Package 'MatchingFrontier'

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Type Package

Title R Package for Calculating the Balance-Sample Size Frontier

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Description Implements methods from King, Lucas, and Nielsen

Imports igraph

LazyData true

License GPL-3

R topics documented:

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estimateEffects   *Estimate Effects on the Frontier*

Description

estimateEffects() is used to estimate the effect of the treatment along the entire frontier.

Usage

```
estimateEffects(frontier.object, formula)
```

Arguments

frontier.object

An object generated by makeFrontier().

formula   An object of class formula (or one that can be coerced to that class). This will be passed to lm().

Examples

```
## Not run:
data(lalonde)
match.on <- colnames(lalonde)[!(colnames(lalonde) %in% c('re78', 'treat'))]
my.frontier <- makeFrontier(dataset = lalonde,
                            treatment = 'treat',
                            outcome = 're78',
                            match.on = match.on)
my.estimates <- estimateEffects(my.frontier, 're78 ~ treat')

## End(Not run)
```

---

generateDataset   *Generate a data set that is on the balance - sample size frontier.*

Description

generateDataset() allows the user to export a data set that sits on the frontier.

Usage

```
generateDataset(frontier.object, number.to.prune)
```

Arguments

`frontier.object`

> An object generated by `makeFrontier()`.

`number.to.prune`

> The number of observations that are to be pruned. If the user selects an undefined point, `generateDataset` returns a dataset from the nearest defined point on the frontier.

Examples

```
## Not run:
data(lalonde)
match.on <- colnames(lalonde)[!(colnames(lalonde) %in% c('re78', 'treat'))]
my.frontier <- makeFrontier(dataset = lalonde,
                            treatment = 'treat',
                            outcome = 're78',
                            match.on = match.on)
my.dataset <- generateDataset(my.frontier, 1000)

## End(Not run)
```

---

lalonde *Modified Lalonde dataset*

Description

This is a modified version of the Lalonde experimental dataset used for explanatory purposes only.

Usage

```
data(lalonde)
```

Format

A data frame with 16437 observations on the following 11 variables.

`treat` treatment variable indicator

`age` age

`education` years of education

`black` race indicator variable

`married` marital status indicator variable

`nodegree` indicator variable for not possessing a degree

`re74` real earnings in 1974

`re75` real earnings in 1975

`re78` real earnings in 1978 (post-treatment outcome)

`hispanic` ethnic indicator variable

| makeFrontier | *Compute the balance - sample size frontier.* |

Description

makeFrontier() computes the balance - frontier sample size and can be used with estimateEffects to estimate effects along the balance - sample size frontier.

Usage

```
makeFrontier(dataset, treatment, outcome, match.on, QOI = "FSATT", metric = "Mahal", ratio = "variable
```

Arguments

dataset	The data set contain containing the treatment, outcome, and variable to match on.
treatment	The name of the treatment.
outcome	The name of the outcome.
match.on	A vector of colnames indicating which variables are to be matched on.
QOI	The quantity of interest to be estimated. By default, feasible sample average treatment effect on the treated or FSATT. The other option is SATT (sample average treatment effect on the treated).
metric	The metric used to measure imbalance. Defaults to average mahalanobis distance to nearest match. The other option is L1.
ratio	Variable or fixed ratio. See King, Lucas, and Nielsen for details.
breaks	Can be used with L1 to provide user-specified breaks.

Examples

```
## Not run:
data(lalonde)
match.on <- colnames(lalonde)[!(colnames(lalonde) %in% c('re78', 'treat'))]
my.frontier <- makeFrontier(dataset = lalonde,
                            treatment = 'treat',
                            outcome = 're78',
                            match.on = match.on)

## End(Not run)
```

---

plotEstimates	*Plot estimates along the frontier.*

Description

plotEstimates() plots estimates along the frontier.

Usage

```
plotEstimates(frontier.object, estimates.object, xlab = "Number of Observations Pruned", ylab = "Esti
```

Arguments

frontier.object
                An object generated by makeFrontier()

estimates.object
                An object generated by estimateEffects()

xlab   The label for the x-axis. Defaults to 'Number of Observations Pruned'.

ylab   The label for the y-axis. Defaults to Estimate'.

main   The main label. Defaults to 'Effects Plot'.

...   Additional arguments to be passed to plot.

Details

plotEstimates() wraps plot and uses ... to pass additional arguments to the base plot() function, like color, axis range, etc.

Examples

```
## Not run:
data(lalonde)
match.on <- colnames(lalonde)[!(colnames(lalonde) %in% c('re78', 'treat'))]
my.frontier <- makeFrontier(dataset = lalonde,
                            treatment = 'treat',
                            outcome = 're78',
                            match.on = match.on)
my.estimates <- estimateEffects(my.frontier, 're78 ~ treat')
plotEstimates(my.frontier, my.estimates)

## End(Not run)
```

---

plotFrontier   *Plot the balance - sample size frontier.*

Description

plotFrontier() plots the balance - sample size frontier.

Usage

```
plotFrontier(frontier.object, xlab = "Number of Observations Pruned", ylab = "AMD", main = "Frontier F
```

Arguments

frontier.object

> An object generated by makeFrontier()

xlab	The label for the x-axis. Defaults to 'Number of Observations Pruned'.
ylab	The label for the y-axis. Defaults to Estimate'.
main	The main label. Defaults to 'Effects Plot'.
...	Additional arguments to be passed to plot.

Details

plotEstimates() wraps plot and uses . . . to pass additional arguments to the base plot() function, like color, axis range, etc.

Examples

```
## Not run:
data(lalonde)
match.on <- colnames(lalonde)[!(colnames(lalonde) %in% c('re78', 'treat'))]
my.frontier <- makeFrontier(dataset = lalonde,
                            treatment = 'treat',
                            outcome = 're78',
                            match.on = match.on)
my.estimates <- estimateEffects(my.frontier, 're78 ~ treat')
plotFrontier(my.frontier)

## End(Not run)
```

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