Package: RSTr (via r-universe)

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Description Takes Poisson or Binomial discrete spatial data and runs a Gibbs sampler for a variety of Spatiotemporal Conditional Autoregressive (CAR) models. Includes measures to prevent estimate over-smoothing through a restriction of model informativeness for select models. Also provides tools to load output and get median estimates. Implements methods from Besag, York, and Mollié (1991) ``Bayesian image restoration, with two applications in spatial statistics" <doi:10.1007/BF00116466>, Gelfand and Vounatsou (2003) ``Proper multivariate conditional autoregressive models for spatial data analysis" <doi:10.1093/biostatistics/4.1.11>, Quick et al. (2017) ``Multivariate spatiotemporal modeling of age-specific stroke mortality" <doi:10.1214/17-AOAS1068>, and Quick et al. (2021) ``Evaluating the informativeness of the Besag-York-Mollié CAR model" <doi:10.1016/j.sste.2021.100420>.

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Description

Takes Poisson or Binomial discrete spatial data and runs a Gibbs sampler for a variety of Spatiotemporal Conditional Autoregressive (CAR) models. Includes measures to prevent estimate oversmoothing through a restriction of model informativeness for select models. Also provides tools to load output and get median estimates. Implements methods from Besag, York, and Mollié (1991) "Bayesian image restoration, with two applications in spatial statistics" <doi:10.1007/BF00116466>, Gelfand and Vounatsou (2003) "Proper multivariate conditional autoregressive models for spatial data analysis" <doi:10.1093/biostatistics/4.1.11>, Quick et al. (2017) "Multivariate spatiotemporal modeling of age-specific stroke mortality" <doi:10.1214/17-AOAS1068>, and Quick et al. (2021) "Evaluating the informativeness of the Besag-York-Mollié CAR model" <doi:10.1016/j.sste.2021.100420>.

Details

The RSTr package uses Bayesian spatiotemporal modeling to spatially smooths discrete small-area event rates using information from neighboring spatial regions. See ‘browseVignettes("RSTr")‘ for a series of tutorials on basic usage of the RSTr functions.

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References

Besag, J., York, J., and Mollié, A. (1991). Bayesian Image Restoration with Two Applications in Spatial Statistics (with Discussion). Annals of the Institute of Statistical Mathematics, 43, 1–59. doi:10.1007/BF00116466

Gelfand, A. E., & Vounatsou, P. (2003). Proper multivariate conditional autoregressive models for spatial data analysis. Biostatistics, 4(1), 11–25. doi:10.1093/biostatistics/4.1.11

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Quick, et al. (2021). Evaluating the informativeness of the Besag-York-Mollié CAR model. Spatial and Spatio-temporal Epidemiology, 37, 100420. doi:10.1016/j.sste.2021.100420

`add_neighbors` *Add neighbors to adjacency information*

Description

Modifies `adjacency` to indicate that `neighs` they should be treated as neighbors.

Usage

```
add_neighbors(adjacency, neighs)
```

Arguments

adjacency	Adjacency information generated by spdep::poly2nb().
neighs	A vector of regions to mark as adjacent. Accepts a vector of indices or names assigned to adjacency.

Details

add_neighbors() is useful when adjacency information generated by spdep::poly2nb() indicates lone regions without links/neighbors, particularly in island counties such as the Hawaiian islands, Nantucket in Massachusetts, or San Juan in Washington. Note that add_neighbors() marks all listed counties as adjacent, so if you have a set of chaining counties where the first may not be connected to the last, several instances of add_neighbors() will be needed.

Value

A modified adjacency list.

Examples

```
if (requireNamespace("sf", quietly = TRUE) &&
    requireNamespace("spdep", quietly = TRUE)) {

  mamap <- sf::st_as_sf(mamap[order(mamap$GEOID), ])
  ma_adj <- spdep::poly2nb(mamap)
  new_neighs <- c(1, 4, 10) # attach regions 1, 4, and 10
  ma_adj <- add_neighbors(ma_adj, new_neighs)

  # Add neighbors by FIPS code instead of index
  ma_adj <- suppressWarnings(spdep::poly2nb(mamap))
  names(ma_adj) <- mamap$GEOID
  ma_adj <- add_neighbors(ma_adj, neighs = c("25001", "25007", "25019"))

  ma_adj <- suppressWarnings(spdep::poly2nb(mamap))
  ma_adj <- add_neighbors(ma_adj, c(1, 4)) # only attach 1 and 4
  ma_adj <- add_neighbors(ma_adj, c(4, 10)) # only attach 4 and 10
}
```

---

age_standardize *Age-standardize model objects*

Description

Generate instructions for age-standardizing samples using a standard population for an RSTr model object.

Usage

```
age_standardize(RSTr_obj, std_pop, new_name, groups = NULL)
```

Arguments

RSTr_obj	An RSTr model object.
std_pop	A vector of standard populations.
new_name	The name to assign to the age-standardized group.
groups	A vector of either indices for each group or a vector of strings for each group name. If set to NULL, will use all groups in the dataset.

Value

An RSTr object with age-standardized parameters.

Examples

```
std_pop <- c(113154, 100640, 95799)
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar("test", data_min, adj_min, tempdir(), show_plots = FALSE, verbose = FALSE)
# age-standardize by all age groups
mod_mst <- age_standardize(mod_mst, std_pop, "35-64")
# Add onto age-standardized estimates. Age-standardize only by the first two age groups
mod_mst <- age_standardize(mod_mst, std_pop[1:2], "35-54", groups = 1:2)
```

---

aggregate_count *Aggregate count arrays*

Description

Sums counts over event/population arrays. Useful when manually generating group-aggregated/age-standardized estimates and a population threshold is needed for suppression.

Usage

```
aggregate_count(
  count,
  margin,
  groups = NULL,
  bind_new = FALSE,
  new_name = NULL
)
```

Arguments

count	The array to aggregate.
margin	For arrays, The margin on which the groups of interest are stratified.
groups	A vector of either indices for each group or a vector of strings for each group name. If set to NULL, will use all groups in the dataset.

bind_new	If set to TRUE, will bind an array to the original sample dataset. Otherwise, will generate a standalone array of samples.
new_name	The name to assign to the age-standardized group.

Value

An array of aggregated count data.

Examples

```
margin_time <- 3
# aggregate population from all years for each county-group
pop_7988 <- aggregate_count(miheart$n, margin_time)
# aggregate population from 1980-1984 for each county-group
pop_8084 <- aggregate_count(miheart$n, margin_time, groups = as.character(1980:1984))
# bind aggregated pop from all years to population data
pop_agg <- aggregate_count(miheart$n, margin_time, bind_new = TRUE, new_name = "1979-1988")
```

---

aggregate_samples *Aggregate samples by non-age group*

Description

Consolidates a set of samples over non-age groups using a population array to create weighted-average samples.

Usage

```
aggregate_samples(
  sample,
  pop,
  margin,
  groups = NULL,
  bind_new = FALSE,
  new_name = NULL
)
```

Arguments

sample	an array of samples imported with load_samples()
pop	The population array to be used for weighted averages.
margin	For arrays, The margin on which the groups of interest are stratified.
groups	A vector of either indices for each group or a vector of strings for each group name. If set to NULL, will use all groups in the dataset.
bind_new	If set to TRUE, will bind an array to the original sample dataset. Otherwise, will generate a standalone array of samples.
new_name	The name to assign to the age-standardized group.

Details

aggregate_samples() is only meant for non-age group data, such as spatial regions, time periods, or other sociodemographic groups (race, sex, etc.). If you are interested in consolidating samples by age group, use age_standardize() instead. Additionally, if you plan on doing age-standardization along with aggregating by other groups, always aggregate groups first before doing age-standardization to ensure that the samples are properly standardized.

Value

An array of weighted-average samples.

Examples

```
pop <- miheart$n[1:2, 1:3, 1:3]
time_margin <- 3
# calculate prevalence by aggregating over time periods
samples_3564 <- aggregate_samples(minsample, pop, margin = time_margin)
# calculate prevalence of only the first two time periods
samples_3554 <- aggregate_samples(minsample, pop, time_margin, groups = 1:2)
# bind prevalence samples to original samples
samples_prev <- aggregate_samples(
  minsample,
  pop,
  time_margin,
  bind_new = TRUE,
  new_name = "1979-1981"
)
```

---

car *Create CAR model*

Description

*car() generates an RSTr model object, samples, and estimates for either an MSTCAR, MCAR, RCAR, or CAR model.

Usage

```
car(
  name,
  data,
  adjacency,
  dir = tempdir(),
  seed = NULL,
  perc_ci = 0.95,
  iterations = 6000,
  burn = 2000,
  show_plots = TRUE,
```

```
  verbose = TRUE,
  ignore_checks = FALSE,
  method = c("binomial", "poisson"),
  impute_bounds = NULL,
  inits = NULL,
  priors = NULL
)

rcar(
  name,
  data,
  adjacency,
  dir = tempdir(),
  seed = NULL,
  perc_ci = 0.95,
  A = NULL,
  m0 = NULL,
  iterations = 6000,
  burn = 2000,
  show_plots = TRUE,
  verbose = TRUE,
  ignore_checks = FALSE,
  method = c("binomial", "poisson"),
  impute_bounds = NULL,
  inits = NULL,
  priors = NULL
)

mcar(
  name,
  data,
  adjacency,
  dir = tempdir(),
  seed = NULL,
  perc_ci = 0.95,
  iterations = 6000,
  burn = 2000,
  show_plots = TRUE,
  verbose = TRUE,
  ignore_checks = FALSE,
  method = c("binomial", "poisson"),
  impute_bounds = NULL,
  inits = NULL,
  priors = NULL
)

mstcar(
  name,
```

```
  data,
  adjacency,
  dir = tempdir(),
  seed = NULL,
  perc_ci = 0.95,
  iterations = 6000,
  burn = 2000,
  show_plots = TRUE,
  verbose = TRUE,
  ignore_checks = FALSE,
  method = c("binomial", "poisson"),
  impute_bounds = NULL,
  inits = NULL,
  priors = NULL,
  update_rho = FALSE
)
```

Arguments

name	Name of model and corresponding folder.
data	Dataset including mortality (Y) and population (n) information.
adjacency	Dataset including adjacency information.
dir	Directory where model will live.
seed	Set of random seeds to use for data replication.
perc_ci	The percentage of the desired estimate credible interval. Defaults to 95 percent (0.95).
iterations	The number of iterations to run the model for.
burn	The number of iterations to use for model burn-in.
show_plots	If set to FALSE, suppresses traceplots.
verbose	If set to FALSE, suppresses model progress messages.
ignore_checks	If set to TRUE, skips model validation.
method	Run model with either Binomial data or Poisson data.
impute_bounds	If counts are suppressed for privacy reasons, impute_bounds is the lower/upper bound of suppression, typically 0 or 1 and 10, respectively.
inits	Optional list of initial conditions for each parameter.
priors	Optional list of priors for updates.
A	For RCAR models, describes maximum intensity of smoothing between regions.
m0	For RCAR models, baseline neighbor count by region.
update_rho	For MSTCAR models, controls whether rho update is performed.

Value

An RSTr model object.

Examples

```
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
# MSTCAR model
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar(
  name = "test",
  data = data_min,
  adjacency = adj_min,
  dir = tempdir(),
  show_plots = FALSE,
  verbose = FALSE
)
```

---

get_estimates *Extract estimates from RSTr model object*

Description

Gathers model and estimate information for an RSTr model object, exported as a long table. Estimate rates and their respective credible intervals are displayed by default in rates per 100,000.

Usage

```
get_estimates(RSTr_obj, rates_per = 1e+05, standardized = TRUE)
```

Arguments

RSTr_obj	An RSTr model object.
rates_per	The desired scaling for estimate rates.
standardized	If RSTr_obj contains age-standardized rates, shows the age-standardized rates. If set to FALSE, always shows the non-age-standardized rates.

Value

A long table containing region/group/time period names, estimates, credible intervals, relative precisions, and the associated event/population counts.

Examples

```
std_pop <- c(113154, 100640, 95799)
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar("test", data_min, adj_min, tempdir(), show_plots = FALSE, verbose = FALSE)
estimates_table <- get_estimates(mod_mst)
mod_mst <- age_standardize(mod_mst, std_pop, "35-64")
estimates_table_as <- get_estimates(mod_mst)
```

get_medians *Generate medians, credible intervals, and relative precisions*

Description

`get_medians()` generates median estimates for array of samples loaded from `load_samples()`.

`get_credible_interval()` generates the credible interval of each estimate using samples loaded from `load_samples()`.

`get_relative_precision()` generates the relative precision of each estimate using samples loaded from `load_samples()`. The relative precision for an estimate is defined as the ratio of the estimate's median divided by the width of its credible interval.

Usage

```
get_medians(sample)

get_credible_interval(sample, perc_ci = 0.95)

get_relative_precision(medians, ci)
```

Arguments

`sample`	array of samples generated by `load_samples`.
`perc_ci`	Number from 0 to 1. Determines width of credible interval.
`medians`	Array of medians generated from samples.
`ci`	Credible interval generated by `get_credible_interval()`.

Value

An `array` of estimates/credible intervals/relative precisions.

Examples

```
minmedians <- get_medians(minsample)
minci <- get_credible_interval(minsample)
# Reducing perc_ci narrows the credible interval
minci_75 <- get_credible_interval(minsample, perc_ci = 0.75)
# low relative precision due to small data size
minrp <- get_relative_precision(minmedians, minci)
# reducing CI increases relative precision
minrp_75 <- get_relative_precision(minmedians, minci_75)
# find estimates with low relative precision
low_rp <- minrp_75 < 1
```

load_model *Load model*

Description

load_model() imports an RSTr object with name name in directory dir.

Usage

```
load_model(name, dir = tempdir())
```

Arguments

name	The name of the model to load.
dir	The directory in which the model lives.

Value

An RSTr model object.

Examples

```
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar("test", data_min, adj_min, tempdir(), show_plots = FALSE, verbose = FALSE)
mod_mst <- load_model(name = "test", dir = tempdir())
```

load_samples *Load MCMC samples*

Description

load_samples() gathers samples saved for model RSTr_obj. By default, loads the rate estimate samples lambda, but any model parameters can be loaded. Users can also specify a burn-in period.

Usage

```
load_samples(RSTr_obj, param = "lambda", burn = NULL)
```

Arguments

RSTr_obj	RSTr model object to load in samples from.
param	Which parameter samples to load.
burn	Number of burn-in samples to discard.

Value

An array of samples from model RSTr_obj.

Examples

```
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar("test", data_min, adj_min, tempdir(), show_plots = FALSE, verbose = FALSE)
samples <- load_samples(mod_mst) * 1e5
```

---

long_to_list_matrix *Generate count data for RSTr object*

Description

long_to_list_matrix() converts a long table featuring event counts across regions and other optional margins into a list that is readable by *car().

Usage

```
long_to_list_matrix(
  table,
  event,
  population,
  region,
  group = NULL,
  time = NULL
)
```

Arguments

table	A table containing event and mortality counts stratified by group/region/time.
event	The column containing event counts.
population	The column containing population counts.
region	The column containing region names.
group	An optional column containing sociodemographic group names.
time	An optional column containing time period names.

Details

long_to_list_matrix() will sum along any group/time stratifications that aren't specified; for example, if your dataset contains time periods and time is not specified in long_to_list_matrix(), the output will be a sum of all time periods. Filter data by desired groups and time periods before running long_to_list_matrix().

Value

A `list` of mortality and population counts organized into multi-dimensional arrays.

Examples

```
ma_data <- maexample[!is.na(maexample$Year), ]
# Generates data from 1979-1981 stratified by sex
ma_data_mst <- long_to_list_matrix(ma_data, Deaths, Population, County.Code, Sex.Code, Year.Code)
ma_data_79 <- ma_data[ma_data$Year == 1979, ]
# Generates 1979 data stratified by sex
ma_data_m <- long_to_list_matrix(ma_data_79, Deaths, Population, County.Code, Sex.Code)
# Generates 1979 data summarized for all sexes
ma_data_u <- long_to_list_matrix(ma_data_79, Deaths, Population, County.Code)
```

---

maexample *Massachusetts Heart Attack Mortality Data*

Description

An example dataset from CDC WONDER containing counts for Myocardial Infarction (ICD-9 code 410.0) deaths in all 14 Massachusetts counties for individuals in 2 sex groups across 3 years.

Usage

```
maexample
```

Format

'maexample' a data frame with 117 rows and 10 variables:

Notes Dataset notes, starts at line 85

Year Year label

Year.Code Year label

County County name

County.Code County FIPS code

Sex Sex group

Sex Abbreviated sex group

Deaths Death count

Population Population count

Crude.Rate Crude rate generated by death and population count

Source

<https://wonder.cdc.gov/cmf-icd9.html>

`mamap` *Massachusetts Shapefile*

Description

A dataset containing U.S. Census TIGER shape data for Massachusetts

Usage

```
mamap
```

Format

'mamap' a data frame with 14 rows and 13 variables:

STATEFP State FIPS code

COUNTYFP County FIPS code

COUNTYNS County GNIS code

AFFGEOID Census Unique Identifier

GEOID Census Unique Identifier, truncated

NAME County Name

NAMELSAD County LSAD code

STUSPS Abbreviated State Name

STATE_NAME State Name

LSAD State LSAD code

ALAND amount of land in square meters

AWATER amount of water in square meters

geometry shape data for each county

Source

<https://www.census.gov/geographies/mapping-files/time-series/geo/tiger-line-file.html>

miadj *Michigan Adjacency Data*

Description

A dataset containing the adjacency structure for each county in Michigan

Usage

```
miadj
```

Format

'miadj' a list containing neighbor adjacency vectors.

miheart *Michigan Heart Attack Mortality Data*

Description

A dataset containing counts for Myocardial Infarction (ICD-9 code 410.0) deaths in all 83 Michigan counties for individuals in 6 age groups across 10 years. This dataset also contains the corresponding population counts.

Usage

```
miheart
```

Format

'miheart' a list with two array objects:

Y death count (0-1005)

n population count (26-292828)

Source

<https://wonder.cdc.gov/cmf-icd9.html>

minsample *Samples Generated for Michigan data*

Description

A 4-dimensional `array` of samples generated by the MSTCAR Gibbs sampler for use in testing and examples

Usage

```
minsample
```

Format

'minsample' a small sample dataset to be used in examples, generated by an MSTCAR model with two regions, three age groups, and three time periods.

minsplit *Age- and Sex-stratified Samples for Michigan data*

Description

A 4-dimensional `array` of samples generated by the MSTCAR Gibbs sampler for demonstration with `split_sample_groups()`

Usage

```
minsplit
```

Format

'minsplit' a small sample dataset to be used for demonstration with `split_sample_groups()`. Generated by an MSTCAR model with two regions, six age-sex groups, and three time periods.

`mishp` *Michigan Shapefile*

Description

A dataset containing U.S. Census TIGER shape data for Michigan

Usage

```
mishp
```

Format

'mishp' a data frame with 83 rows and 13 variables:

STATEFP State FIPS code

COUNTYFP County FIPS code

COUNTYNS County GNIS code

AFFGEOID Census Unique Identifier

GEOID Census Unique Identifier, truncated

NAME County Name

NAMELSAD County LSAD code

STUSPS Abbreviated State Name

STATE_NAME State Name

LSAD State LSAD code

ALAND amount of land in square meters

AWATER amount of water in square meters

geometry shape data for each county

Source

<https://www.census.gov/geographies/mapping-files/time-series/geo/tiger-line-file.html>

split_sample_groups *Split sample groups*

Description

Sequesters stratified sociodemographic group margin into individual array margins.

Usage

```
split_sample_groups(sample, new_groups, delimiter = "_")
```

Arguments

sample	an array of samples imported with load_samples()
new_groups	A string vector of names for each new group.
delimiter	A character that specifies the break between group categories.

Details

When using aggregate_samples() or standardize_samples(), the group/age margin must only feature groups of similar type, e.g., you cannot age-standardize with groups that specify both age and race. split_sample_groups() sequesters each category of group into its own margin to allow group-aggregation and age-standardization of these multiply-stratified groups. Ensure that the delimiter character is only used to split groups. E.g., for an age-sex group named 35-64_m, "_" will split the margins with names "35-64" and "m", whereas for a group named 35_64_m, split_sample_group() will fail.

Value

An array of samples with separate margins for stratified groups.

Examples

```
dimnames(minsplit)[2] # Can't age-standardize due to age-sex stratification
new_groups = c("age", "sex")
delimiter = "_"
sample_split <- split_sample_groups(minsplit, new_groups, delimiter)
dimnames(sample_split)[2:3] # can now age-standardize
std_pop <- c(113154, 100640, 95799)
age_margin <- 2
sample_as <- standardize_samples(sample_split, std_pop, age_margin)
```

`standardize_samples` *Age-standardize samples*

Description

Age-standardizes samples using a standard population.

Usage

```
standardize_samples(
  sample,
  std_pop,
  margin,
  groups = NULL,
  bind_new = FALSE,
  new_name = NULL
)
```

Arguments

`sample`	an `array` of samples imported with `load_samples()`
`std_pop`	A vector of standard populations.
`margin`	For `arrays`, The margin on which the groups of interest are stratified.
`groups`	A vector of either indices for each group or a vector of strings for each group name. If set to `NULL`, will use all groups in the dataset.
`bind_new`	If set to `TRUE`, will bind an `array` to the original sample dataset. Otherwise, will generate a standalone array of samples.
`new_name`	The name to assign to the age-standardized group.

Value

An `array` of age-standardized samples.

Examples

```
std_pop <- c(113154, 100640, 95799)
age_margin <- 2
# age-standardize by all age groups
samples_3564 <- standardize_samples(minsample, std_pop, age_margin)
# age-standardize only by the first two age groups
samples_3554 <- standardize_samples(minsample, std_pop[1:2], age_margin, groups = 1:2)
# bind age-standardized samples to original samples
samples_as <- standardize_samples(
  minsample,
  std_pop,
  age_margin,
  bind_new = TRUE,
```

```
  new_name = "35-64"
)
```

`suppress_estimates` *Suppress estimates based on reliability criteria*

Description

Generates instructions for suppressing estimates for an `RSTr` model object with a given relative precision and population/event threshold.

Usage

```
suppress_estimates(RSTr_obj, threshold = 0, type = c("population", "event"))
```

Arguments

`RSTr_obj`	An `RSTr` model object.
`threshold`	The population/event suppression threshold.
`type`	Determines whether suppression threshold is based on population counts or event counts.

Details

While the `threshold` argument is optional, population/event thresholds are necessary for non-restricted models. Population/event thresholds should only be omitted for restricted CAR models, such as the RCAR.

Value

An `RSTr` model object with suppressed estimates.

Examples

```
std_pop <- c(113154, 100640, 95799)
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar("test", data_min, adj_min, tempdir(), show_plots = FALSE, verbose = FALSE)
mod_mst <- suppress_estimates(mod_mst, threshold = 1000, type = "population")
estimates_table <- get_estimates(mod_mst)
```

update_model *Update model*

Description

update_model() generates additional samples for model RSTr_obj.

Usage

```
update_model(RSTr_obj, iterations = 6000, show_plots = TRUE, verbose = TRUE)
```

Arguments

RSTr_obj	The RSTr model object to generate samples for.
iterations	Number of iterations to run.
show_plots	If set to FALSE, hides traceplots.
verbose	If set to FALSE, hides progress bar and other messages.

Value

An RSTr model object.

Examples

```
data_min <- lapply(miheart, \(x) x[1:2, 1:3, 1:3])
adj_min <- list(2, 1)
on.exit(unlink(file.path(tempdir(), "test"), recursive = TRUE), add = TRUE)
mod_mst <- mstcar("test", data_min, adj_min, tempdir(), show_plots = FALSE, verbose = FALSE)
mod_mst <- update_model(mod_mst, iterations = 1000, show_plots = FALSE, verbose = FALSE)
```

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