

# Package ‘MatchItSE’

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**Type** Package

**Title** Calculates SE for Matched Samples from 'MatchIt'

**Version** 1.0

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**Description** Contains various methods for Standard Error estimation for 'MatchIt' objects.

**URL** <https://github.com/thorstenhenke/MatchItSE>

**BugReports** <https://github.com/thorstenhenke/MatchItSE/issues>

**License** GPL (>= 2)

**Depends** R (>= 3.3.1)

**Imports** Rcpp (>= 0.12.4), methods

**Suggests** optmatch

**Enhances** MatchIt

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 5.0.1

**Encoding** UTF-8

**NeedsCompilation** yes

**Repository** CRAN

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abadie_imbens_se	<i>Abadie Imben's Standard Error for the ATT</i>
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### Description

Calculate the SE for the ATT with Abadie & Imben's method.

### Usage

```
abadie_imbens_se(obj, Y)
```

### Arguments

obj	MatchIt Object
Y	Response Vector

### Value

SE for the ATT of Y

### References

Abadie, A., Drukker, D., Herr, J.L. & Imbens, G. (2004). Implementing matching estimators for average treatment effects in Stata. *The Stata Journal* (4), pp. 290 - 311.

### Examples

```
## Not run:  
library(MatchIt)  
data("lalonde")  
m.out <- matchit(treat ~ educ + black, data = lalonde)  
att(obj = m.out, Y = lalonde$re78)  
abadie_imbens_se(obj = m.out, Y = lalonde$re78)  
  
## End(Not run)
```

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add_model_matrix	<i>Rebuilds the model matrix for MatchIt objects</i>
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## Description

In order to use estimate Standard Errors with the Abadie and Imben's method the MatchIt object needs to have a model matrix. The model matrix is created based on the subclasses given by the full matching procedure.

## Usage

```
add_model_matrix(fit)
```

## Arguments

fit	MatchIt Object
-----	----------------

## Details

This function is experimental! Most methods for estimating standard errors are only documented for NN matching. Please use with caution!

## Value

MatchIt Object with added model matrix

## Examples

```
## Not run:
library(MatchIt)
data('lalonge')
m.out <- matchit(treat ~ educ + black, data = lalonge, method = 'full')
att(obj = m.out, Y = lalonge$re78)
abadie_imbens_se(m.out, lalonge$re78) # FAILS!
m.out <- add_model_matrix(m.out)
abadie_imbens_se(m.out, lalonge$re78)

## End(Not run)
```

att *Average Treatment Effect for the Treated (ATT)*

---

**Description**

Calculate the ATT for a given MatchIt object and a given response vector.

**Usage**

```
att(obj, Y)
```

**Arguments**

obj	MatchIt Object
Y	Response Vector

**Value**

The ATT for Y

**Examples**

```
## Not run:  
library(MatchIt)  
data("lalonde")  
m.out <- matchit(treat ~ educ + black, data = lalonde)  
att(obj = m.out, Y = lalonde$re78)  
  
## End(Not run)
```

---

bootstrap.se *Non-parametric bootstrap Standard Error for the ATT*

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**Description**

Calculate the SE for the ATT with a non-parametric bootstrap method.

**Usage**

```
bootstrap.se(obj, Y, max.iter = 1000)
```

**Arguments**

obj	MatchIt Object
Y	Response Vector
max.iter	Maximum bootstrap Iterations. Default is 1000.

**Value**

SE for the ATT of Y

**Examples**

```
## Not run:
library(MatchIt)
data("lalonge")
m.out <- matchit(treat ~ educ + black, data = lalonge)
att(obj = m.out, Y = lalonge$re78)
bootstrap.se(obj = m.out, Y = lalonge$re78)

## End(Not run)
```

---

lechner\_se

*Lechner's Standard Error for the ATT*


---

**Description**

Calculates the Standard Error for the Average Treatment Effect with Lechner's method.

**Usage**

```
lechner_se(obj, Y)
```

**Arguments**

obj	MatchIt Object
Y	Response Vector

**Value**

SE for the ATT of Y

**References**

Lechner, M. (2001). Identification and estimation of causal effects of multiple treatments under the conditional independence assumption. In M. Lechner & F. Pfeiffer (Eds.), *Econometric Evaluation of Labour Market Policies* (pp. 43-58). Physica-Verlag: Heidelberg.

**Examples**

```
## Not run:
library(MatchIt)
data("lalonge")
m.out <- matchit(treat ~ educ + black, data = lalonge)
att(obj = m.out, Y = lalonge$re78)
lechner_se(obj = m.out, Y = lalonge$re78)

## End(Not run)
```

---

 MatchItSE

*MatchItSE: methods for Standard Error estimation*


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### Description

Contains auxiliary functions for calculating Standard Errors for matched samples from the MatchIt package. Please note, that Matchit does not estimate Standard Errors by intention, since matching is seen by the package's authors as a data preprocessing step.

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 zelig\_se

*Parametric bootstrap Standard Error for the ATT*


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### Description

Calculates the Standard Error for the Average Treatment Effect with a parametric bootstrap method. This procedure mimics the output of the zelig packages as shown on pages 12 and 13 in the MatchIt vignette.

### Usage

```
zelig_se(obj, Y)
```

### Arguments

obj	MatchIt Object
Y	Response Vector

### Value

SE for the ATT of Y

### References

[MatchIt vignette](#)

### Examples

```
## Not run:
library(MatchIt)
data("lalonge")
m.out <- matchit(treat ~ educ + black, data = lalonge)
att(obj = m.out, Y = lalonge$re78)
zelig_se(obj = m.out, Y = lalonge$re78)

## End(Not run)
```

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