Package ‘saeTrafo’

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Type Package

Title Transformations for Unit-Level Small Area Models

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Description The aim of this package is to offer new methodology for unit-level small area models under transformations and limited population auxiliary information. In addition to this new methodology, the widely used nested error regression model without transformations (see “An Error-Components Model for Prediction of County Crop Areas Using Survey and Satellite Data” by Battese, Harter and Fuller (1988) <doi:10.1080/01621459.1988.10478561>) and its well-known uncertainty estimate (see “The estimation of the mean squared error of small-area estimators” by Prasad and Rao (1990) <doi:10.1080/01621459.1995.10476570>) are provided. In this package, the log transformation and the data-driven log-shift transformation are provided. If a transformation is selected, an appropriate method is chosen depending on the respective input of the population data: Individual population data (see “Empirical best prediction under a nested error model with log transformation” by Molina and Martín (2018) <doi:10.1214/17-aos1608>) but also aggregated population data (see “Estimating regional income indicators under transformations and access to limited population auxiliary information” by Würz, Schmid and Tzavidis <unpublished>) can be entered. Especially under limited data access, new methodologies are provided in ‘saeTrafo’. Several options are available to assess the used model and to judge, present and export its results. For a detailed description of the package and the methods used see the corresponding vignette.

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URL https://github.com/NoraWuerz/saeTrafo

LazyData true

Encoding UTF-8

Imports nlme, emdi, stats, sfsmisc, parallelMap, MuMIn, ggplot2, moments, openxlsx, reshape2, HLMdiag, gridExtra, stringr, readODS
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**compare_plot**

*Shows plots for the comparison of estimates*

### Description

Function `compare_plot` is a generic function used to produce plots comparing point and existing MSE/CV estimates of direct and model-based estimation for the Mean.

Methods `compare_plot.NER` produce plots comparing point and existing MSE/CV estimates of direct and model-based estimation from `NER_Trafo`. The direct and model-based point estimates are compared by a scatter plot and a line plot. If the input arguments MSE and CV are set to TRUE, two extra plots are created, respectively: the MSE/CV estimates of the direct and model-based estimates are compared by boxplots and scatter plots.

### Usage

```r
compare_plot(
  model,  # a model object of type 'NER', representing point and optional MSE estimates.
  direct,  # an object of type 'direct' from 'emdi', representing point and MSE estimates.
  MSE = FALSE,
  CV = FALSE,
  label = "orig",
  color = c("blue", "lightblue3"),
  shape = c(16, 16),
  line_type = c("solid", "solid"),
  gg_theme = NULL,
  ...
)
```

```r
## S3 method for class 'NER'
compare_plot(
  model = NULL,
  direct = NULL,
  MSE = FALSE,
  CV = FALSE,
  label = "orig",
  color = c("blue", "lightblue3"),
  shape = c(16, 16),
  line_type = c("solid", "solid"),
  gg_theme = NULL,
  ...
)
```

### Arguments

- `model` a model object of type ‘NER’, representing point and optional MSE estimates.
- `direct` an object of type ‘direct’ from ‘emdi’, representing point and MSE estimates.

For more information on how to generate direct estimates, please see `direct`.
MSE optional logical. If TRUE, the MSE estimates of the direct and model-based estimates are compared via boxplots and scatter plots.

CV optional logical. If TRUE, the coefficient of variation estimates of the direct and model-based estimates are compared via boxplots and scatter plots.

label argument that enables to customize title and axis labels. There are three options to label the evaluation plots: (i) original labels ("orig"), (ii) axis labels but no title ("no_title"), (iii) neither axis labels nor title ("blank").

color a vector with two elements. The first color determines the color for the regression line in the scatter plot and the color for the direct estimates in the remaining plots. The second color specifies the color of the intersection line in the scatter plot and the color for the model-based estimates in the remaining plots. Defaults to c("blue", "lightblue3").

shape a numeric vector with two elements. The first shape determines the shape of the points in the scatterplot and the shape of the points for the direct estimates in the remaining plots. The second shape determines the shape for the points for the model-based estimates. The options are numbered from 0 to 25. Defaults to c(16, 16).

line_type a character vector with two elements. The first line type determines the line type for the regression line in the scatter plot and the line type for the direct estimates in the remaining plots. The second line type specifies the line type of the intersection line in the scatter plot and the line type for the model-based estimates in the remaining plots. The options are: "twodash", "solid", "longdash", "dotted", "dotdash", "dashed" and "blank". Defaults to c("solid", "solid").

gg_theme theme list from package ggplot2. For using this argument, package ggplot2 must be loaded via library(ggplot2). See also Example 2.

... further arguments passed to or from other methods.

Details

Since all of the comparisons need a direct estimator, the plots are only created for in-sample domains.

Value

Plots comparing direct and model-based estimators for the Mean obtained by ggplot.

A scatter plot and a line plot comparing direct and model-based estimators for each selected indicator obtained by ggplot. If the input arguments MSE and CV are set to TRUE two extra plots are created, respectively: the MSE/CV estimates of the direct and model-based estimates are compared by boxplots and scatter plots.

See Also

saeTrafoObject, direct, NER_Trafo
Examples

# Examples for creating plots to compare the 'saeTrafo' object with direct
# estimates (produced by the package emdi)

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
    self_emp1 + unempl_ben + age_ben + surv_ben +
    sick_ben + dis_ben + rent + fam_allow + house_allow +
    cap_inv + tax_adj,
    smp_domains = "district",
    pop_area_size = pop_area_size,
    pop_mean = pop_mean, pop_cov = pop_cov,
    smp_data = eusilcA_smp, MSE = TRUE)

# Get direct estimates from the R-package emdi
require(emdi)
library(emdi)
emdi_direct <- direct(y = "eqIncome", smp_data = eusilcA_smp,
    smp_domains = "district", weights = "weight",
    var = TRUE, na.rm = TRUE)

# Please detach emdi or use saeTrafo::compare_plot

# Example 1: Comparison plots with uncertainty assessment plots
# (for MSE and CV)
saeTrafo::compare_plot(model = NER_model, direct = emdi_direct, MSE = TRUE,
    CV = TRUE)

# Example 2: Personalize comparison plots using the options provided with
# this function and ggplot themes
require(ggplot2)
library(ggplot2)
saeTrafo::compare_plot(model = NER_model, direct = emdi_direct, MSE = TRUE,
    CV = TRUE, label = "no_title",
    color = c("orange", "green"), shape = c(1,2),
    line_type = c("dotted", "dashed"),
    gg_theme = theme(
        text = element_text(size = 20, color = "blue"),
        panel.border = element_rect(linetype = "dashed",
        fill = "NA")))
Description

Function `compare_pred` is a generic function used to compare predictions of two model objects.

Method `compare_pred.saeTrafo` compares predictions of two `saeTrafo` objects or a `saeTrafo` object and an `emdi` object.

Usage

```r
compare_pred(object1, object2, MSE = FALSE, ...)
```

## S3 method for class 'saeTrafo'

```r
compare_pred(object1, object2, MSE = FALSE, ...)
```

Arguments

- **object1**: an object of type `saeTrafo`.
- **object2**: an object of type `saeTrafo` or `emdi` (`emdiObject`).
- **MSE**: optional logical. If `TRUE`, MSE estimates are returned. Defaults to `FALSE` and than point estimates are returned.
- **...**: further arguments passed to or from other methods.

Value

Data frame containing the point estimates or the MSE estimates (if `MSE` is set to `TRUE`) of both objects. If column names are duplicated, the suffixes `_1` and `_2` are added to their names. `_1` and `_2` standing for object1 and object2, respectively.

See Also

- `emdi`
- `NER_Trafo`
- `saeTrafoObject`

Examples

```r
# Example comparing two 'saeTrafo' objects

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model 1
NER_model_1 <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
```
estimators

self_empl + unempl_ben + age_ben + surv_ben +
sick_ben + dis_ben + rent + fam_allow +
house_allow + cap_inv + tax_adj,
smp_domains = "district",
pop_area_size = pop_area_size,
pop_mean = pop_mean, pop_cov = pop_cov,
smp_data = eusilcA_smp, MSE = TRUE)

# Nested error regression model 2
NER_model_2 <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
self_empl + unempl_ben + age_ben + surv_ben,
smp_domains = "district",
pop_area_size = pop_area_size,
pop_mean = pop_mean, pop_cov = pop_cov,
smp_data = eusilcA_smp, MSE = TRUE)

# Generate a data frame for the comparison of point estimates
compare_pred(NER_model_1, NER_model_2)

# Generate a data frame for the comparison of MSE estimates
compare_pred(NER_model_1, NER_model_2, MSE = TRUE)

---

### Description

Function `estimators` is a generic function used to present point and mean squared error (MSE) estimates. Furthermore, it calculates from both the coefficients of variation (CV).

Method `estimators.saeTrafo` presents point and MSE estimates. Coefficients of variation are calculated using these estimators. The returned object is suitable for printing with the method `print.estimators.saeTrafo`.

### Usage

```r
estimators(object, MSE, CV, ...)
```

### Arguments

- **object**: an object of type 'saeTrafo', representing point and, if chosen, MSE estimates.
- **MSE**: optional logical. If TRUE, MSE estimates are added to the data frame of point estimates. Defaults to FALSE.
- **CV**: optional logical. If TRUE, coefficients of variation are added to the data frame of point estimates. Defaults to FALSE.
- **...**: other parameters that can be passed to function `estimators`. 

---

<table>
<thead>
<tr>
<th>estimators</th>
<th>Presents point, MSE and CV estimates</th>
</tr>
</thead>
</table>

---

## Arguments

- **object**: an object of type 'saeTrafo', representing point and, if chosen, MSE estimates.
- **MSE**: optional logical. If TRUE, MSE estimates are added to the data frame of point estimates. Defaults to FALSE.
- **CV**: optional logical. If TRUE, coefficients of variation are added to the data frame of point estimates. Defaults to FALSE.
- **...**: other parameters that can be passed to function `estimators`. 

**Details**

Objects of class 'estimators.saeTrafo' have methods for following generic functions: head and tail (for default documentation, see `head`, `tail`), as.matrix (for default documentation, see `matrix`), as.data.frame (for default documentation, see `as.data.frame`), subset (for default documentation, see `subset`).

**Value**

The return of `estimators.saeTrafo` is an object of type 'estimators.saeTrafo' with point and/or MSE estimates and/or calculated CV’s from `saeTrafoObject$ind` and, if chosen, `saeTrafoObject$MSE`. These objects contain two elements, one data frame `ind` and a character naming the indicator or indicator group `ind_name`.

**See Also**

`saeTrafoObject`, `NER_Trafo`

**Examples**

```r
# Example for presenting point, MSE, and CV estimates for a 'saeTrafo' object

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash + self_empl + unempl_ben + age_ben + surv_ben + sick_ben + dis_ben + rent + fam_allow + house_allow + cap_inv + tax_adj, smp_domains = "district", pop_area_size = pop_area_size, pop_mean = pop_mean, pop_cov = pop_cov, smp_data = eusilcA_smp, MSE = TRUE)

sae_mean <- estimators(NER_model, MSE = TRUE, CV = TRUE)
class(sae_mean)

# use generic functions for estimators.saeTrafo object
print(sae_mean)
head(sae_mean)
tail(sae_mean)
as.matrix(sae_mean)
as.data.frame(sae_mean)
subset(sae_mean)
```
**Description**

The data set is synthetic EU-SILC data based on the data set `eusilcP` from package `simFrame`. The data set is reduced to 17 variables containing three regional variables for the states and districts.

**Usage**

`eusilcA_pop`

**Format**

A data frame with 25000 observations and 17 variables:

- `eqIncome` numeric; a simplified version of the equivalized household income.
- `eqsize` numeric; the equivalized household size according to the modified OECD scale.
- `gender` factor; the person’s gender (levels: male and female).
- `cash` numeric; employee cash or near cash income (net).
- `self_empl` numeric; cash benefits or losses from self-employment (net).
- `unempl_ben` numeric; unemployment benefits (net).
- `age_ben` numeric; old-age benefits (net).
- `surv_ben` numeric; survivor’s benefits (net).
- `sick_ben` numeric; sickness benefits (net).
- `dis_ben` numeric; disability benefits (net).
- `rent` numeric; income from rental of a property or land (net).
- `fam_allow` numeric; family/children related allowances (net).
- `house_allow` numeric; housing allowances (net).
- `cap_inv` numeric; interest, dividends, profit from capital investments in unincorporated business (net).
- `tax_adj` numeric; repayments/receipts for tax adjustment (net).
- `state` factor; state (nine levels).
- `district` factor; districts (94 levels).
Description

The data set is a simple random sample of data set `eusilcA_pop` which is based on `eusilcP` from package `simFrame`.

Usage

eusilcA_smp

Format

A data frame with 1000 observations and 18 variables:

- `eqIncome` numeric; a simplified version of the equivalized household income.
- `eqsize` numeric; the equivalized household size according to the modified OECD scale.
- `gender` factor; the person’s gender (levels: male and female).
- `cash` numeric; employee cash or near cash income (net).
- `self_empl` numeric; cash benefits or losses from self-employment (net).
- `unempl_ben` numeric; unemployment benefits (net).
- `age_ben` numeric; old-age benefits (net).
- `surv_ben` numeric; survivor’s benefits (net).
- `sick_ben` numeric; sickness benefits (net).
- `dis_ben` numeric; disability benefits (net).
- `rent` numeric; income from rental of a property or land (net).
- `fam_allow` numeric; family/children related allowances (net).
- `house_allow` numeric; housing allowances (net).
- `cap_inv` numeric; interest, dividends, profit from capital investments in unincorporated business (net).
- `tax_adj` numeric; repayments/receipts for tax adjustment (net).
- `state` factor; state (nine levels).
- `district` factor; districts (94 levels).
- `weight` numeric; constant weight.


**Description**

Method `fixef.NER` extracts the fixed effects from an 'saeTrafo' object of class 'NER'.

**Usage**

```r
## S3 method for class 'NER'
fixef(object, ...)  
## S3 method for class 'NER'
fixed.effects(object, ...)
```

**Arguments**

- `object`: an object of type 'NER'.
- `...`: additional arguments that are not used in this method.

**Details**

The alias `fixed.effects` can also be used instead of `fixef`. The generic function `fixef` is imported from package `nlme` and re-exported to make the S3-methods available, even though the `nlme` package itself is not loaded or attached. For default documentation, see `fixed.effects`.

**Value**

A vector containing the fixed effects is returned.

**See Also**

`NER_Trafo`, `fixed.effects`

**Examples**

```r
# Example to extract fixed effects

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
                        self_empl + unempl_ben + age_ben + surv_ben +
```
sick_ben + dis_ben + rent + fam_allow + house_allow +
cap_inv + tax_adj,
smp_domains = "district",
pop_area_size = pop_area_size,
pop_mean = pop_mean, pop_cov = pop Cov,
smp_data = eusilcA_smp)

fixef(NER_model)

---

**getDescription**

**Extract 'saeTrafo' object data**

**Description**

Method `getDescription` extracts the data frame used to fit the model.

**Usage**

```r
## S3 method for class 'NER'
getDescription(object, ...)
```

**Arguments**

- `object`:
  - an object of type `NER`.
- `...`:
  - additional arguments that are not used in this method.

**Details**

The generic function `getDescription` is imported from package `nlme` and re-exported to make the S3-methods available, even though the `nlme` package itself is not loaded or attached. For default documentation, see `getDescription`.

**Value**

Data frame used to fit the model. For `NER` the (untransformed) sample data is returned.

**See Also**

`NER_Trafo, getDescription`

**Examples**

```r
# Example to extract object data

# Load Data
data("eusilcA_smp")
data("pop_area_size")
```
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
    self_empl + unempl_ben + age_ben + surv_ben +
    sick_ben + dis_ben + rent + fam_allow + house_allow +
    cap_inv + tax_adj,
    smp_domains = "district",
    pop_area_size = pop_area_size,
    pop_mean = pop_mean, pop_cov = pop_cov,
    smp_data = eusilcA_smp)

data(NER_model)

groups(NER_model)

groups <- extract grouping factors from an 'saeTrafo' object

Description

Method getGroups.NER extracts grouping factors from a 'saeTrafo' object.

Usage

## S3 method for class 'NER'
getGroups(object, ...)

Arguments

object an object of type "NER".

... additional arguments that are not used in this method.

Details

The generic function getGroups is imported from package nlme and re-exported to make the S3-methods available, even though the nlme package itself is not loaded or attached. For default documentation, see getGroups.

Value

A vector containing the grouping factors.

See Also

NER_Trafo, getGroups
Examples

# Example to extract grouping factors

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
                        self_empl + unempl_ben + age_ben + surv_ben +
sick_ben + dis_ben + rent + fam_allow + house_allow +
cap_inv + tax_adj,
smp_domains = "district",
pop_area_size = pop_area_size,
pop_mean = pop_mean, pop_cov = pop_cov,
smp_data = eusilcA_smp)

getGroups(NER_model)

getGroupsFormula

Extract grouping formula from a 'saeTrafo' object

Description

Method getGroupsFormula.NER extracts the grouping formula from an 'saeTrafo' object.

Usage

## S3 method for class 'NER'
getGroupsFormula(object, ...)

Arguments

object an object of type "NER".
...
additional arguments that are not used in this method.

Details

The generic function getGroupsFormula is imported from package nlme and re-exported to make
the S3-methods available, even though the nlme package itself is not loaded or attached. For default
documentation, see getGroupsFormula.

Value

A one-sided formula.
getResponse

See Also

NER_Trafo getGroupsFormula

Examples

# Example to extract grouping formula

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
  self_empl + unempl_ben + age_ben + surv_ben +
  sick_ben + dis_ben + rent + fam_allow + house_allow +
  cap_inv + tax_adj,
  smp_domains = "district",
  pop_area_size = pop_area_size,
  pop_mean = pop_mean, pop_cov = pop_cov,
  smp_data = eusilcA_smp)

groupsFormula(NER_model)

gresponse

Extract response variable from an 'saeTrafo' object

Description

Method getResponse.NER extracts the response variable from a 'saeTrafo' object.

Usage

## S3 method for class 'NER'
gresponse(object, ...)

Arguments

object an object of type "NER".
... additional arguments that are not used in this method.

Details

The generic function getResponse is imported from package nlme and re-exported to make the S3-methods available, even though the nlme package itself is not loaded or attached. For default documentation, see getResponse.
Value

Vector containing the response variable.

See Also

NER_Trafo, getResponse

Examples

# Example to extract the response variable

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
self_empl + unempl_ben + age_ben + surv_ben +
sick_ben + dis_ben + rent + fam_allow + house_allow +
cap_inv + tax_adj,
smp_domains = "district",
pop_area_size = pop_area_size,
pop_mean = pop_mean, pop_cov = pop_cov,
smp_data = eusilcA_smp)

getResponse(NER_model)

---

getVarCov

Extract variance-covariance matrix from an 'saeTrafo' object

Description

Method getVarCov.NER extracts the variance-covariance matrix from a fitted model of class 'NER'.

Usage

## S3 method for class 'NER'
getVarCov(obj, individuals = 1, type = "random.effects", ...)

Arguments

obj an object of type 'NER'.
individuals vector of levels of the in-sample domains can be specified for the types "conditional" or "marginal".
getVarCov

type

a character that determines the type of variance-covariance matrix. Types that
can be chosen (i) random-effects variance-covariance matrix ("random.effects"),
(ii) conditional variance-covariance matrix ("conditional"), (iii) marginal variance-
covariance matrix ("marginal"). Defaults to "random.effects".

... additional arguments that are not used in this method.

Details

The generic function getVarCov is imported from package nlme and re-exported to make the S3-
methods available, even though the nlme package itself is not loaded or attached. For default
documentation, see getVarCov.

Value

A variance-covariance matrix or a list of variance-covariance matrices, if more than one individ-
ual is selected. For method getVarCov.NER, the dimensions of the matrices are 1 x 1 for type
"random.effects" and number of in-sample domains x number of in-sample domains for types
"conditional" and "marginal".

See Also

NER_Trafo, getVarCov

Examples

# Example to extract variance-covariance matrix

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
  self_empl + unempl_ben + age_ben + surv_ben +
  sick_ben + dis_ben + rent + fam_allow + house_allow +
  cap_inv + tax_adj,
  smp_domains = "district",
  pop_area_size = pop_area_size,
  pop_mean = pop_mean, pop_cov = pop_cov,
  smp_data = eusilcA_smp)

getVarCov(NER_model)
Method intervals.NER provides the approximate confidence intervals on the coefficients (fixed effects) of an 'saeTrafo' object.

Usage

## S3 method for class 'NER'
intervals(object, level = 0.95, parm = NULL, ...)

Arguments

- **object**: an object of type 'NER'.
- **level**: an optional numeric value with the confidence level for the intervals. Defaults to 0.95.
- **parm**: vector of names to specify which parameters are to be given confidence intervals. If NULL, all parameters are taken into account. Defaults to NULL.
- **...**: additional arguments that are not used in this method.

Details

The generic function intervals is imported from package nlme and re-exported to make the S3-methods available, even though the nlme package itself is not loaded or attached. For default documentation, see intervals.

Value

A matrix with rows corresponding to the parameters and columns containing the lower confidence limits (lower), the estimated values (est.), and upper confidence limits (upper).

See Also

NER_Trafo, intervals

Examples

# Example to extract confidence intervals on coefficients

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
load_shapeaustria

NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
            self_empl + unempl_ben + age_ben + surv_ben +
            sick_ben + dis_ben + rent + fam_allow + house_allow +
            cap_inv + tax_adj,
            smp_domains = "district",
            pop_area_size = pop_area_size,
            pop_mean = pop_mean, pop_cov = pop_cov,
            smp_data = eusilcA_smp)

intervals(NER_model)

load_shapeaustria Loading the shape file for Austrian districts

Description

The function simplifies to load the shape file for Austrian districts.

Usage

load_shapeaustria()

Details

The shape file contains the borders of Austrian districts. Thus, it can be used for the visualization of estimation results for Austrian districts.

Value

A shape file of class SpatialPolygonsDataFrame.

map_plot Visualizes regional disaggregated estimates on a map

Description

Function map_plot creates spatial visualizations of the estimates obtained by small area estimation methods.
Usage

map_plot(
  object,
  MSE = FALSE,
  CV = FALSE,
  map_obj = NULL,
  map_dom_id = NULL,
  map_tab = NULL,
  color = c("white", "red4"),
  scale_points = NULL,
  guide = "colourbar",
  return_data = FALSE
)

Arguments

object an object of type saeTrafo, containing the estimates to be visualized.
MSE optional logical. If TRUE, the MSE is also visualized. Defaults to FALSE.
CV optional logical. If TRUE, the CV is also visualized. Defaults to FALSE.
map_obj an SpatialPolygonsDataFrame object as defined by the sp package on which the data should be visualized.
map_dom_id a character string containing the name of a variable in map_obj that indicates the domains.
map_tab a data.frame object with two columns that match the domain variable from the census data set (first column) with the domain variable in the map_obj (second column). This should only be used if the IDs in both objects differ.
color a vector of length 2 defining the lowest and highest color in the plots.
scale_points a numeric vector of length two. This scale will be used for every plot.
guide character passed to scale_fill_gradient from ggplot2. Possible values are "none", "colourbar", and "legend". Defaults to "colourbar".
return_data if set to TRUE, a fortified data frame including the map data as well as the chosen indicators is returned. Customized maps can easily be obtained from this data frame via the package ggplot2. Defaults to FALSE.

Value

Creates the plots demanded and, if selected, a fortified data.frame containing the mapdata and chosen indicators.

See Also

readShapePoly, sp, NER_Trafo, saeTrafoObject
Examples

# Examples for creating maps to visualize the 'saeTrafo' estimates

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
                        self_empl + unempl_len + age_len + surv_len +
                        sick_len + dis_len + rent + fam_allow + house_allow +
                        cap_inv + tax_adj,
                        smp_domains = "district",
                        pop_area_size = pop_area_size,
                        pop_mean = pop_mean, pop_cov = pop_cov,
                        smp_data = eusilcA_smp, MSE = TRUE)

# Load shape file
load_shapeaustria()

# Example 1: Map plots with uncertainty plots (for MSE and CV)
map_plot(NER_model, MSE = TRUE, CV = TRUE, map_obj = shape_austria_dis,
         map_dom_id = "PB")

# Example 2: Personalize map plot for point estimates
map_plot(NER_model, map_obj = shape_austria_dis, map_dom_id = "PB",
         color = c("white", "darkblue"),
         scale_points = c(0, max(NER_model$ind$Mean)))

# Example 3: More options to personalize map plot by using return_data = TRUE
# and ggplot2
require(ggplot2)
library(ggplot2)
data_plot <- map_plot(NER_model, map_obj = shape_austria_dis, map_dom_id = "PB",
                      return_data = TRUE)
ggplot(data_plot, aes(long, lat, group = group, fill = Mean)) +
geom_polygon(color = "black") +
coord_equal() +
theme_void() +
ggtitle("Personalized map") +
scale_fill_gradient2(low = "red", mid = "white", high = "darkgreen",
                    midpoint = 20000)

# Example 4: Create a suitable mapping table to use numerical identifiers of
# the shape file

# First find the right order
dom_ord <- match(shape_austria_dis$data$PB, NER_model$ind$Domain)
# Create the mapping table based on the order obtained above
map_tab <- data.frame(pop_data_id = NER_model$ind$Domain[dom_ord],
                     shape_id = shape_austria_dis@data$BKZ)

# Create map plot for mean indicator - point and CV estimates but no MSE
# using the numerical domain identifiers of the shape file
map_plot(object = NER_model, MSE = FALSE, CV = TRUE,
          map_obj = shape_austria_dis,
          map_dom_id = "BKZ", map_tab = map_tab)

---

NER_Trafo

## Nested error regression Model under transformations

### Description

Function NER_Trafo estimates small area means based on the (transformed) nested error regression (NER) model (Battese et al., 1988). In contrast to the empirical best predictor of Molina and Rao (2010), which is implemented in the package emdi (ebp), no unit-level population data are required.

NER_Trafo supports the log as well as the data-driven log-shift transformation. Especially for skewed variables, (data-driven) transformations are useful to meet the model assumptions for the error terms. If a transformation is chosen and aggregates (means and covariance) are simultaneously provided for the population, point estimates are produced by the method of Wuerz et al. (2022), which uses kernel density estimation to resolve the issue of not having access to population micro-data. In the case that population data are available at unit-level and the log or log-shift transformation is selected, the bias-correction of Berg and Chandra (2014) and Molina and Martín (2018) is applied. For this data situation, more methods and options are provided in the package emdi. If only population means are available and the log or log-shift transformation is selected, a bias-correction due to the transformation is added but for the lack of access to population data no correction is available. Therefore, a part of the bias is disregarded.

Additionally, analytically mean squared errors (MSE) are calculated in the case of no transformation following Prasad and Rao (1990). For the log and log-shift transformation, a parametric bootstrap procedure proposed by Wuerz et al. (2022) following Gonzalez-Manteiga et al. (2008) is applied. Please note that this can only be determined if covariance data are also provided. If population data is available on unit-level a bootstrap procedure as described in Molina and Martín (2018) is applied.

### Usage

NER_Trafo(
  fixed,
  pop_area_size = NULL,
  pop_mean = NULL,
  pop_cov = NULL,
)
pop_data = NULL,
pop_domains = NULL,
smp_data,
smp_domains,
threshold = 30,
B = 50,
transformation = "log.shift",
interval = "default",
MSE = FALSE,
parallel_mode = ifelse(grepl("windows", .Platform$OS.type), "socket", "multicore"),
cpus = 1,
seed = 123
)

Arguments

fixed a two-sided linear formula object describing the fixed-effects part of the nested error linear regression model with the dependent variable on the left of a \texttt{~} operator and the explanatory variables on the right, separated by + operators. The argument corresponds to the argument \texttt{fixed} in function \texttt{lme}.

pop_area_size a named numeric vector containing the number of individuals within each domain. This numeric vector is named with the domain names.

pop_mean a named list. Each element of the list contains the population means for the p covariates for a specific domain. The list is named with the respective domain name. The numeric vector within the list is named with the covariate names. The covariates right of the \texttt{~} operator in \texttt{fixed} need to comprise.

pop_cov a named list. Each element of the list contains the domain-specific covariance matrix for p covariates for a specific domain. The list is named with the respective domain name. The matrix within the list has row and column names with the respective covariate names. The covariates right of the \texttt{~} operator in \texttt{fixed} need to comprise. If \texttt{pop_cov} is not available only a bias-correction due to the transformation is added but for the lack of access to population data a correction is not possible. Additionally, no MSE could be determined.

pop_data a data frame that needs to comprise the variables named on the right of the \texttt{~} operator in \texttt{fixed}, i.e. the explanatory variables, and \texttt{pop_domains}. Please note, if population data is available other methods using unit-level population data, like \texttt{ebp}, could be applied.

pop_domains a character string containing the name of a variable that indicates domains in the population data. The variable can be numeric or a factor but needs to be of the same class as the variable named in \texttt{smp_domains}. Only needed if population data are given.

smp_data a data frame that needs to comprise all variables named in \texttt{fixed} and \texttt{smp_domains}.

smp_domains a character string containing the name of a variable that indicates domains in the sample data. The variable can be numeric or a factor but needs to be of the same class as the variable named in \texttt{pop_domains}.

threshold a numeric value indicating the threshold for using pooled domain data (for domains with sample sizes below the threshold) or non pooled domain data (for
domains with sample sizes above the threshold) for the density estimation within the approach of Wuerz et al. (2022). Defaults to 30.

B  a number determining the number of bootstrap replications in the parametric bootstrap approach. The number must be greater than 1. Defaults to 50. For practical applications, values larger than 200 are recommended.

transformation  a character string. Three different transformation types for the dependent variable can be chosen (i) no transformation ("no"); (ii) log transformation ("log"); (iii) Log-Shift transformation ("log.shift"). Defaults to "log.shift".

interval  a string equal to 'default' or a numeric vector containing a lower and upper limit determining an interval for the estimation of the optimal parameter for the log-shift transformation. The interval is passed to function optimize for the optimization. Defaults to an interval based on the range of y. If the convergence fails, it is often advisable to choose a smaller more suitable interval. For right skewed distributions, the negative values may be excluded.

MSE  optional logical. If TRUE, MSE estimates are provided. Defaults to FALSE.

parallel_mode  modus of parallelization, defaults to an automatic selection of a suitable mode, depending on the operating system, if the number of cpus is chosen higher than 1. For details, see parallelStart.

cpus  number determining the kernels that are used for the parallelization. Defaults to 1. For details, see parallelStart.

seed  an integer to set the seed for the random number generator. For the usage of random number generation, see Details. If seed is set to NULL, seed is chosen randomly. Defaults to 123.

Details

For the parametric bootstrap and the density estimation approach random number generation is used. Thus, a seed is set by the argument seed.

Value

An object of class 'NER', 'saeTrafo' that provides estimators for regional means optionally corresponding MSE estimates. Several generic functions have methods for the returned object. For a full list and descriptions of the components of objects of class 'saeTrafo', see saeTrafoObject.

References


See Also

saeTrafoObject, lme.estimators.saeTrafo, plot.saeTrafo, summaries.saeTrafo

Examples

# Examples for (transformed) nested error regression model

# Load Data
data("eusilcA_pop")data("eusilcA_smp")data("pop_area_size")data("pop_mean")data("pop_cov")

# formula object for all examples
formula <- eqIncome ~ gender + eqsize + cash + self_empl + unempl_ben + age_ben + surv_ben + sick_ben + dis_ben + rent + fam_allow + house_allow + cap_inv + tax_adj

# For all four examples, no MSEs/variances are determined in order to avoid long run times. These can be obtained with MSE = TRUE.

# Example 1: No transformation - classical NER
NER_model_1 <- NER_Trafo(fixed = formula, transformation = "no", smp_domains = "district", smp_data = eusilcA_smp, pop_area_size = pop_area_size, pop_mean = pop_mean)

# Example 2: Log-shift transformation and population aggregates
# (means and covariances) with changed threshold
NER_model_2 <- NER_Trafo(fixed = formula, smp_domains = "district", smp_data = eusilcA_smp, pop_area_size = pop_area_size, pop_mean = pop_mean, pop_cov = pop_cov, threshold = 50)
# Example 3: Log-shift transformation and population data
# A bias-corrections which need unit-level population data are applied

NER_model_3 <- NER_Trafo(fixed = formula,
                         smp_domains = "district", smp_data = eusilcA_smp,
                         pop_data = eusilcA_pop, pop_domains = "district")

# Example 4: Log-shift transformation and population aggregates
# (only means (!) - Therefore, no MSE estimation is available, bias is
# disregarded)
NER_model_4 <- NER_Trafo(fixed = formula,
                         smp_domains = "district", smp_data = eusilcA_smp,
                         pop_area_size = pop_area_size, pop_mean = pop_mean)

---

**plot.saeTrafo**

*Plots for an 'saeTrafo' object*

**Description**

Diagnostic plots of the nested error regression model (see also `NER_Trafo`) are obtained. These include Q-Q plots and density plots of residuals and random effects, a Cook’s distance plot for detecting outliers and the log-likelihood of the estimation of the optimal parameter in log-shift transformations. The return depends on the transformation, such that a plot for the optimal parameter is only returned in case if a transformation with transformation parameter is chosen. The range of the x-axis is optional but necessary to change if there are convergence problems. All plots are obtained by `ggplot`.

**Usage**

```r
## S3 method for class 'saeTrafo'
plot(
  x,
  label = "orig",
  color = c("blue", "lightblue3"),
  gg_theme = NULL,
  cooks = TRUE,
  range = NULL,
  ...
)
```

**Arguments**

- `x`: an object of type 'NER', representing point and, if chosen, MSE estimates obtained by the (transformed) nested error regression model (see also `NER_Trafo`).
label argument that enables to customize title and axis labels. There are three instant options to label the diagnostic plot: (i) original labels ("orig"), (ii) axis labels but no title ("no_title"), (iii) neither axis labels nor title ("blank"), (iv) individual labels by a list that needs to have below structure. Six elements can be defined called qq_res, qq_ran, d_res, d_ran, cooks and opt_lambda for the six different plots and these list elements need to have three elements each called title, y_lab and x_lab. Only the labels for the plots that should be different to the original need to be specified. Please see the details section for an example with the default labels.

color a character vector with two elements. The first element defines the color for the line in the QQ-plots, for the Cook’s Distance plot and for the optimal parameter plot. The second element defines the color for the densities.

gg_theme theme list from package ggplot2. For using this argument, package ggplot2 must be loaded via library(ggplot2).

cooks optional logical. If TRUE, a Cook’s distance plot is returned. The used method mdffits.default from the package HLMdiag struggles when data sets get large. In these cases, cooks should be set to FALSE. It defaults to TRUE.

range optional sequence determining the range of the x-axis for plots of the optimal transformation parameter that defaults to NULL. In that case a range of the default interval is used for the plots of the optimal parameter. This leads in some cases to convergence problems such that it should be changed to e.g. the selected interval. The default value depends on the chosen data driven transformation and equals the default interval for the estimation of the optimal parameter.

... optional arguments passed to generic function.

Details

The default settings of the label argument are as follows:

```
list(  
  qq_res = c(title="Error term", y_lab="Quantiles of pearson residuals", x_lab="Theoretical quantiles"),  
  qq_ran = c(title="Random effect", y_lab="Quantiles of random effects", x_lab="Theoretical quantiles"),  
  d_res = c(title="Density - Pearson residuals", y_lab="Density", x_lab="Pearson residuals"),  
  d_ran = c(title="Density - Standardized random effects", y_lab="Density", x_lab="Standardized random effects"),  
  cooks = c(title="Cook’s Distance Plot", y_lab="Cook’s Distance", x_lab="Index"),  
  opt_lambda = c(title="Log-Shift - REML", y_lab="Log-Likelihood", x_lab="expression(lambda)"))
```

Value

Two Q-Q plots in one grid, two density plots, a Cook’s distance plot and a likelihood plot for the optimal parameter of transformations with transformation parameter obtained by ggplot.
See Also

saeTrafoObject, NER_Trafo

Examples

# Examples for diagnostic plots

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
                       self_empl + unempl_ben + age_ben + surv_ben +
                       sick_ben + dis_ben + rent + fam_allow + house_allow +
                       cap_inv + tax_adj,
smp_domains = "district",
pop_area_size = pop_area_size,
pop_mean = pop_mean, pop_cov = pop_cov,
smp_data = eusilcA_smp)

# Example 1: Default diagnostic plot
plot(NER_model)

# Example 2: Creation of diagnostic plots without labels and titles,
# different colors and without Cook's distance plot.
plot(NER_model, label = "no_title", color = c("red", "yellow"),
     cooks = FALSE)

---

pop_area_size  Aggregates from simulated eusilc population data: domain sizes

Description

This data contains aggregates from eusilcA_pop which is based on eusilcP from package simFrame.

Usage

pop_area_size
Format

A named numeric vector containing the number of individuals within each domain. This numeric vector is named with the domain names.

Description

This data contains aggregates from `eusilcA_pop` which is based on `eusilcP` from package `simFrame`.

Usage

`pop_cov`

Format

A named list. Each element of the list contains the domain-specific covariance matrix for `p` covariates for a specific domain. The list is named with the respective domain name. The matrix within the list has row and column names with the respective covariate names. The covariates right of the `~` operator in `fixed` need to comprise.

Description

This data contains aggregates from `eusilcA_pop` which is based on `eusilcP` from package `simFrame`.

Usage

`pop_mean`

Format

A named list. Each element of the list contains the population means for the `p` covariates for a specific domain. The list is named with the respective domain name. The numeric vector within the list is named with the covariate names. The covariates right of the `~` operator in `fixed` need to comprise.
**predict.NER**

*Predictions from 'saeTrafo' objects*

**Description**

Method `predict.NER` extracts the direct estimates, the empirical best linear unbiased or empirical best predictors for all domains from an 'saeTrafo' object.

**Usage**

```r
## S3 method for class 'NER'
predict(object, ...)```

**Arguments**

- `object` an object of type 'saeTrafo'.
- `...` additional arguments that are not used in this method.

**Value**

Data frame with domain predictors.

**See Also**

`saeTrafoObject, NER_Trafo`

**Examples**

```
# Examples for Predictions from 'saeTrafo' objects

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
                        self_empl + unempl_ben + age_ben + surv_ben +
                        sick_ben + dis_ben + rent + fam_allow + house_allow +
                        cap_inv + tax_adj,
                        smp_domains = "district",
                        pop_area_size = pop_area_size,
                        pop_mean = pop_mean, pop_cov = pop_cov,
                        smp_data = eusilcA_smp)

predict(NER_model)
```
Quantile-quantile plots for an 'saeTrafo' object

Description
Normal quantile-quantile plots of the underlying model (see NER_Trafo) are obtained. The plots are obtained by ggplot.

Usage

```r
## S3 method for class 'saeTrafo'
qqnorm(y, color = c("blue", "lightblue3"), gg_theme = NULL, ...)
```

Arguments

- `y`: a model object of type 'saeTrafo' (see NER_Trafo).
- `color`: a character vector with two elements. The first element defines the color for the line in the Q-Q plots, for the Cook’s Distance plot and for the Box-Cox plot. The second element defines the color for the densities.
- `gg_theme`: theme list from package ggplot2. For using this argument, package ggplot2 must be loaded via library(ggplot2). See also Example 2.
- `...`: optional arguments passed to generic function.

Value
Two Q-Q plots in one grid obtained by ggplot.

See Also

saeTrafoObject, NER_Trafo

Examples

```r
# Examples for Quantile-quantile plots

# Load Data
data("eusilcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
  self_empl + unempl_ben + age_ben + surv_ben +
  sick_ben + dis_ben + rent + fam_allow + house_allow +
  cap_inv + tax_adj,
  smp_domains = "district",
  ...)
```
```r
# Example 1: Default Quantile-quantile plots
qqnorm(NER_model)

# Example 2: Personalized plot using theme
require("ggplot2")
library(ggplot2)
qqnorm(NER_model,
    color = c("red", "darkgreen"),
    gg_theme = theme(panel.background = element_rect(fill = NA),
                     panel.grid.major = element_line(colour = "grey50"),
                     panel.ontop = TRUE)
)
```

## S3 method for class 'NER'
ranef(object, ...)

## S3 method for class 'NER'
random.effects(object, ...)

### Arguments
- **object**: an object of type "NER".
- **...**: additional arguments that are not used in this method.

### Details
The alias `random.effects` can also be used instead of `ranef`. The generic function `ranef` is imported from package `nlme` and re-exported to make the S3-methods available, even though the `nlme` package itself is not loaded or attached. For default documentation, see `random.effects`.

### Value
A vector containing the estimated random effects at domain level is returned.
The R Package 'saeTrafo' for Estimating unit-level Small Area Models under Transformations

Description

The package saeTrafo supports estimating regional means based on the nested error regression model (Battese et al., 1988). Therefore, point estimation and mean squared error estimation (Prasad and Rao, 1990) for the classical model is offered. In addition to the classical model, the logarithmic and the data-driven log-shift transformation are provided. The core function NER_Trafo allows several options to enter population data: Either individual population data or only aggregates can be entered. If full population data is given, the method of Molina and Martín (2018) is applied. Compared to other small area packages, these transformations are accessible in the absence of population micro-data. Only population aggregates (mean values, population sizes and preferably also covariances) need to be supplied. The methodology for point and mean squared error estimates is described in Wuerz et al. (2022) and is made available in a user-friendly way within saeTrafo.

Details

The estimation function is called NER_Trafo. For this function, several methods are available such as estimators.saeTrafo and summaries.saeTrafo. For a full list, please see saeTrafoObject. Furthermore, functions map_plot and write.excel help to visualize and export results. An overview of all currently provided functions can be requested by library(help=saeTrafo).
References


saeTrafoObject Fitted saeTrafoObject

Description

An object of class 'saeTrafo' that represents point predictions of domain-specific means. Optionally, it also contains corresponding MSE estimates. Objects of these classes have methods for various generic functions. See Details for more information.

Details

Objects of class 'saeTrafo' and subclass 'NER' have the following methods: compare_pred, estimators, plot.saeTrafo, predict.NER, qnorm.saeTrafo, compare_plot, getData, getGroups, getGroupsFormula, getResponse, plot (for documentation, see plot.saeTrafo), print, qnorm (for documentation, see qnorm.saeTrafo) and summary (for documentation, see summaries.saeTrafo), coef (for default documentation, see coef), confint (for default documentation, see confint), family (for default documentation, see family), fitted (for default documentation, see fitted.values), fixef, formula (for default documentation, see formula), getVarCov, intervals, logLik (for default documentation, see logLik), nobs (for default documentation, see nobs), ranef, residuals (for default documentation, see residuals), terms (for default documentation, see terms), vcov (for default documentation, see vcov) sigma (for default documentation, see sigma)

Value

The following components are always included in an 'saeTrafo' object but not always filled:

call the function call that produced the object.
fixed for details, see fixed in NER_Trafo.
framework a list with components that describe the data setup, e.g., number of domains in the sample.
ind data frame containing estimates for the mean per domain.
method character returning the method for the estimation approach used to fit the linear mixed model and for the the optimal lambda, in our case "reml".

model list containing a selection of model components.

MSE data frame containing MSE estimates corresponding to the mean predictions in ind per domain if MSE is selected in function call. If MSE, MSE is NULL.

transformation character or list containing information about applied transformation.

transform_param a list with two elements, optimal_lambda and shift_par, where the first contains the optimal parameter for a transformation with transformation parameter or NULL for no and log transformation and the second the potential shift parameter for the log transformation and NULL for no transformation.

successful_bootstraps a numeric returning the number of successful bootstraps. If MSE = FALSE in the function call or transformation = "no", successful_bootstraps is NULL.

See Also

NER_Trafo, lme, lmeObject

summarizes.saeTrafo

Summarizes an 'saeTrafo' object

Description

Additional information about the data and model in small area estimation methods and components of an 'saeTrafo' object are extracted. The returned object is suitable for printing with the print function.

Usage

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

Arguments

object an object of type 'NER', representing point and MSE estimates.

... additional arguments that are not used in this method.

Value

an object of type 'summary.NER' with information about the sample and population data, the usage of transformation, normality tests and information of the model fit.

See Also

saeTrafoObject, NER_Trafo, r.squaredGLMM, skewness, kurtosis, shapiro.test
write.excel  

Exports an 'saeTrafo' Object to an Excel file or OpenDocument Spreadsheet

Description

Function write.excel enables the user to export point and MSE estimates as well as diagnostics from the summary to an Excel file. The user can choose if the results should be reported in one or several Excel sheets. Furthermore, a selection of indicators can be specified. Respectively the function write.ods enables the export to OpenDocument Spreadsheets. Note that while write.excel will create a single document write.ods will create a group of files.

Usage

```r
write.excel(
  object,
  file = "excel_output.xlsx",
  MSE = FALSE,
  CV = FALSE,
  split = FALSE
)

write.ods(
  object,
  file = "ods_output.ods",
  MSE = FALSE,
  CV = FALSE,
  split = FALSE
)
```

Arguments

- **object**: an object of type 'saeTrafo', representing point and MSE estimates.
- **file**: path and filename of the spreadsheet to create. It should end on .xlsx or .ods respectively.
- **MSE**: logical. If TRUE, the MSE of the saeTrafoObject is exported. Defaults to FALSE.
- **CV**: logical. If TRUE, the CV of the saeTrafoObject is exported. Defaults to FALSE.
- **split**: logical. If TRUE, point estimates, MSE and CV are written to different sheets in the Excel file. In write.ods TRUE will result in different files for point estimates and their precision. Defaults to FALSE.

Details

These functions create an Excel file via the package openxlsx and ODS files via the package read-ODS. Both packages require a zip application to be available to R. If this is not the case the authors of openxlsx suggest the first of the following two ways.
write.excel

- Install Rtools from: http://cran.r-project.org/bin/windows/Rtools/ and modify the system PATH during installation.
- If Rtools is installed, but no system path variable is set. One can set such a variable temporarily to R by a command like: Sys.setenv("R_ZIPCMD" = "PathToTheRToolsFolder/bin/zip.exe").

To check if a zip application is available they recommend the command `shell("zip")`.

Value

An Excel file is created in your working directory, or at the given path. Alternatively multiple ODS files are created at the given path.

See Also

`saeTrafoObject, NER_Trafo`

Examples

# Examples for exporting 'saeTrafoObject' to an 'Excel' file or 'OpenDocument'
# Spreadsheet

## Not run:
# Load Data
data("euislcA_smp")
data("pop_area_size")
data("pop_mean")
data("pop_cov")

# Nested error regression model
NER_model <- NER_Trafo(fixed = eqIncome ~ gender + eqsize + cash +
                        self_empl + unempl_ben + age_ben + surv_ben +
                        sick_ben + dis_ben + rent + fam_allow + house_allow +
                        cap_inv + tax_adj,
                        smp_domains = "district",
                        pop_area_size = pop_area_size,
                        pop_mean = pop_mean, pop_cov = pop_cov,
                        smp_data = euislcA_smp, MSE = TRUE)

# Example 1: Export estimates for all indicators and uncertainty measures and
# diagnostics to Excel
write.excel(NER_model, file = "excel_output.xlsx", MSE = TRUE, CV = TRUE)

# Example 2: Single Excel sheets for point, MSE and CV estimates
write.excel(NER_model, file = "excel_output_split.xlsx", MSE = TRUE,
            CV = TRUE, split = TRUE)

# Example 3: Same as example 1 but for an ODS output
write.ods(NER_model, file = "ods_output_all.ods", MSE = TRUE, CV = TRUE)

## End(Not run)
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