Package 'tipsae'

August 19, 2022

Title Tools for Handling Indices and Proportions in Small Area
Estimation

Version 0.0.7

Description It allows for mapping proportions and indicators defined on the unit interval. It implements Beta-based small area methods comprising the classical Beta regression models, the Flexible Beta model and Zero and/or One Inflated extensions (Janicki 2020 <doi:10.1080/03610926.2019.1570266>). Such methods, developed within a Bayesian framework through Stan <https://mc-stan.org/>, come equipped with a set of diagnostics and complementary tools, visualizing and exporting functions. A Shiny application with a user-friendly interface can be launched to further simplify the process.

License GPL-3

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SystemRequirements GNU make

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R topics documented:

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tipsae-package	*The 'tipsae' Package.*

Description

It provides tools for mapping proportions and indicators defined on the unit interval, widely used to measure, for instance, unemployment, educational attainment and also disease prevalence. It implements Beta-based small area methods, particularly indicated for unit interval responses, comprising the classical Beta regression models, the Flexible Beta model and Zero and/or One Inflated extensions. Such methods, developed within a Bayesian framework, come equipped with a set of diagnostics and complementary tools, visualizing and exporting functions. A customized parallel computing is built-in to reduce the computational time. The features of the tipsae package assist the user in carrying out a complete SAE analysis through the entire process of estimation, validation and results presentation, making the application of Bayesian algorithms and complex SAE methods straightforward. A Shiny application with a user-friendly interface can be launched to further simplify the process.

Author(s)

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References

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Morris M, Wheeler-Martin K, Simpson D, Mooney SJ, Gelman A, DiMaggio C (2019). "Bayesian hierarchical spatial models: Implementing the Besag York Mollié model in stan." *Spatial and Spatio-Temporal Epidemiology*, **31**, 100301.

De Nicolò S, Ferrante MR, Pacei S (2021). "Put Inequality on the Map: Small Area Estimation of Inequality Measures using a Beta Mixture." Working Paper.

Chang W, Cheng J, Allaire JJ, Sievert C, Schloerke B, Xie Y, Allen J, McPherson J, Dipert A, Borges B (2021). "shiny: Web Application Framework for R." R package version 1.6.0, https://CRAN.R-project.org/package=shiny.

| benchmark | *Benchmarking Procedure for Model-Based Estimates* |

Description

The `benchmark()` function gives the chance to perform a benchmarking procedure on model-based estimates. Benchmarking could target solely the point estimates (single benchmarking) or, alternatively, also the ensemble variability (double benchmarking). Furthermore, an estimate of the overall posterior risk is provided, aggregated for all areas. This value is only yielded when in-sample areas are treated and a single benchmarking is performed.

Usage

```
benchmark(
  x,
  bench,
  share,
```

```
        method = c("raking", "ratio", "double"),
        H = NULL,
        time = NULL,
        areas = NULL
    )
```

Arguments

x	Object of class `summary_fitsae`.
bench	A numeric value denoting the benchmark for the whole set of areas or a subset of areas.
share	A numeric vector of areas weights, in case of proportions it denotes the population shares.
method	The method to be specified among `"raking"`, `"ratio"` and `"double"`, see details.
H	A numeric value denoting an additional benchmark, to be specified when the `"double"` method is selected, corresponding to the ensemble variability.
time	A character string indicating the time period to be considered, in case of temporal models, where a benchmark can be specified only for one time period at a time.
areas	If NULL (default option), benchmarking is done on the whole set of areas, alternatively it can be done on a subset of them by indicating a vector containing the names of subset areas.

Details

The function allows performing three different benchmarking methods, according to the argument method.

- The `"ratio"` and `"raking"` methods provide benchmarked estimates that minimize the posterior expectation of the weighted squared error loss, see Datta et al. (2011) and `tipsae` vignette.
- The `"double"` method accounts for a further benchmark on the weighted ensemble variability, where H is a prespecified value of the estimators variability.

Value

A `benchmark_fitsae` object being a list of the following elements:

bench_est A vector including the benchmarked estimates for each considered domain.

post_risk A numeric value indicating an estimate of the overall posterior risk, aggregated for all areas. This value is only yielded when in-sample areas are treated and a single benchmarking is performed.

method The benchmarking method performed as selected in the input argument.

time The time considered as selected in the input argument.

areas The areas considered as selected in the input argument.

data_obj A list containing input objects including in-sample and out-of-sample relevant quantities.

model_settings A list summarizing all the assumptions of the model: sampling likelihood, presence of intercept, dispersion parametrization, random effects priors and possible structures.

model_estimates Posterior summaries of target parameters for in-sample areas.

model_estimates_oos Posterior summaries of target parameters for out-of-sample areas.

is_oos Logical vector defining whether each domain is out-of-sample or not.

direct_est Vector of direct estimates for in-sample areas.

References

Datta GS, Ghosh M, Steorts R, Maples J (2011). "Bayesian benchmarking with applications to small area estimation." *Test*, **20**(3), 574–588.

See Also

summary.fitsae to produce the input object.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
              # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)

# creating a subset of the areas whose estimates have to be benchmarked
subset <- c("RIMINI", "RICCIONE", "RUBICONE", "CESENA - VALLE DEL SAVIO")

# creating population shares of the subset areas
pop <- emilia_cs$pop[emilia_cs$id %in% subset]
shares_subset <- pop / sum(pop)

# perform benchmarking procedure
bmk_subset <- benchmark(x = summ_beta,
                        bench = 0.13,
                        share = shares_subset,
                        method = "raking",
                        areas = subset)

# check benchmarked estimates and posterior risk
bmk_subset$bench_est
```

```
bmk_subset$post_risk
```

___

density.summary_fitsae

Density Plot Function for a summary_fitsae *Object*

___

Description

The method density() provides, in a grid (default) or sequence, the density plot of direct estimates versus HB model estimates and the density plot of standardized posterior means of the random effects versus standard normal.

Usage

```
## S3 method for class 'summary_fitsae'
density(x, grid = TRUE, ...)
```

Arguments

x	Object of class summary_fitsae.
grid	Logical indicating whether plots are displayed in a grid (TRUE) or in sequence (FALSE).
...	Currently unused.

Value

Two ggplot2 objects in a grid or in sequence.

See Also

[summary.fitsae](#) to produce the input object.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
              # MCMC setting to obtain a fast example. Remove next line for reliable results.
```

```
                        chains = 1, iter = 300, seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)

# visualize estimates and random effect densities via density() function
density(summ_beta)
```

---

emilia   *Poverty in Emilia-Romagna (Italy) Health Districts*

Description

The `emilia` dataset consists of a panel on poverty mapping concerning 38 health districts within the Emilia-Romagna region, located in North-East of Italy, with annual observations recorded from 2014 to 2018.

Usage

```
emilia
```

Format

Dataframe with 190 observations and 8 variables.

`id` Character, name of the health district.

`prov` Character, name of NUTS-3 region related to the district.

`year` Numeric, year of the observation.

`hcr` Numeric, head-count ratio estimate (used as response variable).

`vars` Numeric, sampling variance of head-count ratio estimator.

`n` Numeric, area sample size.

`x` Numeric, fake covariate.

`pop` Numeric, population size of the area.

Details

It has been built starting from model-based estimates and related CV freely available on Emilia-Romagna region website. Since it is used for illustrative purposes only, such estimates are assumed to be unreliable direct estimates, requiring a SAE procedure.

Examples

```
library(tipsae)
data("emilia")
```

---

emilia_cs   *Poverty in Emilia-Romagna (Italy) Health Districts in 2016*

Description

The `emilia` dataset consists of a dataset on poverty mapping concerning 38 health districts within the Emilia-Romagna region, located in North-East of Italy, with observations recorded in 2016.

Usage

```
emilia_cs
```

Format

Dataframe with 38 area observations and 8 variables.

`id` Character, name of the health district.

`prov` Character, name of NUTS-3 region related to the district.

`year` Numeric, year of the observation.

`hcr` Numeric, head-count ratio estimate (used as response variable).

`vars` Numeric, sampling variance of head-count ratio estimator.

`n` Numeric, area sample size.

`x` Numeric, fake covariate.

`pop` Numeric, population size of the area.

Details

It has been built starting from model-based estimates and related CV freely available on Emilia-Romagna region website. Since it is used for illustrative purposes only, such estimates are assumed to be unreliable direct estimates, requiring a SAE procedure.

See Also

emilia for the panel dataset including observation from 2014 to 2018.

Examples

```
library(tipsae)
data("emilia_cs")
```

---

emilia_shp   *Shapefile of Emilia-Romagna (Italy) Health Districts*

Description

The `emilia_shp` shapefile consists of a `SpatialPolygonsDataFrame` object of 38 health districts within the Emilia-Romagna region, located in the North-East of Italy.

Usage

```
emilia_shp
```

Format

A shapefile of class `SpatialPolygonsDataFrame`.

COD_DIS_SA Code of the health district.

NAME_DISTRICT Name of the health district. It can be linked to the variable `id` in emilia and emilia_cs

See Also

emilia and emilia_cs for the provided datasets.

Examples

```
library(tipsae)
data("emilia_shp")
```

---

export   *Exporting Results of a Small Area Model Fitting*

Description

The function `export()` allows for exporting model estimates in CSV format.

Usage

```
export(x, file, type = "all", ...)
```

Arguments

x	An object of class `estimates_fitsae`.
file	A character string indicating the path (if different from the working directory) and filename of the CSV to be created. It should end with .csv.
type	An option between `"in"`, `"out"` and `"all"`, indicating whether to export only in or out-of-sample areas or both.
...	Additional arguments of `write.csv` function from `utils` package can be indicated.

Value

A CSV file is created in the working directory, or at the given path, exporting the `estimates_fitsae` object given as input.

See Also

`extract` to produce the input object and `write.csv`.

Examples

```
## Not run:
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
                    seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)

# extract model estimates
HB_estimates <- extract(summ_beta)

# export model estimates
export(HB_estimates, file = "results.csv", type = "all")

## End(Not run)
```

---

extract   *Extract Posterior Summaries of Target Parameters*

Description

The extract() function provides the posterior summaries of target parameters, including model-based estimates, and possibly benchmarked estimates, related to a fitted small area model.

Usage

```
extract(x)
```

Arguments

x   An object of class summary_fitsae or benchmark_fitsae.

Value

An object of class estimates_fitsae, being a list of two data frames, distinguishing between $in_sample and $out_of_sample areas, which gathers domains name, direct and HB estimates, as well as posterior summaries of target parameters. When the input is a benchmark_fitsae object, benchmarked estimates are also included.

See Also

[summary.fitsae](#) and [benchmark](#) to produce the input object.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
              # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)

# extract model estimates
HB_estimates <- extract(summ_beta)
head(HB_estimates)
```

---

fit_sae   *Fitting a Small Area Model*

Description

fit_sae() is used to fit Beta-based small area models, such as the classical Beta, zero and/or one
inflated Beta and Flexible Beta models. The random effect part can incorporate either a temporal
and/or a spatial dependency structure devoted to the prior specification settings. In addition, differ-
ent prior assumptions can be specified for the unstructured random effects, allowing for robust and
shrinking priors and different parametrizations can be set up.

Usage

```
fit_sae(
  formula_fixed,
  data,
  domains = NULL,
  disp_direct,
  type_disp = c("neff", "var"),
  domain_size = NULL,
  likelihood = c("beta", "flexbeta", "Infbeta0", "Infbeta1", "Infbeta01"),
  prior_reff = c("normal", "t", "VG"),
  spatial_error = FALSE,
  spatial_df = NULL,
  temporal_error = FALSE,
  temporal_variable = NULL,
  adapt_delta = 0.95,
  max_treedepth = 10,
  init = "0",
  ...
)
```

Arguments

formula_fixed	An object of class "formula" specifying the linear regression fixed part at the linking level.
data	An object of class "data.frame" containing all relevant quantities.
domains	Data column name displaying the domain names. If NULL (default), the domains are denoted with a progressive number.
disp_direct	Data column name displaying given values of sampling dispersion for each domain. In out-of-sample areas, dispersion must be NA.
type_disp	Parametrization of the dispersion parameter. The choices are variance ("var") or $\phi_d + 1$ ("neff") parameter.
domain_size	Data column name indicating domain sizes (optional). In out-of-sample areas, sizes must be NA.

likelihood	Sampling likelihood to be used. The choices are "beta" (default), "flexbeta", "Infbeta0", "Infbeta1" and "Infbeta01".
prior_reff	Prior distribution of the unstructured random effect. The choices are: "normal", "t", "VG".
spatial_error	Logical indicating whether to include a spatially structured random effect.
spatial_df	Object of class SpatialPolygonsDataFrame with the shapefile of the studied region. Required if spatial_error = TRUE.'
temporal_error	Logical indicating whether to include a temporally structured random effect.
temporal_variable	
	Data column name indicating temporal variable. Required if temporal_error = TRUE.
adapt_delta	HMC option: target average proposal acceptance probability. See stan documentation.
max_treedepth	HMC option: target average proposal acceptance probability. See stan documentation.
init	Initial values specification. See the detailed documentation for the init argument in stan.
...	Arguments passed to sampling (e.g. iter, chains).

Value

A list of class fitsae containing the following objects:

model_settings A list summarizing all the assumptions of the model: sampling likelihood, presence of intercept, dispersion parametrization, random effects priors and possible structures.

data_obj A list containing input objects including in-sample and out-of-sample relevant quantities.

stanfit A stanfit object, outcome of sampling function containing full posterior draws. For details, see stan documentation.

pars_interest A vector containing the names of parameters whose posterior samples are stored.

call Image of the function call that produced the fitsae object.

References

Janicki R (2020). "Properties of the beta regression model for small area estimation of proportions and application to estimation of poverty rates." *Communications in Statistics-Theory and Methods*, **49**(9), 2264–2284.

Carpenter B, Gelman A, Hoffman MD, Lee D, Goodrich B, Betancourt M, Brubaker M, Guo J, Li P, Riddell A (2017). "Stan: A probabilistic programming language." *Journal of Statistical Software*, **76**(1), 1–32.

Morris M, Wheeler-Martin K, Simpson D, Mooney SJ, Gelman A, DiMaggio C (2019). "Bayesian hierarchical spatial models: Implementing the Besag York Mollié model in stan." *Spatial and Spatio-Temporal Epidemiology*, **31**, 100301.

De Nicolò S, Ferrante MR, Pacei S (2021). "Put Inequality on the Map: Small Area Estimation of Inequality Measures using a Beta Mixture." Working Paper.

See Also

sampling for sampler options and summary.fitsae for handling the output.

Examples

```
library(tipsae)

# loading toy cross sectional dataset
data("emilia_cs")

# fitting a cross sectional model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
             # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)


# Spatio-temporal model: it might require time to be fitted
## Not run:
# loading toy panel dataset
data("emilia")
# loading the shapefile of the concerned areas
data("emilia_shp")

# ordering the shapefile consistently with the dataset order
emilia_shp@data <- emilia_shp@data[match(unique(emilia$id), emilia_shp@data$NAME_DISTRICT),]

# fitting a spatio-temporal model
fit_ST <- fit_sae(formula_fixed = hcr ~ x,
                  domains = "id",
                  disp_direct = "vars",
                  type_disp = "var",
                  domain_size = "n",
                  data = emilia,
                  spatial_error = TRUE,
                  spatial_df = emilia_shp,
                  temporal_error = TRUE,
                  temporal_variable = "year",
                  max_treedepth = 15,
                  seed = 0)

## End(Not run)
```

---

map   *Map Relevant Quantities from a Small Area Model*

---

map 15

Description

The map() function enables to plot maps containing relevant model outputs by accounting for their geographical dimension. The shapefile of the area must be provided via a SpatialPolygonsDataFrame object.

Usage

```
map(
  x,
  spatial_df,
  spatial_id_domains,
  match_names = NULL,
  color_palette = c("snow2", "deepskyblue4"),
  quantity = c("HB_est", "Direct_est", "SD"),
  time = NULL
)
```

Arguments

x   An object of class summary_fitsae or benchmark_fitsae.

spatial_df   A object of class SpatialPolygonsDataFrame (spatial polygons object) from sp package, accounting for the geographical dimension of the domains.

spatial_id_domains

                    A character string indicating the name of spatial_df variable containing area denominations, in order to correctly match the areas.

match_names   An encoding two-columns data.frame: the first with the original data coding (domains) and the second one with corresponding spatial_df object labels. This argument has to be specified only if spatial_df object labels do not match the ones provided through the original dataset.

color_palette   A vector with two color strings denoting the extreme bounds of colors range to be used.

quantity   A string indicating the quantity to be mapped. When a summary_fitsae is given as input, it can be selected among "HB_est" (model-based estimates), "SD"(posterior standard deviations) and "Direct_est"(direct estimates). While when a benchmark_fitsae class object is given as input, this argument turns automatically to "Bench_est", displaying the benchmarked estimates.

time   A string indicating the year of interest for the quantities to be treated, in case of temporal or spatio-temporal objects.

Value

A map ggplot2 object with colors scaled legend.

See Also

[summary.fitsae](#) to produce the input object and [SpatialPolygonsDataFrame](#) to manage the shapefile.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
            # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)

# load shapefile of concerned areas
data("emilia_shp")

# plot the map using model diagnostics and areas shapefile
map(x = summ_beta,
    spatial_df = emilia_shp,
    spatial_id_domains = "NAME_DISTRICT")
```

---

plot.benchmark_fitsae   *Plot Method for* benchmark_fitsae *Object*

Description

The method plot() provides the boxplots of original and benchmarked estimates in comparison with the benchmark value. Note that share weights are not considered.

Usage

```
## S3 method for class 'benchmark_fitsae'
plot(x, ...)
```

Arguments

x   A benchmark_fitsae object.

...   Currently unused.

Value

A ggplot2 object.

See Also

[benchmark](#) to produce the input object.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
              # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)

# creating a subset of the areas whose estimates have to be benchmarked
subset <- c("RIMINI", "RICCIONE", "RUBICONE", "CESENA - VALLE DEL SAVIO")

# creating population shares of the subset areas
pop <- emilia_cs$pop[emilia_cs$id %in% subset]
shares_subset <- pop / sum(pop)

# perform benchmarking procedure
bmk_subset <- benchmark(x = summ_beta,
                        bench = 0.13,
                        share = shares_subset,
                        method = "raking",
                        areas = subset)
plot(bmk_subset)
```

---

plot.smoothing_fitsae   *Plot Method for* smoothing_fitsae *Object*

Description

The plot() method provides (a) the boxplot of variance estimates, when effective sample sizes are estimated through kish method; (b) a scatterplot of both original and smoothed estimates versus the area sample sizes, when variance smoothing is performed through methods ols and gls.

Usage

```
## S3 method for class 'smoothing_fitsae'
plot(x, size = 2.5, alpha = 0.8, ...)
```

Arguments

x	A `smoothing_fitsae` object.
size	Aesthetic option denoting the size of scatterplots points, see [`geom_point`](#) documentation.
alpha	Aesthetic option denoting the opacity of scatterplots points, see [`geom_point`](#) documentation.
...	Currently unused.

Value

A `ggplot2` object.

See Also

[`smoothing`](#) to produce the input object.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# perform smoothing procedure
smoo <- smoothing(emilia_cs, direct_estimates = "hcr", area_id = "id",
                  raw_variance = "vars", areas_sample_sizes = "n",
                  var_function = NULL, method = "ols")
plot(smoo)
```

---

plot.summary_fitsae　　　　*Plot Method for a* `summary_fitsae` *Object*

Description

The generic method `plot()` provides, in a grid (default) or sequence, (a) a scatterplot of direct estimates versus model-based estimates, visually capturing the shrinking process, (b) a Bayesian P-values histogram, (c) a boxplot of standard deviation reduction values, and, if areas sample sizes are provided as input in `fit_sae()`, (d) a scatterplot of model residuals versus sample sizes, in order to check for design-consistency i.e., as long as sizes increase residuals should converge to zero.

Usage

```
## S3 method for class 'summary_fitsae'
plot(
  x,
  size = 2.5,
  alpha = 0.8,
  n_bins = 15,
  grid = TRUE,
  label_names = NULL,
  ...
)
```

Arguments

x	Object of class `summary_fitsae`.
size	Aesthetic option denoting the size of scatterplots points, see [geom_point](#) documentation.
alpha	Aesthetic option denoting the opacity of scatterplots points, see [geom_point](#) documentation.
n_bins	Denoting the number of bins used for histogram.
grid	Logical indicating whether plots are displayed in a grid (`TRUE`) or in sequence (`FALSE`).
label_names	Character string indicating the model name to display in boxplot x-axis label.
...	Currently unused.

Value

Four `ggplot2` objects in a grid.

See Also

[summary.fitsae](#) to produce the input object.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
            # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)

# check model diagnostics
summ_beta <- summary(fit_beta)
```

```
# visualize diagnostics via plot() method
plot(summ_beta)
```

---

runShiny_tipsae   *Lauch Shiny App to Performs Small Area Estimation*

Description

The command launches a Shiny application that assists the user from the data loading step to the export of the outputs. See the vignette for further details.

Usage

```
runShiny_tipsae()
```

Value

No value returned.

Examples

```
library(tipsae)

# Starting the Shiny application
if(interactive()){
 runShiny_tipsae()
}
```

---

smoothing   *Variance Smoothing and Effective Sample Sizes Estimation*

Description

The `smoothing()` function implements three methods, all yielding refined estimates of either variance or effective sample size, to account for indicators with different variance functions. The output estimates are ready to be used as known parameters in an area-level model, and they need to be added to the analysed `data.frame` object. All the implemented methods enable the estimation of the effective sample sizes, whereas `"ols"` and `"gls"` also perform a variance smoothing procedure.

Usage

```
smoothing(
  data,
  direct_estimates,
  area_id = NULL,
  raw_variance = NULL,
  areas_sample_sizes = NULL,
  additional_covariates = NULL,
  method = c("ols", "gls", "kish"),
  var_function = NULL,
  survey_data = NULL,
  survey_area_id = NULL,
  weights = NULL,
  sizes = NULL
)
```

Arguments

data   A data.frame object including the direct estimates.

direct_estimates
                     Character string specifying the variable in data denoting the direct estimates.

area_id   Character string indicating the variable with domain names included in data, to be specified if method "kish" is selected.

raw_variance   Character string indicating the variable name for raw variance estimates included in data object, to be specified if methods "ols" or "gls" are selected.

areas_sample_sizes
                     Character string indicating the variable name for domain sample sizes included in data object, to be specified if methods "ols" or "gls" are selected.

additional_covariates
                     A vector of character strings indicating the variable names of possible additional covariates, included in data, to be added to the smoothing procedure if methods "ols" or "gls" are selected.

method   The method to be used. The choices are "kish","ols" and "gls".

var_function   An object of class function denoting the variance function of the response variable. The default option (NULL) matches the proportion case being equal to function(x) x * (1 - x).

survey_data   An additional dataset to be specified when method "kish" is selected, defined at sampling unit level (e.g., households) and comprising sampling weights, unit sizes and domain names.

survey_area_id   Character string indicating the variable denoting the domain names included in the survey_data object.

weights   Character string indicating the variable including sampling weights in survey_data object.

sizes   Character string indicating the variable including unit sizes in survey_data object.

Value

An object of class smoothing_fitsae, being a list of vectors including dispersion parameters esti-
mates: both the variances and the effective sample sizes. When "ols" or "gls" method has been
selected, the list incorporates also an object of class gls from nlme package.

References

Kish L (1992). "Weighting for Unequal Pi." *Journal of Official Statistics*, **8**(2), 183.

Fabrizi E, Ferrante MR, Pacei S, Trivisano C (2011). "Hierarchical Bayes multivariate estimation
of poverty rates based on increasing thresholds for small domains." *Computational Statistics &
Data Analysis*, **55**(4), 1736–1747.

See Also

gls for details on estimation procedure for "ols" and "gls" methods.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# perform smoothing procedure
smoo <- smoothing(emilia_cs, direct_estimates = "hcr", area_id = "id",
                  raw_variance = "vars", areas_sample_sizes = "n",
                  var_function = NULL, method = "ols")
```

---

summary.fitsae   *Summary Method for* fitsae *Objects*

Description

Summarizing the small area model fitting through the distributions of estimated parameters and
derived diagnostics using posterior draws.

Usage

```
## S3 method for class 'fitsae'
summary(
  object,
  probs = c(0.025, 0.25, 0.5, 0.75, 0.975),
  compute_loo = TRUE,
  ...
)
```

Arguments

object	An instance of class `fitsae`.
probs	A numeric vector of [quantile](#)s of interest. The default is `c(0.025,0.25,0.5,0.75,0.975)`.
compute_loo	Logical, indicating whether to compute [loo](#) diagnostics or not.
...	Currently unused.

Details

If printed, the produced summary displays:

- Posterior summaries about the fixed effect coefficients and the scale parameters related to unstructured and possible structured random effects.
- Model diagnostics summaries of (a) model residuals; (b) standard deviation reductions; (c) Bayesian P-values obtained with the MCMC samples.
- Shrinking Bound Rate.
- [loo](#) information criteria and related diagnostics from the loo package.

Value

A list of class `summary_fitsae` containing diagnostics objects:

raneff A list of `data.frame` objects storing the random effects posterior summaries divided for each type: `$unstructured`, `$temporal`, and `$spatial`.

fixed_coeff Posterior summaries of fixed coefficients.

var_comp Posterior summaries of model variance parameters.

model_estimates Posterior summaries of the parameter of interest θ_d for each in-sample domain d.

model_estimates_oos Posterior summaries of the parameter of interest θ_d for each out-of-sample domain d.

is_oos Logical vector defining whether each domain is out-of-sample or not.

direct_est Vector of input direct estimates.

post_means Model-based estimates, i.e. posterior means of the parameter of interest θ_d for each domain d.

sd_reduction Standard deviation reduction, see details section.

sd_dir Standard deviation of direct estimates, given as input if `type_disp="var"`.

loo The object of class loo, for details see loo package documentation.

shrink_rate Shrinking Bound Rate, see details section.

residuals Residuals related to model-based estimates.

bayes_pvalues Bayesian p-values obtained via MCMC samples, see details section.

y_rep An array with values generated from the posterior predictive distribution, enabling the implementation of posterior predictive checks.

diag_summ Summaries of residuals, standard deviation reduction and Bayesian p-values across the whole domain set.

data_obj A list containing input objects including in-sample and out-of-sample relevant quantities.

model_settings A list summarizing all the assumptions of the input model: sampling likelihood, presence of intercept, dispersion parametrization, random effects priors and possible structures.

call Image of the function call that produced the input fitsae object.

References

Janicki R (2020). "Properties of the beta regression model for small area estimation of proportions and application to estimation of poverty rates." *Communications in Statistics-Theory and Methods*, **49**(9), 2264–2284.

Vehtari A, Gelman A, Gabry J (2017). "Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC." *Statistics and Computing*, **27**(5), 1413–1432.

See Also

`fit_sae` to estimate the model and the generic methods `plot.summary_fitsae` and `density.summary_fitsae`, and functions `map`, `benchmark` and `extract`.

Examples

```
library(tipsae)

# loading toy dataset
data("emilia_cs")

# fitting a model
fit_beta <- fit_sae(formula_fixed = hcr ~ x, data = emilia_cs, domains = "id",
                    type_disp = "var", disp_direct = "vars", domain_size = "n",
              # MCMC setting to obtain a fast example. Remove next line for reliable results.
                    chains = 1, iter = 300, seed = 0)

# check model diagnostics via summary() method
summ_beta <- summary(fit_beta)
summ_beta
```

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