Package ‘PanelMatch’

June 4, 2024

Type Package

Title Matching Methods for Causal Inference with Time-Series Cross-Sectional Data

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Description Implements a set of methodological tools that enable researchers to apply matching methods to time-series cross-sectional data. Imai, Kim, and Wang (2023) <http://web.mit.edu/insong/www/pdf/tscs.pdf> proposes a nonparametric generalization of the difference-in-differences estimator, which does not rely on the linearity assumption as often done in practice. Researchers first select a method of matching each treated observation for a given unit in a particular time period with control observations from other units in the same time period that have a similar treatment and covariate history. These methods include standard matching methods based on propensity score and Mahalanobis distance, as well as weighting methods. Once matching and refinement is done, treatment effects can be estimated with standard errors. The package also offers diagnostics for researchers to assess the quality of their results.

License GPL (>= 3)

Imports Rcpp (>= 0.12.5), data.table, ggplot2, CBPS, stats, graphics, MASS, Matrix, doParallel, foreach, methods

Depends R (>= 2.14.0)

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BugReports https://github.com/insongkim/PanelMatch/issues

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### R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>balance_scatter</td>
<td>2</td>
</tr>
<tr>
<td>dem</td>
<td>4</td>
</tr>
<tr>
<td>DisplayTreatment</td>
<td>5</td>
</tr>
<tr>
<td>enforce_lead_restrictions</td>
<td>7</td>
</tr>
<tr>
<td>get_covariate_balance</td>
<td>8</td>
</tr>
<tr>
<td>get_set_treatment_effects</td>
<td>10</td>
</tr>
<tr>
<td>handle_moderating_variable</td>
<td>11</td>
</tr>
<tr>
<td>matched_set</td>
<td>12</td>
</tr>
<tr>
<td>PanelEstimate</td>
<td>13</td>
</tr>
<tr>
<td>PanelMatch</td>
<td>16</td>
</tr>
<tr>
<td>perunitSum</td>
<td>19</td>
</tr>
<tr>
<td>perunitSum_Dit</td>
<td>20</td>
</tr>
<tr>
<td>placebo_test</td>
<td>21</td>
</tr>
<tr>
<td>plot.matched.set</td>
<td>22</td>
</tr>
<tr>
<td>plot.PanelEstimate</td>
<td>24</td>
</tr>
<tr>
<td>print.matched.set</td>
<td>25</td>
</tr>
<tr>
<td>summary.matched.set</td>
<td>26</td>
</tr>
<tr>
<td>summary.PanelEstimate</td>
<td>27</td>
</tr>
</tbody>
</table>

**Index** 28

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**Description**

Visualizing the standardized mean differences for covariates via a scatter plot.
### balance_scatter

#### Usage

```r
balance_scatter(
  matched_set_list,
  xlim = c(0, 0.8),
  ylim = c(0, 0.8),
  main = "Standardized Mean Difference of Covariates",
  pchs = c(2, 3),
  covariates,
  data,
  x.axis.label = "Before refinement",
  y.axis.label = "After refinement",
  ...
)
```

#### Arguments

- **matched_set_list**
  - a list of one or more matched.set objects
- **xlim**
  - xlim of the scatter plot. This is the same as the xlim argument in `plot()`
- **ylim**
  - ylim of the scatter plot. This is the same as the ylim argument in `plot()`
- **main**
  - title of the scatter plot. This is the same as the main argument in `plot()`
- **pchs**
  - one or more pch indicators for the symbols on the scatter plot. You should specify a pch symbol for each matched.set you specify in matched_set_list. See `plot()` for more information
- **covariates**
  - variables for which balance is displayed
- **data**
  - the same time series cross sectional data set used to create the matched sets.
- **x.axis.label**
  - x axis label
- **y.axis.label**
  - y axis label
- **...**
  - optional arguments to be passed to `plot()`

#### Details

`balance_scatter` visualizes the standardized mean differences for each covariate. Although users can use the scatter plot in a variety of ways, it is recommended that the x-axis refers to balance for covariates before refinement, and y-axis refers to balance after refinement. Users can utilize parameters powered by `plot()` in base R to further customize the figure.

#### Author(s)

In Song Kim <insong@mit.edu>, Erik Wang <haixiao@Princeton.edu>, Adam Rauh <amrauh@umich.edu>, and Kosuke Imai <imai@harvard.edu>
Examples

dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
# get a matched set without refinement
sets0 <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
 treatment = "dem", refinement.method = "none",
 data = dem.sub, match.missing = FALSE,
 size.match = 5, qoi = "att",
 outcome.var = "y",
 lead = 0:4, forbid.treatment.reversal = FALSE)

# get a matched set with refinement using propensity score matching, setting the
# size of matched set to 5
sets1 <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
 treatment = "dem", refinement.method = "ps.match",
 data = dem.sub, match.missing = FALSE,
 covs.formula = ~ tradewb,
 size.match = 5, qoi = "att",
 outcome.var = "y",
 lead = 0:4, forbid.treatment.reversal = FALSE)

# get another matched set with refinement using propensity score weighting
sets2 <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
 treatment = "dem", refinement.method = "ps.weight",
 data = dem.sub, match.missing = FALSE,
 covs.formula = ~ tradewb,
 size.match = 10, qoi = "att",
 outcome.var = "y",
 lead = 0:4, forbid.treatment.reversal = FALSE)

# use the function to produce the scatter plot
balance_scatter(matched_set_list = list(sets0$att, sets1$att, sets2$att),
 data = dem.sub,
 covariates = c("y", "tradewb"))

# add legend
legend(x = 0, y = 0.8,
 legend = c("mahalanobis",
 "PS weighting"),
y.intersp = 0.65,
x.intersp = 0.3,
xjust = 0,
pch = c(1, 3), pt.cex = 1,
bty = "n", ncol = 1, cex = 1, bg = "white")

dem

*Country-level Democracy indicator*
Description
A dataset containing the democracy indicator for 184 countries from 1960 to 2010

Format
A data.frame containing 9384 rows and 3 variables

Details
- wbcode2. World Bank country ID. Integer.
- dem. binary indicator of democracy as defined in Acemoglu et al (2019).
- y. log of GDP per capita in 2000 constant dollars (multiplied by 100). Numeric.
- tradewb. Exports plus imports as a share of GDP from World Bank. Numeric.

Source

DisplayTreatment

DisplayTreatment visualizes the treatment distribution across units and time in a panel data set

Usage
DisplayTreatment(
  unit.id,
  time.id,
  treatment,
  data,
  color.of.treated = "red",
  color.of.untreated = "blue",
  title = "Treatment Distribution \n Across Units and Time",
  xlab = "Time",
  ylab = "Unit",
  x.size = NULL,
  y.size = NULL,
  legend.position = "none",
  x.angle = NULL,
  y.angle = NULL,
  legend.labels = c("not treated", "treated"),
  decreasing = FALSE,
matched.set = NULL,
show.set.only = FALSE,
hide.x.tick.label = FALSE,
hide.y.tick.label = FALSE,
gradient.weights = FALSE,
dense.plot = FALSE
)

Arguments

unit.id Name of the unit identifier variable as a character string
time.id Name of the time identifier variable as a character string
treatment Name of the treatment variable as a character string
data data.frame that contains the time series cross sectional data used for matching and estimation. Unit and time data must be integers. Time data must also be formatted as sequential integers that increase by one.
color.of.treated Color of the treated observations provided as a character string (this includes hex values). Default is red.
color.of.untreated Color of the untreated observations provided as a character string (this includes hex values). Default is blue.
title Title of the plot provided as character string
xlab Character label of the x-axis
ylab Character label of the y-axis
x.size Numeric size of the text for xlab or x axis tick labels. Assign x.size = NULL to use built in ggplot2 method of determining label size. When the length of the time period is long, consider setting to NULL and adjusting size and ratio of the plot.
y.size Numeric size of the text for ylab or y axis tick labels. Assign y.size = NULL to use built in ggplot2 method of determining label size. When the number of units is large, consider setting to NULL and adjusting size and ratio of the plot.
legend.position Position of the legend. Provide this according to ggplot2 standards.
x.angle Angle (in degrees) of the tick labels for x-axis
y.angle Angle (in degrees) of the tick labels for y-axis
legend.labels Character vector of length two describing the labels of the legend to be shown in the plot. ggplot2 standards are used.
decreasing Logical. Determines if display order should be increasing or decreasing by the amount of treatment received. Default is decreasing = FALSE.
matched.set a matched.set object (optional) containing a single treated unit and a set of matched controls. If provided, this set will be highlighted on the resulting plot.
show.set.only logical. If TRUE, only the treated unit and control units contained in the provided matched.set object will be shown on the plot. Default is FALSE. If no matched.set is provided, then this argument will have no effect.
enforce_lead_restrictions

enforce_lead_restrictions check treatment and control units for treatment reversion in the lead window. Treated units must stay treated and control units must stay in control (according to the specified qoi).

Description

enforce_lead_restrictions check treatment and control units for treatment reversion in the lead window. Treated units must stay treated and control units must stay in control (according to the specified qoi).

Value

DisplayTreatment returns a treatment variation plot (using ggplot2 geom_tile() or geom_raster()), which visualizes the variation of treatment across unit and time.

Author(s)

In Song Kim <insong@mit.edu>, Erik Wang <haixiao@Princeton.edu>, Adam Rauh <amrauh@umich.edu>, and Kosuke Imai <imai@harvard.edu>

Examples

DisplayTreatment(unit.id = "wbcode2",
                 time.id = "year", legend.position = "none",
                 xlab = "year", ylab = "Country Code",
                 treatment = "dem", data = dem)
Usage

enforce_lead_restrictions(
    matched_sets,
    ordered.data,
    max.lead,
    t.var,
    id.var,
    treatment.var
)

Arguments

matched_sets  matched.set object
ordered.data   parsed data as data.frame object
max.lead       The largest lead value (e.g. the biggest F)
t.var          string specifying the time variable
id.var         string specifying the unit id variable
treatment.var  string specifying the treatment variable.

Value

matched.set object with the matched sets that meet the conditions

Description

Calculate covariate balance for user specified covariates across matched sets. Balance is assessed by taking the average of the difference between the values of the specified covariates for the treated unit(s) and the weighted average of the control units across all matched sets. Results are standardized and are expressed in standard deviations. Balance is calculated for each period in the specified lag window.

Usage

gcov_balance(
    matched.sets,
    data,
    covariates,
    use.equal.weights = FALSE,
    plot = FALSE,
    reference.line = TRUE,
    legend = TRUE,
    ylab = "SD",
)
get_covariate_balance

include.treatment.period = TRUE,
legend.position = "topleft",
...)

Arguments

matched.sets A matched.set object
data The time series cross sectional data set (as a data.frame object) used to produce the matched.set object. This data set should be identical to the one passed to PanelMatch() and PanelEstimate() to ensure consistent results.
covariates a character vector, specifying the names of the covariates for which the user is interested in calculating balance.
use.equal.weights logical. If set to TRUE, then equal weights will be assigned to control units, rather than using whatever calculated weights have been assigned. This is helpful for assessing the improvement in covariate balance as a result of refining the matched sets.
plot logical. When TRUE, a plot showing the covariate balance calculation results will be shown. When FALSE, no plot is made, but the results of the calculations are returned. default is FALSE
reference.line logical indicating whether or not a horizontal line should be present on the plot at y = 0. Default is TRUE.
legend logical indicating whether or not a legend identifying the variables should be included on the plot. Default is TRUE.
ylab Label for y axis. Default is "SD". This is the same as the ylab argument to plot().
include.treatment.period logical. Default is TRUE. When TRUE, covariate balance measures for the period during which treatment occurs is included. These calculations are not included when FALSE. Users may wish to leave this period off in some circumstances. For instance, one would expect covariate balance to be poor during this period when treatment is continuous and a lagged outcome is included in the refinement formula.
legend.position position of legend. See documentation for graphics::legend. Default is "topleft"
...

Additional graphical parameters to be passed to the plot function in base R.

Examples

dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
#add some additional data to data set for demonstration purposes
dem.sub$adata <- runif(runif(nrow(dem.sub)))

pm.obj <- PanelMatch(lead = 0:3, lag = 4, time.id = "year", unit.id = "wbcode2", treatment = "dem",
outcome.var = "y", refinement.method = "ps.match",
data = dem.sub, match.missing = TRUE,
Description

Calculates the treatment effect size at the matched set level

Usage

get_set_treatment_effects(pm.obj, data, lead)

Arguments

pm.obj an object of class PanelMatch
data data.frame with the time series cross sectional data used for matching, refinement, and estimation
lead integer (or integer vector) indicating the time period(s) in the future for which the treatment effect size will be calculated. Calculations will be made for the period t + lead, where t is the time of treatment. If more than one lead value is provided, then calculations will be performed for each value.

Details

Calculate the size of treatment effects for each matched set.

Value

a list equal in length to the number of lead periods specified to the lead argument. Each element in the list is a vector of the matched set level effects.

Examples

dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
treatment = "dem", refinement.method = "ps.match",
data = dem.sub, match.missing = TRUE,
covs.formula = ~ I(lag(tradewb, 1:4)),
size.match = 5, qoi = "att",
outcome.var = "y", lead = 0:4, forbid.treatment.reversal = FALSE,
placebo.test = FALSE)
handle_moderating_variable handles moderating variable calculations: In practice, this just involves slicing the data up according to the moderator, calling PanelEstimate() and putting everything back together. This function creates the sets of objects on which PanelEstimate() will be called. It identifies the set of valid values the moderating variable can take on.

Description

handle_moderating_variable handles moderating variable calculations: In practice, this just involves slicing the data up according to the moderator, calling PanelEstimate() and putting everything back together. This function creates the sets of objects on which PanelEstimate() will be called. It identifies the set of valid values the moderating variable can take on.

Usage

handle_moderating_variable(
  ordered.data,
  att.sets,
  atc.sets,
  PM.object,
  moderator,
  unit.id,
  time.id,
  qoi.in
)

Arguments

   ordered.data   data.frame
   att.sets      matched.set object for the ATT or ART
   atc.sets      matched.set object for the ATC
   PM.object     PanelMatch object
   moderator     string specifying the name of the moderating variable
   unit.id       string specifying the unit id variable
   time.id       string specifying the time id variable
   qoi.in        string specifying the QOI

Value

Character vector of valid moderating variable values
**Description**

matched_set is a constructor for the matched_set class.

**Usage**

matched_set(matchedsets, id, t, L, t.var, id.var, treatment.var)

**Arguments**

- **matchedsets**: a list of treated units and matched control units. Each element in the list should be a vector of control unit ids.
- **id**: A vector containing the ids of treated units
- **t**: A vector containing the times of treatment for treated units.
- **L**: integer specifying the length of the lag window used in matching
- **t.var**: string specifying the time variable
- **id.var**: string specifying the unit id variable
- **treatment.var**: string specifying the treatment variable.

The constructor function returns a matched_set object. matched_set objects are a modified lists. Each element in the list is a vector of ids corresponding to the control unit ids in a matched set. Additionally, these vectors might have additional attributes – "weights". These correspond to the weights assigned to each control unit, as determined by the specified refinement method. Each element in the list also has a name, which corresponds to the unit id of the treated unit and time of treatment, concatenated together and separated by a period. matched_set objects also have a number of methods defined: summary, plot, and `\[`. matched_set objects can be modified manually as long as these conventions (and conventions about other attributes) are maintained. It is important to note that matched_set objects are distinct from PanelMatch objects. matched_set objects are often contained within PanelMatch objects.

**Details**

Users should never need to use this function by itself. See below for more about matched_set objects.

**Value**

matched_set objects have additional attributes. These reflect the specified parameters when using the PanelMatch function:

- **lag**: an integer value indicating the length of treatment history to be used for matching. Treated and control units are matched based on whether or not they have exactly matching treatment histories in the lag window.
PanelEstimate

estimates a causal quantity of interest, including the average treatment effect for treated or control units (att and atc, respectively), the average effect of treatment reversal on reversed units (art), or average treatment effect (ate), as specified in PanelMatch(). This is done by estimating the counterfactual outcomes for each treated unit using matched sets. Users will provide matched sets that were obtained by the PanelMatch function and obtain point estimates via a weighted average computation with weighted bootstrap standard errors. Point estimates and standard errors will be produced for each period in the lead window specified by the lead argument from PanelMatch(). Users may run multiple estimations by providing lists of each argument to the function. However, in this format, every argument must be explicitly specified in each configuration and must adhere to the same data types/structures outlined below.

Usage

PanelEstimate(
    sets,
    data,
    number.iterations = 1000,
    df.adjustment = FALSE,
    confidence.level = 0.95,
    moderator = NULL,
    se.method = "bootstrap",
    pooled = FALSE,
)
include.placebo.test = FALSE,
parallel = FALSE,
num.cores = 1
)

Arguments

sets A PanelMatch object attained via the PanelMatch() function.
data The same time series cross sectional data set provided to the PanelMatch() function used to produce the matched sets.

number.iterations If using bootstrapping for calculating standard errors, this is the number of bootstrap iterations. Provide as integer. If se.method is not equal to "bootstrap", this argument has no effect.
df.adjustment A logical value indicating whether or not a degree-of-freedom adjustment should be performed for the standard error calculation. The default is FALSE. This parameter is only available for the bootstrap method of standard error calculation.

confidence.level A numerical value specifying the confidence level and range of interval estimates for statistical inference. The default is .95.
moderator The name of a moderating variable, provided as a character string. If a moderating variable is provided, the returned object will be a list of PanelEstimate objects. The names of the list will reflect the different values of the moderating variable. More specifically, the moderating variable values will be converted to syntactically proper names using make.names().

se.method Method used for calculating standard errors, provided as a character string. Users must choose between "bootstrap", "conditional", and "unconditional" methods. Default is "bootstrap". "bootstrap" uses a block bootstrapping procedure to calculate standard errors. The conditional method calculates the variance of the estimator, assuming independence across units but not across time. The unconditional method also calculates the variance of the estimator analytically, but makes no such assumptions about independence across units. When the quantity of interest is "att", "atc", or "art", all methods are available. Only "bootstrap" is available for the ate. If pooled argument is TRUE, then only bootstrap is available.
pooled Logical. If TRUE, estimates and standard errors are returned for treatment effects pooled across the entire lead window. Only available for se.method = "bootstrap"

include.placebo.test Logical. If TRUE, a placebo test is run and returned in the results. The placebo test uses the same specifications for calculating standard errors as the main results. That is, standard errors are calculated according to the user provided se.method and confidence.level arguments (and, if applicable, parallelization specifications). If these are invalid for some reason, an error will be thrown.

parallel Logical. If TRUE and se.method = "bootstrap", bootstrap procedure will be parallelized. Default is FALSE. If se.method is not set to bootstrap, this option does nothing.
num.cores

Integer. Specifies the number of cores to use for parallelization. If se.method = `"bootstrap"' and parallel = TRUE, then this option will take effect. Otherwise, it will do nothing.

Value

PanelEstimate returns a list of class ‘PanelEstimate’ containing the following components:

estimates

the point estimates of the quantity of interest for the lead periods specified

se.method

The method used to calculate standard errors. This is the same as the argument provided to the function.

bootstrapped.estimates

the bootstrapped point estimate values, when applicable

bootstrap.iterations

the number of iterations used in bootstrapping, when applicable

method

refinement method used to create the matched sets from which the estimates were calculated

lag

See PanelMatch() argument lag for more information.

lead

The lead window sequence for which PanelEstimate() is producing point estimates and standard errors.

confidence.level

the confidence level

qoi

the quantity of interest

matched.sets

the refined matched sets used to produce the estimations

standard.error

the standard error(s) of the point estimates

pooled

Logical indicating whether or not estimates were calculated for individual lead periods or pooled.

placebo.test

if include.placebo.test = TRUE, a placebo test is conducted using placebo_test() and returned as a list. See documentation for placebo_test() for more about each individual item.

Author(s)

In Song Kim <insong@mit.edu>, Erik Wang <haixiao@Princeton.edu>, Adam Rauh <amrauh@umich.edu>, and Kosuke Imai <imai@harvard.edu>

References

Imai, Kosuke, In Song Kim, and Erik Wang (2023)

Examples

dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
treatment = "dem", refinement.method = "ps.match",
data = dem.sub, match.missing = TRUE, covs.formula = ~ tradewb,
PanelMatch

Description
Create refined/weighted sets of treated and control units

Usage
PanelMatch(
  lag,
  time.id,
  unit.id,
  treatment,
  outcome.var,
  refinement.method,
  data,
  qoi,
  size.match = 10,
  match.missing = TRUE,
  covs.formula = NULL,
  lead = 0,
  verbose = FALSE,
  exact.match.variables = NULL,
  forbid.treatment.reversal = FALSE,
  matching = TRUE,
  listwise.delete = FALSE,
  use.diagonal.variance.matrix = FALSE,
  restrict.control.period = NULL,
  placebo.test = FALSE
)

Arguments
- **lag**: An integer value indicating the length of treatment history periods to be matched on.
- **time.id**: A character string indicating the name of the time variable in the data. This data currently must be formatted as sequential integers.
- **unit.id**: A character string indicating the name of unit identifier in the data. This data must be integer.

Example:
```r
size.match = 5, qoi = "att", outcome.var = "y",
lead = 0:4, forbid.treatment.reversal = TRUE)
PE.results <- PanelEstimate(sets = PM.results, data = dem.sub, se.method = "unconditional")
```
treatment A character string indicating the name of the treatment variable in the data. The treatment must be a binary indicator variable (integer with 0 for the control group and 1 for the treatment group).

outcome.var A character string identifying the outcome variable.

refinement.method A character string specifying the matching or weighting method to be used for refining the matched sets. The user can choose "mahalanobis", "ps.match", "CBPS.match", "ps.weight", "CBPS.weight", or "none". The first three methods will use the size.match argument to create sets of at most size.match closest control units. Choosing "none" will assign equal weights to all control units in each matched set.

data A data.frame object containing time series cross sectional data. Time data must be sequential integers that increase by 1. Unit identifiers must be integers. Treatment data must be binary.

qoi quantity of interest, provided as a string: att (average treatment effect on treated units), atc (average treatment effect of treatment on the control units) art (average effect of treatment reversal for units that experience treatment reversal), or ate (average treatment effect).

size.match An integer dictating the number of permitted closest control units in a matched set after refinement. This argument only affects results when using a matching method ("mahalanobis" or any of the refinement methods that end in ".match"). This argument is not needed and will have no impact if included when a weighting method is specified (any refinement.method that includes "weight" in the name).

match.missing Logical variable indicating whether or not units should be matched on the patterns of missingness in their treatment histories. Default is TRUE. When FALSE, neither treated nor control units are allowed to have missing treatment data in the lag window.

covs.formula One sided formula object indicating which variables should be used for matching and refinement. Argument is not needed if refinement.method is set to "none" If the user wants to include lagged variables, this can be done using a function, "lag()", which takes two, unnamed, positional arguments. The first is the name of the variable which you wish to lag. The second is the lag window, specified as an integer sequence in increasing order. For instance, I(lag(x, 1:4)) will then add new columns to the data for variable "x" for time t-1, t-2, t-3, and t-4 internally and use them for defining/measuring similarity between units. Other transformations using the I() function, such as I(x^2) are also permitted. The variables specified in this formula are used to define the similarity/distances between units.

lead integer sequence specifying the lead window, for which qoi point estimates (and standard errors) will ultimately be produced. Default is 0 (which corresponds to contemporaneous treatment effect).

verbose option to include more information about the matched.set object calculations, like the distances used to create the refined sets and weights.

exact.match.variables character vector giving the names of variables to be exactly matched on. These
should be time invariant variables. Exact matching for time varying covariates is not currently supported.

forbid.treatment.reversal
Logical. For the ATT, it indicates whether or not it is permissible for treatment to reverse in the specified lead window. This is defined analogously for the ART. It is not valid for the ATC or ATE. When set to TRUE, only matched sets for treated units where treatment is applied continuously in the lead window are included in the results. Default is FALSE.

matching
logical indicating whether or not any matching on treatment history should be performed. This is primarily used for diagnostic purposes, and most users will never need to set this to FALSE. Default is FALSE.

listwise.delete
TRUE/FALSE indicating whether or not missing data should be handled using listwise deletion or the package's default missing data handling procedures. Default is FALSE.

use.diagonal.variance.matrix
TRUE/FALSE indicating whether or not a regular covariance matrix should be used in mahalanobis distance calculations during refinement, or if a diagonal matrix with only covariate variances should be used instead. In many cases, setting this to TRUE can lead to better covariate balance, especially when there is high correlation between variables. Default is FALSE. This argument is only necessary when refinement.method = mahalanobis and will have no impact otherwise.

restrict.control.period
(optional) integer specifying the number of pre-treatment periods that treated units and potentially matched control units should be non-NULL and in the control state. For instance, specifying 4 would mean that the treatment history cannot contain any missing data or treatment from t-4 to t.

placebo.test
logical TRUE/FALSE. indicates whether or not you want to be able to run a placebo test. This will add additional requirements on the data – specifically, it requires that no unit included in the matching/refinement process can have missing outcome data over the lag window. Additionally, you should not use the outcome variable in refinement when placebo.test = TRUE.

Details
PanelMatch identifies a matched set for each treated observation. Specifically, for a given treated unit, the matched set consists of control observations that have an identical treatment history up to a number of lag time periods. Researchers must specify lag. A further refinement of the matched set may be performed by setting a maximum size of each matched set, size.match (the maximum number of control units that can be matched to a treated unit). Users can also specify covariates that should be used to identify similar control units and a method for defining similarity/distance between units. This is done via the covs.formula and refinement.method arguments, respectively, which are explained in more detail below.

Value
PanelMatch() returns an object of class "PanelMatch". This is a list that contains a few specific elements: First, a matched.set object(s) that has the same name as the provided qoi if the qoi is
"att", "art", or "atc". If qoi = "ate" then two matched.set objects will be attached, named "att" and "atc." Please consult the documentation for matched.set() to read more about the structure and usage of matched.set objects. Also, see the vignette page about matched.set objects for more information about these objects: vignette("matched_set_objects", package = "PanelMatch"). The PanelMatch object also has some additional attributes:

- qoi: The qoi specified in the original function call
- lead: the lead window specified in the original function call
- forbid.treatment.reversal: logical value matching the forbid.treatment.reversal parameter provided in the function call.
- outcome.var: character string matching the outcome variable provided in the original function call.

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References

Imai, Kosuke, In Song Kim, and Erik Wang (2023)

Examples

dem.sub <- dem[ dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
treatment = "dem", refinement.method = "ps.match",
data = dem.sub, match.missing = TRUE,
covs.formula = ~ tradewb,
size.match = 5, qoi = "att",
outcome.var = "y", lead = 0:4, forbid.treatment.reversal = FALSE)

perunitSum

This is a low level function that is used to calculate a value associated with each unit. This value is a weighted summation of the dependent variable, based on the Wit values discussed in Imai et al. (2023)

Description

perunitSum This is a low level function that is used to calculate a value associated with each unit. This value is a weighted summation of the dependent variable, based on the Wit values discussed in Imai et al. (2023)
Usage

perunitSum(udf, lead.in, dependent.in, qoi_in)

Arguments

- **udf**: data.frame
- **lead.in**: integer. A particular lead value
- **dependent.in**: string specifying the dependent variable name
- **qoi_in**: string specifying the QOI

Value

Named vector containing the per-unit sums.

---

**perunitSum_Dit**

*perunitSum_Dit Similar to perunitSum, this is a low level helper function for calculating specific values defined in Imai et al. (2023). This focuses on Dit rather than Wit*

Description

perunitSum_Dit Similar to perunitSum, this is a low level helper function for calculating specific values defined in Imai et al. (2023). This focuses on Dit rather than Wit

Usage

perunitSum_Dit(udf, qoi_in)

Arguments

- **udf**: data.frame
- **qoi_in**: string specifying the QOI

Value

Named vector containing the per-unit sums.
**Description**

Calculates results for a placebo test

**Usage**

```r
placebo_test(
  pm.obj,
  data,
  lag.in = NULL,
  number.iterations = 1000,
  confidence.level = 0.95,
  plot = FALSE,
  se.method = "bootstrap",
  parallel = FALSE,
  num.cores = 1,
  ...
)
```

**Arguments**

- `pm.obj`: an object of class `PanelMatch`
- `data`: data.frame with the original data
- `lag.in`: integer indicating earliest the time period(s) in the future for which the placebo test change in outcome will be calculated. Calculations will be made over the period \( t - \max(lag) \) to \( t-2 \), where \( t \) is the time of treatment. The results are similar to those returned by `PanelEstimate()`, except \( t-1 \) is used as the period of comparison, rather than the lead window. If not specified, the placebo test is conducted for periods from \( t - \max(lag) \) to \( t-2 \).
- `number.iterations`: integer specifying the number of bootstrap iterations
- `confidence.level`: confidence level for the calculated standard error intervals
- `plot`: logical indicating whether or not a plot should be generated, or just return the raw data from the calculations
- `se.method`: character string describing the type of standard error to be used. Valid inputs include "bootstrap", "conditional" and "unconditional". When the QOI is ATE, only bootstrap can be used.
- `parallel`: Logical. If TRUE and `se.method = "bootstrap"`, bootstrap procedure will be parallelized. Default is FALSE. If `se.method` is not set to bootstrap, this option does nothing.
plot.matched.set

plot.matched.set

plot.matched.set  Plot the distribution of the sizes of matched sets.

Description

A plot method for creating a histogram of the distribution of the sizes of matched sets. This method accepts all standard optional `hist` arguments via the `...` argument. By default, empty matched sets (treated units that could not be matched with any control units) are noted as a vertical bar at x = 0 and not included in the regular histogram. See the `include.empty.sets` argument for more information about this.

Usage

```r
## S3 method for class 'matched.set'
plot(
  x,
  ...,
)```
```r
border = NA,
col = "grey",
ylab = "Frequency of Size",
xlab = "Matched Set Size",
lwd = NULL,
main = "Distribution of Matched Set Sizes",
freq = TRUE,
include.empty.sets = FALSE
)
```

**Arguments**

- `x` a matched.set object
- `...` optional arguments to be passed to `hist()`
- `border` default is NA. This is the same argument as the standard argument for `hist()`
- `col` default is "grey". This is the same argument as the standard argument for `hist()`
- `ylab` default is "Frequency of Size". This is the same argument as the standard argument for `hist()`
- `xlab` default is "Matched Set Size". This is the same argument as the standard argument for `hist()`
- `lwd` default is NULL. This is the same argument as the standard argument for `hist()`
- `main` default is "Distribution of Matched Set Sizes". This is the same argument as the standard argument for `hist()`
- `freq` default is TRUE. See `freq` argument in `hist()` function for more.
- `include.empty.sets` logical value indicating whether or not empty sets should be included in the histogram. default is FALSE. If FALSE, then empty sets will be noted as a separate vertical bar at x = 0. If TRUE, empty sets will be included as normal sets.

**Examples**

```r
dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
treatment = "dem", refinement.method = "ps.match",
data = dem, match.missing = TRUE,
covs.formula = ~ I(lag(tradewb, 1:4)) + I(lag(y, 1:4)),
size.match = 5, qoi = "att",
outcome.var = "y", lead = 0:4, forbid.treatment.reversal = FALSE)
plot(PM.results$att)
plot(PM.results$att, include.empty.sets = TRUE)
```
plot.PanelEstimate

Plot point estimates and standard errors from a PanelEstimate calculation.

Description

The `plot.PanelEstimate` method takes an object returned by the `PanelEstimate` function and plots the calculated point estimates and standard errors over the specified lead time period. The only mandatory argument is an object of the `PanelEstimate` class.

Usage

```r
## S3 method for class 'PanelEstimate'
plot(
x, ylab = "Estimated Effect of Treatment", xlab = "Time", main = "Estimated Effects of Treatment Over Time", ylim = NULL, pch = NULL, cex = NULL, bias.corrected = FALSE, ...
)
```

Arguments

- `x` a `PanelEstimate` object
- `ylab` default is "Estimated Effect of Treatment." This is the same argument as the standard argument for `plot()`
- `xlab` default is "Time". This is the same argument as the standard argument for `plot()`
- `main` default is "Estimated Effects of Treatment Over Time". This is the same argument as the standard argument for `plot`.
- `ylim` default is NULL. This is the same argument as the standard argument for `plot()`
- `pch` default is NULL. This is the same argument as the standard argument for `plot()`
- `cex` default is NULL. This is the same argument as the standard argument for `plot()`
- `bias.corrected` logical indicating whether or not bias corrected estimates should be plotted. Default is FALSE. This argument only applies for standard errors calculated with the bootstrap.
- `...` Additional optional arguments to be passed to `plot()`.
Examples

    dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
    # create subset of data for simplicity
    PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
                              treatment = "dem", refinement.method = "mahalanobis",
                              data = dem.sub, match.missing = TRUE,
                              covs.formula = ~ tradewb,
                              size.match = 5, qoi = "att",
                              outcome.var = "y", lead = 0:4, forbid.treatment.reversal = FALSE)
    PE.results <- PanelEstimate(sets = PM.results, data = dem.sub, se.method = "unconditional")
    plot(PE.results)

print.matched.set

Print matched.set objects.

Description

Print matched.set objects.

Usage

    ## S3 method for class 'matched.set'
    print(x, ..., verbose = FALSE)

Arguments

    x
    a matched.set object

    ...    
    additional arguments to be passed to print

    verbose
    logical indicating whether or not output should be printed in expanded/raw list
    form. The verbose form is not recommended unless the data set is small. Default
    is FALSE

Examples

    dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
    # create subset of data for simplicity
    PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
                              treatment = "dem", refinement.method = "ps.match",
                              data = dem, match.missing = TRUE,
                              covs.formula = ~ I(lag(tradewb, 1:4)) + I(lag(y, 1:4)),
                              size.match = 5, qoi = "att",
                              outcome.var = "y", lead = 0:4, forbid.treatment.reversal = FALSE)
    print(PM.results$att)
summary.matched.set  
*Summarize information about a matched.set object and the matched sets contained within them.*

**Description**
A method for viewing summary data about the sizes of matched sets and metadata about how they were created. This method accepts all standard summary arguments.

**Usage**
## S3 method for class 'matched.set'
summary(object, ..., verbose = TRUE)

**Arguments**
- **object**  a matched.set object
- ...  Optional additional arguments to be passed to the summary function
- **verbose**  Logical value specifying whether or not a longer, more verbose summary should be calculated and returned. Default is TRUE.

**Value**
list object with either 5 or 1 element(s), depending on whether or not verbose is set to TRUE or not.

- **overview**  A data.frame object containing information about the treated units (unit id, time of treatment), and the number of matched control units with weights zero and above.

- **set.size.summary**  a summary object summarizing the minimum, maximum, and IQR of matched set sizes

- **number.of.treated.units**  The number of unit, time pairs that are considered to be "treated" units

- **num.units.empty.set**  The number of units treated at a particular time that were not able to be matched to any control units

- **lag**  The size of the lag window used for matching on treatment history. This affects which treated and control units are matched.

**Examples**
```r
dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
treatment = "dem", refinement.method = "ps.match",
data = dem.sub, match.missing = TRUE,
covs.formula = ~ I(lag(tradewb, 1:4)) + I(lag(y, 1:4)),
```
summary.PanelEstimate

summary.PanelEstimate

---

### Description

summary.PanelEstimate takes an object returned by PanelEstimate, and returns a summary table of point estimates and confidence intervals.

### Usage

```r
## S3 method for class 'PanelEstimate'
summary(object, verbose = TRUE, bias.corrected = FALSE, ...)
```

### Arguments

- **object**: A PanelEstimate object
- **verbose**: logical indicating whether or not output should be printed in an expanded form. Default is TRUE.
- **bias.corrected**: logical indicating whether or not bias corrected estimates should be provided. Default is FALSE. This argument only applies for standard errors calculated with the bootstrap.
- **...**: optional additional arguments. Currently, no additional arguments are supported.

### Examples

```r
dem.sub <- dem[dem[, "wbcode2"] <= 100, ]
# create subset of data for simplicity
PM.results <- PanelMatch(lag = 4, time.id = "year", unit.id = "wbcode2",
treatment = "dem", refinement.method = "ps.weight",
data = dem.sub, match.missing = TRUE,
covs.formula = ~ tradewb,
size.match = 5, qoi = "att",
outcome.var = "y", lead = 0:4, forbid.treatment.reversal = FALSE)
PE.results <- PanelEstimate(sets = PM.results, data = dem.sub, se.method = "unconditional")
summary(PE.results)
```
Index

* dataset
  dem, 4

balance_scatter, 2
dem, 4
DisplayTreatment, 5
enforce_lead_restrictions, 7
get_covariate_balance, 8
get_set_treatment_effects, 10
handle_moderating_variable, 11
matched_set, 12
PanelEstimate, 13
PanelMatch, 16
perunitSum, 19
perunitSum_Dit, 20
placebo_test, 21
plot.matched.set, 22
plot.PanelEstimate, 24
print.matched.set, 25
summary.matched.set, 26
summary.PanelEstimate, 27