

# Package ‘MLFS’

April 20, 2022

**Type** Package

**Title** Machine Learning Forest Simulator

**Version** 0.4.2

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**Description** Climate-sensitive forest simulator based on the principles of machine learning. It stimulates all key processes in the forest: radial growth, height growth, mortality, crown recession, regeneration and harvesting. The method for predicting tree heights was described by Skudnik and Jevšenak (2022) <doi:10.1016/j.foreco.2022.120017>, while the method for predicting basal area increments (BAI) was described by Jevšenak and Skudnik (2021) <doi:10.1016/j.foreco.2020.118601>.

**License** GPL-3

**Imports** brnn(>= 0.6), ranger(>= 0.13.1), reshape2 (>= 1.4.4), pscl (>= 1.5.5), naivebayes(>= 0.9.7), magrittr(>= 1.5), dplyr(>= 0.7.0),tidyr (>= 1.1.3), tidyselect(>= 1.0.0)

**Encoding** UTF-8

**LazyData** true

**Depends** R(>= 3.4)

**NeedsCompilation** no

**Repository** CRAN

**RoxygenNote** 7.1.2

**Date/Publication** 2022-04-20 08:22:37 UTC

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add\_stand\_variables    *add\_stand\_variables*

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## Description

This function adds two variables to existing data frame of individual tree measurements: 1) stand basal area and 2) the number of trees per hectare

## Usage

```
add_stand_variables(df)
```

## Arguments

**df**                    a data frame with individual tree measurements that include basal area and the upscale factors. All trees should also be described with plotID and year variables

**Value**

a data frame with added stand variables: total stand basal area and the number of trees per hectare

**Examples**

```
data(data_v1)
data_v1 <- add_stand_variables(df = data_v1)
```

---

BAI_prediction	<i>BAI_prediction</i>
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---

**Description**

The Basal Area Increment BAI sub model that is run within the MLFS

**Usage**

```
BAI_prediction(
  df_fit,
  df_predict,
  species_n_threshold = 100,
  site_vars,
  include_climate,
  eval_model_BAI = TRUE,
  rf_mtry = NULL,
  k = 10,
  blocked_cv = TRUE,
  measurement_thresholds = NULL,
  area_correction = NULL
)
```

**Arguments**

<code>df_fit</code>	a data frame with Basal Area Increments (BAI) and all independent variables as specified with the formula
<code>df_predict</code>	data frame which will be used for BAI predictions
<code>species_n_threshold</code>	a positive integer defining the minimum number of observations required to treat a species as an independent group
<code>site_vars</code>	a character vector of variable names which are used as site descriptors
<code>include_climate</code>	logical, should climate variables be included as predictors
<code>eval_model_BAI</code>	logical, should the the BAI model be evaluated and returned as the output

rf_mtry	a number of variables randomly sampled as candidates at each split of a random forest model for predicting basal area increments (BAI). If NULL, default settings are applied.
k	the number of folds to be used in the k fold cross-validation
blocked_cv	logical, should the blocked cross-validation be used in the evaluation phase?
measurement_thresholds	data frame with two variables: 1) DBH_threshold and 2) weight. This information is used to assign the correct weights in BAI and increment sub-model; and to upscale plot-level data to hectares.
area_correction	an optional data frame with three variables: 1) plotID and 2) DBH_threshold and 3) the correction factor to be multiplied by weight for this particular category

### Value

a list with four elements:

1. \$predicted\_BAI - a data frame with calculated basal area increments (BAI)
2. \$eval\_BAI - a data frame with predicted and observed basal area increments (BAI), or a character string indicating that BAI model was not evaluated
3. \$rf\_model\_species - the output model for BAI (species level)
4. \$rf\_model\_speciesGroups - the output model for BAI (species group level)

```
# add BA to measurement thresholds measurement_thresholds$BA_threshold <- ((measurement_thresholds$DBH_threshold
* pi)/10000
```

```
BAI_outputs <- BAI_prediction(df_fit = data_BAI, df_predict = data_v6, site_vars = c("slope",
"elevation", "northness", "siteIndex"), rf_mtry = 3, species_n_threshold = 100, include_climate
= TRUE, eval_model_BAI = FALSE, k = 10, blocked_cv = TRUE, measurement_thresholds =
measurement_thresholds)
```

```
# get the ranger objects BAI_outputs_model_species <- BAI_outputs$rf_model_species BAI_outputs_model_groups
<- BAI_outputs$rf_model_speciesGroups
```

### Examples

```
library(MLFS)
data(data_BAI)
data(data_v6)
data(measurement_thresholds)
```

---

calculate_BAL	<i>calculate_BAL</i>
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---

**Description**

This function calculates the competition index BAL (Basal Area in Large trees) and adds it to the table of individual tree measurements that include basal area and the upscale factors. All trees should also be described with plotID and year variables

**Usage**

```
calculate_BAL(df)
```

**Arguments**

`df` a data frame with individual tree measurements that include basal area and the upscale factors. All trees should also be described with plotID and year variables

**Value**

a data frame with calculated basal area in large trees (BAL)

**Examples**

```
data(data_v1)
data_v1 <- calculate_BAL(df = data_v1)
```

---

crownHeight_prediction	<i>crownHeight_prediction</i>
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---

**Description**

Model for predicting crown height

**Usage**

```
crownHeight_prediction(  
  df_fit,  
  df_predict,  
  site_vars = site_vars,  
  species_n_threshold = 100,  
  k = 10,  
  eval_model_crownHeight = TRUE,  
  crownHeight_model = "lm",
```

```

    BRNN_neurons = 3,
    blocked_cv = TRUE
  )

```

### Arguments

<code>df_fit</code>	data frame with tree heights and basal areas for individual trees
<code>df_predict</code>	data frame which will be used for predictions
<code>site_vars</code>	optional, character vector with names of site variables
<code>species_n_threshold</code>	a positive integer defining the minimum number of observations required to treat a species as an independent group
<code>k</code>	the number of folds to be used in the k fold cross-validation
<code>eval_model_crownHeight</code>	logical, should the crown height model be evaluated and returned as the output
<code>crownHeight_model</code>	character string defining the model to be used for crown heights. Available are ANN with Bayesian regularization ( <code>brnn</code> ) or linear regression ( <code>lm</code> )
<code>BRNN_neurons</code>	positive integer defining the number of neurons to be used in the <code>brnn</code> method.
<code>blocked_cv</code>	logical, should the blocked cross-validation be used in the evaluation phase?

### Value

a list with four elements:

1. `$predicted_crownHeight` - a data frame with imputed crown heights
2. `$eval_crownHeight` - a data frame with predicted and observed crown heights, or a character string indicating that crown height model was not evaluated
3. `$model_species` - the output model for crown heights (species level)
4. `$model_speciesGroups` - the output model for crown heights (species group level)

### Examples

```

library(MLFS)
data(data_tree_heights)
data(data_v3)

# A) Example with linear model
Crown_h_predictions <- crownHeight_prediction(df_fit = data_tree_heights,
  df_predict = data_v3,
  crownHeight_model = "lm",
  site_vars = c(),
  species_n_threshold = 100,
  k = 10, blocked_cv = TRUE,
  eval_model_crownHeight = TRUE)

predicted_df <- Crown_h_predictions$predicted_crownHeight # df with imputed heights
evaluation_df <- Crown_h_predictions$eval_crownHeight # df with evaluation results

```

```
# B) Example with non-linear BRNN model
Crown_h_predictions <- crownHeight_prediction(df_fit = data_tree_heights,
  df_predict = data_v3,
  crownHeight_model = "brnn",
  BRNN_neurons = 3,
  site_vars = c(),
  species_n_threshold = 100,
  k = 10, blocked_cv = TRUE,
  eval_model_crownHeight = TRUE)
```

---

data_BAI	<i>An example of joined national forest inventory data, site descriptors, and climate data that is used as a fitting data frame for BAI sub model</i>
----------	---

---

## Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for BAI sub model. To make examples running more quickly, we keep only one tree species: PINI.

## Usage

```
data_BAI
```

## Format

A data frame with 135 rows and 25 variables:

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**year** year in which plot was visited

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**species** species name

**height** tree height in meters

**crownHeight** crown height in meters

**protected** logical, 1 if protected, otherwise 0

**slope** slope on a plot

**elevation** plot elevation

**northness** plot northness, 1 is north, 0 is south

**siteIndex** a proxy for site index, higher value represents more productive sites

**BA** basal area of individual trees in m2

**weight** upscale weight to calculate hectare values  
**stand\_BA** Total stand basal area  
**stand\_n** The number of trees in a stand  
**BAL** Basal Area in Large trees  
**p\_BA** basal area of individual trees in m2 from previous simulation step  
**p\_height** tree height in meters from previous simulation step  
**p\_crownHeight** crown height in meters from previous simulation step  
**p\_weight** upscale weight to calculate hectare values from previous simulation step  
**BAI** basal area increment  
**p\_sum** monthly precipitation sum  
**t\_avg** monthly mean temperature

---

data\_climate

*An example of climate data*

---

### Description

This is simulated monthly climate data, and consists of precipitation sum and mean temperature

### Usage

data\_climate

### Format

A data frame with 16695 rows and 5 variables:

**plotID** a unique identifier for plot  
**year** year  
**month** month  
**t\_avg** monthly mean temperature  
**p\_sum** monthly precipitation sum



---

`data_final_cut_weights`*An example of data\_final\_cut\_weights*

---

**Description**

Each species should have one weight that is multiplied with the probability of being harvested when final\_cut is applied

**Usage**`data_final_cut_weights`**Format**

A data frame with 36 rows and 6 variables:

**species** species name as used in data\_NFI

**step\_1** final cut weight applied in step 1

**step\_2** final cut weight applied in step 2

**step\_3** final cut weight applied in step 3

**step\_4** final cut weight applied in step 4

**step\_5** final cut weight applied in step 5 and all subsequent steps

---

`data_ingrowth`*An example of data\_ingrowth suitable for the MLFS*

---

**Description**

An example of plot-level data with plotID, stand variables and site descriptors, and the two target variables describing the number of ingrowth trees for inner (ingrowth\_3) and outer (ingrowth\_15) circles

**Usage**`data_ingrowth`

**Format**

A data frame with 365 rows and 11 variables:

**plotID** a unique identifier for plot

**year** year in which plot was visited

**stand\_BA** Total stand basal area

**stand\_n** The number of trees in a stand

**BAL** Basal Area in Large trees

**slope** slope on a plot

**elevation** plot elevation

**siteIndex** a proxy for site index, higher value represents more productive sites

**northness** plot northness, 1 is north, 0 is south

**ingrowth\_3** the number of new trees in inner circle

**ingrowth\_15** the number of new trees in outer circle

---

data_mortality	<i>An example of joined national forest inventory data, site descriptors, and climate data that is used as a fitting data frame for mortality sub model</i>
----------------	---

---

**Description**

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for mortality sub model

**Usage**

```
data_mortality
```

**Format**

A data frame with 6394 rows and 25 variables:

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**year** year in which plot was visited

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**species** species name

**height** tree height in meters

**crownHeight** crown height in meters

**protected** logical, 1 if protected, otherwise 0

**slope** slope on a plot  
**elevation** plot elevation  
**northness** plot northness, 1 is north, 0 is south  
**siteIndex** a proxy for site index, higher value represents more productive sites  
**BA** basal area of individual trees in m2  
**weight** upscale weight to calculate hectare values  
**stand\_BA** Total stand basal area  
**stand\_n** The number of trees in a stand  
**BAL** Basal Area in Large trees  
**p\_BA** basal area of individual trees in m2 from previous simulation step  
**p\_height** tree height in meters from previous simulation step  
**p\_crownHeight** crown height in meters from previous simulation step  
**p\_weight** upscale weight to calculate hectare values from previous simulation step  
**BAI** basal area increment  
**p\_sum** monthly precipitation sum  
**t\_avg** monthly mean temperature

---

 data\_NFI

*An example of national forest inventory data*


---

### Description

This is simulated data that reassemble the national forest inventory

### Usage

data\_NFI

### Format

A data frame with 11984 rows and 10 variables:

**plotID** a unique identifier for plot  
**treeID** a unique identifier for tree  
**year** year in which plot was visited  
**speciesGroup** identifier for species group  
**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)  
**DBH** diameter at breast height in cm  
**species** species name  
**height** tree height in meters  
**crownHeight** crown height in meters  
**protected** logical, 1 if protected, otherwise 0

---

data_site	<i>An example of site descriptors</i>
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**Description**

This is simulated data describing site descriptors

**Usage**

data\_site

**Format**

A data frame with 371 rows and 5 variables:

**plotID** a unique identifier for plot

**slope** slope on a plot

**elevation** plot elevation

**northness** plot northness, 1 is north, 0 is south

**siteIndex** a proxy for site index, higher value represents more productive sites

---

data_tariffs	<i>An example of table with one-parametric volume functions (adapted uniform French tariffs)</i>
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---

**Description**

The adapted uniform French tariffs are typically used in Slovenia to determine tree volume based on tree DBH

**Usage**

data\_tariffs

**Format**

A data frame with 1196 rows and 4 variables:

**tarifa\_class** tariff class for a particular species on this plot

**plotID** plot identifier

**species** species name as used in data\_NFI

**v45** volume of tree with DBH 45 cm

---

data\_thinning\_weights *An example of data\_thinning\_weights*

---

### Description

Each species should have one weight that is multiplied with the probability of being harvested when thinning is applied

### Usage

```
data_thinning_weights
```

### Format

A data frame with 36 rows and 6 variables:

**species** species name as used in data\_NFI

**step\_1** thinning weight applied in step 1

**step\_2** thinning weight applied in step 2

**step\_3** thinning weight applied in step 3

**step\_4** thinning weight applied in step 4

**step\_5** thinning weight applied in step 5 and all subsequent steps

---

data\_tree\_heights *An example of data with individual tree and crown heights that can be used as a fitting data frame for predicting tree and crown heights in MLFS*

---

### Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for some specific functions

### Usage

```
data_tree_heights
```

**Format**

A data frame with 2741 rows and 8 variables:

**plotID** a unique identifier for plot  
**treeID** a unique identifier for tree  
**year** year in which plot was visited  
**speciesGroup** identifier for species group  
**species** species name  
**height** tree height in meters  
**crownHeight** crown height in meters  
**BA** basal area of individual trees in m2

---

data_v1	<i>An example of joined national forest inventory and site data that is used within the MLFS</i>
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---

**Description**

This is simulated data that reassemble the national forest inventory and simulated data. We use it to show how to run examples for some specific functions

**Usage**

data\_v1

**Format**

A data frame with 11984 rows and 15 variables:

**plotID** a unique identifier for plot  
**treeID** a unique identifier for tree  
**year** year in which plot was visited  
**speciesGroup** identifier for species group  
**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)  
**species** species name  
**height** tree height in meters  
**crownHeight** crown height in meters  
**protected** logical, 1 if protected, otherwise 0  
**slope** slope on a plot  
**elevation** plot elevation  
**northness** plot northness, 1 is north, 0 is south  
**siteIndex** a proxy for site index, higher value represents more productive sites  
**BA** basal area of individual trees in m2  
**weight** upscale weight to calculate hectare values

---

data_v2	<i>An example of joined national forest inventory and site data that is used within the MLFS</i>
---------	--

---

### Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for tree and crown height predictions

### Usage

data\_v2

### Format

A data frame with 6948 rows and 14 variables:

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**year** year in which plot was visited

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**species** species name

**height** tree height in meters

**crownHeight** crown height in meters

**BA** basal area of individual trees in m2

**weight** upscale weight to calculate hectare values

**p\_BA** basal area of individual trees in m2 from previous simulation step

**p\_weight** upscale weight to calculate hectare values from previous simulation step

**p\_height** tree height in meters from previous simulation step

**p\_crownHeight** crown height in meters from previous simulation step

---

data_v3	<i>An example of joined national forest inventory and site data that is used within the MLFS</i>
---------	--

---

### Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for tree and crown height predictions. The difference between data\_v2 and data\_v3 is that in data\_v3, tree heights are already predicted

### Usage

data\_v3

### Format

A data frame with 6948 rows and 14 variables:

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**year** year in which plot was visited

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**species** species name

**height** tree height in meters

**crownHeight** crown height in meters

**BA** basal area of individual trees in m2

**weight** upscale weight to calculate hectare values

**p\_BA** basal area of individual trees in m2 from previous simulation step

**p\_height** tree height in meters from previous simulation step

**p\_crownHeight** crown height in meters from previous simulation step

**p\_weight** upscale weight to calculate hectare values from previous simulation step

**volume** tree volume in m3

**p\_volume** tree volume in m3 from previous simulation step



---

data_v4	<i>An example of joined national forest inventory and site data that is used within the MLFS</i>
---------	--

---

### Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for predicting tree mortality. Mortality occurs in the middle of a simulation step, so all variables have the preposition 'mid'

### Usage

data\_v4

### Format

A data frame with 6855 rows and 41 variables:

**year** year in which plot was visited

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**species** species name

**slope** slope on a plot

**elevation** plot elevation

**northness** plot northness, 1 is north, 0 is south

**siteIndex** a proxy for site index, higher value represents more productive sites

**p\_sum** monthly precipitation sum

**t\_avg** monthly mean temperature

**BA\_mid** basal area of individual trees in m2 in the middle of a simulation step

**BAI\_mid** basal area increment in the middle of a simulation step

**weight\_mid** upscale weight to calculate hectare values in the middle of a simulation step

**height\_mid** tree height in meters in the middle of a simulation step

**crownHeight\_mid** crown height in meters in the middle of a simulation step

**volume\_mid** tree volume in m3 in the middle of a simulation step

**BAL\_mid** Basal Area in Large trees the middle of a simulation step

**stand\_BA\_mid** Total stand basal area the middle of a simulation step

**stand\_n\_mid** The number of trees in a stand the middle of a simulation step

---

data_v5	<i>An example of joined national forest inventory and site data that is used within the MLFS</i>
---------	--

---

### Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for simulating harvesting.

### Usage

data\_v5

### Format

A data frame with 5949 rows and 10 variables:

**species** species name

**year** year in which plot was visited

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**volume\_mid** tree volume in m3 in the middle of a simulation step

**weight\_mid** upscale weight to calculate hectare values in the middle of a simulation step

**BA\_mid** basal area of individual trees in m2 in the middle of a simulation step

**protected** logical, 1 if protected, otherwise 0

---

data_v6	<i>An example of joined national forest inventory and site data that is used within the MLFS</i>
---------	--

---

### Description

This is simulated data that reassemble the national forest inventory data. We use it to show how to run examples for simulating Basal Area Increments (BAI) and the ingrowth of new trees. To make examples running more quickly, we keep only one tree species: PINI

### Usage

data\_v6

**Format**

A data frame with 186 rows and 27 variables:

**species** species name

**year** year in which plot was visited

**plotID** a unique identifier for plot

**treeID** a unique identifier for tree

**speciesGroup** identifier for species group

**code** status of a tree: 0 (normal), 1(harvested), 2(dead), 3 (ingrowth)

**height** tree height in meters

**crownHeight** crown height in meters

**protected** logical, 1 if protected, otherwise 0

**slope** slope on a plot

**elevation** plot elevation

**northness** plot northness, 1 is north, 0 is south

**siteIndex** a proxy for site index, higher value represents more productive sites

**BA** basal area of individual trees in m2

**weight** upscale weight to calculate hectare values

**stand\_BA** Total stand basal area

**stand\_n** The number of trees in a stand

**BAL** Basal Area in Large trees

**p\_BA** basal area of individual trees in m2 from previous simulation step

**p\_height** tree height in meters from previous simulation step

**p\_crownHeight** crown height in meters from previous simulation step

**p\_weight** upscale weight to calculate hectare values from previous simulation step

**BAI** basal area increment

**p\_sum** monthly precipitation sum

**t\_avg** monthly mean temperature

**volume** tree volume in m3

**p\_volume** tree volume in m3 from previous simulation step

---

df\_volume\_parameters *An example table with parameters and equations for n-parametric volume functions*

---

### Description

Volume functions can be specified for each species and plot separately, also limited to specific DBH interval. The factor variables (vol\_factor, h\_factor and DBH\_factor) are used to control the input and output units.

### Usage

```
df_volume_parameters
```

### Format

A data frame with 6 rows and 14 variables:

**species** species name as used in data\_NFI. The category REST is used for all species without specific equation

**equation** equation for selected volume function

**vol\_factor** will be multiplied with the volume

**h\_factor** will be multiplied with tree height

**d\_factor** will be divided with tree DBH

**DBH\_min** lower interval threshold for considered trees

**DBH\_max** upper interval threshold for considered trees

**a** parameter a for volume equation

**b** parameter b for volume equation

**c** parameter c for volume equation

**d** parameter d for volume equation

**e** parameter e for volume equation

**f** parameter f for volume equation

**g** parameter g for volume equation

---

form_factors	<i>An example table with form factors used to calculate tree volume</i>
--------------	---

---

**Description**

Form factors can be specified per species, plot or per species and plot

**Usage**

```
form_factors
```

**Format**

A data frame with 1199 rows and 3 variables:

**plotID** a unique identifier for plot

**species** species name as used in data\_NFI

**form** for factor used to calculate tree volume

---

height_prediction	<i>height_prediction</i>
-------------------	--------------------------

---

**Description**

Height model

**Usage**

```
height_prediction(  
  df_fit,  
  df_predict,  
  species_n_threshold = 100,  
  height_model = "naslund",  
  BRNN_neurons = 3,  
  height_pred_level = 0,  
  eval_model_height = TRUE,  
  blocked_cv = TRUE,  
  k = 10  
)
```

**Arguments**

<code>df_fit</code>	data frame with tree heights and basal areas for individual trees
<code>df_predict</code>	data frame which will be used for predictions
<code>species_n_threshold</code>	a positive integer defining the minimum number of observations required to treat a species as an independent group
<code>height_model</code>	character string defining the model to be used for height prediction. If 'brnn', then ANN method with Bayesian Regularization is applied. In addition, all 2- and 3- parametric H-D models from lmfor R package are available.
<code>BRNN_neurons</code>	positive integer defining the number of neurons to be used in the brnn method.
<code>height_pred_level</code>	integer with value 0 or 1 defining the level of prediction for height-diameter (H-D) models. The value 1 defines a plot-level prediction, while the value 0 defines regional-level predictions. Default is 0. If using 1, make sure to have representative plot-level data for each species.
<code>eval_model_height</code>	logical, should the height model be evaluated and returned as the output
<code>blocked_cv</code>	logical, should the blocked cross-validation be used in the evaluation phase?
<code>k</code>	the number of folds to be used in the k fold cross-validation

**Value**

a list with four elements:

1. `$data_height_predictions` - a data frame with imputed tree heights
2. `$data_height_eval` - a data frame with predicted and observed tree heights, or a character string indicating that tree heights were not evaluated
3. `$model_species` - the output model for tree heights (species level)
4. `$model_speciesGroups` - the output model for tree heights (species group level)

**Examples**

```
library(MLFS)
data(data_tree_heights)
data(data_v2)

# A) Example with the BRNN method
h_predictions <- height_prediction(df_fit = data_tree_heights,
                                  df_predict = data_v2,
                                  species_n_threshold = 100,
                                  height_pred_level = 0,
                                  height_model = "brnn",
                                  BRNN_neurons = 3,
                                  eval_model_height = FALSE,
                                  blocked_cv = TRUE, k = 10
                                  )
```

```
predicted_df <- h_predictions$data_height_predictions # df with imputed heights
evaluation_df <- h_predictions$data_height_eval # df with evaluation results
```

---

```
ingrowth_parameter_list
```

*An example data of ingrowth\_parameter\_list*

---

### Description

This is a list with two ingrowth levels: 3 (inner circle) and 15 (outer circle). In each list there are deciles of DBH distributions that are used to simulate DBH for new trees, separately for each ingrowth category

### Usage

```
ingrowth_parameter_list
```

### Format

A list with 2 elements:

**3** deciles of DBH distribution for ingrowth category 3

**15** deciles of DBH distribution for ingrowth category 15

---

```
ingrowth_table
```

*An example data of ingrowth\_table*

---

### Description

Ingrowth table is used within the ingrowth sub model to correctly simulate different ingrowth levels and associated upscale weights

### Usage

```
ingrowth_table
```

### Format

A data frame with 2 rows and 4 variables:

**code** ingrowth codes

**DBH\_threshold** a DBH threshold for particular ingrowth category

**DBH\_max** maximum DBH for a particular ingrowth category

**weight** the upscale weight for particular measurement category

---

max_size_data	<i>An example of data with maximum allowed BA that is used in the mortality sub model</i>
---------------	---

---

### Description

This is simulated max\_size\_data and used for examples in mortality sub model

### Usage

max\_size\_data

### Format

A data frame with 36 rows and 2 variables:

**species** species name

**BA\_max** The maximum allowed basal area (BA) for each individual species

---

measurement_thresholds	<i>An example of measurement_thresholds table</i>
------------------------	---

---

### Description

An example of measurement\_thresholds table resulting from concentric plots as used in Slovenian NFI

### Usage

measurement\_thresholds

### Format

A data frame with 2 rows and 2 variables:

**DBH\_threshold** a DBH threshold for particular measurement category

**weight** the upscale weight for particular measurement category



---

MLFS

*MLFS*


---

## Description

Machine Learning Forest Simulator

## Usage

```
MLFS(
  data_NFI,
  data_site,
  data_tariffs = NULL,
  data_climate = NULL,
  df_volumeF_parameters = NULL,
  thinning_weights_species = NULL,
  final_cut_weights_species = NULL,
  thinning_weights_plot = NULL,
  final_cut_weights_plot = NULL,
  form_factors = NULL,
  form_factors_level = "species_plot",
  uniform_form_factor = 0.42,
  sim_steps,
  volume_calculation = "volume_functions",
  merchantable_whole_tree = "merchantable",
  sim_harvesting = TRUE,
  sim_mortality = TRUE,
  sim_ingrowth = TRUE,
  sim_crownHeight = TRUE,
  harvesting_sum = NULL,
  forest_area_ha = NULL,
  harvest_sum_level = NULL,
  plot_upscale_type = NULL,
  plot_upscale_factor = NULL,
  mortality_share = NA,
  mortality_share_type = "volume",
  mortality_model = "glm",
  ingrowth_model = "ZIF_poiss",
  BAI_rf_mtry = NULL,
  ingrowth_rf_mtry = NULL,
  mortality_rf_mtry = NULL,
  nb_laplace = 0,
  harvesting_type = "final_cut",
  share_thinning = 0.8,
  final_cut_weight = 10,
  thinning_small_weight = 1,
  species_n_threshold = 100,
```

```

height_model = "brnn",
crownHeight_model = "brnn",
BRNN_neurons_crownHeight = 1,
BRNN_neurons_height = 3,
height_pred_level = 0,
include_climate = FALSE,
select_months_climate = c(1, 12),
set_eval_mortality = TRUE,
set_eval_crownHeight = TRUE,
set_eval_height = TRUE,
set_eval_ingrowth = TRUE,
set_eval_BAI = TRUE,
k = 10,
blocked_cv = TRUE,
max_size = NULL,
max_size_increase_factor = 1,
ingrowth_codes = c(3),
ingrowth_max_DBH_percentile = 0.9,
measurement_thresholds = NULL,
area_correction = NULL,
export_csv = FALSE,
sim_export_mode = TRUE,
include_mortality_BAI = TRUE,
intermediate_print = FALSE
)

```

### Arguments

<code>data_NFI</code>	data frame with individual tree variables
<code>data_site</code>	data frame with site descriptors. This data is related to <code>data_NFI</code> based on the 'plotID' column
<code>data_tariffs</code>	optional, but mandatory if volume is calculated using the one-parametric tariff functions. Data frame with plotID, species and V45. See details.
<code>data_climate</code>	data frame with climate data, covering the initial calibration period and all the years which will be included in the simulation
<code>df_volumeF_parameters</code>	optional, data frame with species-specific volume function parameters
<code>thinning_weights_species</code>	data frame with thinning weights for each species. The first column represents species code, each next column consists of species-specific thinning weights applied in each simulation step
<code>final_cut_weights_species</code>	data frame with final cut weights for each species. The first column represents species code, each next column consists of species-specific final cut weights applied in each simulation step
<code>thinning_weights_plot</code>	data frame with harvesting weights related to plot IDs, used for thinning

<code>final_cut_weights_plot</code>	data frame with harvesting weights related to plot IDs, used for final cut
<code>form_factors</code>	optional, data frame with species-specific form factors
<code>form_factors_level</code>	character, the level of specified form factors. It can be 'species', 'plot' or 'species_plot'
<code>uniform_form_factor</code>	numeric, uniform form factor to be used for all species and plots. Only if <code>form_factors</code> are not provided
<code>sim_steps</code>	The number of simulation steps
<code>volume_calculation</code>	character string defining the method for volume calculation: 'tariffs', 'volume_functions', 'form_factors' or 'slo_2p_volume_functions'
<code>merchantable_whole_tree</code>	character, 'merchantable' or 'whole_tree'. It indicates which type of volume functions will be used. This parameter is used only for volume calculation using the 'slo_2p_volume_functions'.
<code>sim_harvesting</code>	logical, should harvesting be simulated?
<code>sim_mortality</code>	logical, should mortality be simulated?
<code>sim_ingrowth</code>	logical, should ingrowth be simulated?
<code>sim_crownHeight</code>	logical, should crown heights be simulated? If TRUE, a <code>crownHeight</code> column is expected in <code>data_NFI</code>
<code>harvesting_sum</code>	a value, or a vector of values defining the harvesting sums through the simulation stage. If a single value, then it is used in all simulation steps. If a vector of values, the first value is used in the first step, the second in the second step, etc.
<code>forest_area_ha</code>	the total area of all forest which are subject of the simulation
<code>harvest_sum_level</code>	integer with value 0 or 1 defining the level of specified harvesting sum: 0 for plot level and 1 for regional level
<code>plot_upscale_type</code>	character defining the upscale method of plot level values. It can be 'area' or 'upscale factor'. If 'area', provide the forest area represented by all plots in hectares ( <code>forest_area_ha</code> argument). If 'factor', provide the fixed factor to upscale the area of all plots. Please note: <code>forest_area_ha/plot_upscale_factor</code> = number of unique plots. This argument is important when harvesting sum is defined on regional level.
<code>plot_upscale_factor</code>	numeric value to be used to upscale area of each plot
<code>mortality_share</code>	a value, or a vector of values defining the proportion of the volume which is to be the subject of mortality. If a single value, then it is used in all simulation steps. If a vector of values, the first value is used in the first step, the second in the second step, and so on.

mortality_share_type	character, it can be 'volume' or 'n_trees'. If 'volume' then the mortality share relates to total standing volume, if 'n_trees' then mortality share relates to the total number of standing trees
mortality_model	model to be used for mortality prediction: 'glm' for generalized linear models; 'rf' for random forest algorithm; 'naiveBayes' for Naive Bayes algorithm
ingrowth_model	model to be used for ingrowth predictions. 'glm' for generalized linear models (Poisson regression), 'ZIF_pois' for zero inflated Poisson regression and 'rf' for random forest
BAI_rf_mtry	a number of variables randomly sampled as candidates at each split of a random forest model for predicting basal area increments (BAI). If NULL, default settings are applied.
ingrowth_rf_mtry	a number of variables randomly sampled as candidates at each split of a random forest model for predicting ingrowth. If NULL, default settings are applied
mortality_rf_mtry	a number of variables randomly sampled as candidates at each split of a random forest model for predicting mortality. If NULL, default settings are applied
nb_laplace	value used for Laplace smoothing (additive smoothing) in naive Bayes algorithm. Defaults to 0 (no Laplace smoothing)
harvesting_type	character, it could be 'random', 'final_cut', 'thinning' or 'combined'. The latter combines 'final_cut' and 'thinning' options, where the share of each is specified with the argument 'share_thinning'
share_thinning	numeric, a number or a vector of numbers between 0 and 1 that specifies the share of thinning in comparison to final_cut. Only used if harvesting_type is 'combined'
final_cut_weight	numeric value affecting the probability distribution of harvested trees. Greater value increases the share of harvested trees having larger DBH. Default is 10.
thinning_small_weight	numeric value affecting the probability distribution of harvested trees. Greater value increases the share of harvested trees having smaller DBH. Default is 1.
species_n_threshold	a positive integer defining the minimum number of observations required to treat a species as an independent group
height_model	character string defining the model to be used for height prediction. If brnn, then ANN method with Bayesian Regularization is applied.
crownHeight_model	character string defining the model to be used for crown heights. Available are ANN with Bayesian regularization (brnn) or linear regression (lm)
BRNN_neurons_crownHeight	a positive integer defining the number of neurons to be used in the brnn method for predicting crown heights

BRNN_neurons_height	a positive integer defining the number of neurons to be used in the brnn method for predicting tree heights
height_pred_level	integer with value 0 or 1 defining the level of prediction for height-diameter (H-D) models. The value 1 defines a plot-level prediction, while the value 0 defines regional-level predictions. Default is 0. If using 1, make sure to have representative plot-level data for each species.
include_climate	logical, should climate variables be included as predictors
select_months_climate	vector of subset months to be considered. Default is c(1,12), which uses all months.
set_eval_mortality	logical, should the mortality model be evaluated and returned as the output
set_eval_crownHeight	logical, should the crownHeight model be evaluated and returned as the output
set_eval_height	logical, should the height model be evaluated and returned as the output
set_eval_ingrowth	logical, should the the ingrowth model be evaluated and returned as the output
set_eval_BAI	logical, should the the BAI model be evaluated and returned as the output
k	the number of folds to be used in the k fold cross-validation
blocked_cv	logical, should the blocked cross-validation be used in the evaluation phase?
max_size	a data frame with the maximum values of DBH for each species. If a tree exceeds this value, it dies. If not provided, the maximum is estimated from the input data. Two columns must be present, i.e. 'species' and 'DBH_max'
max_size_increase_factor	numeric value, which will be used to increase the max DBH for each species, when the maximum is estimated from the input data. If the argument 'max_size' is provided, the 'max_size_increase_factor' is ignored. Default is 1. To increase maximum for 10 percent, use 1.1.
ingrowth_codes	numeric value or a vector of codes which refer to ingrowth trees
ingrowth_max_DBH_percentile	which percentile should be used to estimate the maximum simulated value of ingrowth trees?
measurement_thresholds	data frame with two variables: 1) DBH_threshold and 2) weight. This information is used to assign the correct weights in BAI and increment sub-model; and to upscale plot-level data to hectares.
area_correction	optional data frame with three variables: 1) plotID and 2) DBH_threshold and 3) the correction factor to be multiplied by weight for this particular category.
export_csv	logical, if TRUE, at each simulation step, the results are saved in the current working directory as csv file

<code>sim_export_mode</code>	logical, if FALSE, the results of the individual simulation steps are not merged into the final export table. Therefore, output element 1 ( <code>\$sim_results</code> ) will be empty. This was introduced to allow simulations when using larger data sets and long term simulations that might exceed the available RAM. In such cases, we recommend setting the argument <code>export_csv = TRUE</code> , which will export each simulation step to the current working directory.
<code>include_mortality_BAI</code>	logical, should basal area increments (BAI) be used as independent variable for predicting individual tree mortality?
<code>intermediate_print</code>	logical, if TRUE intermediate steps will be printed while MLFS is running

### Value

a list of class `mlfs` with at least 15 elements:

1. `$sim_results` - a data frame with the simulation results
2. `$height_eval` - a data frame with predicted and observed tree heights, or a character string indicating that tree heights were not evaluated
3. `$crownHeight_eval` - a data frame with predicted and observed crown heights, or character string indicating that crown heights were not evaluated
4. `$mortality_eval` - a data frame with predicted and observed probabilities of dying for all individual trees, or character string indicating that mortality sub-model was not evaluated
5. `$ingrowth_eval` - a data frame with predicted and observed number of new ingrowth trees, separately for each ingrowth level, or character string indicating that ingrowth model was not evaluated
6. `$BAI_eval` - a data frame with predicted and observed basal area increments (BAI), or character string indicating that BAI model was not evaluated
7. `$height_model_species` - the output model for tree heights (species level)
8. `$height_model_speciesGroups` - the output model for tree heights (species group level)
9. `$crownHeight_model_species` - the output model for crown heights (species level)
10. `$crownHeight_model_speciesGroups` - the output model for crown heights (species group level)
11. `$mortality_model` - the output model for mortality
12. `$BAI_model_species` - the output model for basal area increments (species level)
13. `$BAI_model_speciesGroups` - the output model for basal area increments (species group level)
14. `$max_size` - a data frame with maximum allowed diameter at breast height (DBH) for each species
15. `$ingrowth_model_3` - the output model for ingrowth (level 1) – the output name depends on ingrowth codes
16. `$ingrowth_model_15` - the output model for ingrowth (level 2) – optional and the output name depends on ingrowth codes

## Examples

```
library(MLFS)

# open example data
data(data_NFI)
data(data_site)
data(data_climate)
data(df_volume_parameters)
data(measurement_thresholds)

test_simulation <- MLFS(data_NFI = data_NFI,
  data_site = data_site,
  data_climate = data_climate,
  df_volumeF_parameters = df_volume_parameters,
  form_factors = volume_functions,
  sim_steps = 2,
  sim_harvesting = TRUE,
  harvesting_sum = 100000,
  harvest_sum_level = 1,
  plot_upscale_type = "factor",
  plot_upscale_factor = 1600,
  measurement_thresholds = measurement_thresholds,
  ingrowth_codes = c(3,15),
  volume_calculation = "volume_functions",
  select_months_climate = seq(6,8),
  intermediate_print = FALSE
)
```

---

predict\_ingrowth      *predict\_ingrowth*

---

## Description

ingrowth model for predicting new trees within the MLFS

## Usage

```
predict_ingrowth(
  df_fit,
  df_predict,
  site_vars = site_vars,
  include_climate = include_climate,
  eval_model_ingrowth = TRUE,
  k = 10,
  blocked_cv = TRUE,
  ingrowth_model = "glm",
  rf_mtry = NULL,
```

```

  ingrowth_table = NULL,
  DBH_distribution_parameters = NULL
)

```

### Arguments

<code>df_fit</code>	a plot-level data with plotID, stand variables and site descriptors, and the two target variables describing the number of ingrowth trees for inner ( <code>ingrowth_3</code> ) and outer ( <code>ingrowth_15</code> ) circles
<code>df_predict</code>	data frame which will be used for ingrowth predictions
<code>site_vars</code>	a character vector of variable names which are used as site descriptors
<code>include_climate</code>	logical, should climate variables be included as predictors
<code>eval_model_ingrowth</code>	logical, should the the ingrowth model be evaluated and returned as the output
<code>k</code>	the number of folds to be used in the k fold cross-validation
<code>blocked_cv</code>	logical, should the blocked cross-validation be used in the evaluation phase?
<code>ingrowth_model</code>	model to be used for ingrowth predictions. 'glm' for generalized linear models (Poisson regression), 'ZIF_pois' for zero inflated Poisson regression and 'rf' for random forest
<code>rf_mtry</code>	a number of variables randomly sampled as candidates at each split of a random forest model for predicting ingrowth. If NULL, default settings are applied.
<code>ingrowth_table</code>	a data frame with 4 variables: ( <code>ingrowth</code> ) code, <code>DBH_threshold</code> , <code>DBH_max</code> and <code>weight</code> . Ingrowth table is used within the ingrowth sub model to correctly simulate different ingrowth levels and associated upscale weights
<code>DBH_distribution_parameters</code>	A list with deciles of DBH distributions that are used to simulate DBH for new trees, separately for each ingrowth category

### Value

a list with four elements:

1. `$predicted_ingrowth` - a data frame with newly added trees based on the ingrowth predictions
2. `$eval_ingrowth` - a data frame with predicted and observed number of new trees, separately for each ingrowth level, or character string indicating that ingrowth model was not evaluated
3. `$mod_ing_3` - the output model for predicting the ingrowth of trees with code 3
4. `$mod_ing_15` - the output model for predicting the ingrowth of trees with code 15 (the output name depends on the code used for this particular ingrowth level)

### Examples

```

library(MLFS)

data(data_v6)

```



```

data(data_ingrowth)
data(ingrowth_table)
data(ingrowth_parameter_list)

ingrowth_outputs <- predict_ingrowth(
  df_fit = data_ingrowth,
  df_predict = data_v6,
  site_vars = c("slope", "elevation", "northness", "siteIndex"),
  include_climate = TRUE,
  eval_model_ingrowth = FALSE,
  rf_mtry = 3,
  k = 10, blocked_cv = TRUE,
  ingrowth_model = 'rf',
  ingrowth_table = ingrowth_table,
  DBH_distribution_parameters = ingrowth_parameter_list)

```

---

predict_mortality	<i>predict_mortality</i>
-------------------	--------------------------

---

### Description

This sub model first fits a binary model to derive the effects of individual tree, site and climate variables on mortality; and afterwards predict the probability of dying for each tree from df\_predict

### Usage

```

predict_mortality(
  df_fit,
  df_predict,
  df_climate,
  mortality_share = NA,
  mortality_share_type = "volume",
  include_climate,
  site_vars,
  select_months_climate = c(6, 8),
  mortality_model = "rf",
  nb_laplace = 0,
  sim_crownHeight = FALSE,
  k = 10,
  eval_model_mortality = TRUE,
  blocked_cv = TRUE,
  sim_mortality = TRUE,
  sim_step_years = 5,
  rf_mtry = NULL,
  df_max_size = NULL,
  ingrowth_codes = 3,
  include_mortality_BAI = TRUE,

```

```

    intermediate_print = FALSE
  )

```

### Arguments

**df\_fit** a data frame with individual tree data and site descriptors where code is used to specify a status of each tree

**df\_predict** data frame which will be used for mortality predictions

**df\_climate** data frame with monthly climate data

**mortality\_share** a value defining the proportion of the volume which is to be the subject of mortality

**mortality\_share\_type** character, it can be 'volume' or 'n\_trees'. If 'volume' then the mortality share relates to total standing volume, if 'n\_trees' then mortality share relates to the total number of standing trees

**include\_climate** logical, should climate variables be included as predictors

**site\_vars** a character vector of variable names which are used as site descriptors

**select\_months\_climate** vector of subset months to be considered. Default is c(1,12), which uses all months.

**mortality\_model** logical, should the mortality model be evaluated and returned as the output

**nb\_laplace** value used for Laplace smoothing (additive smoothing) in naive Bayes algorithm. Defaults to 0 (no Laplace smoothing).

**sim\_crownHeight** logical, should crown heights be considered as a predictor variable? If TRUE, a crownHeight column is expected in data\_NFI

**k** the number of folds to be used in the k fold cross-validation

**eval\_model\_mortality** logical, should the mortality model be evaluated and returned as the output

**blocked\_cv** logical, should the blocked cross-validation be used in the evaluation phase?

**sim\_mortality** logical, should mortality be simulated?

**sim\_step\_years** the simulation step in years

**rf\_mtry** number of variables randomly sampled as candidates at each split of a random forest model. If NULL, default settings are applied.

**df\_max\_size** a data frame with the maximum BA values for each species. If a tree exceeds this value, it dies.

**ingrowth\_codes** numeric value or a vector of codes which refer to ingrowth trees

**include\_mortality\_BAI** logical, should basal area increments (BAI) be used as independent variable for predicting individual tree mortality?

**intermediate\_print** logical, if TRUE intermediate steps will be printed while the mortality sub model is running

**Value**

a list with three elements:

1. \$predicted\_mortality - a data frame with updated tree status (code) based on the predicted mortality
2. \$eval\_mortality - a data frame with predicted and observed probabilities of dying for all individual trees, or character string indicating that mortality sub-model was not evaluated
3. \$model\_output - the output model for mortality

**Examples**

```
data("data_v4")
data("data_mortality")
data("max_size_data")

mortality_outputs <- predict_mortality(
  df_fit = data_mortality,
  df_predict = data_v4,
  mortality_share_type = 'volume',
  df_climate = data_climate,
  site_vars = c("slope", "elevation", "northness", "siteIndex"),
  sim_mortality = TRUE,
  mortality_model = 'naiveBayes',
  nb_laplace = 0,
  sim_crownHeight = TRUE,
  mortality_share = 0.02,
  include_climate = TRUE,
  select_months_climate = c(6,7,8),
  eval_model_mortality = TRUE,
  k = 10, blocked_cv = TRUE,
  sim_step_years = 6,
  df_max_size = max_size_data,
  ingrowth_codes = c(3,15),
  include_mortality_BAI = TRUE)

df_predicted <- mortality_outputs$predicted_mortality
df_evaluation <- mortality_outputs$eval_mortality

# confusion matrix
table(df_evaluation$mortality, round(df_evaluation$mortality_pred, 0))
```

---

simulate\_harvesting     *A sub model to simulate harvesting within the MLFS*

---

**Description**

Harvesting is based on probability sampling, which depends on the selected parameters and the seize of a tree. Bigger trees have higher probability of being harvested when final cut is applied, while smaller trees have higher probability of being sampled in the case of thinning.

**Usage**

```
simulate_harvesting(
  df,
  harvesting_sum,
  df_thinning_weights_species = NULL,
  df_final_cut_weights_species = NULL,
  df_thinning_weights_plot = NULL,
  df_final_cut_weights_plot = NULL,
  harvesting_type = "random",
  share_thinning = 0.8,
  final_cut_weight = 1e+07,
  thinning_small_weight = 1e+05,
  harvest_sum_level = 1,
  plot_upscale_type,
  plot_upscale_factor,
  forest_area_ha
)
```

**Arguments**

**df** a data frame with individual tree data, which include basal areas in the middle of a simulation step, species name and code

**harvesting\_sum** a value, or a vector of values defining the harvesting sums through the simulation stage. If a single value, then it is used in all simulation steps. If a vector of values, the first value is used in the first step, the second in the second step, etc.

**df\_thinning\_weights\_species** data frame with thinning weights for each species. The first column represents species code, each next column consists of species-specific thinning weights

**df\_final\_cut\_weights\_species** data frame with final cut weights for each species. The first column represents species code, each next column consists of species-specific final cut weights

**df\_thinning\_weights\_plot** data frame with harvesting weights related to plot IDs, used for thinning

**df\_final\_cut\_weights\_plot** data frame with harvesting weights related to plot IDs, used for final cut

**harvesting\_type** character, it could be 'random', 'final\_cut', 'thinning' or 'combined'. The latter combines 'final\_cut' and 'thinning' options, where the share of each is specified with the argument 'share\_thinning'

**share\_thinning** numeric, a number between 0 and 1 that specifies the share of thinning in comparison to final\_cut. Only used if harvesting\_type is 'combined'

**final\_cut\_weight** numeric value affecting the probability distribution of harvested trees. Greater value increases the share of harvested trees having larger DBH. Default is 10.

**thinning\_small\_weight** numeric value affecting the probability distribution of harvested trees. Greater value increases the share of harvested trees having smaller DBH. Default is 1.

harvest\_sum\_level  
integer with value 0 or 1 defining the level of specified harvesting sum: 0 for plot level and 1 for regional level

plot\_upscale\_type  
character defining the upscale method of plot level values. It can be 'area' or 'upscale factor'. If 'area', provide the forest area represented by all plots in hectares (forest\_area\_ha argument). If 'factor', provide the fixed factor to upscale the area of all plots. Please note: forest\_area\_ha/plot\_upscale\_factor = number of unique plots. This argument is important when harvesting sum is defined on regional level.

plot\_upscale\_factor  
numeric value to be used to upscale area of each plot

forest\_area\_ha the total area of all forest which are subject of the simulation

**Value**

a data frame with updated status (code) of all individual trees based on the simulation of harvesting

**Examples**

```
library(MLFS)
data(data_v5)

data_v5 <- simulate_harvesting(df = data_v5,
  harvesting_sum = 5500000,
  harvesting_type = "combined",
  share_thinning = 0.50,
  harvest_sum_level = 1,
  plot_upscale_type = "factor",
  plot_upscale_factor = 1600,
  final_cut_weight = 5,
  thinning_small_weight = 1)
```

---

volume\_form\_factors    *volume\_form\_factors*

---

**Description**

The calculation of individual tree volume using form factors, which can be defined per species, per plot, or per species and per plot

**Usage**

```
volume_form_factors(
  df,
  form_factors = NULL,
```

```

  form_factors_level = "species",
  uniform_form_factor = 0.42
)

```

### Arguments

**df** data frame with tree heights and basal areas for individual trees

**form\_factors** data frame with for factors for species, plot or both

**form\_factors\_level** character, the level of specified form factors. It can be 'species', 'plot' or 'species\_plot'

**uniform\_form\_factor** a uniform form factor to be applied to all trees. If specified, it overwrites the argument 'form\_factors'

### Value

a data frame with calculated volume for all trees

### Examples

```

library(MLFS)
data(data_v3)
data(form_factors)

data_v3 <- volume_form_factors(df = data_v3, form_factors = form_factors,
  form_factors_level = "species_plot")

summary(data_v3)

```

---

volume_functions	<i>volume_functions</i>
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---

### Description

The calculation of individual tree volume using the n-parameter volume functions for the MLFS

### Usage

```
volume_functions(df, df_volumeF_parameters = NULL)
```

### Arguments

**df** data frame with tree heights and basal areas for individual trees

**df\_volumeF\_parameters** data frame with equations and parameters for n-parametric volume functions

**Value**

a data frame with calculated volume for all trees

**Examples**

```
library(MLFS)
data(data_v3)
data(df_volume_parameters)

data_v3 <- volume_functions(df = data_v3,
  df_volumeF_parameters = df_volume_parameters)
```

---

volume_tariffs	<i>volume_tariffs</i>
----------------	-----------------------

---

**Description**

One-parameter volume functions (tariffs) for the MLFS.

**Usage**

```
volume_tariffs(df, data_tariffs)
```

**Arguments**

df	data frame with tree heights and basal areas for individual trees
data_tariffs	data frame with plot- and species-specific parameters for the calculations of tree volume

**Value**

a data frame with calculated volume for all trees

**Examples**

```
data(data_v3)
data(data_tariffs)
data_v3 <- volume_tariffs(df = data_v3, data_tariffs = data_tariffs)
```

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