Package ‘TriMatch’

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License GPL (>= 2)
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This package provides functions to estimate and visualize propensity score analyses including matching for non-binary treatments.

**Author(s)**

Jason Bryer <jason@bryer.org>

**See Also**

PSAgraphics multilevelPSA
as.data.frame.list  

Convert a list of vectors to a data frame.

Description

This function will convert a list of vectors to a data frame. This function will handle three different types of lists of vectors. First, if all the elements in the list are named vectors, the resulting data frame will have a number of columns equal to the number of unique names across all vectors. In cases where some vectors do not have names in other vectors, those values will be filled with NA.

Usage

```r
## S3 method for class 'list'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

- `x`: a list to convert to a data frame.
- `row.names`: a vector equal to `length(x)` corresponding to the row names. If NULL, the row names will be set to `names(x)`.
- `optional`: not used.
- `...`: other parameters passed to `data.frame`.

Details

The second case is when all the vectors are of the same length. In this case, the resulting data frame is equivalent to applying `rbind` across all elements.

The third case handled is when there are varying vector lengths and not all the vectors are named. This condition should be avoided. However, the function will attempt to convert this list to a data frame. The resulting data frame will have a number of columns equal to the length of the longest vector. For vectors with length less than this will fill the row with NA's. Note that this function will print a warning if this condition occurs.

Value

a data frame.

Author(s)

Jason Bryer jason@bryer.org

References

http://stackoverflow.com/questions/4227223/r-list-to-data-frame
Examples

```r
test1 <- list(c(a='a', b='b', c='c'), c(a='d', b='e', c='f'))
as.data.frame(test1)

# This will print a warning.
test2 <- list(c('a', 'b', 'c'), c('d', 'e', 'f'))
as.data.frame(test2)

# This will throw an error.
test3 <- list(Row1=c(a='a', b='b', c='c'), Row2=c(var1='d', var2='e', var3='f'))
as.data.frame(test3)

# This will print a warning.
test4 <- list(Row1=letters[1:5], Row2=letters[1:7], Row3=letters[8:14])
as.data.frame(test4)

# This will throw an error.
test5 <- list(letters[1:10], letters[11:20])
as.data.frame(test5)

# This will throw an error.
test6 <- list(list(letters), letters)
as.data.frame(test6)
```

**balance.plot**  
*Balance plot for the given covariate.*

**Description**

If the covariate is numeric, boxplots will be drawn with red points for the mean and green error bars for the standard error. For non-numeric covariates a barplot will be drawn.

**Usage**

```r
balance.plot(x, covar, model, nstrata = attr(attr(tmatch, "triangle.psa"), "nstrata"), label = "Covariate", ylab = "", xlab = NULL, se.ratio = 2, print = TRUE, legend.position = "top", x.axis.labels, x.axis.angle = -45, ...)
```

**Arguments**

- **x**: results from `trimatch`.
- **covar**: vector of the covariate to check balance of.
- **model**: an integer between 1 and 3 indicating from which model the propensity scores will be used.
boxdiff.plot

nstrata number of strata to use.
label label for the legend.
ylab label of the y-axis.
xlab label of the x-axis.
se.ratio a multiplier for how large standard error bars will be.
print print the output if the Friedman Rank Sum Test and repeated measures ANOVA (for continuous variables).
legend.position the position of the legend. See theme.
x.axis.labels labels for the x-axis.
x.axis.angle angle for x-axis labels.
... parameters passed to plot.balance.plots.

Details
A Friedman rank sum test will be performed for all covariate types, printed, and stored as an attribute to the returned object named friedman. If a continuous covariate a repeated measures ANOVA will also be performed, printed, and returned as an attribute named rmanova.

Value
a ggplot2 figure or a list of ggplot2 figures if covar is a data frame.

boxdiff.plot

Returns a ggplot2 box plot of the differences.

Description
A boxplot of differences between each pair of treatments.

Usage
boxdiff.plot(tmatch, out, plot.mean = TRUE, ordering = attr(tmatch, "match.order"), ci.width = 0.5)

Arguments

tmatch the results from trimatch.
out a vector of the outcome measure of interest.
plot.mean logical indicating whether the means should be plotted.
ordering specify the order for doing the paired analysis, that is analysis will be conducted as: ordering[1] ~ ordering[2], ordering[1] ~ ordering[3], and ordering[2] ~ ordering[3].
ci.width the width for the confidence intervals.
covariateBalance

Value

a ggplot2 boxplot of the differences.

covariateBalance Calculate covariate effect size differences before and after stratification.

Description

This function is modified from the cv.bal.psa function in the PSAgraphics package.

Usage

covariateBalance(covariates, treatment, propensity, strata = NULL,
    int = NULL, tree = FALSE, minsize = 2, universal.psd = TRUE,
    trM = 0, absolute.es = TRUE, trt.value = NULL, use.trt.var = FALSE,
    verbose = FALSE, xlim = NULL, plot.strata = TRUE, ...)

Arguments

covariates dataframe of interest
treatment binary vector of 0s and 1s (necessarily? what if character, or 1, 2?)
propensity PS scores from some method or other.
strata either a vector of strata number for each row of covariate, or one number n
    in which case it is attempted to group rows by ps scores into n strata of size
    approximately 1/n. This does not seem to work well in the case of few specific
    propensity values, as from a tree.
int either a number m used to divide [0,1] into m equal length subintervals, or a vec-
    tor of cut points between 0 an 1 defining the subintervals (perhaps as suggested
    by loess.psa). In either case these subintervals define strata, so strata can be of
    any size.
tree logical, if unique ps scores are few, as from a recursively partitioned tree, then
    TRUE will force each ps value to define a stratum.
minsize smallest allowable stratum-treatment size. If violated, strata is removed.
universal.psd If 'TRUE', forces standard deviations used to be unadjusted for stratification.
trM trimming proportion for mean calculations.
absolute.es logical, if 'TRUE' routine uses absolute values of all effect sizes.
trt.value allows user to specify which value is active treatment, if desired.
use.trt.var logical, if true then Rubin-Stuart method using only treatment variance with be
    used in effect size calculations.
verbose logical, controls output that is visibly returned.
xlim limits for the x-axis.
plot.strata logical indicating whether to print strata.
... currently unused.
data.frame.to.list

Details

Note: effect sizes are calculated as treatment 1 - treatment 0, or treatment B - treatment A.

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data.frame.to.list  Convert a list of vectors to a data frame.

Description

This function will convert a list of vectors to a data frame. This function will handle three different
types of lists of vectors. First, if all the elements in the list are named vectors, the resulting data
frame will have have a number of columns equal to the number of unique names across all vectors.
In cases where some vectors do not have names in other vectors, those values will be filled with NA.

Usage

data.frame.to.list(...)  

Arguments

... other parameters passed to data.frame.

Details

The second case is when all the vectors are of the same length. In this case, the resulting data frame
is equivalent to applying rbind across all elements.

The third case handled is when there are varying vector lengths and not all the vectors are named.
This condition should be avoided. However, the function will attempt to convert this list to a data
frame. The resulting data frame will have a number of columns equal to the length of the longest
vector. For vectors with length less than this will fill the row with NAs. Note that this function will
print a warning if this condition occurs.

Value

a data frame.

References

http://stackoverflow.com/questions/4227223/r-list-to-data-frame
distance.euclid | Euclidean distance calculation.

**Description**

This method uses a simple Euclidean distance calculation for determining the distances between two matches. That is, $|ps1 - ps2|$.

**Usage**

```
distance.euclid(x, grouping, id, groups, caliper, nmatch = Inf)
```

**Arguments**

- `x` : vector of propensity scores.
- `grouping` : vector or factor identifying group membership.
- `id` : vector corresponding to unique identifier for each element in `x` and `grouping`.
- `groups` : vector of length two indicating the unique groups to calculate the distance between. The first element will be the rows, the second columns.
- `caliper` : a scaler indicating the caliper to use for matching within each step.
- `nmatch` : number of smallest distances to retain.

**Value**

a list of length equal to `x`. Each element of the list is a named numeric vector where the values correspond to the distance and the name to the `id`.

---

distances.plot | Barplot for the sum of distances.

**Description**

Barplot for the sum of distances.

**Usage**

```
distances.plot(tmatch, caliper = 0.25, label = FALSE)
```

**Arguments**

- `tmatch` : the results of `trimatch`.
- `caliper` : a vector indicating where vertical lines should be drawn as a factor of the standard deviation. Rosenbaum and Rubin (1985) suggested one quarter of one standard deviation.
- `label` : label the bars that exceed the minimum caliper.
See Also
  triangle.match

Description
This function will create a ggplot2 figure with propensity scores on the x-axis and the outcome on the y-axis. Three Loess regression lines will be plotted based upon the propensity scores from model. Since each model produces propensity scores for two of the three groups, the propensity score for the third group in each matched triplet will be the mean of the other two. If model is not specified, the default will be to use the model that estimates the propensity scores for the first two groups in the matching order.

Usage
loess3.plot(tmatch, outcome, model, ylab = "Outcome",
  plot.connections = FALSE, connections.color = "black",
  connections.alpha = 0.2, plot.points = geom_point, points.alpha = 0.1,
  points.palette = "Dark2", ...)

Arguments
tmatch the results of trimatch.
outcome a vector representing the outcomes.
model an integer between 1 and 3 indicating from which model the propensity scores will be used.
ylab the label for the y-axis.
plot.connections boolean indicating whether lines will be drawn connecting each matched triplet.
connections.color the line color of connections.
connections.alpha number between 0 and 1 representing the alpha levels for connection lines.
plot.points a ggplot2 function for plotting points. Usually geom_point or geom_jitter. If NULL no points will be drawn.
points.alpha number between 0 and 1 representing the alpha level for the points.
points.palette the color palette to use. See scale_colour_brewer and http://colorbrewer2.org/ for more information.
... other parameters passed to geom_smooth and stat_smooth.

Value
a ggplot2 figure.
**maximumTreat**

This method will return at least one treatment from groups one and two within the caliper.

**Description**

This method will attempt to return enough rows to use each treatment (the first two groups in the matching order) at least once. Assuming treat1 is the first group in the match order and treat2 the second, all duplicate treat1 rows are removed. Next, all treat2 units not in present in after removing duplicate treat1 units are identified. For each of those treat2 units, the matched triplet with the smallest overall distances where treat2 is one of the matched units is retained.

**Usage**

```r
maximumTreat(tmatch, ...)```

**Arguments**

- `tmatch`: initial results from `trimatch` that contains all possible matches within the specified caliper.
- `...`: currently unused.

**merge.triangle.matches**

Merges outcomes with the matched set.

**Description**

The `y` parameter should be a subset of the original data used.

**Usage**

```r
# S3 method for class 'triangle.matches'
merge(x, y, ...)```

**Arguments**

- `x`: the result of `trimatch`
- `y`: another data frame or vector to merge with.
- `...`: unused

**Value**

`x` with the additional column(s) added.
merge.triangle.psa  Merges covariate(s) with the results of trips.

Description
The y parameter should be a subset of the original data used.

Usage
```r
## S3 method for class 'triangle.psa'
merge(x, y, ...)
```

Arguments
- `x` the result of trips
- `y` another data frame or vector to merge with.
- `...` unused

Value
`x` with the additional column(s) added.

multibalance.plot  Multiple covariate balance assessment plot.

Description
A graphic based upon cv.bal.psa function in the PSAgraphics package. This graphic plots the effect sizes for multiple covariates before and after propensity score adjustment.

Usage
```r
multibalance.plot(tpsa, tmatch, grid = TRUE, cols)
```

Arguments
- `tpsa` results of trips.
- `tmatch` results of trimatch.
- `grid` if TRUE, then a grid of three plots for each model will be displayed.
- `cols` character vector of covariates (i.e. column names) from the original data to include in the plot. By default all covariates used in the logistic regression model are used.

Value
a ggplot2 figure.
Results from the 1987 National Medical Expenditure Study

Description

This file was originally prepared by Anders Corr (corr@fas.harvard.edu) who reports on December 8, 2007 that the resulting numbers closely match with those reported in the published article. It was later modified by Jason Bryer (jason@bryer.org) to an R data object to be included in this package. See http://imai.princeton.edu/research/pscore.html for more information.

Format

A data frame with 9,708 observations of 12 variables.

Author(s)

United States Department of Health and Human Services. Agency for Health Care Policy and Research

Source

http://imai.princeton.edu/research/pscore.html

References


OneToN

This method will use a M1-to-M2-to-1 matching.

Description

In this method, M2 corresponds to the number of times a treat1 unit can be matched with a treat2 unit. The M1 parameter corresponds to the number of times a treat1 unit can be used in total.

Usage

OneToN(tmatch, M1 = 2, M2 = 1, ...)

This method will use a M1-to-M2-to-1 matching.
parallel.plot

Arguments

- **tmatch**: Initial results from `trimatch` that contains all possible matches within the specified caliper.
- **M1**: A scaler indicating the number of unique subjects in group one to retain. This applies only to the first group in the matching order.
- **M2**: A scaler indicating the number of unique matches to retain. This applies to the first two groups in the matching order.
- **...**: Currently unused.

**Description**

Creates a `ggplot2` figure of a parallel coordinate plot.

**Usage**

```r
parallel.plot(tmatch, outcome)
```

Arguments

- **tmatch**: Results from `trimatch`.
- **outcome**: Vector of the outcome

**perpPt**

Internal method for plotting. Finds a point d distance from x, y

**Description**

Internal method for plotting. Finds a point d distance from x, y

**Usage**

```r
perpPt(x, y, d = 0.05)
```

Arguments

- **x**: x coordinate
- **y**: y coordinate
- **d**: The distance
**plot.balance.plots**  
*Prints a grid of balance plots.*

**Description**

Prints a grid of balance plots.

**Usage**

```r
## S3 method for class 'balance.plots'
plot(x, rows, cols, byrow = TRUE,
     plot.sequence = seq_along(bplots), ...)
```

**Arguments**

- `x`: the results of `balance.plot` when a data frame is specified.
- `rows`: if `covar` is a data frame of covariates, the number of rows in the grid of figures.
- `cols`: if `covar` is a data frame of covariates, the number of columns in the grid of figures.
- `byrow`: if TRUE (default), plots will be drawn by rows, otherwise by columns.
- `plot.sequence`: the sequence (or subset) of plots to draw.
- `...`: currently unused.

---

**plot.triangle.matches**  
*Triangle plot drawing matched triplets.*

**Description**

This plot function adds a layer to `plot.triangle.psa` drawing matched triplets. If `p` is supplied, this function will simply draw on top of the pre-existing plot, otherwise `plot.triangle.psa` will be called first.

**Usage**

```r
## S3 method for class 'triangle.matches'
plot(x, sample = 0.05,
     rows = sample(nrow(tmatch), nrow(tmatch) * sample), line.color = "black",
     line.alpha = 0.5, point.color = "black", point.size = 3, p, ...)
```
Arguments

- **x**: matched triplets from `link{triangle.match}`.
- **sample**: an number between 0 and 1 representing the percentage of matched triplets to draw.
- **rows**: an integer vector corresponding to the rows in `tmatch` to draw.
- **line.color**: the line color.
- **line.alpha**: the alpha for the lines.
- **point.color**: color of matched triplet points.
- **point.size**: point size for matched triplets.
- **p**: a ggplot to add the match lines. If NULL, then `plot.triangle.psa`.
- **...**: other parameters passed to `plot.triangle.psa`.

Details

If this function calls `plot.triangle.psa`, it will only draw line segments and points for those data rows that were used in the matching procedure. That is, data elements not matched will be excluded from the figure. To plot all segments and points regardless if used in matching, set `p = plot(tpsa)`.

Value

- a ggplot2 graphic.

See Also

- `plot.triangle.psa`
- `triangle.match`

Description

Triangle plot showing the fitted values (propensity scores) for three different models.

Usage

```r
## S3 method for class 'triangle.psa'
plot(x, point.alpha = 0.3, point.size = 1.5,
     legend.title = "Treatment", text.size = 4, draw.edges = FALSE,
     draw.segments = TRUE, edge.alpha = 0.2, edge.color = "grey",
     edge.labels = c("Model 1", "Model 2", "Model 3"), sample = c(1), ...)
```
Arguments

x the results from `trips`.
point.alpha alpha level for points.
point.size point size.
legend.title title for the legend.
text.size text size.
draw.edges draw edges of the triangle.
draw.segments draw segments connecting points across two models.
edge.alpha alpha level for edges if drawn.
edge.color the color for edges if drawn.
edge.labels the labels to use for each edge of the triangle.
sample a vector of length 1 or 3 representing the sample of points to plot. The position of each element corresponds to the groups as returned by `attr(tpsa, 'groups')`. If equal to one, all points will be plotted. Values less than one will plot a percentage of points. Values greater than one exactly that number of points will be plotted.

... currently unused.

Value

ggplot2 figure

See Also

triangle.psa

print.balance.plots  Print the results of `balance.plot` for a data frame of covariates.

Description

Print the results of `balance.plot` for a data frame of covariates.

Usage

```r
## S3 method for class 'balance.plots'
print(x, ...)
```

Arguments

x the results of `balance.plot` when a data frame is specified.
... parameters passed to `plot.balance.plots` and `summary.balance.plots`. 
### print.triangle.plot

**Print method for plot.triangle.psa.** The primary purpose is to suppress the "Removed n rows containing missing values" warning printed by ggplot2.

#### Description

Print method for `plot.triangle.psa`. The primary purpose is to suppress the "Removed n rows containing missing values" warning printed by ggplot2.

#### Usage

```r
## S3 method for class 'triangle.plot'
print(x, ...)  
```

#### Arguments

- `x`: a plot from `plot.triangle.psa`.
- `...`: other parameters passed to ggplot2.

### print.trimatch.summary

**Prints the results of summary.triangle.matches.**

#### Description

This is an S3 generic function to print the results of `summary.triangle.matches`.

#### Usage

```r
## S3 method for class 'trimatch.summary'
print(x, ...)  
```

#### Arguments

- `x`: results of `summary.triangle.matches`.
- `...`: multiple results of `summary.triangle.matches`. These must be named. For example,"Method 1" = summary(tmath, outcome).
segment1

*Internal method for plotting. Position along the left side segment*

**Description**

Internal method for plotting. Position along the left side segment

**Usage**

segment1(d)

**Arguments**

- **d**: the distance

---

segment2

*Internal method for plotting. Position along the right side segment*

**Description**

Internal method for plotting. Position along the right side segment

**Usage**

segment2(d)

**Arguments**

- **d**: the distance

---

star

*Returns significance level.*

**Description**

Returns the significance level as stars, or NA if a non-numeric value is passed in.

**Usage**

star(x)

**Arguments**

- **x**: p-value.
summary.balance.plots  Prints a summary table of the test statistics of each balance plot.

Description

The balance.plot function will create a grid of balance plots if a data frame is provided. The returned object is a list of ggplot2 figures with the statistical tests (i.e. Friedmen Rank Sum tests and if a continuous variable, repeated measures ANOVA as well) saved as attributes. This function will return a data frame combining all of those results.

Usage

```r
## S3 method for class 'balance.plots'
summary(object, ...)```

Arguments

- `object` the results of balance.plot when a data frame is specified.
- `...` currently unused.

Value

a data frame

summary.triangle.matches  Provides a summary of the matched triplets including analysis of outcome measure if provided.

Description

If an outcome measure is provided this function will perform a Freidman Rank Sum Test and repeated measures ANOVA. If either test has a statistically significant difference (as determined by the value of the p parameter), a Pairwise Wilcoxon Rank Sum Test will also be provided.

Usage

```r
## S3 method for class 'triangle.matches'
summary(object, outcome, p = 0.05,
         ordering = attr(object, "match.order"), ...)```
Arguments

- **object**: result of `trimatch`.
- **outcome**: vector representing the outcome measure.
- **p**: threshold of the p value to perform a
- **ordering**: specify the order for doing the paired analysis, that is analysis will be conducted as: ordering[1] - ordering[2], ordering[1] - ordering[3], and ordering[2] - ordering[3].
- **...**: parameters passed to other statistical tests.

Value

- a `trimatch.summary` object.

See Also

- `friedman.test`, `ezANOVA`, `pairwise.wilcox.test`

---

**summary.triangle.psa**

*Prints the summary results of the logistic regression models.*

**Description**

The `trips` function estimates three separate logistic regression models for each pair of groups. This function will print a combined table of the three summaries.

**Usage**

```r
## S3 method for class 'triangle.psa'
summary(object, ...)
```

**Arguments**

- **object**: the results of `trips`.
- **...**: currently unused.
summary.unmatched

Provides a summary of unmatched subjects.

Description
Will return as a list and print the percentage of total unmatched rows and percent by treatment.

Usage
```r
## S3 method for class 'unmatched'
summary(object, digits = 3, ...)
```

Arguments
- `object`: results of `unmatched`
- `digits`: number of digits to print.
- `...`: currently unused.

Value
- a list of summary results.

trimatch

Creates matched triplets.

Description
Create matched triplets by minimizing the total distance between matched triplets within a specified caliper.

Usage
```r
trimatch(tpsa, caliper = 0.25, nmatch = c(15), match.order, exact,
method = maximumTreat, ...)
```

Arguments
- `tpsa`: the results from `trips`
- `caliper`: a vector of length one or three indicating the caliper to use for matching within each step. This is expressed in standardized units such that .25 means that matches must be within .25 of one standard deviation to be kept, otherwise the match is dropped.
number of closest matches to retain before moving to next edge. This can be Inf in which case all matches within the caliper will be retained through to the next step. For large datasets, evaluating all possible matches within the caliper could be time consuming.

match.order character vector of length three indicating the order in which the matching algorithm will processes. The default is to use start with the group the middle number of subjects, followed by the smallest, and then the largest.

exact a vector or data frame of representing covariates for exact matching. That is, matched triplets will first be matched exactly on these covariates before evaluating distances.

method This is a function that specifies which matched triplets will be retained. If NULL, all matched triplets within the specified caliper will be returned (equivalent to caliper matching in two group matching). The default is maximumTreat that attempts include each treatment at least once. Another option is OneToN which mimicks the one-to-n matching where treatments are matched to multiple control units.

other parameters passed to method.

Details

The trips function will estimate the propensity scores for three models. This method will then find the best matched triplets based upon minimizing the summed differences between propensity scores across the three models. That is, the algorithm works as follows:

- The first subject from model 1 is selected.
- The nmatch[1] smallest distances are selected using propensity scores from model 1.
- For each of the matches identified, the subjects propensity score from model 2 is retrieved.
- The nmatch[2] smallest distances are selected using propensity score from model 3.
- For each of those matches identified, the subjects propensity score from model 2 is retrieved.
- The distances is calculated from the first and last subjects propensity scores from model 2.
- The three distances are summed.
- The triplet with the smallest overall distance is selected and returned.

Examples

```
## Not run:
data(turoing)
formu <- ~ Gender + Ethnicity + Military + ESL + EdMother + EdFather + Age + Employment + Income + Transfer + GPA
tpsa <- trips(tutoring, tutoring$trait, formu)
tmatch <- trimatch(tpsa, status=FALSE)

## End(Not run)
```
trimatch.apply2

Recursive function to find possible matched triplets using the apply functions.

Description

Internal method. This version does not use the exact matching. Instead, this function should be called separately for each grouping.

Usage

trimatch.apply2(tpsa, caliper, nmatch, match.order, sd1, sd2, sd3)

Arguments

tpsa the results from trips

caliper a vector of length one or three indicating the caliper to use for matching within each step. This is expressed in standardized units such that .25 means that matches must be within .25 of one standard deviation to be kept, otherwise the match is dropped.
nmatch number of closest matches to retain before moving to next edge. This can be Inf in which case all matches within the caliper will be retained through to the next step. For large datasets, evaluating all possible matches within the caliper could be time consuming.

match.order character vector of length three indicating the order in which the matching algorithm will processes. The default is to use start with the group the middle number of subjects, followed by the smallest, and then the largest.
sd1 standard deviation for propensity scores from model 1.
sd2 standard deviation for propensity scores from model 2.
sd3 standard deviation for propensity scores from model 3.

trips Estimates propensity scores for three groups

Description

The propensity score is

\[ e(X) = P(W = 1|X) \]

This function will estimate the propensity scores for each pair of groups (e.g. two treatments and one control).
Usage

```r
trips(thedata, treat, formu = ~., groups = unique(treat), nstrata = 5,
method = "logistic", ...)
```

Arguments

- **thedata**: the data frame.
- **treat**: vector or factor indicating the treatment/control assignment for the data. Length must be equal to `nrow(thedata)`.
- **formu**: the logistic regression formula. Note that the dependent variable should not be specified and will be modified.
- **groups**: a vector of exactly length three corresponding the values in `treat` for each control/treatment.
- **nstrata**: the number of strata marks to plot on the edge.
- **method**: the method to use to estimate the propensity scores. Current options are logistic or randomForest.
- **...**: other parameters passed to `glm`.

Details

\[ PS_1 = e(X_{T_1C}) = Pr(z = 1 | X_{T_1C}) \]
\[ PS_2 = e(X_{T_2C}) = Pr(z = 1 | X_{T_2C}) \]
\[ PS_3 = e(X_{T_2T_1}) = Pr(z = 1 | X_{T_2T_1}) \]

Examples

```r
## Not run:
data(tutoring)
formu <- ~ Gender + Ethnicity + Military + ESL + EdMother + EdFather + Age +
        Employment + Income + Transfer + GPA
tpsa <- trips(tutoring, tutoring$ treat, formu)
head(tpsa)
## End(Not run)
```
Results from a study examining the effects of tutoring services on course grades.

Description

- **treat**: Treatment indicator.
- **Course**: The course id the student was enrolled in.
- **Grade**: The course grade the student earned (4=A, 3=B, 2=C, 1=D, 0=F or W).
- **Gender**: Gender of the student.
- **Ethnicity**: Ethnicity of the student, either White, Black, or Other.
- **Military**: Is the student an active military student.
- **ESL**: English second language student.
- **EdMother**: Education level of the mother (1 = did not finish high school; 2 = high school grad; 3 = some college; 4 = earned associate degree; 5 = earned baccalaureate degree; 6 = Earned Master’s degree; 7 = earned doctorate).
- **EdFather**: Education level of the father (levels same as EdMother).
- **Age**: Age at the start of the course.
- **Employment**: Employment level at college enrollment (1 = No; 2 = part-time; 3 = full-time).
- **Income**: Household income level at college enrollment (1 = <25K; 2 = <35K; 3 = <45K; 4 = <55K; 5 = <70K; 6 = <85K; 7 = <100K; 8 = <120K; 9 = >120K).
- **Transfer**: Number of transfer credits at the start of the course.
- **GPA**: GPA as of the start of the course.
- **GradeCode**: Letter grade.
- **Level**: Level of the course, either Lower or Upper.
- **ID**: Randomly assigned student ID.

Format

A data frame with 17 variables.
unmatched

Returns rows from trips that were not matched by trimatch.

Description

This function returns a subset of trips that were not matched by trimatch. All data frame methods work with the returned object but special summary function will provided relevant information.

Usage

unmatched(tmatch)

Arguments

tmatch the results of trimatch.

Value

a data frame of unmatched rows.
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