Package ‘spatialRF’

October 14, 2022

Title Easy Spatial Modeling with Random Forest
Version 1.1.4
URL https://blasbenito.github.io/spatialRF/

BugReports https://github.com/BlasBenito/spatialRF/issues/

Description Automatic generation and selection of spatial predictors for spatial regression with Random Forest. Spatial predictors are surrogates of variables driving the spatial structure of a response variable. The package offers two methods to generate spatial predictors from a distance matrix among training cases: 1) Moran’s Eigenvector Maps (MEMs; Dray, Legendre, and Peres-Neto 2006 <DOI:10.1016/j.ecolmodel.2006.02.015>): computed as the eigenvectors of a weighted matrix of distances; 2) RFsp (Hengl et al. <DOI:10.7717/peerj.5518>): columns of the distance matrix used as spatial predictors. Spatial predictors help minimize the spatial autocorrelation of the model residuals and facilitate an honest assessment of the importance scores of the non-spatial predictors. Additionally, functions to reduce multicollinearity, identify relevant variable interactions, tune random forest hyperparameters, assess model transferability via spatial cross-validation, and explore model results via partial dependence curves and interaction surfaces are included in the package. The modelling functions are built around the highly efficient ‘ranger’ package (Wright and Ziegler 2017 <DOI:10.18637/jss.v077.i01>).

License GPL-3
Depends R (>= 2.10)
Imports dplyr, ggplot2, magrittr, stats, tibble, utils, foreach, doParallel, ranger, rlang, tidyr, tidyselect, huxtable, patchwork, viridis
Suggests testthat, spelling
Encoding UTF-8
LazyData true
RoxygenNote 7.2.1
Language en-US
NeedsCompilation no

Author Blas M. Benito [aut, cre, cph]
(<https://orcid.org/0000-0001-5105-7232>)
Maintainer  Blas M. Benito <blasbenito@gmail.com>
Repository  CRAN
Date/Publication  2022-08-19 16:00:02 UTC

R topics documented:

- auc ................................................................. 3
- auto_cor ......................................................... 4
- auto_vif ......................................................... 5
- beowulf_cluster ................................................ 7
- case_weights ..................................................... 9
- default_distance_thresholds ................................. 10
- distance_matrix ............................................... 10
- double_center_distance_matrix ......................... 11
- filter_spatial_predictors .................................. 12
- get_evaluation .................................................. 13
- get_importance ............................................... 14
- get_importance_local ....................................... 15
- get_moran ...................................................... 16
- get_performance .............................................. 17
- get_predictions ............................................... 18
- get_residuals ................................................... 19
- get_response_curves ....................................... 20
- get_spatial_predictors ...................................... 21
- is_binary ......................................................... 22
- make_spatial_fold .......................................... 23
- make_spatial_folds ........................................ 25
- mem .............................................................. 27
- mem_multithreshold ......................................... 28
- moran ............................................................ 29
- moran_multithreshold ....................................... 30
- objects_size .................................................. 32
- optimization_function .................................... 33
- pca ............................................................ 34
- pca_multithreshold ......................................... 35
- plant_richness_df .......................................... 36
- plot_evaluation ............................................... 37
- plot_importance ............................................... 39
- plot_moran ..................................................... 40
- plot_optimization .......................................... 42
- plot_residuals_diagnostics ................................ 43
- plot_response_curves ...................................... 45
- plot_response_surface ..................................... 46
- plot_training_df ............................................. 48
- plot_training_df_moran ................................... 49
- plot_tuning ..................................................... 51
- prepare_importance_spatial ............................... 52
**auc**

Area under the ROC curve

**Description**

Computes the area under the ROC curve in models with binary responses.

**Usage**

```r
auc(o, p)
```

**Arguments**

- `o` Numeric vector with observations, must have the same length as `p`.
- `p` Numeric vector with predictions, must have the same length as `o`.

**Value**

Numeric, AUC value.
auto_cor

Multicollinearity reduction via Pearson correlation

Description
Computes the correlation matrix among a set of predictors, orders the correlation matrix according to a user-defined preference order, and removes variables one by one, taking into account the preference order, until the remaining ones are below a given Pearson correlation threshold. **Warning:** variables in `preference.order` not in `colnames(x)`, and non-numeric columns are removed silently from `x` and `preference.order`. The same happens with rows having NA values (`.na.omit()` is applied). The function issues a warning if zero-variance columns are found.

Usage
```r
auto_cor(
x = NULL,
preference.order = NULL,
cor.threshold = 0.5,
verbose = TRUE
)
```

Arguments
- `x` A data frame with predictors, or the result of `auto_vif()` Default: `NULL`
- `preference.order` Character vector indicating the user’s order of preference to keep variables. Doesn’t need to contain If not provided, variables in `x` are prioritised by their column order. Default: `NULL`
- `cor.threshold` Numeric between 0 and 1, with recommended values between 0.5 and 0.9. Maximum Pearson correlation between any pair of the selected variables. Default: `0.50`
- `verbose` Logical. if `TRUE`, describes the function operations to the user. Default: `TRUE`

Details
Can be chained together with `auto_vif()` through pipes, see the examples below.
auto_vif

Value

List with three slots:

- cor: correlation matrix of the selected variables.
- selected.variables: character vector with the names of the selected variables.
- selected.variables.df: data frame with the selected variables.

See Also

auto_vif()

Examples

if(interactive()){

#load data
data(plant_richness_df)

#on a data frame
out <- auto_cor(x = plant_richness_df[, 5:21])

#getting the correlation matrix
out$cor

#getting the names of the selected variables
out$selected.variables

#getting the data frame of selected variables
out$selected.variables.df

#on the result of auto_vif
out <- auto_vif(x = plant_richness_df[, 5:21])
out <- auto_cor(x = out)

#with pipes
out <- plant_richness_df[, 5:21] %>%
auto_vif() %>%
auto_cor()

}

auto_vif Multicollinearity reduction via Variance Inflation Factor
auto_vif

Description

Selects predictors that are not linear combinations of other predictors by using computing their variance inflation factors (VIF). Allows the user to define an order of preference for the selection of predictors. **Warning**: variables in `preference.order` not in `colnames(x)`, and non-numeric columns are removed silently from `x` and `preference.order`. The same happens with rows having NA values (`na.omit()` is applied). The function issues a warning if zero-variance columns are found.

Usage

```r
auto_vif(
  x = NULL,
  preference.order = NULL,
  vif.threshold = 5,
  verbose = TRUE
)
```

Arguments

- **x**: A data frame with predictors or the result of `auto_cor()`. Default: NULL.
- **preference.order**: a character vector with columns names of `x` ordered by the user preference, Default: NULL.
- **vif.threshold**: Numeric between 2.5 and 10 defining the selection threshold for the VIF analysis. Higher numbers result in a more relaxed variable selection. Default: 5.
- **verbose**: Logical. if TRUE, describes the function operations to the user. Default:: TRUE

Details

This function has two modes of operation:

- 1. When the argument `preference.order` is NULL, the function removes on each iteration the variable with the highest VIF until all VIF values are lower than `vif.threshold`.
- 2. When `preference.order` is provided, the variables are selected by giving them priority according to their order in `preference.order`. If there are variables not in `preference.order`, these are selected as in option 1. Once both groups of variables have been processed, all variables are put together and selected by giving priority to the ones in `preference.order`. This method preserves the variables desired by the user as much as possible.

Can be chained together with `auto_cor()` through pipes, see the examples below.

Value

List with three slots:

- **vif**: data frame with the names of the selected variables and their respective VIF scores.
- **selected.variables**: character vector with the names of the selected variables.
- **selected.variables.df**: data frame with the selected variables.
beowulf_cluster

**See Also**

`auto_cor()`

**Examples**

```r
if(interactive()){

# loading data
data(plant_richness_df)

# on a data frame
out <- auto_vif(x = plant_richness_df[, 5:21])

# getting out the vif data frame
out$vif

# getting the names of the selected variables
out$selected.variables

# getting the data frame of selected variables
out$selected.variables.df

# on the result of auto_cor
out <- auto_cor(x = plant_richness_df[, 5:21])
out <- auto_vif(x = out)

# with pipes
out <- plant_richness_df[, 5:21] %>%
   auto_cor() %>%
   auto_vif()
}
```

---

**beowulf_cluster**

*Defines a beowulf cluster*

**Description**

Defines a Beowulf cluster from the IPs of the machines in the cluster, the number of cores of each machine, and the user name. The returned cluster has to be registered with `doParallel::registerDoParallel()`.

**Usage**

```r
beowulf_cluster(
    cluster.ips = NULL,
    cluster.cores = NULL,
    cluster.user = Sys.info()["user"],
    cluster.port = "11000",
    outfile = NULL
)
```
Arguments

- **cluster.ips**: Character vector with the IPs of the machines in the cluster. The first machine will be considered the main node of the cluster, and will generally be the machine on which the R code is being executed. Default: NULL.

- **cluster.cores**: Numeric integer vector, number of cores on each machine. Default: NULL.

- **cluster.user**: Character string, name of the user (should be the same throughout machines), Defaults to the current system user.

- **cluster.port**: Character, port used by the machines in the cluster to communicate. The firewall in all computers must allow traffic from and to such port. Default: "11000"

- **outfile**: Where to direct the messages provided by the workers. When working on a local computer, "" prints the worker’s messages in the console. A text file path will append worker’s messages on the given file. Default: /dev/null en Linux and nul: on windows.

Value

A list ready to be used as input for the spec argument of the function **makeCluster**.

Examples

```r
if(interactive()){
  beowulf.cluster <- beowulf_cluster(
    cluster.ips = c(
      "10.42.0.1",
      "10.42.0.34",
      "10.42.0.104"
    ),
    cluster.cores = c(7, 4, 4),
    cluster.user = "blas",
    cluster.port = "11000"
  )

doParallel::registerDoParallel(cl = beowulf.cluster)

#PARALLELIZED foreach LOOP HERE

parallel::stopCluster(cl = beowulf.cluster)
}
```
case_weights

Generates case weights for binary data

Description

When the data is binary, setting the `ranager` argument `case.weights` helps to minimize the issues produced by class imbalance. This function takes a binary response variable and returns a vector of weights populated with the values $1/#zeros$ and $1/#ones$. It is used internally by the function `rf()`.

Usage

case_weights(data = NULL, dependent.variable.name = NULL)

Arguments

data Data frame with a response variable and a set of predictors. Default: NULL
dependent.variable.name Character string with the name of the response variable. Must be in the column names of `data`. Default: NULL

Value

A vector with a length equal to `nrow(data)` with the respective weights of the cases.

Examples

```r
if(interactive()){

data <- data.frame(
  response = c(0, 0, 0, 1, 1)
)

case_weights(
  data = data,
  dependent.variable.name = "response"
)
}
```
default_distance_thresholds

Default distance thresholds to generate spatial predictors

Description
Generates four distance thresholds, from 0 to max(distance.matrix)/2.

Usage
default_distance_thresholds(distance.matrix = NULL)

Arguments
distance.matrix
Distance matrix. Default: NULL.

Value
A numeric vector with distance thresholds.

Examples
if(interactive()){
  #loading example distance matrix
data(distance_matrix)
  #computing set of default distance thresholds
default_distance_thresholds(distance_matrix)
}

distance_matrix
Matrix of distances among ecoregion edges.

Description
Distance matrix (in km) among the edges of the American ecoregions described in the plant_richness_df dataset.

Usage
data(distance_matrix)
**double_center_distance_matrix**

**Format**

A numeric matrix with 227 rows and columns.

**See Also**

plant_richness_df

---

**double_center_distance_matrix**

*Double centers a distance matrix*

**Description**

Generates a double-centered matrix (row and column means are zero) from the weights of a distance matrix (see weights_from_distance_matrix()) and a distance threshold. This is a required step before the computation of Moran’s Eigenvector Maps.

**Usage**

```r
double_center_distance_matrix (  
  distance.matrix = NULL,  
  distance.threshold = 0  
)
```

**Arguments**

- **distance.matrix**
  - Distance matrix. Default: NULL.
- **distance.threshold**
  - Numeric, positive, in the range of values of x. Distances below this value in the distance matrix are set to 0. Default: 0.

**Value**

A double-centered matrix of the same dimensions as x.

**See Also**

weights_from_distance_matrix().mem().mem_multithreshold()

**Examples**

```r
if(interactive()){

  #loading the distance matrix
  data(distance_matrix)

  x <- double_center_distance_matrix(
```
**filter_spatial_predictors**

Removes redundant spatial predictors

**Description**

Removes spatial predictors that are pair-wise correlated with other spatial predictors (which happens when there are several close distance thresholds), and spatial predictors correlated with non-spatial predictors.

**Usage**

```r
filter_spatial_predictors(
  data = NULL,
  predictor.variable.names = NULL,
  spatial.predictors.df = NULL,
  cor.threshold = 0.5
)
```

**Arguments**

- `data` Data frame with a response variable and a set of predictors. Default: `NULL`
- `predictor.variable.names` Character vector with the names of the predictive variables. Every element of this vector must be in the column names of `data`. Default: `NULL`
- `spatial.predictors.df` Data frame of spatial predictors.
- `cor.threshold` Numeric between 0 and 1, maximum Pearson correlation between any pair of the selected variables. Default: `0.5`

**Value**

A data frame with non-redundant spatial predictors.

**Examples**

```r
if(interactive()){  
  #loading data
  data("distance_matrix")
  data("plant_richness_df")
}
get_evaluation

Get evaluation data frame from a cross-validated model

Description
Returns performance metrics produced by rf_evaluate().

Usage
get_evaluation(model)

Arguments
model A model fitted with rf_evaluate().

Value
A data frame with evaluation scores. The following columns are shown:

- **model**: Identifies the given model. The values are "Full", (original model introduced into rf_evaluate()), "Training" (model trained on an independent training spatial fold), and "Testing" (predictive performance of the training model on an independent testing spatial fold). The performance values of the "Testing" model represent the model performance on unseen data, and hence its ability to generalize.
- **metric**: Four values representing different evaluation metrics, "rmse", "nrmse", "r.squared", and "pseudo.r.squared".
- **mean, sd, min, and max**: Average, standard deviation, minimum, and maximum of each metric across the evaluation (cross-validation) iterations.

See Also
rf_evaluate(), plot_evaluation(), print_evaluation()
Examples

if(interactive()){

    # loading data
    data(plant_richness_df)
    data(distance_matrix)

    # fitting a random forest model
    rf.model <- rf(
        data = plant_richness_df,
        dependent.variable.name = "richness_species_vascular",
        predictor.variable.names = colnames(plant_richness_df)[5:21],
        distance.matrix = distance_matrix,
        distance.thresholds = 0,
        n.cores = 1,
        verbose = FALSE
    )

    # evaluating the model with spatial cross-validation
    rf.model <- rf_evaluate(
        model = rf.model,
        xy = plant_richness_df[, c("x", "y")],
        n.cores = 1,
        verbose = FALSE
    )

    # getting evaluation results from the model
    x <- get_evaluation(rf.model)
    x
}

get_importance

get_importance(model)

Arguments

model A model fitted with rf(), rf_repeat(), or rf_spatial(). Default: NULL

Value

A data frame with variable names and importance scores.
See Also

`rf()`, `rf_repeat()`, `rf_spatial()`, `plot_importance()`, `print_importance()`.

Examples

```r
if(interactive()){
  data(plant_richness_df)
  data(distance_matrix)

  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1,
    verbose = FALSE
  )

  x <- get_importance(rf.model)
  x
}
```

Description

Gets local importance scores from `rf()`, `rf_repeat()`, and `rf_spatial()` models.

Usage

```r
get_importance_local(model)
```

Arguments

- `model` A model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`. Default: NULL

Value

A data frame with variable names and local importance scores.

See Also

`rf()`, `rf_repeat()`, `rf_spatial()`, `plot_importance()`, `print_importance()`.
get_moran

Examples

if(interactive()){

  # loading example data
  data(plant_richness_df)
  data(distance_matrix)

  # fitting a random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1,
    verbose = FALSE
  )

  # getting importance scores
  x <- get_importance_local(rf.model)
  x

}

get_moran

Gets Moran’s I test of model residuals

Description

Returns the Moran’s I test on the residuals of a model produced by rf(), rf_repeat(), or rf_spatial().

Usage

get_moran(model)

Arguments

model

A model fitted with rf(), rf_repeat(), or rf_spatial()

Value

A data frame with Moran’s I test results produced by moran_multithreshold().

See Also

moran(), moran_multithreshold(), plot_moran(), print_moran().
get_performance

Examples

```r
if(interactive()){

#loading example data
data(plant_richness_df)
data(distance_matrix)

#fitting a random forest model
rf.model <- rf(
data = plant_richness_df,
dependent.variable.name = "richness_species_vascular",
predictor.variable.names = colnames(plant_richness_df)[5:21],
distance.matrix = distance_matrix,
distance.thresholds = c(0, 1000, 2000),
n.cores = 1,
verbose = FALSE
)

#getting Moran's I of the residuals
x <- get_moran(rf.model)
}
```

get_performance

*Gets out-of-bag performance scores from a model*

Description

Returns the performance slot of an `rf()`, `rf_repeat()`, or `rf_spatial()` model computed on the out-of-bag data.

Usage

`get_performance(model)`

Arguments

- `model` Model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`.

Value

A data frame with four columns:

- `metric` Name of the performance metric.
- `median` Value of the performance metric. Truly a median only if the model is fitted with `rf_repeat()`.
- `median_absolute_deviation` median absolute deviation (MAD), only if the model is fitted with `rf_repeat()`, and NA otherwise.
See Also

`print_performance()`

Examples

```r
if(interactive()){
    #loading example data
data(plant_richness_df)
data(distance.matrix)

    #fitting random forest model
rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1,
    verbose = FALSE
)

    #getting model performance
x <- get_performance(rf.model)
x
}
```

---

**get_predictions**  
*Gets model predictions*

**Description**

Returns model predictions from a model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`.

**Usage**

`get_predictions(model)`

**Arguments**

- `model`: A model produced by `rf()`, `rf_repeat()`, or `rf_spatial()`.

**Value**

A vector with predictions, or median of the predictions across repetitions if the model was fitted with `rf_repeat()`.
get_residues

Examples

if(interactive()){

  #loading example data
  data(plant_richness_df)

  #fitting a random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    n.cores = 1,
    verbose = FALSE
  )

  #get vector of predictions
  x <- get_predictions(rf.model)
  x

}

get_residues

Gets model residuals

Description

Returns the residuals of models fitted with rf(), rf_repeat(), or rf_spatial().

Usage

get_residues(model)

Arguments

model  A model fitted with rf(), rf_repeat(), or rf_spatial().

Value

A vector with model residuals, or the median of model residuals across repetitions if the model was fitted with rf_repeat().

Examples

if(interactive()){

  #load example data
  data(plant_richness_df)

  #fit random forest model

get_response_curves

Description

Generates and returns the data required to plot the response curves of a model fitted with \texttt{rf()}, \texttt{rf_repeat()}, or \texttt{rf_spatial()}.

Usage

```r
get_response_curves(
  model = NULL,
  variables = NULL,
  quantiles = c(0.1, 0.5, 0.9),
  grid.resolution = 200,
  verbose = TRUE
)
```

Arguments

- **model** A model fitted with \texttt{rf()}, \texttt{rf_repeat()}, or \texttt{rf_spatial()}.
- **variables** Character vector, names of predictors to plot. If \texttt{NULL}, the most important variables (importance higher than the median) in \texttt{model} are selected. Default: \texttt{NULL}.
- **quantiles** Numeric vector with values between 0 and 1, argument \texttt{probs} of \texttt{quantile}. Quantiles to set the other variables to. Default: \texttt{c(0.1, 0.5, 0.9)}
- **grid.resolution** Integer between 20 and 500. Resolution of the plotted curve Default: \texttt{100}
- **verbose** Logical, if TRUE the plot is printed. Default: \texttt{TRUE}

Details

All variables that are not plotted in a particular response curve are set to the values of their respective quantiles, and the response curve for each one of these quantiles is shown in the plot.
get_spatial_predictors

Value

A data frame with the following columns:

- **response**: Predicted values of the response, obtained with stats::predict().
- **predictor**: Values of the given predictor.
- **quantile**: Grouping column, values of the quantiles at which the other predictors are set to generate the response curve.
- **model**: Model number, only relevant if the model was produced with rf_repeat().
- **predictor.name**: Grouping variable, name of the predictor.
- **response.name**: Grouping variable, name of the response variable.

See Also

plot_response_curves()

Examples

if(interactive()){

  #loading example data
  data(plant_richness_df)

  #fitting random forest model
  out <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    n.cores = 1,
    verbose = FALSE
  )

  #getting data frame with response curves
  p <- get_response_curves(out)
  head(p)
}

---

get_spatial_predictors

*Gets the spatial predictors of a spatial model*

Description

Returns spatial predictors from a model fitted with rf_spatial() in order of importance.

Usage

get_spatial_predictors(model)
is_binary

Checks if dependent variable is binary with values 1 and 0

Description

Returns TRUE if dependent.variable.name is a binary variable with the values 1 and 0.

Usage

is_binary(data = NULL, dependent.variable.name = NULL)

Arguments

data Data frame with a response variable and a set of predictors. Default: NULL

dependent.variable.name Character string with the name of the response variable. Must be in the column names of data. Default: NULL
**make_spatial_fold**

**Value**

Logical.

**Examples**

```r
if(interactive()){
    #dummy data frame
data <- data.frame(
        response = c(0, 0, 0, 1, 1)
    )

    #checking if response is binary
    is_binary(
        data = data,
        dependent.variable.name = "response"
    )
}
```

**Description**

Used internally by `make_spatial_folds()` and `rf_evaluate()`. Uses the coordinates of a point `xy.i` to generate two spatially independent data folds from the data frame `xy`. It does so by growing a rectangular buffer from `xy.i` until a number of records defined by `training.fraction` is inside the buffer. The indices of these records are then stored as "training" in the output list. The indices of the remaining records outside of the buffer are stored as "testing". These training and testing records can be then used to evaluate a model on independent data via cross-validation.

**Usage**

```r
make_spatial_fold(
    data = NULL,
    dependent.variable.name = NULL,
    xy.i = NULL,
    xy = NULL,
    distance.step.x = NULL,
    distance.step.y = NULL,
    training.fraction = 0.8
)
```
make_spatial_fold

Arguments

data
   Data frame with a response variable and a set of predictors. Default: NULL

dependent.variable.name
   Character string with the name of the response variable. Must be in the column names of data. Default: NULL

xy.i
   One row data frame with at least three columns: "x" (longitude), "y" (latitude), and "id" (integer, id of the record). Can be a row of xy. Default: NULL.

xy
   A data frame with at least three columns: "x" (longitude), "y" (latitude), and "id" (integer, index of the record). Default: NULL.

distance.step.x
   Numeric, distance step used during the growth in the x axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the x coordinates).

distance.step.y
   Numeric, distance step used during the growth in the y axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the y coordinates).

training.fraction
   Numeric, fraction of the data to be included in the training fold, Default: 0.8.

Value

A list with two slots named training and testing with the former having the indices of the training records selected from xy, and the latter having the indices of the testing records.

See Also

make_spatial_folds(), rf_evaluate()

Examples

if(interactive()){

   #loading example data
data(plant_richness_df)

   #getting case coordinates
xy <- plant_richness_df[, 1:3]
colnames(xy) <- c("id", "x", "y")

   #building a spatial fold centered in the first pair of coordinates
out <- make_spatial_fold(
   xy.i = xy[1, ],
   xy = xy,
   training.fraction = 0.6
)

   #indices of the training and testing folds
out$training
out$testing
#plotting the data
plot(xy[, c("x", "y")], type = "n", xlab = "", ylab = "")
#plots training points
points(xy[out$training, c("x", "y")], col = "red4", pch = 15)
#plots testing points
points(xy[out$testing, c("x", "y")], col = "blue4", pch = 15)
#plots xy.i
points(xy[1, c("x", "y")], col = "black", pch = 15, cex = 2)

make_spatial_folds

Makes training and testing spatial folds

Description

Applies make_spatial_fold() to every record in a data frame xy.selected to generate as many spatially independent folds over the dataset xy as rows are in xy.selected.

Usage

make_spatial_folds(
  data = NULL,
  dependent.variable.name = NULL,
  xy.selected = NULL,
  xy = NULL,
  distance.step.x = NULL,
  distance.step.y = NULL,
  training.fraction = 0.75,
  n.cores = parallel::detectCores() - 1,
  cluster = NULL
)

Arguments

data
  Data frame with a response variable and a set of predictors. Default: NULL
dependent.variable.name
  Character string with the name of the response variable. Must be in the column names of data. Default: NULL
xy.selected
  Data frame with at least three columns: "x" (longitude), "y" (latitude), and "id" (integer, id of the record). Usually a subset of xy. Usually the result of applying thinning() or thinning_til_n() to 'xy'. Default: NULL.
xy
  data frame with at least three columns: "x" (longitude), "y" (latitude), and "id" (integer, index of the record). Default: NULL.
distance.step.x
  Numeric, distance step used during the growth in the x axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the x coordinates).
make_spatial_folds

### distance.step.y

Numeric, distance step used during the growth in the y axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the y coordinates).

### training.fraction

Numeric, fraction of the data to be included in the growing buffer as training data. Default: 0.75

### n.cores

Integer, number of cores to use for parallel execution. Creates a socket cluster with `parallel::makeCluster()`, runs operations in parallel with `foreach` and `%dopar%`, and stops the cluster with `parallel::clusterStop()` when the job is done. Default: `parallel::detectCores() - 1`

### cluster

A cluster definition generated with `parallel::makeCluster()`. If provided, overrides `n.cores`. When `cluster = NULL` (default value), and `model` is provided, the cluster in `model`, if any, is used instead. If this cluster is NULL, then the function uses `n.cores` instead. The function does not stop a provided cluster, so it should be stopped with `parallel::stopCluster()` afterwards. The cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the `model` argument, or using the `>%` pipe. Default: NULL

### Value

A list with as many slots as rows are in `xy.selected`. Each slot has two slots named `training` and `testing`, with the former having the indices of the training records selected from `xy`, and the latter having the indices of the testing records.

### See Also

`make_spatial_fold()`, `rf_evaluate()`

### Examples

```r
if(interactive()){

  # loading example data
  data(plant_richness_df)

  # getting case coordinates
  xy <- plant_richness_df[, 1:3]
  colnames(xy) <- c("id", "x", "y")

  # thinning til 20 cases
  xy.selected <- thinning_til_n(xy = xy, n = 20)

  # making spatial folds centered on these 20 cases
  out <- make_spatial_folds(xy.selected = xy.selected, xy = xy,
}
mem

**Moran’s Eigenvector Maps of a distance matrix**

Description

Computes the positive Moran’s Eigenvector Maps of a distance matrix.

Usage

```r
mem(
  distance.matrix = NULL,
  distance.threshold = 0,
  colnames.prefix = "mem"
)
```

Arguments

- `distance.matrix`: Distance matrix. Default: `NULL`.
- `distance.threshold`: Numeric vector with distance thresholds defining different neighborhood extents within the distance matrix, Default: 0
- `colnames.prefix`: Character, name prefix for the output columns. Default: "mem"

Details

Takes the distance matrix `x`, double-centers it with `double_center_distance_matrix()`, applies `eigen`, and returns eigenvectors with positive normalized eigenvalues (a.k.a Moran’s Eigenvector Maps, or MEMs). These MEMs are later used as spatial predictors by `rf.spatial()`.

Value

A data frame with positive Moran’s Eigenvector Maps.
See Also

mem_multithreshold(), rf_spatial()

Examples

if(interactive()){

  #loading example distance matrix
data(distance_matrix)

  #Moran's Eigenvector Maps of the distance matrix
  mem <- mem(x = distance_matrix)
}

mem_multithreshold  Moran's Eigenvector Maps for different distance thresholds

Description

Computes Moran's Eigenvector Maps of a distance matrix (using \texttt{mem()}) over different distance thresholds.

Usage

\begin{verbatim}
mem_multithreshold(
  distance.matrix = NULL,
  distance.thresholds = NULL,
  max.spatial.predictors = NULL
)
\end{verbatim}

Arguments

\begin{description}
\item[distance.matrix] Distance matrix. Default: \texttt{NULL}.
\item[distance.thresholds] Numeric vector with distance thresholds defining neighborhood in the distance matrix, Default: \texttt{NULL}.
\item[max.spatial.predictors] Maximum number of spatial predictors to generate. Only useful to save memory when the distance matrix \texttt{x} is very large. Default: \texttt{NULL}.
\end{description}

Details

The function takes the distance matrix \texttt{x}, computes its weights at difference distance thresholds, double-centers the resulting weight matrices with \texttt{double_center_distance_matrix()}, applies \texttt{eigen} to each double-centered matrix, and returns eigenvectors with positive normalized eigenvalues for different distance thresholds.
Value

A data frame with as many rows as the distance matrix x containing positive Moran’s Eigenvector Maps. The data frame columns are named "spatial_predictorDISTANCE_COLUMN", where DISTANCE is the given distance threshold, and COLUMN is the column index of the given spatial predictor.

Examples

if(interactive()){
  #loading example data
  data(distance_matrix)

  #computing Moran's eigenvector maps for 0, 1000, and 2000 km
  mem.df <- mem_multithreshold(
    distance.matrix = distance_matrix,
    distance.thresholds = c(0, 1000, 2000)
  )
  head(mem.df)
}

---

moran Moran’s I test

Description

Computes the spatial correlation coefficient (Moran’s I) of a vector given a distance matrix, and a distance threshold used to define "neighborhood".

Usage

moran(
  x = NULL, 
  distance.matrix = NULL, 
  distance.threshold = NULL, 
  verbose = TRUE
)

Arguments

- **x**: Numeric vector, generally model residuals, Default: NULL
- **distance.matrix**: Distance matrix among cases in x. The number of rows of this matrix must be equal to the length of x. Default: NULL
- **distance.threshold**: numeric value in the range of values available in distance.matrix. Distances below such threshold are set to 0. Default: NULL (which defaults to 0).
- **verbose**: Logical, if TRUE, prints a Moran’s I plot. Default: TRUE
moran_multithreshold

Details

Inspired in the Moran.I() function of the ape package.

Value

A list with three named slots:

- test: Data frame with observed and expected Moran’s I values, p-value, and interpretation.
- plot: Moran’s plot of the vector x against the spatial lags of x.
- plot.df: Data used in the Moran’s plot.

See Also

moran_multithreshold()

Examples

if(interactive()){
  #loading example data
data(distance_matrix)
data(plant_richness)

  #Moran's I of the response variable
  out <- moran(
    x = plant_richness$richness_species_vascular,
    distance.matrix = distance_matrix
  )
  out
}

Arguments

x Numeric vector, generally model residuals, Default: NULL

distance.matrix Distance matrix among cases in x. The number of rows of this matrix must be
equal to the length of x. Default: NULL

distance.thresholds Numeric vector, distances below each value are set to 0 on separated copies
of the distance matrix for the computation of Moran’s I at different neigh-
borhood distances. If NULL, it defaults to seq(0, max(distance.matrix)/4,
length.out = 2). Default: NULL

verbose Logical, if TRUE, plots Moran’s I values for each distance threshold. Default: TRUE

Details

Using different distance thresholds helps to take into account the uncertainty about what "neighbor-
bhood" means in ecological systems (1000km in geological time means little, but 100m might be
quite a long distance for a tree to disperse seeds over), and allows to explore spatial autocorrelation
of model residuals for several minimum-distance criteria at once.

Value

A named list with the slots:

• df: Data frame with the results of Moran per distance threshold.
• plot: A plot of Moran’s I across distance thresholds.
• max.moran: Maximum value of Moran’s I across thresholds.
• max.moran.distance.threshold: Distance threshold with the maximum Moran’s I value.

See Also

moran()

Examples

if(interactive()){

#loading example data
data(distance_matrix)
data(plant_richness)

#computing Moran's I for the response variable at several reference distances
out <- moran_multithreshold(
  x = plant_richness$richness_species_vascular,
  distance.matrix = distance_matrix,
  distance.thresholds = c(0, 100, 1000, 10000),
  plot = TRUE
)

out

Objects size

Description

Shows the size of the objects currently in the R environment. Helps to locate large objects cluttering
the R environment and/or causing memory problems during the execution of large workflows.

Usage

objects_size(n = 10)

Arguments

n Number of objects to show, Default: 10

Value

A data frame with the row names indicating the object name, the field ‘Type’ indicating the object
type, ‘Size’ indicating the object size, and the columns ‘Length/Rows’ and ‘Columns’ indicating the
object dimensions if applicable.

Examples

if(interactive()){

#creating dummy objects
x <- matrix(runif(100), 10, 10)
y <- matrix(runif(10000), 100, 100)

#reading their in-memory size
objects_size()

}"
optimization_function

**optimization_function**  
*Optimization equation to select spatial predictors*

**Description**

Optimizes the selection of spatial predictors using two different methods: "moran.i", and "p.value".

**Usage**

```r
optimization_function(
  x = NULL,
  weight.r.squared = NULL,
  weight.penalization.n.predictors = NULL,
  optimization.method = "moran.i"
)
```

**Arguments**

- `x` Optimization data frame generated internally by `select.spatial.predictors_sequential()` or `select.spatial.predictors_recursive()`. Default: `NULL`
- `weight.r.squared` Numeric between 0 and 1, weight of R-squared in the optimization process. Default: `NULL`
- `weight.penalization.n.predictors` Numeric between 0 and 1, weight of the penalization on the number of introduced spatial predictors. Default: `NULL`
- `optimization.method` Character, one of "moran.i", and "p.value". Default: "moran.i"

**Details**

The method "moran.i" tries to maximize $1 - \text{Moran's I}$ while taking into account the R-squared of the model and a penalization on the number of introduced spatial predictors through the expression

$$(1 - \text{Moran's I}) + w_1 \cdot \text{r.squared} - w_2 \cdot \text{penalization}$$

The method "p.value" uses a binary version of the p-values of Moran's I (1 if $\geq 0.05$, 0 otherwise), and uses the expression

$$\max(1 - \text{Moran's I, binary p-value}) + w_1 \cdot \text{r.squared} - w_2 \cdot \text{penalization}$$

The "moran.i" method generally selects more spatial predictors than the "p.value" method.

**Value**

A numeric vector with the optimization criteria.

**See Also**

`select.spatial.predictors_recursive()`, `select.spatial.predictors_sequential()`
**pca**

*Principal Components Analysis*

**Description**

Extracts all factors of a principal component analysis of a matrix or data frame. Just a convenient wrapper for `prcomp`.

**Usage**

```r
pca(
  x = NULL,
  colnames.prefix = "pca_factor"
)
```

**Arguments**

- `x`: numeric matrix or data frame, Default: NULL
- `colnames.prefix`: character, name prefix for the output columns, Default: 'pca_factor'

**Details**

Columns in `x` with zero variance are removed before computing the PCA.

**Value**

A data frame with the PCA factors of `x`.

**See Also**

`pca_multithreshold()`

**Examples**

```r
if(interactive()){
  #load example distance matrix
data(distance_matrix)

  #PCA of the distance matrix
  out <- pca(x = distance_matrix)
  out
}
```
pca_multithreshold

PCA of a distance matrix over distance thresholds

Description

Computes PCA factors of a distance matrix over different distance thresholds to generate spatial predictors for a model fitted with rf_spatial().

Usage

pca_multithreshold(
  distance.matrix = NULL,
  distance.thresholds = NULL,
  max.spatial.predictors = NULL
)

Arguments

distance.matrix
  Distance matrix. Default: NULL

distance.thresholds
  Numeric vector with distance thresholds defining neighborhood in the distance matrix, Default: 0

max.spatial.predictors
  Integer, maximum number of spatial predictors to generate. Only useful when the distance matrix x is very large. Default: NULL

Details

The distance matrix is converted into weights with weights_from_distance_matrix() before computing the PCA. This produces more meaningful spatial predictors than using the distance matrix as is.

Value

A data frame with the PCA factors of the thresholded matrix. The data frame columns are named "spatial_predictor_DISTANCE_COLUMN", where DISTANCE is the given distance threshold, and COLUMN is the column index of the given predictor.

See Also

pca()
Examples

if(interactive()){

#loading example distance matrix
load(distance_matrix)

#PCA factors of the distance matrix for two reference distances
x <- pca_multithreshold(
  distance.matrix = distance_matrix,
  distance.thresholds = c(0, 1000)
)
head(x)

}

plant_richness_df  

Description

Richness of vascular plants of the American ecoregions as defined in Ecoregions 2017.

Usage

data(plant_richness_df)

Format

A data frame with 227 rows and 22 columns:

- ecoregion_id: Id of the ecoregion.
- x: Longitude in degrees (WGS84).
- y: Latitude in degrees (WGS84).
- richness_species_vascular: Number of vascular species found in the ecoregion. Response variable.
- bias_area_km2: Area of the ecoregion in squared kilometers.
- bias_species_per_record: Number of species divided by the number of spatial GBIF records available in the ecoregion as a measure of sampling bias.
- climate_aridity_index_average: Average of the ecoregion.
- climate_hypervolume: Volume of the climatic envelope of the ecoregion, computed with the hypervolume package.
- climate_velocity_lgm_average: Average climate velocity of the ecoregion since the Last Glacial Maximum.
- neighbors_count: Number of immediate neighbors of the ecoregion as a measure of connectivity/isolation.
- neighbors_percent_shared_edge: Percentage of shared edge with the neighbors as a measure of connectivity/isolation.
- human_population_density: Population density of the ecoregion.
- topography_elevation_average: Average elevation of the ecoregion.
- landcover_herbs_percent_average: Average cover percentage of herbs extracted from MODIS Vegetation Continuous Fields.
- fragmentation_cohesion: Geographic fragmentation index of the ecoregion as computed with the R package landscapemetrics.
- fragmentation_division: Another fragmentation index.
- neighbors_area: Total area of the ecoregions's immediate neighbors.
- human_population: Human population in the ecoregion.
- human_footprint_average: Average human footprint in the ecoregion.
- climate_bio1_average: Average mean annual temperature.
- climate_bio15_minimum: Average precipitation seasonality.

See Also

distance_matrix

plot_evaluation  Plots the results of a spatial cross-validation

Description

Plots the results of an spatial cross-validation performed with rf_evaluate().

Usage

plot_evaluation(model,
    fill.color = viridis::viridis(3,
        option = "F",
        alpha = 0.8,
        direction = -1
    ),
    line.color = "gray30",
    verbose = TRUE,
    notch = TRUE
)
plot_evaluation

Arguments

model
A model resulting from rf_evaluate().

fill.color
Character vector with three hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. viridis::viridis(3)). Default: viridis::viridis(3, option = "F", alpha = 0.8, direction = -1)

line.color
Character string, color of the line produced by ggplot2::geom_smooth(). Default: "gray30"

verbose
Logical, if TRUE the plot is printed. Default: TRUE

notch
Logical, if TRUE, boxplot notches are plotted. Default: TRUE

Value
A ggplot.

See Also

rf_evaluate(), get_evaluation(), print_evaluation().

Examples

if(interactive()){

#loading example data
data(plant_richness_df)
data(distance_matrix)

#fitting a random forest model
rf.model <- rf(
  data = plant_richness_df,
  dependent.variable.name = "richness_species_vascular",
  predictor.variable.names = colnames(plant_richness_df)[5:21],
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  n.cores = 1,
  verbose = FALSE
)

#evaluating the model with spatial cross-validation
rf.model <- rf_evaluate(
  model = rf.model,
  xy = plant_richness_df[, c("x", "y")],
  n.cores = 1
)

#plotting the evaluation results
plot_evaluation(rf.model)
}
plot_importance

Plots the variable importance of a model

Description

Plots variable importance scores of \texttt{rf()}, \texttt{rf_repeat()}, and \texttt{rf.spatial()} models. Distributions of importance scores produced with \texttt{rf_repeat()} are plotted using \texttt{ggplot2::geom_violin}, which shows the median of the density estimate rather than the actual median of the data. However, the violin plots are ordered from top to bottom by the real median of the data to make small differences in median importance easier to spot. This function does not plot the result of \texttt{rf_importance()} yet, but you can find it under \texttt{model$importance$cv.per.variable.plot}.

Usage

\begin{verbatim}
plot_importance(
  model,
  fill.color = viridis::viridis(
    100,
    option = "F",
    direction = -1,
    alpha = 1,
    end = 0.9
  ),
  line.color = "white",
  verbose = TRUE
)
\end{verbatim}

Arguments

- \texttt{model}:
  A model fitted with \texttt{rf()}, \texttt{rf_repeat()}, or \texttt{rf.spatial()}, or a data frame with variable importance scores (only for internal use within the package functions).

- \texttt{fill.color}:
  Character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. \texttt{viridis::viridis(100)}). Default: \texttt{viridis::viridis(100, option = "F", direction = -1, alpha = 0.8, end = 0.9)}

- \texttt{line.color}:
  Character string, color of the line produced by \texttt{ggplot2::geom_smooth()}. Default: "white"

- \texttt{verbose}:
  Logical, if \texttt{TRUE}, the plot is printed. Default: \texttt{TRUE}

Value

- A \texttt{ggplot}.

See Also

- \texttt{print_importance()}, \texttt{get_importance()}
Examples

if(interactive()){

  # loading example data
  data(plant_richness_df)
  data(distance_matrix)

  # fitting a random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1,
    verbose = FALSE
  )

  # plotting variable importance scores
  plot_importance(model = rf.model)
}

plot_moran

Plots a Moran’s I test of model residuals

Description

Plots the results of spatial autocorrelation tests for a variety of functions within the package. The x axis represents the Moran’s I estimate, the y axis contains the values of the distance thresholds, the dot sizes represent the p-values of the Moran’s I estimate, and the red dashed line represents the theoretical null value of the Moran’s I estimate.

Usage

plot_moran(
  model,
  point.color = viridis::viridis(
    100,
    option = "F",
    direction = -1
  ),
  line.color = "gray30",
  option = 1,
  ncol = 1,
  verbose = TRUE
)
Arguments

- **model**: A model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`, or a data frame generated by `moran()`. Default: NULL
- **point.color**: Colors of the plotted points. Can be a single color name (e.g. "red4"), a character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. `viridis::viridis(100)`). Default: `viridis::viridis(100, option = "F")`
- **line.color**: Character string, color of the line produced by `ggplot2::geom_smooth()`. Default: "gray30"
- **option**: Integer, type of plot. If 1 (default) a line plot with Moran’s I and p-values across distance thresholds is returned. If 2, scatterplots of residuals versus lagged residuals per distance threshold and their corresponding slopes are returned. In models fitted with `rf_repeat()`, the residuals and lags of the residuals are computed from the median residuals across repetitions. Option 2 is disabled if x is a data frame generated by `moran()`.
- **ncol**: Number of columns of the plot. Only relevant when option = 2. Argument ncol of `wrap_plots`.
- **verbose**: Logical, if TRUE, the resulting plot is printed. Default: TRUE

Value

A ggplot.

See Also

`moran()`, `moran_multithreshold()`

Examples

```r
if(interactive()){

  #loading example data
data(plant_richness_df)
data(distance.matrix)

  #fitting a random forest model
rf.model <- rf(
  data = plant_richness_df, 
  dependent.variable.name = "richness_species_vascular", 
  predictor.variable.names = colnames(plant_richness_df)[5:21], 
  distance.matrix = distance_matrix, 
  distance.thresholds = c(0, 1000, 2000), 
  n.cores = 1, 
  verbose = FALSE
)

  #Incremental/multiscale Moran's I
plot_moran(rf.model)
```
# Moran's scatterplot
plot_moran(rf.model, option = 2)


---

**plot_optimization**  
*Optimization plot of a selection of spatial predictors*

**Description**

Plots optimization data frames produced by `select.spatial.predictors_sequential()` and `select.spatial.predictors_recursive()`.

**Usage**

```r
plot_optimization(
  model,
  point.color = viridis::viridis(100, option = "F", direction = -1),
  verbose = TRUE
)
```

**Arguments**

- **model**: A model produced by `rf.spatial()`, or an optimization data frame produced by `select.spatial.predictors_sequential()` or `select.spatial.predictors_recursive()`.
- **point.color**: Colors of the plotted points. Can be a single color name (e.g. "red4"), a character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. `viridis::viridis(100)`). Default: `viridis::viridis(100, option = "F", direction = -1)`
- **verbose**: Logical, if TRUE the plot is printed. Default: TRUE

**Details**

If the method used to fit a model with `rf.spatial()` is "hengl", the function returns nothing, as this method does not require optimization.

**Value**

A ggplot.
Examples

if(interactive()){

#loading example data
data(distance_matrix)
data(plant_richness_df)

#names of the response and predictors
dependent.variable.name <- "richness_species_vascular"
predictor.variable.names <- colnames(plant_richness_df)[5:21]

#spatial model
model <- rf_spatial(
  data = plant_richness_df,
  dependent.variable.name = dependent.variable.name,
  predictor.variable.names = predictor.variable.names,
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  method = "mem.moran.sequential",
  n.cores = 1,
  seed = 1
)

#plotting selection of spatial predictors
plot_optimization(model = model)

}

plot_residuals_diagnostics

Plot residuals diagnostics

Description

Plots normality and autocorrelation tests of model residuals.

Usage

plot_residuals_diagnostics(
  model,
  point.color = viridis::viridis(100, option = "F"),
  line.color = "gray10",
  fill.color = viridis::viridis(4, option = "F", alpha = 0.95)[2],
  option = 1,
  ncol = 1,
  verbose = TRUE
)
plot_residuals_diagnostics

Arguments

- **model**: A model produced by `rf()`, `rf_repeat()`, or `rf_spatial()`.

- **point.color**: Colors of the plotted points. Can be a single color name (e.g. "red4"), a character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. `viridis::viridis(100)`). Default: `viridis::viridis(100, option = "F")`.

- **line.color**: Character string, color of the line produced by `ggplot2::geom_smooth()`. Default: "gray30"

- **fill.color**: Character string, fill color of the bars produced by `ggplot2::geom_histogram()`. Default: `viridis::viridis(4, option = "F", alpha = 0.95)`[2]

- **option**: (argument of `plot_moran()`) Integer, type of plot. If 1 (default) a line plot with Moran's I and p-values across distance thresholds is returned. If 2, scatterplots of residuals versus lagged residuals per distance threshold and their corresponding slopes are returned. In models fitted with `rf_repeat()`, the residuals and lags of the residuals are computed from the median residuals across repetitions. Option 2 is disabled if `x` is a data frame generated by `moran()`.

- **ncol**: (argument of `plot_moran()`) Number of columns of the Moran's I plot if option = 2.

- **verbose**: Logical, if TRUE, the resulting plot is printed. Default: TRUE

Value

A patchwork object.

Examples

```r
if(interactive()){

  # load example data
  data(plant_richness_df)
  data(distance_matrix)

  # fit a random forest model
  x <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    n.cores = 1
  )

  # residuals diagnostics
  plot_residuals_diagnostics(x)
}
```
plot_response_curves

Plots the response curves of a model.

Description

Plots the response curves of models fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`.

Usage

```r
plot_response_curves(
  model = NULL,
  variables = NULL,
  quantiles = c(0.1, 0.5, 0.9),
  grid.resolution = 200,
  line.color = viridis::viridis(length(quantiles), option = "F", end = 0.9),
  ncol = 2,
  show.data = FALSE,
  verbose = TRUE
)
```

Arguments

- **model**: A model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`.
- **variables**: Character vector, names of predictors to plot. If NULL, the most important variables (importance higher than the median) in x are selected. Default: NULL.
- **quantiles**: Numeric vector with values between 0 and 1, argument `probs` of `quantile`. Quantiles to set the other variables to. Default: c(0.1, 0.5, 0.9)
- **grid.resolution**: Integer between 20 and 500. Resolution of the plotted curve. Default: 100
- **line.color**: Character vector with colors, or function to generate colors for the lines representing quantiles. Must have the same number of colors as quantiles are defined. Default: `viridis::viridis(length(quantiles), option = "F", end = 0.9)`
- **ncol**: Integer, argument of `wrap_plots`. Defaults to the rounded squared root of the number of plots. Default: 2
- **show.data**: Logical, if TRUE, the observed data is plotted along with the response curves. Default: FALSE
- **verbose**: Logical, if TRUE the plot is printed. Default: TRUE

Details

All variables that are not plotted in a particular response curve are set to the values of their respective quantiles, and the response curve for each one of these quantiles is shown in the plot. When the input model was fitted with `rf_repeat()` with `keep.models = TRUE`, then the plot shows the median of all model runs, and each model run separately as a thinner line. The output list can be plotted all at once with `patchwork::wrap_plots(p)` or `cowplot::plot_grid(plotlist = p)`, or one by one by extracting each plot from the list.
plot_response_surface

Plots the response surfaces of a random forest model

Description

Plots response surfaces for any given pair of predictors in a rf(), rf_repeat(), or rf_spatial() model.

Usage

plot_response_surface(
  model = NULL,
  a = NULL,
  b = NULL,
  quantiles = 0.5,
  grid.resolution = 100,
  point.size.range = c(0.5, 2.5),
  point.alpha = 1,
  fill.color = viridis::viridis(100, option = "F", direction = -1, alpha = 0.9),
  point.color = "gray30",
  verbose = TRUE
)

Value

A list with slots named after the selected variables, with one ggplot each.

See Also

plot_response_surface()

Examples

if(interactive()){

  #loading example data
  data(plant_richness_df)

  #fitting a random forest model
  m <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    n.cores = 1,
    verbose = FALSE
  )

  #response curves of most important predictors
  plot_response_curves(model = m)
}

plot_response_surface

Plots the response surfaces of a random forest model

Plot the response surfaces of a random forest model.
Arguments

model  A model fitted with rf(), rf_repeat(), or rf_spatial(). Default NULL
a      Character string, name of a model predictor. If NULL, the most important variable in model is selected. Default: NULL
b      Character string, name of a model predictor. If NULL, the second most important variable in model is selected. Default: NULL
quantiles Numeric vector between 0 and 1. Argument probs of the function quantile. Quantiles to set the other variables to. Default: 0.5
grid.resolution Integer between 20 and 500. Resolution of the plotted surface Default: 100
point.size.range Numeric vector of length 2 with the range of point sizes used by geom_point. Using c(-1, -1) removes the points. Default: c(0.5, 2.5)
point.alpha Numeric between 0 and 1, transparency of the points. Setting it to 0 removes all points. Default: 1.
fill.color Character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. viridis::viridis(100)). Default: viridis::viridis(100, option = "F", direction = -1, alpha = 0.9)
point.color Character vector with a color name (e.g. "red4"). Default: gray30
verbose Logical, if TRUE the plot is printed. Default: TRUE

Details

All variables that are not a or b in a response curve are set to the values of their respective quantiles to plot the response surfaces. The output list can be plotted all at once with patchwork::wrap_plots(p) or cowplot::plot_grid(plotlist = p), or one by one by extracting each plot from the list.

Value

A list with slots named after the selected quantiles, each one with a ggplot.

See Also

plot_response_curves()

Examples

if(interactive()){
  #load example data
data(plant_richness_df)

  #fit random forest model
out <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
predictor.variable.names = colnames(plant_richness_df)[5:21],
plot_training_df

n.cores = 1,
verbose = FALSE
)

#plot interactions between most important predictors
plot_response_surfaces(x = out)
}

plot_training_df
Scatterplots of a training data frame

Description

Plots the dependent variable against each predictor.

Usage

plot_training_df(
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  ncol = 4,
  method = "loess",
  point.color = viridis::viridis(100, option = "F"),
  line.color = "gray30"
)

Arguments

data: Data frame with a response variable and a set of predictors. Default: NULL

dependent.variable.name: Character string with the name of the response variable. Must be in the column names of data. If the dependent variable is binary with values 1 and 0, the argument case.weights of ranger is populated by the function case_weights(). Default: NULL

predictor.variable.names: Character vector with the names of the predictive variables. Every element of this vector must be in the column names of data. Optionally, the result of auto_cor() or auto_vif() Default: NULL

ncol: Number of columns of the plot. Argument ncol of wrap_plots.

method: Method for geom_smooth, one of: "lm", "glm", "gam", "loess", or a function, for example mgcv::gam Default: 'loess'

point.color: Colors of the plotted points. Can be a single color name (e.g. "red4"), a character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. viridis::viridis(100)). Default: viridis::viridis(100, option = "F")
line.color  Character string, color of the line produced by ggplot2::geom_smooth(). Default: "gray30"

Value  A wrap_plots object.

Examples
if(interactive()){
  # load example data
  data(plant_richness_df)
  # scatterplot of the training data
  plot_training_data(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21]
  )
}

plot_training_df_moran

Moran’s I plots of a training data frame

Description
Plots the Moran’s I test of the response and the predictors in a training data frame.

Usage
plot_training_df_moran(
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  distance.matrix = NULL,
  distance.thresholds = NULL,
  fill.color = viridis::viridis(100, option = "F", direction = -1),
  point.color = "gray30"
)

Arguments
data  Data frame with a response variable and a set of predictors. Default: NULL
dependent.variable.name
Character string with the name of the response variable. Must be in the column names of data. If the dependent variable is binary with values 1 and 0, the argument case.weights of ranger is populated by the function case_weights(). Default: NULL

predictor.variable.names
Character vector with the names of the predictive variables. Every element of this vector must be in the column names of data. Optionally, the result of auto_cor() or auto_vif() Default: NULL

distance.matrix
Squared matrix with the distances among the records in data. The number of rows of distance.matrix and data must be the same. If not provided, the computation of the Moran’s I of the residuals is omitted. Default: NULL

distance.thresholds
Numeric vector, distances below each value are set to 0 on separated copies of the distance matrix for the computation of Moran’s I at different neighborhood distances. If NULL, it defaults to seq(0, max(distance.matrix)/4, length.out = 2). Default: NULL

fill.color
Character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. viridis::viridis(100)). Default: viridis::viridis(100, option = "F", direction = -1)

point.color
Character vector with a color name (e.g. "red4"). Default: gray30

Value
A ggplot2 object.

Examples
if(interactive()){

  #load example data
data(plant_richness_df)
data(distance_matrix)

  #plot Moran's I of training data
plot_moran_training_data(
  data = plant_richness_df,
  dependent.variable.name = "richness_species_vascular",
  predictor.variable.names = colnames(plant_richness_df)[5:21],
  distance.matrix = distance_matrix,
  distance.thresholds = c(0, 2000, 4000, 6000, 8000)
)
}
plot_tuning

Plots a tuning object produced by rf_tuning()

Description

Plots the tuning of the hyperparameters num.trees, mtry, and min.node.size performed by rf_tuning().

Usage

plot_tuning(
  model,
  point.color = viridis::viridis(100, option = "F"),
  verbose = TRUE
)

Arguments

model A model fitted with rf_tuning(). Default: NULL
point.color Colors of the plotted points. Can be a single color name (e.g. "red4"), a character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. viridis::viridis(100)). Default: viridis::viridis(100, option = "F")
verbose Logical, if TRUE, the plot is printed. Default: TRUE

Value

A ggplot.

See Also

rf_tuning()

Examples

if(interactive()){  
#load example data  
data(plant_richness_df)
  
#fit random forest model  
rf.model <- rf(  
data = plant_richness_df,  
dependent.variable.name = "richness_species_vascular",  
predictor.variable.names = colnames(plant_richness_df)[5:21],

)
```

prepare_importance_spatial

Prepares variable importance objects for spatial models

Description
Prepares variable importance data frames and plots for models fitted with `rf_spatial()`.

Usage
```r
prepare_importance_spatial(model)
```  
Arguments
- **model**: An importance data frame with spatial predictors, or a model fitted with `rf_spatial()`.

Value
A list with importance data frames in different formats depending on whether the model was fitted with `rf()` or `rf_repeat()`.

Examples
```r
if(interactive()){

  # loading example data
  data(distance_matrix)
  data(plant_richness_df)

  # fitting spatial model
  model <- rf_spatial(
```
data = plant_richness_df,
dependent.variable.name = "richness_species_vascular",
predictor.variable.names = colnames(plant_richness_df)[5:21],
distance.matrix = distance_matrix,
distance.thresholds = 0,
n.cores = 1
)

# preparing the importance data frame
importance <- prepare_importance_spatial(model)
names(importance)

Description
Custom print method for random forest models

Usage
## S3 method for class 'rf'
print(x, ...)

Arguments
x A model fitted with rf(), rf_repeat(), or rf_spatial().
...
Additional arguments for print methods.

Value
Prints model details to the console.

See Also
print_evaluation(), print_importance(), print_moran(), print_performance()

Examples
if(interactive()){

# loading example data
data("plant_richness_df")
data("distance_matrix")

# fitting random forest model
rf.model <- rf(
data = plant_richness_df,
  dependent.variable.name = "richness_species_vascular",
  predictor.variable.names = colnames(plant_richness_df)[5:21],
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  n.cores = 1
)

# printing model summary
print(rf.model)
}

print_evaluation

Prints cross-validation results

Description
Prints the results of an spatial cross-validation performed with rf_evaluate().

Usage
print_evaluation(model)

Arguments
model A model resulting from rf_evaluate().

Value
A table printed to the standard output.

See Also
plot_evaluation().get_evaluation()

Examples
if(interactive()){

  # loading example data
  data(plant_richness_df)
  data(distance_matrix)

  # fitting random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1
  )

  # printing model summary
  print(rf.model)
}
#evaluation with spatial cross-validation
rf.model <- rf_evaluate(
  model = rf.model,
  xy = plant_richness_df[, c("x", "y")],
  n.cores = 1
)

#checking evaluation results
print_evaluation(rf.model)

print_importance

Prints variable importance

Description

Prints variable importance scores from rf, rf_repeat, and rf_spatial models.

Usage

print_importance(
  model,
  verbose = TRUE
)

Arguments

model A model fitted with rf, rf_repeat, or rf_spatial.
verbose Logical, if TRUE, variable importance is returned. Default: TRUE

Value

A table printed to the standard output.

See Also

plot_importance(), get_importance()
Examples

```r
if(interactive()){
  # loading example data
  data(plant_richness_df)
  data(distance_matrix)

  # fitting a random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1,
    verbose = FALSE
  )

  # printing variable importance scores
  print_importance(model = rf.model)
}
```

---

**print_moran**  
*Prints results of a Moran’s I test*

Description

Prints the results of a Moran’s I test on the residuals of a model.

Usage

```r
print_moran(
  model,
  caption = NULL,
  verbose = TRUE
)
```

Arguments

- `model`  
  A model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`.
- `caption`  
  Character, caption of the output table, Default: NULL
- `verbose`  
  Logical, if TRUE, the resulting table is printed into the console, Default: TRUE

Value

Prints a table in the console using the huxtable package.
See Also

moran(), moran_multithreshold(), get_moran(), plot_moran()

Examples

if(interactive()){
  #loading example data
  data(plant_richness_df)
  data(distance.matrix)

  #fitting random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = c(0, 1000, 2000),
    n.cores = 1,
    verbose = FALSE
  )

  #printing Moran's I of model's residuals
  print_moran(rf.model)
}

Description

Prints the performance slot of a model fitted with rf(), rf_repeat(), or rf_spatial(). For models fitted with rf_repeat() it shows the median and the median absolute deviation of each performance measure.

Usage

print_performance(model)

Arguments

model Model fitted with rf(), rf_repeat(), or rf_spatial().

Value

Prints model performance scores to the console.
\textit{rank\_spatial\_predictors}

\textbf{See Also}

\texttt{print\_performance()}, \texttt{get\_performance()}

\textbf{Examples}

\begin{verbatim}
if(interactive()){

  #loading example data
  data(plant_richness_df)
  data(distance.matrix)

  #fitting a random forest model
  rf.model <- rf(
      data = plant_richness_df,
      dependent.variable.name = "richness\_species\_vascular",
      predictor.variable.names = colnames(plant_richness_df)[5:21],
      distance.matrix = distance_matrix,
      distance.thresholds = 0,
      n.cores = 1,
      verbose = FALSE
    )

  #printing performance scores
  print_performance(rf.model)
}

\end{verbatim}

\textit{rank\_spatial\_predictors}

\textit{Ranks spatial predictors}

\textbf{Description}

Ranks spatial predictors generated by \texttt{mem\_multithreshold()} or \texttt{pca\_multithreshold()} by their effect in reducing the Moran’s I of the model residuals (\texttt{ranking.method = “effect”}), or by their own Moran’s I (\texttt{ranking.method = “moran”}).

In the former case, one model of the type \(y \sim \text{predictors} + \text{spatial\_predictor\_X}\) is fitted per spatial predictor, and the Moran’s I of this model’s residuals is compared with the one of the model without spatial predictors (\(y \sim \text{predictors}\)), to finally rank the spatial predictor from maximum to minimum difference in Moran’s I.

In the latter case, the spatial predictors are ordered by their Moran’s I alone (this is the faster option).

In both cases, spatial predictors that are redundant with others at a Pearson correlation > 0.5 and spatial predictors with no effect (no reduction of Moran’s I or Moran’s I of the spatial predictor equal or lower than 0) are removed.

This function has been designed to be used internally by \texttt{rf\_spatial()} rather than directly by a user.
Usage

```r
rank_spatial_predictors(
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  distance.matrix = NULL,
  distance.thresholds = NULL,
  ranger.arguments = NULL,
  spatial.predictors.df = NULL,
  ranking.method = c("moran", "effect"),
  reference.moran.i = 1,
  verbose = FALSE,
  n.cores = parallel::detectCores() - 1,
  cluster = NULL
)
```

Arguments

- **data**: Data frame with a response variable and a set of predictors. Default: NULL
- **dependent.variable.name**: Character string with the name of the response variable. Must be in the column names of `data`. Default: NULL
- **predictor.variable.names**: Character vector with the names of the predictive variables. Every element of this vector must be in the column names of `data`. Default: NULL
- **distance.matrix**: Squared matrix with the distances among the records in `data`. The number of rows of `distance.matrix` and `data` must be the same. If not provided, the computation of the Moran’s I of the residuals is omitted. Default: NULL
- **distance.thresholds**: Numeric vector with neighborhood distances. All distances in the distance matrix below each value in `distance.thresholds` are set to 0 for the computation of Moran’s I. If NULL, it defaults to `seq(0, max(distance.matrix), length.out = 4)`. Default: NULL
- **ranger.arguments**: List with ranger arguments. See `rf` or `rf_repeat` for further details.
- **spatial.predictors.df**: Data frame of spatial predictors.
- **ranking.method**: Character, method used by to rank spatial predictors. The method "effect" ranks spatial predictors according how much each predictor reduces Moran’s I of the model residuals, while the method "moran" ranks them by their own Moran’s I. Default: "moran".
- **reference.moran.i**: Moran’s I of the residuals of the model without spatial predictors. Default: 1
- **verbose**: Logical, if TRUE, messages and plots generated during the execution of the function are displayed, Default: TRUE
n.cores  Integer, number of cores to use for parallel execution. Creates a socket cluster with `parallel::makeCluster()`, runs operations in parallel with `foreach` and `%dopar%`, and stops the cluster with `parallel::clusterStop()` when the job is done. Default: `parallel::detectCores() - 1`

cluster  A cluster definition generated with `parallel::makeCluster()`. If provided, overrides `n.cores`. When `cluster = NULL` (default value), and `model` is provided, the cluster in `model`, if any, is used instead. If this cluster is `NULL`, then the function uses `n.cores` instead. The function does not stop a provided cluster, so it should be stopped with `parallel::stopCluster()` afterwards. The cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the `model` argument, or using the `%>%` pipe. Default: `NULL`

Value

A list with four slots:

- `method`: Character, name of the method used to rank the spatial predictors.
- `criteria`: Data frame with two different configurations depending on the ranking method. If `ranking.method = "effect"`, the columns contain the names of the spatial predictors, the r-squared of the model, the Moran’s I of the model residuals, the difference between the Moran’s I of the model including the given spatial predictor, and the Moran’s I of the model fitted without spatial predictors, and the interpretation of the Moran’s I value. If `ranking.method = "moran"`, only the name of the spatial predictor and it’s Moran’s I are in the output data frame.
- `ranking`: Ordered character vector with the names of the spatial predictors selected.
- `spatial.predictors.df`: data frame with the selected spatial predictors in the order of the ranking.

Examples

```r
if(interactive()){

  #loading distance matrix
data(distance_matrix)

  #computing Moran's Eigenvector Maps
  mem.df <- mem(
    distance.matrix = distance_matrix[1:50, 1:50],
    distance.threshold = 0
  )

  #ranking by the Moran's I of the spatial predictor
  rank <- rank_spatial_predictors(
    distance.matrix = distance_matrix[1:50, 1:50],
    distance.thresholds = 0,
    spatial.predictors.df = mem.df,
    ranking.method = "moran",
    n.cores = 1
  )
}
```
# checking Moran's I of MEMs
rank$criteria

# checking rank of MEMs
rank$ranking

rescale_vector

## Description
Rescales a numeric vector into a new range.

## Usage

```r
rescale_vector(
  x = NULL,
  new.min = 0,
  new.max = 1,
  integer = FALSE
)
```

## Arguments

- **x**: Numeric vector. Default: `NULL`
- **new.min**: New minimum value. Default: `0`
- **new.max**: New maximum value. Default: `1`
- **integer**: Logical, if `TRUE`, coerces the output to integer. Default: `FALSE`

## Value
A numeric vector of the same length as `x`, but with its values rescaled between `new.min` and `new.max`.

## Examples

```r
if(interactive()){  
  out <- rescale_vector(  
    x = rnorm(100),
    new.min = 0,
    new.max = 100,
    integer = TRUE
  )
  out
}
```
residuals_diagnostics  Normality test of a numeric vector

Description
Applies a Shapiro-Wilks test to a numeric vector, and plots the qq plot and the histogram.

Usage
residuals_diagnostics(residuals, predictions)

Arguments
residuals   Numeric vector, model residuals.
predictions Numeric vector, model predictions.

Details
The function shapiro.test() has a hard limit of 5000 cases. If the model residuals have more than 5000 cases, then sample(x = residuals, size = 5000) is applied to the model residuals before the test.

Value
A list with four slots:
- w  W statistic returned by shapiro.test().
- p.value  p-value of the Shapiro test.
- interpretation  Character vector, one of "x is normal", "x is not normal".
- plot A patchwork plot with the qq plot and the histogram of x.

See Also
ggplot.aes.geom_qq_line.ggtheme.labs.geom_freqpoly.geom_abline.plot_annotation

Examples
if(interactive()){
  residuals_diagnostics(
    residuals = runif(100),
    predictions = runif(100)
  )
}
}
residuals_test  Normality test of a numeric vector

Description

Applies a Shapiro-Wilks test to a numeric vector, and returns a list with the statistic W, its p-value, and a character string with the interpretation.

Usage

residuals_test(residuals)

Arguments

residuals Numeric vector, model residuals.

Value

A list with four slots:

- **w**: W statistic returned by `shapiro.test()`.
- **p.value**: p-value of the Shapiro test.
- **interpretation**: Character vector, one of "x is normal", "x is not normal".
- **plot**: A patchwork plot with the qq plot and the histogram of x.

See Also

ggplot, aes, geom_qq_line, ggtheme, labs, geom_freqpoly, geom_abline, plot_annotation

Examples

```r
if(interactive()){
    residuals_test(residuals = runif(100))
}
```

rf  Random forest models with Moran’s I test of the residuals

Description

A convenient wrapper for `ranger` that completes its output by providing the Moran’s I of the residuals for different distance thresholds, the rmse and nrmse (as computed by `root_mean_squared_error()`), and variable importance scores based on a scaled version of the data generated by `scale`.
Usage

\[
\text{rf}( \\
\quad \text{data} = \text{NULL}, \\
\quad \text{dependent.variable.name} = \text{NULL}, \\
\quad \text{predictor.variable.names} = \text{NULL}, \\
\quad \text{distance.matrix} = \text{NULL}, \\
\quad \text{distance.thresholds} = \text{NULL}, \\
\quad \text{xy} = \text{NULL}, \\
\quad \text{ranger.arguments} = \text{NULL}, \\
\quad \text{scaled.importance} = \text{FALSE}, \\
\quad \text{seed} = 1, \\
\quad \text{verbose} = \text{TRUE}, \\
\quad \text{n.cores} = \text{parallel::detectCores()} - 1, \\
\quad \text{cluster} = \text{NULL} \\
) \\
\]

Arguments

data
Data frame with a response variable and a set of predictors. Default: NULL
dependent.variable.name
Character string with the name of the response variable. Must be in the column names of data. If the dependent variable is binary with values 1 and 0, the argument case.weights of ranger is populated by the function case_weights(). Default: NULL
predictor.variable.names
Character vector with the names of the predictive variables. Every element of this vector must be in the column names of data. Optionally, the result of auto_cor() or auto_vif(). Default: NULL
distance.matrix
Squared matrix with the distances among the records in data. The number of rows of distance.matrix and data must be the same. If not provided, the computation of the Moran’s I of the residuals is omitted. Default: NULL
distance.thresholds
Numeric vector with neighborhood distances. All distances in the distance matrix below each value in distance.thresholds are set to 0 for the computation of Moran’s I. If NULL, it defaults to seq(0, max(distance.matrix), length.out = 4). Default: NULL
xy
(optional) Data frame or matrix with two columns containing coordinates and named "x" and "y". It is not used by this function, but it is stored in the slot ranger.arguments$xy of the model, so it can be used by rf_evaluate() and rf_tuning(). Default: NULL
ranger.arguments
Named list with ranger arguments (other arguments of this function can also go here). All ranger arguments are set to their default values except for ‘importance’, that is set to ‘permutation’ rather than ‘none’. The ranger arguments x, y, and formula are disabled. Please, consult the help file of ranger if you are not familiar with the arguments of this function.
scaled.importance
Logical, if TRUE, the function scales data with scale and fits a new model to compute scaled variable importance scores. This makes variable importance scores of different models somewhat comparable. Default: FALSE

seed
Integer, random seed to facilitate reproducibility. If set to a given number, the returned model is always the same. Default: 1

verbose
Boolean. If TRUE, messages and plots generated during the execution of the function are displayed. Default: TRUE

n.cores
Integer, number of cores to use. Default: parallel::detectCores() - 1

cluster
A cluster definition generated with parallel::makeCluster(). This function does not use the cluster, but can pass it on to other functions when using the %>% pipe. It will be stored in the slot cluster of the output list. Default: NULL

Details
Please read the help file of ranger for further details. Notice that the formula interface of ranger is supported through ranger.arguments, but variable interactions are not allowed (but check the_feature_engineer()).

Value
A ranger model with several extra slots:

• ranger.arguments: Stores the values of the arguments used to fit the ranger model.

• importance: A list containing a data frame with the predictors ordered by their importance, a ggplot showing the importance values, and local importance scores (difference in accuracy between permuted and non permuted variables for every case, computed on the out-of-bag data).

• performance: performance scores: R squared on out-of-bag data, R squared (cor(observed, predicted) ^ 2), pseudo R squared (cor(observed, predicted)), RMSE, and normalized RMSE (NRMSE).

• residuals: residuals, normality test of the residuals computed with residuals_test(), and spatial autocorrelation of the residuals computed with moran_multithreshold().

Examples
if(interactive()){

#loading example data
data("plant_richness_df")
data("distance_matrix")

#fittind random forest model
out <- rf(
  data = plant_richness_df,
dependent.variable.name = "richness_species_vascular",
predictor.variable.names = colnames(plant_richness_df)[5:21],
distance.matrix = distance_matrix,
distance.thresholds = 0,
)
class(out)

#data frame with ordered variable importance
out$importance$per.variable

#variable importance plot
out$importance$per.variable.plot

#performance
out$performance

#spatial correlation of the residuals
out$spatial.correlation.residuals$per.distance

#plot of the Moran’s I of the residuals for different distance thresholds
out$spatial.correlation.residuals$plot

#predictions for new data as done with ranger models:
predicted <- stats::predict(
  object = out,
  data = plant_richness_df,
  type = "response"
)$predictions

#alternative data input methods
###############################

#ranger.arguments can contain ranger arguments and any other rf argument
my.ranger.arguments <- list(
  data = plant_richness_df,
  dependent.variable.name = "richness_species_vascular",
  predictor.variable.names = colnames(plant_richness_df)[8:21],
  distance.matrix = distance_matrix,
  distance.thresholds = c(0, 1000)
)

#fitting model with these ranger arguments
out <- rf(
  ranger.arguments = my.ranger.arguments,
  n.cores = 1
)

rf_compare

rf_compare
Compares models via spatial cross-validation
rf_compare

Description

Uses rf_evaluate() to compare the performance of several models on independent spatial folds via spatial cross-validation.

Usage

rf_compare(
models = NULL,
xy = NULL,
repetitions = 30,
training.fraction = 0.75,
metrics = c("r.squared", "pseudo.r.squared", "rmse", "nrmse", "auc"),
distance.step = NULL,
distance.step.x = NULL,
distance.step.y = NULL,
fill.color = viridis::viridis(100, option = "F", direction = -1, alpha = 0.8),
line.color = "gray30",
seed = 1,
verbose = TRUE,
n.cores = parallel::detectCores() - 1,
cluster = NULL
)

Arguments

models
Named list with models resulting from rf(), rf.spatial(), rf.tuning(), or rf_evaluate(). Example: models = list(a = model.a, b = model.b). Default: NULL

xy
Data frame or matrix with two columns containing coordinates and named "x" and "y". Default: NULL

repetitions
Integer, number of spatial folds to use during cross-validation. Must be lower than the total number of rows available in the model's data. Default: 30

training.fraction
Proportion between 0.5 and 0.9 indicating the proportion of records to be used as training set during spatial cross-validation. Default: 0.75

metrics
Character vector, names of the performance metrics selected. The possible values are: "r.squared" (cor(obs, pred) ^ 2), "pseudo.r.squared" (cor(obs, pred)),"rmse"(sqrt(sum((obs - pred)^2)/length(obs))),'nrmse"(rmse/(quantile(obs, 0.75) - quantile(obs, 0.25))). Default: c("r.squared", "pseudo.r.squared", "rmse", "nrmse")

distance.step
Numeric, argument distance.step of thinning_til_n(). distance step used during the selection of the centers of the training folds. These fold centers are selected by thinning the data until a number of folds equal or lower than repetitions is reached. Its default value is 1/1000th the maximum distance within records in xy. Reduce it if the number of training folds is lower than expected.
distance.step.x
Numeric, argument distance.step.x of `make.spatial.folds()`. Distance step used during the growth in the x axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the x coordinates).

distance.step.y
Numeric, argument distance.step.x of `make.spatial.folds()`. Distance step used during the growth in the y axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the y coordinates).

fill.color
Character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"), or function generating a palette (e.g. `viridis::viridis(100)`). Default: `viridis::viridis(100, option = "F", direction = -1)`

line.color
Character string, color of the line produced by `ggplot2::geom_smooth()`. Default: "gray30"

seed
Integer, random seed to facilitate reproducibility. If set to a given number, the results of the function are always the same. Default: 1.

verbose
Logical. If TRUE, messages and plots generated during the execution of the function are displayed. Default: TRUE

n.cores
Integer, number of cores to use for parallel execution. Creates a socket cluster with `parallel::makeCluster()`, runs operations in parallel with `foreach` and `%dopar%`, and stops the cluster with `parallel::clusterStop()` when the job is done. Default: `parallel::detectCores() - 1`

cluster
A cluster definition generated with `parallel::makeCluster()`. If provided, overrides `n.cores`. When `cluster = NULL` (default value), and `model` is provided, the cluster in `model`, if any, is used instead. If this cluster is NULL, then the function uses `n.cores` instead. The function does not stop a provided cluster, so it should be stopped with `parallel::stopCluster()` afterwards. The cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the `model` argument, or using the `%>%` pipe. Default: NULL

Value
A list with three slots:

- comparison.df: Data frame with one performance value per spatial fold, metric, and model.
- spatial.folds: List with the indices of the training and testing records for each evaluation repetition.
- plot: Violin-plot of comparison.df.

See Also
`rf_evaluate()`

Examples
```r
if(interactive()){
```
# loading example data
data(distance_matrix)
data(plant_richness_df)

# fitting random forest model
rf.model <- rf(
  data = plant_richness_df,
  dependent.variable.name = "richness_species_vascular",
  predictor.variable.names = colnames(plant_richness_df)[5:21],
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  n.cores = 1
)

# fitting a spatial model with Moran's Eigenvector Maps
rf.spatial <- rf_spatial(
  model = rf.model,
  n.cores = 1
)

# comparing the spatial and non spatial models
comparison <- rf_compare(
  models = list(
    'Non spatial' = rf.model,
    Spatial = rf.spatial
  ),
  xy = plant_richness_df[, c("x", "y")],
  metrics = c("r.squared", "rmse"),
  n.cores = 1
)

---

**rf_evaluate**

Evaluates random forest models with spatial cross-validation

**Description**

Evaluates the performance of random forest on unseen data over independent spatial folds.

**Usage**

```r
rf_evaluate(
  model = NULL,
  xy = NULL,
  repetitions = 30,
  training.fraction = 0.75,
  metrics = c("r.squared", "pseudo.r.squared", "rmse", "nrmse", "auc"),
  distance.step = NULL,
  distance.step.x = NULL,
)```
distance.step.y = NULL,
grow.testing.folds = FALSE,
seed = 1,
verbose = TRUE,
n.cores = parallel::detectCores() - 1,
cluster = NULL
)

Arguments

model Model fitted with `rf()`, `rf_repeat()`, or `rf_spatial()`.
xy Data frame or matrix with two columns containing coordinates and named "x" and "y". If NULL, the function will throw an error. Default: NULL
repetitions Integer, number of spatial folds to use during cross-validation. Must be lower than the total number of rows available in the model's data. Default: 30
training.fraction Proportion between 0.5 and 0.9 indicating the proportion of records to be used as training set during spatial cross-validation. Default: 0.75
metrics Character vector, names of the performance metrics selected. The possible values are: "r.squared" (cor(obs, pred) ^ 2), "pseudo.r.squared" (cor(obs, pred)), "rmse"(sqrt(sum((obs - pred)^2)/length(obs))), "nrmse"(rmse/(quantile(obs, 0.75) - quantile(obs, 0.25))), and "auc" (only for binary responses with values 1 and 0). Default: c("r.squared", "pseudo.r.squared", "rmse", "nrmse")
distance.step Numeric, argument distance.step of `thinning_til_n()`. Distance step used during the selection of the centers of the training folds. These fold centers are selected by thinning the data until a number of folds equal or lower than repetitions is reached. Its default value is 1/1000th the maximum distance within records in xy. Reduce it if the number of training folds is lower than expected.
distance.step.x Numeric, argument distance.step.x of `make_spatial_folds()`. Distance step used during the growth in the x axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the x coordinates).
distance.step.y Numeric, argument distance.step.x of `make_spatial_folds()`. Distance step used during the growth in the y axis of the buffers defining the training folds. Default: NULL (1/1000th the range of the y coordinates).
grow.testing.folds Logic. By default, this function grows contiguous training folds to keep the spatial structure of the data as intact as possible. However, when setting `grow.testing.folds = TRUE`, the argument `training.fraction` is set to `1 - training.fraction`, and the training and testing folds are switched. This option might be useful when the training data has a spatial structure that does not match well with the default behavior of the function. Default: FALSE
seed Integer, random seed to facilitate reproducibility. If set to a given number, the results of the function are always the same. Default: 1.
The evaluation algorithm works as follows: the number of repetitions and the input dataset (stored in model$ranger.arguments$data) are used as inputs for the function thinning_til_n(), that applies thinning() to the input data until as many cases as repetitions are left, and as separated as possible. Each of these remaining records will be used as a "fold center". From that point, the fold grows, until a number of points equal (or close) to training.fraction is reached. The indices of the records within the grown spatial fold are stored as "training" in the output list, and the remaining ones as "testing". Then, for each spatial fold, a "training model" is fitted using the cases corresponding with the training indices, and predicted over the cases corresponding with the testing indices. The model predictions on the "unseen" data are compared with the observations, and the performance measures (R squared, pseudo R squared, RMSE and NRMSE) computed.

Value

A model of the class "rf_evaluate" with a new slot named "evaluation", that is a list with the following slots:

- training.fraction: Value of the argument training.fraction.
- spatial.folds: Result of applying make_spatial_folds() on the data coordinates. It is a list with as many slots as repetitions are indicated by the user. Each slot has two slots named "training" and "testing", each one having the indices of the cases used on the training and testing models.
- per.fold: Data frame with the evaluation results per spatial fold (or repetition). It contains the ID of each fold, its central coordinates, the number of training and testing cases, and the training and testing performance measures: R squared, pseudo R squared (cor( observed, predicted)), rmse, and normalized rmse.
- per.model: Same data as above, but organized per fold and model ("Training", "Testing", and "Full").
- aggregated: Same data, but aggregated by model and performance measure.
Examples

```r
if(interactive()){

  # loading example data
data(plant_richness_df)
data(distance_matrix)

  # fitting random forest model
  rf.model <- rf(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1,
    verbose = FALSE
  )

  # evaluation with spatial cross-validation
  rf.model <- rf_evaluate(
    model = rf.model,
    xy = plant_richness_df[, c("x", "y")],
    n.cores = 1
  )

  # checking evaluation results
  plot_evaluation(rf.model)
  print_evaluation(rf.model)
  x <- get_evaluation(rf.model)
}
```

rf_importance

**Contribution of each predictor to model transferability**

Description

Evaluates the contribution of the predictors to model transferability via spatial cross-validation. The function returns the median increase or decrease in a given evaluation metric (R², pseudo R², RMSE, nRMSE, or AUC) when a variable is introduced in a model, by comparing and evaluating via spatial cross-validation models with and without the given variable. This function was devised to provide importance scores that would be less sensitive to spatial autocorrelation than those computed internally by random forest on the out-of-bag data. This function is experimental.

Usage

```r
rf_importance(
  model = NULL,
  xy = NULL,
```
rf_importance

repetitions = 30,
training.fraction = 0.75,
metric = c("r.squared", "pseudo.r.squared", "rmse", "nrmse", "auc"),
distance.step = NULL,
distance.step.x = NULL,
distance.step.y = NULL,
fill.color = viridis::viridis(100, option = "F", direction = -1, alpha = 1, end = 0.9),
line.color = "white",
seed = 1,
verbose = TRUE,
n.cores = parallel::detectCores() - 1,
cluster = NULL
)

Arguments

model  Model fitted with rf() and/or rf_spatial(). The function doesn’t work with
models fitted with rf_repeat(). Default: NULL

xy  Data frame or matrix with two columns containing coordinates and named "x"
and "y". If NULL, the function will throw an error. Default: NULL

repetitions  Integer, number of spatial folds to use during cross-validation. Must be lower
than the total number of rows available in the model’s data. Default: 30

training.fraction  Proportion between 0.5 and 0.9 indicating the proportion of records to be used
as training set during spatial cross-validation. Default: 0.75

metric  Character, names of the performance metric to use. The possible values are:
"r.squared" (cor(obs, pred)^2), "pseudo.r.squared" (cor(obs, pred)), "rmse"
(sqrt(sum((obs - pred)^2)/length(obs)), "nrmse" (rmse/(quantile(obs, 0.75) - quantile(obs, 0.25))), and "auc" (only for binary responses with
values 1 and 0). Default: "r.squared"

distance.step  Numeric, argument distance.step of thinning_till_n(). distance step used
during the selection of the centers of the training folds. These fold centers
are selected by thinning the data until a number of folds equal or lower than
repetitions is reached. Its default value is 1/1000th the maximum distance
within records in xy. Reduce it if the number of training folds is lower than
expected.

distance.step.x  Numeric, argument distance.step.x of make.spatial.folds(). Distance
step used during the growth in the x axis of the buffers defining the training
folds. Default: NULL (1/1000th the range of the x coordinates).

distance.step.y  Numeric, argument distance.step.x of make.spatial.folds(). Distance
step used during the growth in the y axis of the buffers defining the training
folds. Default: NULL (1/1000th the range of the y coordinates).

fill.color  Character vector with hexadecimal codes (e.g. "#440154FF" "#21908CFF" "#FDE725FF"),
or function generating a palette (e.g. viridis::viridis(100)). Default: viridis::viridis(100,
option = "F", direction = -1, alpha = 0.8, end = 0.9)
**line.color**  
Character string, color of the line produced by `ggplot2::geom_smooth()`. Default: "white"

**seed**  
Integer, random seed to facilitate reproducibility. If set to a given number, the results of the function are always the same. Default: 1.

**verbose**  
Logical. If TRUE, messages and plots generated during the execution of the function are displayed. Default: TRUE

**n.cores**  
Integer, number of cores to use for parallel execution. Creates a socket cluster with `parallel::makeCluster()`, runs operations in parallel with foreach and `%dopar%`, and stops the cluster with `parallel::clusterStop()` when the job is done. Default: `parallel::detectCores() - 1`

**cluster**  
A cluster definition generated with `parallel::makeCluster()`. If provided, overrides `n.cores`. When `cluster = NULL` (default value), and `model` is provided, the cluster in `model`, if any, is used instead. If this cluster is NULL, then the function uses `n.cores` instead. The function does not stop a provided cluster, so it should be stopped with `parallel::stopCluster()` afterwards. The cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the `model` argument, or using the `%>%` pipe. Default: NULL

**Value**

The input model with new data in its "importance" slot. The new importance scores are included in the data frame `model$importance$per.variable`, under the column names "importance.cv" (median contribution to transferability over spatial cross-validation repetitions), "importance.cv.mad" (median absolute deviation of the performance scores over spatial cross-validation repetitions), "importance.cv.percent" ("importance.cv" expressed as a percent, taking the full model’s performance as baseline), and "importance.cv.mad" (median absolute deviation of "importance.cv"). The plot is stored as "cv.per.variable.plot".

**Examples**

```r
if(interactive()){

    #loading example data
data(plant_richness_df)
data(distance_matrix)

    xy <- plant_richness_df[, c("x", "y")]

    #fitting random forest model
    rf.model <- rf(
        data = plant_richness_df,
        dependent.variable.name = "richness_species_vascular",
        predictor.variable.names = colnames(plant_richness_df)[5:21],
        distance.matrix = distance_matrix,
        distance.thresholds = 0,
        n.cores = 1,
        verbose = FALSE
    )
}
```
rf_repeat

#computing predictor contribution to model transferability
rf.model <- rf_importance(rf.model)

rf_repeat

Fits several random forest models on the same data

Description

Fits several random forest models on the same data in order to capture the effect of the algorithm’s stochasticity on the variable importance scores, predictions, residuals, and performance measures. The function relies on the median to aggregate performance and importance values across repetitions. It is recommended to use it after a model is fitted (rf() or rf_spatial()), tuned (rf_tuning()), and/or evaluated (rf_evaluate()). This function is designed to be used after fitting a model with rf() or rf_spatial(), tuning it with rf_tuning() and evaluating it with rf_evaluate().

Usage

rf_repeat(
  model = NULL,
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  distance.matrix = NULL,
  distance.thresholds = NULL,
  xy = NULL,
  ranger.arguments = NULL,
  scaled.importance = FALSE,
  repetitions = 10,
  keep.models = TRUE,
  seed = 1,
  verbose = TRUE,
  n.cores = parallel::detectCores() - 1,
  cluster = NULL
)

Arguments

model A model fitted with rf(). If provided, the data and ranger arguments are taken directly from the model definition (stored in model$ranger.arguments). Default: NULL
data Data frame with a response variable and a set of predictors. Default: NULL
dependent.variable.name
Character string with the name of the response variable. Must be in the column names of data. If the dependent variable is binary with values 1 and 0, the argument case.weights of ranger is populated by the function case_weights(). Default: NULL

predictor.variable.names
Character vector with the names of the predictive variables. Every element of this vector must be in the column names of data. Default: NULL

distance.matrix
Squared matrix with the distances among the records in data. The number of rows of distance.matrix and data must be the same. If not provided, the computation of the Moran’s I of the residuals is omitted. Default: NULL

distance.thresholds
Numeric vector with neighborhood distances. All distances in the distance matrix below each value in distance.thresholds are set to 0 for the computation of Moran’s I. If NULL, it defaults to seq(0, max(distance.matrix), length.out = 4). Default: NULL

xy
(optional) Data frame or matrix with two columns containing coordinates and named "x" and "y". It is not used by this function, but it is stored in the slot ranger.arguments$xy of the model, so it can be used by rf_evaluate() and rf_tuning(). Default: NULL

ranger.arguments
Named list with ranger arguments (other arguments of this function can also go here). All ranger arguments are set to their default values except for ‘importance’, that is set to ’permutation’ rather than ‘none’. Please, consult the help file of ranger if you are not familiar with the arguments of this function.
scaled.importance
Logical. If TRUE, and ‘importance = “permutation”, the function scales ’data’ with scale and fits a new model to compute scaled variable importance scores. Default: FALSE

repetitions
Integer, number of random forest models to fit. Default: 10

keep.models
Logical, if TRUE, the fitted models are returned in the models slot. Set to FALSE if the accumulation of models is creating issues with the RAM memory available. Default: TRUE.

seed
Integer, random seed to facilitate reproducibility. If set to a given number, the results of the function are always the same. Default: 1.

verbose
Logical, if TRUE, messages and plots generated during the execution of the function are displayed. Default: TRUE

n.cores
Integer, number of cores to use for parallel execution. Creates a socket cluster with parallel::makeCluster(), runs operations in parallel with foreach and %dopar%, and stops the cluster with parallel::clusterStop() when the job is done. Default: parallel::detectCores() - 1

cluster
A cluster definition generated with parallel::makeCluster(). If provided, overrides n.cores. When cluster = NULL (default value), and model is provided, the cluster in model, if any, is used instead. If this cluster is NULL, then the function uses n.cores instead. The function does not stop a provided cluster, so it should be stopped with parallel::stopCluster() afterwards. The
cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the model argument, or using the %>% pipe. Default: NULL

Value

A ranger model with several new slots:

- `ranger.arguments`: Stores the values of the arguments used to fit the ranger model.
- `importance`: A list containing a data frame with the predictors ordered by their importance, a ggplot showing the importance values, and local importance scores.
- `pseudo.r.squared`: computed as the correlation between the observations and the predictions.
- `residuals`: residuals, normality test of the residuals computed with `residuals_test()`, and spatial autocorrelation of the residuals computed with `moran_multithreshold()`.

Examples

```r
if(interactive()){
  #loading example data
data(plant_richness_df)
data(distance_matrix)

  #fitting 5 random forest models
  out <- rf_repeat(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    repetitions = 5,
    n.cores = 1
  )

  #data frame with ordered variable importance
  out$importance$per.variable

  #per repetition
  out$importance$per.repetition

  #variable importance plot
  out$importance$per.repetition.plot

  #performance
  out$performance

  #spatial correlation of the residuals for different distance thresholds
}
out$spatial.correlation.residuals$per.distance

#plot of the Moran’s I of the residuals for different distance thresholds
out$spatial.correlation.residuals$plot

#using a model as an input for rf_repeat()
rf.model <- rf(
  data = plant_richness_df,
  dependent.variable.name = "richness_species_vascular",
  predictor.variable.names = colnames(plant_richness_df)[8:21],
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  n.cores = 1
)

#repeating the model 5 times
rf.repeat <- rf_repeat(
  model = rf.model,
  n.cores = 1
)

rf.repeat$performance
rf.repeat$importance$per.repetition.plot

---

**rf_spatial**

### Fits spatial random forest models

**Description**

Fits spatial random forest models using different methods to generate, rank, and select spatial predictors acting as proxies of spatial processes not considered by the non-spatial predictors. The end goal is providing the model with information about the spatial structure of the data to minimize the spatial correlation (Moran’s I) of the model residuals and generate honest variable importance scores.

**Usage**

```r
rf_spatial(
  model = NULL,
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  distance.matrix = NULL,
  distance.thresholds = NULL,
  xy = NULL,
  ranger.arguments = NULL,
```
scaled.importance = TRUE,
method = c("mem.moran.sequential", "mem.effect.sequential", "mem.effectrecursive",
  "hengl", "hengl.moran.sequential", "hengl.effect.sequential",
  "hengl.effectrecursive", "pca.moran.sequential", "pca.effect.sequential",
  "pca.effectrecursive"),
max.spatial.predictors = NULL,
weight.r.squared = NULL,
weight.penalization.n.predictors = NULL,
seed = 1,
verbose = TRUE,
n.cores = parallel::detectCores() - 1,
cluster = NULL
)

Arguments

model
A model fitted with \textit{rf()}. If used, the arguments \textit{data}, \textit{dependent.variable.name},
\textit{predictor.variable.names}, \textit{distance.matrix}, \textit{distance.thresholds}, \textit{ranger.arguments},
and \textit{scaled.importance} are taken directly from the model definition. Default: NULL

data
Data frame with a response variable and a set of predictors. Default: NULL

dependent.variable.name
Character string with the name of the response variable. Must be in the column
names of \textit{data}. If the dependent variable is binary with values 1 and 0, the argu-
ment \textit{case.weights} of \textit{ranger} is populated by the function \textit{case_weights()}. Default: NULL

predictor.variable.names
Character vector with the names of the predictive variables. Every element of
this vector must be in the column names of \textit{data}. Default: NULL

distance.matrix
Squared matrix with the distances among the records in \textit{data}. The number of
rows of \textit{distance.matrix} and \textit{data} must be the same. If not provided, the
computation of the Moran’s I of the residuals is omitted. Default: NULL

distance.thresholds
Numeric vector with distances in the same units as \textit{distance.matrix} Distances
below each distance threshold are set to 0 on separated copies of the distance
matrix to compute Moran’s I at different neighborhood distances. If NULL, it
defaults to seq(0, max(distance.matrix)/2, length.out = 4) (defined by
default_distance_thresholds()). Default: NULL

xy
(optional) Data frame or matrix with two columns containing coordinates and
named ”x” and ”y”. It is not used by this function, but it is stored in the slot
\textit{ranger.arguments}$xy$ of the model, so it can be used by \textit{rf_evaluate()} and
\textit{rf_tuning()}. Default: NULL

ranger.arguments
Named list with \textit{ranger} arguments (other arguments of this function can also go
here). All \textit{ranger} arguments are set to their default values except for ‘import-
ance’, that is set to ‘permutation’ rather than ‘none’. Please, consult the help
file of \textit{ranger} if you are not familiar with the arguments of this function.
scaled.importance

Logical. If TRUE, and 'importance = "permutation"', the function scales 'data' with scale and fits a new model to compute scaled variable importance scores. Default: TRUE

method

Character, method to build, rank, and select spatial predictors. One of:

• "hengl"
• "hengl.moran.sequential" (experimental)
• "hengl.effect.sequential" (experimental)
• "hengl.effect.recursive" (experimental)
• "pca.moran.sequential" (experimental)
• "pca.effect.sequential" (experimental)
• "pca.effect.recursive" (experimental)
• "mem.moran.sequential"
• "mem.effect.sequential"
• "mem.effect.recursive"

max.spatial.predictors

Integer, maximum number of spatial predictors to generate. Useful when memory problems arise due to a large number of spatial predictors, Default: NULL

weight.r.squared

Numeric between 0 and 1, weight of R-squared in the selection of spatial components. See Details, Default: NULL

weight.penalization.n.predictors

Numeric between 0 and 1, weight of the penalization for adding an increasing number of spatial predictors during selection. Default: NULL

seed

Integer, random seed to facilitate reproducibility. Default: 1.

verbose

Logical. If TRUE, messages and plots generated during the execution of the function are displayed, Default: TRUE

n.cores

Integer, number of cores to use for parallel execution. Creates a socket cluster with parallel::makeCluster(), runs operations in parallel with foreach and %dopar% and stops the cluster with parallel::clusterStop() when the job is done. Default: parallel::detectCores() - 1

cluster

A cluster definition generated with parallel::makeCluster(). If provided, overrides n.cores. When cluster = NULL (default value), and model is provided, the cluster in model, if any, is used instead. If this cluster is NULL, then the function uses n.cores instead. The function does not stop a provided cluster, so it should be stopped with parallel::stopCluster() afterwards. The cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the model argument, or using the %>% pipe. Default: NULL

Details

The function uses three different methods to generate spatial predictors ("hengl", "pca", and "mem"), two methods to rank them in order to define in what order they are introduced in the model ("effect" and "moran"), and two methods to select the spatial predictors that minimize the spatial correlation.
of the model residuals ("sequential" and "recursive"). All method names but "hengl" (that uses the complete distance matrix as predictors in the spatial model) are named by combining a method to generate the spatial predictors, a method to rank them, and a method to select them, separated by a point. Examples are "mem.moran.sequential" or "mem.effect.recursive". All combinations are not possible, since the ranking method "moran" cannot be used with the selection method "recursive" (because the logics behind them are very different, see below). Methods to generate spatial predictors:

- "hengl": named after the method RFsp presented in the paper "Random forest as a generic framework for predictive modeling of spatial and spatio-temporal variables", by Hengl et al. (2018), where the authors propose to use the distance matrix among records as predictors in spatial random forest models (RFsp method). In this function, all methods starting with "hengl" use either the complete distance matrix, or select columns of the distance matrix as spatial predictors.

- "mem": Generates Moran’s Eigenvector Maps, that is, the eigenvectors of the double-centered weights of the distance matrix. The method is described in "Spatial modelling: a comprehensive framework for principal coordinate analysis of neighbour matrices (PCNM)", by Dray et al. (2006), and "Statistical methods for temporal and space–time analysis of community composition data", by Legendre and Gauthier (2014).

- "pca": Computes spatial predictors from the principal component analysis of a weighted distance matrix (see `weights_from_distance_matrix()`). This is an experimental method, use with caution.

Methods to rank spatial predictors (see `rank_spatial_predictors()`):

- "moran": Computes the Moran’s I of each spatial predictor, selects the ones with positive values, and ranks them from higher to lower Moran’s I.

- "effect": If a given non-spatial random forest model is defined as $y = p_1 + \ldots + p_n$, being $p_1 + \ldots + p_n$ the set of predictors, for every spatial predictor generated ($spX$) a spatial model $y = p_1 + \ldots + p_n + spX$ is fitted, and the Moran’s I of its residuals is computed. The spatial predictors are then ranked by how much they help to reduce spatial autocorrelation between the non-spatial and the spatial model.

Methods to select spatial predictors:

- "sequential" (see `select_spatial_predictors_sequential()`): The spatial predictors are added one by one in the order they were ranked, and once all spatial predictors are introduced, the best first n predictors are selected. This method is similar to the one employed in the MEM methodology (Moran’s Eigenvector Maps) described in the paper "Spatial modelling: a comprehensive framework for principal coordinate analysis of neighbour matrices (PCNM)", by Dray et al. (2006), and "Statistical methods for temporal and space–time analysis of community composition data", by Legendre and Gauthier (2014). This method generally introduces tens of predictors into the model, but usually offers good results.

- "recursive" (see `select_spatial_predictors_recursive()`): This method tries to find the smallest combination of spatial predictors that reduce the spatial correlation of the model’s residuals the most. The algorithm goes as follows: 1. The first ranked spatial predictor is introduced into the model; 2. the remaining predictors are ranked again using the "effect" method, using the model in 1. as reference. The first spatial predictor in the resulting ranking is then introduced into the model, and the steps 1. and 2. are repeated until spatial predictors
stop having an effect in reducing the Moran’s I of the model residuals. This method takes longer to compute, but generates smaller sets of spatial predictors. This is an experimental method, use with caution.

Once ranking procedure is completed, an algorithm is used to select the minimal subset of spatial predictors that reduce the most the Moran’s I of the residuals: for each new spatial predictor introduced in the model, the Moran’s I of the residuals, it’s p-value, a binary version of the p-value (0 if < 0.05 and 1 if >= 0.05), the R-squared of the model, and a penalization linear with the number of spatial predictors introduced (computed as (1 / total spatial predictors) * introduced spatial predictors) are rescaled between 0 and 1. Then, the optimization criteria is computed as max(1 - Moran’s I, p-value binary) + (weight.r.squared * R-squared) - (weight.penalization.n.predictors * penalization). The predictors from the first one to the one with the highest optimization criteria are then selected as the best ones in reducing the spatial correlation of the model residuals, and used along with data to fit the final spatial model.

Value

A ranger model with several new slots:

- ranger.arguments: Values of the arguments used to fit the ranger model.
- importance: A list containing the vector of variable importance as originally returned by ranger (scaled or not depending on the value of 'scaled.importance'), a data frame with the predictors ordered by their importance, and a ggplot showing the importance values.
- performance: With the out-of-bag R squared, pseudo R squared, RMSE and NRMSE of the model.
- residuals: residuals, normality test of the residuals computed with residuals_test(), and spatial autocorrelation of the residuals computed with moran_multithreshold().
- spatial: A list with four slots:
  - method: Character, method used to generate, rank, and select spatial predictors.
  - names: Character vector with the names of the selected spatial predictors. Not returned if the method is "hengl".
  - optimization: Criteria used to select the spatial predictors. Not returned if the method is "hengl".
  - plot: Plot of the criteria used to select the spatial predictors. Not returned if the method is "hengl".

Examples

```r
if(interactive()){
  #loading example data
data(distance_matrix)
data(plant_richness_df)

  #names of the response and predictors
dependent.variable.name <- "richness_species_vascular"
predictor.variable.names <- colnames(plant_richness_df)[5:21]

  #hengl
model <- rf.spatial(
```
rf_tuning

Tuning of random forest hyperparameters via spatial cross-validation

Description

Finds the optimal set of random forest hyperparameters \texttt{num.trees}, \texttt{mtry}, and \texttt{min.node.size} via grid search by maximizing the model’s R squared, or AUC, if the response variable is binomial, via spatial cross-validation performed with \texttt{rf_evaluate()}. 
Usage

```r
erf_tuning(
    model = NULL,
    num.trees = NULL,
    mtry = NULL,
    min.node.size = NULL,
    xy = NULL,
    repetitions = 30,
    training.fraction = 0.75,
    seed = 1,
    verbose = TRUE,
    n.cores = parallel::detectCores() - 1,
    cluster = NULL
)
```

Arguments

- **model**: A model fitted with `rf()`. If provided, the training data is taken directly from the model definition (stored in `model$ranger.arguments`). Default: `NULL`.
- **num.trees**: Numeric integer vector with the number of trees to fit on each model repetition. Default: `c(500, 1000, 2000)`.
- **mtry**: Numeric integer vector, number of predictors to randomly select from the complete pool of predictors on each tree split. Default: `floor(seq(1, length(predictor.variable.names), length.out = 4))`.
- **min.node.size**: Numeric integer, minimal number of cases in a terminal node. Default: `c(5, 10, 20, 40)`.
- **xy**: Data frame or matrix with two columns containing coordinates and named "x" and "y". If `NULL`, the function will throw an error. Default: `NULL`.
- **repetitions**: Integer, number of independent spatial folds to use during the cross-validation. Default: `30`.
- **training.fraction**: Proportion between 0.2 and 0.9 indicating the number of records to be used in model training. Default: `0.75`.
- **seed**: Integer, random seed to facilitate reproducibility. If set to a given number, the results of the function are always the same. Default: `1`.
- **verbose**: Logical. If `TRUE`, messages and plots generated during the execution of the function are displayed. Default: `TRUE`.
- **n.cores**: Integer, number of cores to use for parallel execution. Creates a socket cluster with `parallel::makeCluster()`, runs operations in parallel with `foreach` and `%dopar%`, and stops the cluster with `parallel::clusterStop()` when the job is done. Default: `parallel::detectCores() - 1`.
- **cluster**: A cluster definition generated with `parallel::makeCluster()`. If provided, overrides n.cores. When `cluster = NULL` (default value), and model is provided, the cluster in model, if any, is used instead. If this cluster is `NULL`, then the function uses n.cores instead. The function does not stop a provided cluster, so it should be stopped with `parallel::stopCluster()` afterwards. The
cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the model argument, or using the %>% pipe. Default: NULL

Value

A model with a new slot named tuning, with a data frame with the results of the tuning analysis.

See Also

rf_evaluate()

Examples

if(interactive()){  
  #loading example data  
data(plant_richness_df)  
data(distance_matrix)

  #fitting model to tune  
  out <- rf(  
    data = plant_richness_df,  
    dependent.variable.name = "richness_species_vascular",  
    predictor.variable.names = colnames(plant_richness_df)[5:21],  
    distance.matrix = distance_matrix,  
    distance.thresholds = 0,  
    n.cores = 1  
  )

  #model tuning  
tuning <- rf_tuning(  
    model = out,  
    num.trees = c(100, 500),  
    mtry = c(2, 8),  
    min.node.size = c(5, 10),  
    xy = plant_richness_df[, c("x", "y")],  
    n.cores = 1  
  )
}

root_mean_squared_error

RMSE and normalized RMSE

Description

Computes the rmse or normalized rmse (nrmse) between two numeric vectors of the same length representing observations and model predictions.
root_mean_squared_error

Usage

root_mean_squared_error(
  o,
  p,
  normalization = c("rmse", "all", "mean", "sd", "maxmin", "iq")
)

Arguments

  o        Numeric vector with observations, must have the same length as p.
  p        Numeric vector with predictions, must have the same length as o.
  normalization character, normalization method, Default: "rmse" (see Details).

Details

The normalization methods go as follows:

- "rmse": RMSE with no normalization.
- "mean": RMSE divided by the mean of the observations (rmse/mean(o)).
- "sd": RMSE divided by the standard deviation of the observations (rmse/sd(o)).
- "maxmin": RMSE divided by the range of the observations (rmse/(max(o) - min(o))).
- "iq": RMSE divided by the interquartile range of the observations (rmse/(quantile(o, 0.75) - quantile(o, 0.25)))

Value

Named numeric vector with either one or 5 values, as selected by the user.

Examples

if(interactive()){
  root_mean_squared_error(
    o = runif(10),
    p = runif(10)
  )
}
select_spatial_predictors_recursive

Finds optimal combinations of spatial predictors

Description

Selects spatial predictors following these steps:

1. Gets the spatial predictors ranked by `rank_spatial_predictors()` and fits a model of the form $y \sim \text{predictors} + \text{best_spatial_predictor}_1$. The Moran’s I of the residuals of this model is used as reference value for the next step.

2. The remaining spatial predictors are introduced again into `rank_spatial_predictors()`, and the spatial predictor with the highest ranking is introduced in a new model of the form $y \sim \text{predictors} + \text{best_spatial_predictor}_1 + \text{best_spatial_predictor}_2$.

3. Steps 1 and 2 are repeated until the Moran’s I doesn’t improve for a number of repetitions equal to the 20 percent of the total number of spatial predictors introduced in the function.

This method allows to select the smallest set of spatial predictors that have the largest joint effect in reducing the spatial correlation of the model residuals, while maintaining the model’s R-squared as high as possible. As a consequence of running `rank_spatial_predictors()` on each iteration, this method includes in the final model less spatial predictors than the sequential method implemented in `select_spatial_predictors_sequential()` would do, while minimizing spatial correlation and maximizing the R-squared of the model as much as possible.

Usage

```r
select_spatial_predictors_recursive(
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  distance.matrix = NULL,
  distance.thresholds = NULL,
  ranger.arguments = NULL,
  spatial.predictors.df = NULL,
  spatial.predictors.ranking = NULL,
  weight.r.squared = 0.25,
  weight.penalization.n.predictors = 0,
  n.cores = parallel::detectCores() - 1,
  cluster = NULL
)
```

Arguments

data Data frame with a response variable and a set of predictors. Default: NULL

dependent.variable.name Character string with the name of the response variable. Must be in the column names of data. Default: NULL
predictor.variable.names
Character vector with the names of the predictive variables. Every element of
this vector must be in the column names of data. Default: NULL
distance.matrix
Squared matrix with the distances among the records in data. The number of
rows of distance.matrix and data must be the same. If not provided, the
computation of the Moran’s I of the residuals is omitted. Default: NULL
distance.thresholds
Numeric vector with neighborhood distances. All distances in the distance ma-
trix below each value in distance.thresholds are set to 0 for the computation
of Moran’s I. If NULL, it defaults to seq(0, max(distance.matrix), length.out = 4).
Default: NULL
ranger.arguments
Named list with ranger arguments (other arguments of this function can also go
here). All ranger arguments are set to their default values except for ‘import-
ance’, that is set to ‘permutation’ rather than ‘none’. Please, consult the help
file of ranger if you are not familiar with the arguments of this function.
spatial.predictors.df
Data frame of spatial predictors.
spatial.predictors.ranking
Ranking of predictors returned by rank_spatial_predictors().
weight.r.squared
Numeric between 0 and 1, weight of R-squared in the optimization index. De-
fault: 0.25
weight.penalization.n.predictors
Numeric between 0 and 1, weight of the penalization for the number of spatial
predictors added in the optimization index. Default: 0
n.cores
Integer, number of cores to use. Default: parallel::detectCores() - 1
cluster
A cluster definition generated by parallel::makeCluster(). Default: NULL

Details
The algorithm works as follows. If the function rank_spatial_predictors() returns 10 ranked
spatial predictors (sp1 to sp10, being sp7 the best one), select_spatial_predictors_recursive() is
going to first fit the model y ~ predictors + sp7. Then, the spatial predictors sp2 to sp9 are
again ranked with rank_spatial_predictors() using the model y ~ predictors + sp7 as refer-
ence (at this stage, some of the spatial predictors might be dropped due to lack of effect). When
the new ranking of spatial predictors is ready (let’s say they are sp5, sp3, and sp4), the best one
(sp5) is included in the model y ~ predictors + sp7 + sp5, and the remaining ones go again to
rank_spatial_predictors() to repeat the process until spatial predictors are depleted.

Value
A list with two slots: optimization, a data frame with the index of the spatial predictor added on
each iteration, the spatial correlation of the model residuals, and the R-squared of the model, and
best.spatial.predictors, that is a character vector with the names of the spatial predictors that
minimize the Moran’s I of the residuals and maximize the R-squared of the model.
Examples

if(interactive()){

  #loading example data
  data(distance_matrix)
  data(plant_richness_df)

  #response and predictor names
  dependent.variable.name = "richness_species_vascular"
  predictor.variable.names = colnames(plant_richness_df)[5:21]

  #non-spatial model
  model <- rf(
    data = plant_richness_df,
    dependent.variable.name = dependent.variable.name,
    predictor.variable.names = predictor.variable.names,
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1
  )

  #preparing spatial predictors
  spatial.predictors <- mem_multithreshold(
    distance.matrix = distance_matrix,
    distance.thresholds = 0
  )

  #ranking spatial predictors
  spatial.predictors.ranking <- rank_spatial_predictors(
    data = plant_richness_df,
    dependent.variable.name = dependent.variable.name,
    predictor.variable.names = predictor.variable.names,
    spatial.predictors.df = spatial.predictors,
    ranking.method = "moran",
    reference.moran.i = model$spatial.correlation.residuals$max.moran,
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    n.cores = 1
  )

  #selecting the best subset of predictors
  selection <- select_spatial_predictors_recursive(
    data = plant_richness_df,
    dependent.variable.name = dependent.variable.name,
    predictor.variable.names = predictor.variable.names,
    distance.matrix = distance_matrix,
    distance.thresholds = 0,
    spatial.predictors.df = spatial.predictors,
    spatial.predictors.ranking = spatial.predictors.ranking,
    n.cores = 1
  )
}
select.spatial.predictors.sequential

Sequential introduction of spatial predictors into a model

Description

Selects spatial predictors by adding them sequentially into a model while monitoring the Moran’s I of the model residuals and the model’s R-squared. Once all the available spatial predictors have been added to the model, the function identifies the first \( n \) predictors that minimize the spatial correlation of the residuals and maximize R-squared, and returns the names of the selected spatial predictors and a data frame with the selection criteria.

Usage

```r
select.spatial.predictors.sequential(
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
  distance.matrix = NULL,
  distance.thresholds = NULL,
  ranger.arguments = NULL,
  spatial.predictors.df = NULL,
  spatial.predictors.ranking = NULL,
  weight.r.squared = 0.75,
  weight.penalization.n.predictors = 0.25,
  verbose = FALSE,
  n.cores = parallel::detectCores() - 1,
  cluster = NULL
)
```

Arguments

- **data**: Data frame with a response variable and a set of predictors. Default: NULL
- **dependent.variable.name**: Character string with the name of the response variable. Must be in the column names of data. Default: NULL
- **predictor.variable.names**: Character vector with the names of the predictive variables. Every element of this vector must be in the column names of data. Default: NULL
select.spatial.predictors_sequential

distance.matrix
Squared matrix with the distances among the records in data. The number of rows of distance.matrix and data must be the same. If not provided, the computation of the Moran's I of the residuals is omitted. Default: NULL

distance.thresholds
Numeric vector with neighborhood distances. All distances in the distance matrix below each value in distance.thresholds are set to 0 for the computation of Moran's I. If NULL, it defaults to seq(0, max(distance.matrix), length.out = 4). Default: NULL

ranger.arguments
Named list with ranger arguments (other arguments of this function can also go here). All ranger arguments are set to their default values except for 'importance', that is set to 'permutation' rather than 'none'. Please, consult the help file of ranger if you are not familiar with the arguments of this function.

spatial.predictors.df
Data frame of spatial predictors.

spatial.predictors.ranking
Ranking of the spatial predictors returned by rank.spatial.predictors().

weight.r.squared
Numeric between 0 and 1, weight of R-squared in the optimization index. Default: 0.75

weight.penalization.n.predictors
Numeric between 0 and 1, weight of the penalization for the number of spatial predictors added in the optimization index. Default: 0.25

verbose
Logical, if TRUE, messages and plots generated during the execution of the function are displayed, Default: FALSE

n.cores
Integer, number of cores to use. Default: parallel::detectCores() - 1

cluster
A cluster definition generated by parallel::makeCluster(). Default: NULL

Details
The algorithm works as follows: If the function rank.spatial.predictors returns 10 spatial predictors (sp1 to sp10, ordered from best to worst), select.spatial.predictors_sequential is going to fit the models y ~ predictors + sp1, y ~ predictors + sp1 + sp2, until all spatial predictors are used in y ~ predictors + sp1 ... sp10. The model with lower Moran's I of the residuals and higher R-squared (computed on the out-of-bag data) is selected, and its spatial predictors returned.

Value
A list with two slots: optimization, a data frame with the index of the spatial predictor added on each iteration, the spatial correlation of the model residuals, and the R-squared of the model, and best.spatial.predictors, that is a character vector with the names of the spatial predictors that minimize the Moran's I of the residuals and maximize the R-squared of the model.

Examples
if(interactive()){
#loading example data
data(distance_matrix)
data(plant_richness_df)

#common arguments
dependent.variable.name = "richness_species_vascular"
predictor.variable.names = colnames(plant_richness_df)[5:21]

#non-spatial model
model <- rf(
  data = plant_richness_df,
  dependent.variable.name = dependent.variable.name,
  predictor.variable.names = predictor.variable.names,
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  n.cores = 1
)

#preparing spatial predictors
spatial.predictors <- mem_multithreshold(
  distance.matrix = distance_matrix,
  distance.thresholds = 0
)

#ranking spatial predictors by their Moran's I (faster option)
spatial.predictors.ranking <- rank_spatial_predictors(
  ranking.method = "moran",
  spatial.predictors.df = spatial.predictors,
  reference.moran.i = model$spatial.correlation.residuals$max.moran,
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  n.cores = 1
)

#selecting the best subset of predictors
selection <- select_spatial_predictors_sequential(
  data = plant_richness_df,
  dependent.variable.name = dependent.variable.name,
  predictor.variable.names = predictor.variable.names,
  distance.matrix = distance_matrix,
  distance.thresholds = 0,
  spatial.predictors.df = spatial.predictors,
  spatial.predictors.ranking = spatial.predictors.ranking,
  n.cores = 1
)

selection$optimization
selection$best.spatial.predictors
plot_optimization(selection$optimization)
**standard_error**

**Standard error of the mean of a numeric vector**

**Description**

Computes the standard error of the mean of a numeric vector as \( \text{round}\left(\sqrt{\text{var}(x)/\text{length}(x)}, 3\right) \)

**Usage**

```r
standard_error(x)
```

**Arguments**

- `x` A numeric vector.

**Details**

The function removes `NA` values before computing the standard error, and rounds the result to 3 decimal places.

**Value**

A numeric value.

**Examples**

```r
if(interactive()){
  standard_error(runif(10))
}
```

---

**statistical_mode**

**Statistical mode of a vector**

**Description**

Computes the mode of a numeric or character vector

**Usage**

```r
statistical_mode(x)
```

**Arguments**

- `x` Numeric or character vector.
the_feature_engineer

Value

Statistical mode of x.

Examples

```r
if(interactive()){
  statistical_mode(c(10, 9, 10, 8))
}
```

Description

Suggests candidate variable interactions and composite features able to improve predictive accuracy over data not used to train the model via spatial cross-validation with `rf_evaluate()`. For a pair of predictors a and b, interactions are built via multiplication (a * b), while composite features are built by extracting the first factor of a principal component analysis performed with `pca()`, after rescaling a and b between 1 and 100. Interactions and composite features are named `a..x..b` and `a..pca..b` respectively.

Candidate variables a and b are selected from those predictors in `predictor.variable.names` with a variable importance above `importance.threshold` (set by default to the median of the importance scores).

For each interaction and composite feature, a model including all the predictors plus the interaction or composite feature is fitted, and it's R squared (or AUC if the response is binary) computed via spatial cross-validation (see `rf_evaluate()`) is compared with the R squared of the model without interactions or composite features.

From all the potential interactions screened, only those with a positive increase in R squared (or AUC when the response is binomial) of the model, a variable importance above the median, and a maximum correlation among themselves and with the predictors in `predictor.variable.names` not higher than `cor.threshold` (set to 0.5 by default) are selected. Such a restrictive set of rules ensures that the selected interactions can be used right away for modeling purposes without increasing model complexity unnecessarily. However, the suggested variable interactions might not make sense from a domain expertise standpoint, so please, examine them with care.

The function returns the criteria used to select the interactions, and the data required to use these interactions a model.

Usage

```r
the_feature_engineer(
  data = NULL,
  dependent.variable.name = NULL,
  predictor.variable.names = NULL,
)```
xy = NULL,
ranger.arguments = NULL,
repetitions = 30,
training.fraction = 0.75,
importance.threshold = 0.75,
cor.threshold = 0.75,
point.color = viridis::viridis(100, option = "F", alpha = 0.8),
seed = NULL,
verbose = TRUE,
n.cores = parallel::detectCores() - 1,
cluster = NULL
)

Arguments

data
Data frame with a response variable and a set of predictors. Default: NULL

dependent.variable.name
Character string with the name of the response variable. Must be in the column
names of data. If the dependent variable is binary with values 1 and 0, the argu-
ment case.weights of ranger is populated by the function case_weights().
Default: NULL

predictor.variable.names
Character vector with the names of the predictive variables, or object of class
"variable_selection" produced by auto_vif() and/or auto_cor(). Every
element of this vector must be in the column names of data. Default: NULL

xy
Data frame or matrix with two columns containing coordinates and named "x"
and "y". If not provided, the comparison between models with and without
variable interactions is not done.

ranger.arguments
Named list with ranger arguments (other arguments of this function can also go
here). All ranger arguments are set to their default values except for 'import-
ance', that is set to 'permutation' rather than 'none'. Please, consult the help
file of ranger if you are not familiar with the arguments of this function.

repetitions
Integer, number of spatial folds to use during cross-validation. Must be lower
than the total number of rows available in the model’s data. Default: 30

training.fraction
Proportion between 0.5 and 0.9 indicating the proportion of records to be used
as training set during spatial cross-validation. Default: 0.75

importance.threshold
Numeric between 0 and 1, quantile of variable importance scores over which to
select individual predictors to explore interactions among them. Larger values
reduce the number of potential interactions explored. Default: 0.75

cor.threshold
Numeric, maximum Pearson correlation between any pair of the selected inter-
actions, and between any interaction and the predictors in predictor.variable.names.
Default: 0.75

point.color
Colors of the plotted points. Can be a single color name (e.g. "red4"), a character
vector with hexadecimal codes (e.g. "#440154FF" ",#21908CFF" ",#E725FF")
or function generating a palette (e.g. `viridis::viridis(100)`). Default: `viridis::viridis(100, option = "F", alpha = 0.8)`

**seed**
Integer, random seed to facilitate reproducibility. If set to a given number, the results of the function are always the same. Default: NULL

**verbose**
Logical. If TRUE, messages and plots generated during the execution of the function are displayed. Default: TRUE

**n.cores**
Integer, number of cores to use for parallel execution. Creates a socket cluster with `parallel::makeCluster()`, runs operations in parallel with foreach and `%dopar%`, and stops the cluster with `parallel::clusterStop()` when the job is done. Default: `parallel::detectCores() - 1`

**cluster**
A cluster definition generated with `parallel::makeCluster()`. If provided, overrides n.cores. When `cluster = NULL` (default value), and `model` is provided, the cluster in `model`, if any, is used instead. If this cluster is NULL, then the function uses n.cores instead. The function does not stop a provided cluster, so it should be stopped with `parallel::stopCluster()` afterwards. The cluster definition is stored in the output list under the name "cluster" so it can be passed to other functions via the `model` argument, or using the `%>%` pipe. Default: NULL

**Value**
A list with seven slots:

- **screening**: Data frame with selection scores of all the interactions considered.
- **selected**: Data frame with selection scores of the selected interactions.
- **df**: Data frame with the computed interactions.
- **plot**: List of plots of the selected interactions versus the response variable. The output list can be plotted all at once with `patchwork::wrap_plots(p)` or `cowplot::plot_grid(plotlist = p)`, or one by one by extracting each plot from the list.
- **data**: Data frame with the response variable, the predictors, and the selected interactions, ready to be used as data argument in the package functions.
- **dependent.variable.name**: Character, name of the response.
- **predictor.variable.names**: Character vector with the names of the predictors and the selected interactions.

**Examples**

```r
if(interactive()){
  #load example data
data(plant_richness_df)

  new.features <- the_feature_engineer(
    data = plant_richness_df,
    dependent.variable.name = "richness_species_vascular",
    predictor.variable.names = colnames(plant_richness_df)[5:21],
    n.cores = 1,
```
thinning

   verbose = TRUE

new.features$screening
new.features$selected
new.features$columns

thinning

Applies thinning to pairs of coordinates

Description

Resamples a set of points with x and y coordinates to impose a minimum distance among nearby points.

Usage

thinning(xy, minimum.distance = NULL)

Arguments

xy A data frame with columns named "x" and "y" representing geographic coordinates.
minimum.distance Numeric, minimum distance to be set between nearby points, in the same units as the coordinates of xy.

Details

Generally used to remove redundant points that could produce pseudo-replication, and to limit sampling bias by disaggregating clusters of points.

Value

A data frame with the same columns as xy with points separated by the defined minimum distance.

See Also

thinning_til_n()
Examples

```r
if(interactive()){

  # load example data
data(plant_richness_df)

  # thinning to points separated by 5 degrees
  plant_richness.thin <- thinning(
    x = plant_richness_df,
    minimum.distance = 5 # points separated by at least 5 degrees
  )

  plant_richness.thin

}
```

---

**thinning_til_n**  
Applies thinning to pairs of coordinates until reaching a given n

### Description

Resamples a set of points with x and y coordinates by increasing the distance step by step until a given sample size is obtained.

### Usage

```r
thinning_til_n(xy, n = 30, distance.step = NULL)
```

### Arguments

- `xy`  
  A data frame with columns named "x" and "y" representing geographic coordinates. Default: NULL

- `n`  
  Integer, number of samples to obtain. Must be lower than `nrow(xy)`. Default: 30

- `distance.step`  
  Numeric, distance step used during the thinning iterations. If NULL, the one percent of the maximum distance among points in `xy` is used. Default: NULL

### Value

A data frame with the same columns as `xy` with a row number close to `n`.

### See Also

`thinning()`
Examples

if(interactive()){  
  #loading example data  
  data(plant_richness_df)  
  #thinning to ~20 records  
  plant_richness.thin <- thinning_til_n(  
    x = plant_richness_df,  
    n = 20  
  )  
  plant_richness.thin  
}

vif  

Variance Inflation Factor of a data frame

Description

Computes the variance inflation factor (VIF) of the columns in a data frame. **Warning:** variables in `preference.order` not in `colnames(x)`, and non-numeric columns are removed silently from `x` and `preference.order`. The same happens with rows having NA values (`na.omit()` is applied). The function issues a warning if zero-variance columns are found.

Usage

`vif(x)`

Arguments

`x`  
Data frame with numeric columns, typically containing a set of model predictors.

Value

A data frame with two columns having the name of the variables in `x` and their respective VIF values.

See Also

`auto_vif()`, `auto_cor()`
weights_from_distance_matrix

Transforms a distance matrix into a matrix of weights

Description
Transforms a distance matrix into weights (1/distance.matrix) normalized by the row sums. Used to compute Moran’s I values and Moran’s Eigenvector Maps. Allows to apply a threshold to the distance matrix before computing the weights.

Usage
weights_from_distance_matrix(
  distance.matrix = NULL,
  distance.threshold = 0
)

Arguments
distance.matrix
  Distance matrix. Default: NULL.
distance.threshold
  Numeric, positive, in the range of values of distance.matrix. Distances below this value in the distance matrix are set to 0., Default: 0.

Value
A weighted distance matrix.

Examples
if(interactive()){
  #loading example distance matrix
data(distance_matrix)

  #computing matrix of weights
distance_matrix.weights <- weights_from_distance_matrix(
    distance_matrix = distance_matrix


weights_from_distance_matrix

)

distance.matrix.weights

}
Index

* datasets
  distance_matrix, 10
  plant_richness_df, 36

  aes, 62, 63
  auc, 3
  auto_cor, 4
  auto_cor(), 6, 7, 48, 50, 64, 95, 99
  auto_vif, 5
  auto_vif(), 4, 5, 48, 50, 64, 95

  beowulf_cluster, 7

  case_weights, 9
  case_weights(), 48, 50, 64, 76, 79, 95

  default_distance_thresholds, 10
  default_distance_thresholds(), 79
  distance_matrix, 10, 37
  double_center_distance_matrix, 11
  double_center_distance_matrix(), 27, 28

  eigen, 27, 28

  filter_spatial_predictors, 12

  geom_abline, 62, 63
  geom_freqpoly, 62, 63
  geom_point, 47
  geom_qq_line, 62, 63
  geom_smooth, 48
  get_evaluation, 13
  get_evaluation(), 38, 54
  get_importance, 14
  get_importance(), 39, 55
  get_importance_local, 15
  get_moran, 16
  get_moran(), 57
  get_performance, 17
  get_performance(), 58
  get_predictions, 18

  get_residuals, 19
  get_response_curves, 20
  get_spatial_predictors, 21
  ggplot, 62, 63
  ggtheme, 62, 63

  huxtable, 56

  is_binary, 22

  labs, 62, 63

  make_spatial_fold, 23
  make_spatial_fold(), 25, 26
  make_spatial_folds, 25
  make_spatial_folds(), 23, 24, 68, 70, 71, 73
  makeCluster, 8
  mem, 27
  mem(), 11, 28
  mem_multithreshold, 28
  mem_multithreshold(), 11, 28, 58
  moran, 29, 31
  moran(), 16, 30, 31, 41, 44, 47
  moran_multithreshold, 30
  moran_multithreshold(), 16, 30, 41, 57, 65, 77, 82
  na.omit, 4, 6, 99

  objects_size, 32
  optimization_function, 33

  pca, 34
  pca(), 35, 94
  pca_multithreshold, 35
  pca_multithreshold(), 34, 58
  plant_richness_df, 10, 11, 36
  plot_annotation, 62, 63
  plot_evaluation, 37
  plot_evaluation(), 13, 54
  plot_importance, 39
INDEX

plot_importance(), 15, 55
plot_moran, 40
plot_moran(), 16, 44, 57
plot_optimization, 42
plot_residuals_diagnostics, 43
plot_response_curves, 45
plot_response_curves(), 21, 47
plot_response_surface, 46
plot_response_surface(), 46
plot_training_df, 48
plot_training_df_moran, 49
plot_tuning, 51
prcomp, 34
prepare_importance_spatial, 52
print.rf, 53
print_evaluation, 54
print_evaluation(), 13, 38, 53
print_importance, 55
print_importance(), 15, 39, 53
print_moran, 56
print_moran(), 16, 53
print_performance, 57
print_performance(), 18, 53, 58
quantile, 20, 45, 47
ranger, 59, 63–65, 76, 79, 88, 91, 95
rank_spatial_predictors, 58, 91
rank_spatial_predictors(), 81, 87, 88, 91
rescale_vector, 61
residuals_diagnostics, 62
residuals_test, 63
residuals_test(), 65, 77, 82
rf, 55, 59, 63
rf(), 9, 14–20, 39, 41, 44–47, 52, 53, 56, 57, 67, 70, 73, 75, 79, 84
rf_compare, 66
rf_evaluate, 69
rf_evaluate(), 13, 23, 24, 26, 37, 38, 54, 64, 67, 68, 75, 76, 79, 83, 85, 94
rf_importance, 72
rf_importance(), 39
rf_repeat, 55, 59, 75
rf_repeat(), 14–21, 39, 41, 44–47, 52, 53, 56, 57, 70, 73
rf.spatial, 55, 78
rf.spatial(), 14–22, 27, 28, 35, 39, 41, 42, 44–47, 52, 53, 56–58, 67, 70, 73, 75
rf_tuning, 83
rf_tuning(), 51, 64, 67, 75, 76, 79
root_mean_squared_error, 85
root_mean_squared_error(), 63
scale, 63, 65, 76, 80
select_spatial_predictors_recursive, 87
select_spatial_predictors_recursive(), 33, 42, 81, 88
select_spatial_predictors_sequential, 90, 91
select_spatial_predictors_sequential(), 33, 42, 81, 87
shapiro.test(), 62, 63
standard_error, 93
statistical_mode, 93
the_feature_engineer, 94
the_feature_engineer(), 65
thinning, 97
thinning(), 25, 71, 98
thinning_til_n, 98
thinning_til_n(), 25, 67, 70, 71, 73, 97
vif, 99
weights_from_distance_matrix, 100
weights_from_distance_matrix(), 11, 35, 81
wrap_plots, 41, 45, 48, 49