Package: rTG (via r-universe)

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Type Package

Title Methods to Analyse Seasonal Radial Tree Growth Data

Version 1.0.3

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Description Methods for comparing different regression algorithms for describing the temporal dynamics of secondary tree growth (xylem and phloem). Users can compare the accuracy of the most common fitting methods usually used to analyse xylem and phloem data, i.e., Gompertz function, Double Gompertz function, General Additive Models (GAMs); and an algorithm newly introduced to the field, i.e., Bayesian Regularised Neural Networks (brnn). The core function of the package is XPSgrowth(), while the results can be interpreted using implemented generic S3 methods, such as plot() and summary().

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Encoding UTF-8

LazyData true

Suggests testthat (>= 3.0.0)

Imports ggplot2(>= 2.2.0), mgcv (>= 1.8-34), knitr(>= 1.19), dplyr(>= 0.1.0), magrittr(>= 1.5), methods

Depends R(>= 3.5), brnn(>= 0.6), minpack.lm (>= 1.2-4)

URL https://github.com/jernejjevsenak/rTG

BugReports https://github.com/jernejjevsenak/rTG/issues

NeedsCompilation no

RoxygenNote 7.1.2

Config/testthat/edition 3

Repository https://jernejjevsenak.r-universe.dev

RemoteUrl https://github.com/jernejjevsenak/rtg

RemoteRef HEAD

RemoteSha 74caf5baaa85a6a86b9eea64704f78764fb924e0

Contents

`data_dendrometers` *data_dendrometers*

Description

A data set with dendrometer data from sugar maple and black spruce from Simoncouche site, Canada.

Usage

```
data_dendrometers
```

Format

A data frame with 718 rows and 6 variables:

site Simoncouche

species sugar maple and black spruce

tree tree identifier

year 2017, 2020

doy day Of a Year

width width expressed in relative terms

Source

Data belongs to Sergio Rossi

data_trees *data_trees*

Description

A dataset with intra-seasonal radial tree growth data. It was collected in three different years, at three sites, each with six trees. Please see references for details.

Usage

```
data_trees
```

Format

A data frame with 945 rows and 7 variables:

Tissue XYLEM or PHLOEM

Species Fagus sylvatica (FASY), Picea abies (PIAB), Quercus pubescens (QUPE)

Site Panska reka (PAN), Karst (KRAS)

Year 2011, 2017

Tree Tree ID indicators ranging from 1 to 6

doy Day Of a Year

width The total number of radial cells / the total ring width

Source

Gričar, J., Prislan, P., De Luis, M., Gryc, V., Hacurová, J., Vavrčík, H., Čufar, K., 2015. Plasticity in variation of xylem and phloem cell characteristics of Norway spruce under different local conditions. Frontiers in plant science 6, 730. Gričar, J., Zavadlav, S., Jyske, T., Lavrič, M., Laakso, T., Hafner, P., Eler, K., Vodnik, D., 2019. Effect of soil water availability on intra-annual xylem and phloem formation and non-structural carbohydrate pools in stem of Quercus pubescens. Tree Physiol. 39, 222-233. Prislan, P., Gričar, J., Čufar, K., de Luis, M., Merela, M., Rossi, S., 2019. Growing season and radial growth predicted for Fagus sylvatica under climate change. Clim. Change 153, 181-197.

parameters *parameters*

Description

data frame with model fitting parameters for different regression methods.

Usage

```
parameters
```

Format

A data frame with 79 rows and 2 variables:

Tissue XYLEM or PHLOEM

Species Fagus sylvatica (FASY), Picea abies (PIAB), Quercus pubescens (QUPE)

Site Panska reka (PAN), Karst (KRAS)

Year 2011, 2017

Tree Tree ID indicators ranging from 1 to 6

gom_a The initial value for the Gompertz parameter a

gom_b The initial value for the Gompertz parameter b

gom_k The initial value for the Gompertz parameter c

brnn_neurons The number of neurons for BRNN method

gam_k The k parameter value for GAM method

gam_sp The sp parameter value for GAM method

`XPSgrowth` *XPSgrowth*

Description

XylemPhloemSeasonalGrowth: This Function fits and compares the selected methods for modeling seasonal xylem and phloem data.

Usage

```
XPSgrowth(
  data_trees,
  parameters = NULL,
  search_initial_gom = FALSE,
  search_initial_double_gom = FALSE,
  fitting_method = c("gompertz", "GAM", "brnn"),
  ID_vars = NULL,
  fitted_save = FALSE,
  add_zeros = TRUE,
  add_zeros_before = "min",
  post_process = TRUE,
  unified_parameters = FALSE,
  gom_a = NA,
  gom_b = NA,
  gom_k = NA,
  d_gom_a1 = NA,
  d_gom_a2 = NA,
  d_gom_b1 = NA,
  d_gom_b2 = NA,
```

```
  d_gom_k1 = NA,
  d_gom_k2 = NA,
  brnn_neurons = NA,
  gam_k = NA,
  gam_sp = NA,
  gom_a_range = seq(0, 3000, by = 500),
  gom_b_range = seq(0.01, 1000, by = 50),
  gom_k_range = seq(0, 500, by = 2),
  d_gom_a1_range = seq(0, 1, by = 0.001),
  d_gom_a2_range = seq(0, 5, by = 0.01),
  d_gom_b1_range = seq(0, 5, by = 0.001),
  d_gom_b2_range = seq(0, 10, by = 0.1),
  d_gom_k1_range = seq(0, 1, by = 0.001),
  d_gom_k2_range = seq(0, 1, by = 0.001)
)
```

Arguments

data_trees	a data frame with ID variables and wood formation data with columns doy and width
parameters	a data frame with ID variables and initial parameter values for the selected methods
search_initial_gom	logical, should the algorithm to search initial Gompertz parameters be applied? This argument also overwrites manually defined Gompertz parameter values
search_initial_double_gom	logical, should the algorithm to search initial parameters for double Gompertz function be applied? This argument also overwrites manually defined parameter values for double Gompertz
fitting_method	vector of one or more methods to be compared: "gompertz", "double_gompertz", "gam", "brnn"
ID_vars	character vector of variables which indicate column names of ID variables
fitted_save	logical, should the fitted curves be saved in current working directory?
add_zeros	logical, should zero observations at the beginning of growing season be added?
add_zeros_before	if 'min' (character) then zeros will be added prior to the first observation in each year. Alternatively, users can specify absolute doy prior which zeros will be added.
post_process	logical, should the post-process algorithm be applied?
unified_parameters	logical, if TRUE, the algorithm will use only manually selected function parameters. See the arguments 'gom_a', 'gom_b', 'd_gom_k', 'd_gom_a1', 'd_gom_a2', 'd_gom_b1', 'd_gom_b2', 'd_gom_k1', 'd_gom_k2', 'brnn_neurons', 'gam_k' and 'gam_sp'. Default is FALSE
gom_a	numeric, the parameter a for the Gompertz function
gom_b	numeric, the parameter b for the Gompertz function

gom_k	numeric, the parameter k for the Gompertz function
d_gom_a1	numeric, the parameter a1 for the double Gompertz function
d_gom_a2	numeric, the parameter a2 for the double Gompertz function
d_gom_b1	numeric, the parameter b1 for the double Gompertz function
d_gom_b2	numeric, the parameter b2 for the double Gompertz function
d_gom_k1	numeric, the parameter k1 for the double Gompertz function
d_gom_k2	numeric, the parameter k2 for the double Gompertz function
brnn_neurons	positive integer, the number of neurons to be used by the BRNN method
gam_k	numeric, the parameter k for General Additive Model (GAM)
gam_sp	numeric, the parameter sp for General Additive Model (GAM)
gom_a_range	a numerical vector of the possible values of the parameter a, which is considered in the search for the initial Gompertz parameter values
gom_b_range	a numerical vector of the possible values of the parameter b, which is considered in the search for the initial Gompertz parameter values
gom_k_range	a numerical vector of the possible values of the parameter k, which is considered in the search for the initial Gompertz parameter values
d_gom_a1_range	A numerical vector representing the range of potential values for the 'a1' parameter within the double Gompertz function.
d_gom_a2_range	A numerical vector representing the range of potential values for the 'a2' parameter within the double Gompertz function.
d_gom_b1_range	A numerical vector representing the range of potential values for the 'b1' parameter within the double Gompertz function.
d_gom_b2_range	A numerical vector representing the range of potential values for the 'b2' parameter within the double Gompertz function.
d_gom_k1_range	A numerical vector representing the range of potential values for the 'k1' parameter within the double Gompertz function.
d_gom_k2_range	A numerical vector representing the range of potential values for the 'k2' parameter within the double Gompertz function.

Value

a list with the following elements:

1. $fitted - a data frame with fitted values
2. $gompertz_initial_parameters - a data frame that contains a curated selection of initial parameter values for the Gompertz function.
3. $gompertz_model_parameters - a data frame with final model coefficients for the Gompertz function.
4. $gompertz_initial_parameters_errors - a data frame with unsuccessful cases of Gompertz grid search.
5. $double_gompertz_initial_parameters - a data frame that contains a curated selection of initial parameter values for the double Gompertz function.

6. $double_gompertz_initial_parameters_errors - a data frame with unsuccessful cases of double Gompertz grid search.
7. $doble_gompertz_model_parameters - a data frame with final model coefficients for the double Gompertz function.

Examples

```
library(rTG)

# 1 Example on xylem and phloem data
data(parameters)
data(data_trees)

# subset data_trees
data_trees <- data_trees[c(1:27),]

# 1a Example using neural network
simulation_1a <- XPSgrowth(data_trees = data_trees,
     parameters = parameters,
     ID_vars = c("Species", "Tissue", "Site", "Year", "Tree"),
     fitting_method = c("brnn"),
     fitted_save = FALSE,
     search_initial_gom = FALSE,
     add_zeros = TRUE,
     add_zeros_before = 'min',
     post_process = TRUE)

## Not run:
#' # 1b Example on double Gompertz function
simulation_1b <- XPSgrowth(data_trees = data_trees,
     parameters = parameters,
     ID_vars = c("Species", "Tissue", "Site", "Year"),
     fitting_method = c("double_gompertz"),
     fitted_save = FALSE,
     search_initial_double_gom = FALSE,
     unified_parameters = TRUE,
     add_zeros = TRUE,
     add_zeros_before = 'min',
     d_gom_a1 = 0.204, d_gom_a2 = 0.240,
     d_gom_b1 = 2.433, d_gom_b2 = 2.900,
     d_gom_k1 = 0.974, d_gom_k2 = 0.963,
     post_process = TRUE)

# 1b Example on Double Gompertz function without initial parameters
simulation_1c <- XPSgrowth(data_trees = data_trees,
     parameters = parameters,
     ID_vars = c("Species", "Tissue", "Site", "Year"),
     fitting_method = c("double_gompertz"),
     fitted_save = FALSE,
     search_initial_double_gom = TRUE,
     post_process = TRUE)
```

```
# Obtain model parameters
simulation_1c$double_gompertz_model_parameters

## End(Not run)

# 2 Example on dendrometer data
data("data_dendrometers")

simulation_2 <- XPSgrowth(data_dendrometers, unified_parameters = TRUE,
                  ID_vars = c("site", "species", "year", "tree"),
                  fitting_method = c("brnn", "gam"),
                  brnn_neurons = 2, gam_k = 9, gam_sp = 0.5,
                  search_initial_gom = TRUE, add_zeros = FALSE,
                  post_process = TRUE)
```

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