE)
summary(att1)

# Run the panel.qtet method on the observational data with no covariates

```

### Arguments

- **iters**
  - The number of iterations to compute bootstrap standard errors. This is only used if se=TRUE

- **alp**
  - The significance level used for constructing bootstrap confidence intervals

- **method**
  - The method for estimating the propensity score when covariates are included

- **plot**
  - Boolean whether or not the estimated QTET should be plotted

- **se**
  - Boolean whether or not to compute standard errors

- **retEachIter**
  - Boolean whether or not to return list of results from each iteration of the bootstrap procedure

- **seedvec**
  - Optional value to set random seed; can possibly be used in conjunction with bootstrapping standard errors.

- **pl**
  - Boolean for whether or not to compute bootstrap error in parallel. Note that computing standard errors in parallel is a new feature and may not work at all on Windows.

- **cores**
  - The number of cores to use if bootstrap standard errors are computed in parallel
Usage

## S3 method for class 'BoundsObj'
summary(object, ...)

Arguments

object A BoundsObj Object
...
Other params (for consistency as generic S3 method, but not used)

Value

summary.BoundsObj Object

summary.QTE

Description

summary.QTE summarizes QTE objects

Usage

## S3 method for class 'QTE'
summary(object, ...)

Arguments

object A QTE Object
...
Other params (to work as generic method, but not used)
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