

Package ‘rTG’

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Type Package

Title Methods to Analyse Seasonal Radial Tree Growth Data

Version 0.2.2

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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 and 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), brnn(>= 0.6), mgcv (>= 1.8-34), knitr(>= 1.19), dplyr(>= 0.1.0), magrittr(>= 1.5)

Depends R(>= 3.5)

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

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

NeedsCompilation no

Repository CRAN

RoxygenNote 7.1.1

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data_trees	<i>data_trees</i>
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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 8 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

Sample A consecutive number of collected sample

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,
  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,
  brnn_neurons = NA,
  gam_k = NA,
  gam_sp = NA
)

```

Arguments

<code>data_trees</code>	a data frame with ID variables and wood formation data with columns DOY and Width
<code>parameters</code>	a data frame with ID variables and initial parameter values for the selected methods
<code>search_initial_gom</code>	logical, should the algorithm to search initial Gompertz parameters be applied?
<code>fitting_method</code>	vector of one or more methods to be compared: "gompertz", "gam", "brnn"
<code>ID_vars</code>	character vector of variables which indicate column names of ID variables
<code>fitted_save</code>	logical, should the fitted curves be saved in current working directory?
<code>add_zeros</code>	logical, should zero observations at the beginning of growing season be added?
<code>add_zeros_before</code>	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.
<code>post_process</code>	logical, should the post-process algorithm be applied?
<code>unified_parameters</code>	logical, if FALSE, the algorithm will use only manually selected function parameters. See the arguments 'gom_a', 'gom_b', 'gom_k', 'brnn_neurons', 'gam_k' and 'gam_sp'. Default is FALSE
<code>gom_a</code>	numeric, the parameter a for the Gompertz function
<code>gom_b</code>	numeric, the parameter b for the Gompertz function
<code>gom_k</code>	numeric, the parameter k for the Gompertz function
<code>brnn_neurons</code>	positive integer, the number of neurons to be used by the BRNN method

<code>gam_k</code>	numeric, the parameter k for General Additive Model (GAM)
<code>gam_sp</code>	numeric, the parameter sp for General Additive Model (GAM)

Value

a list with the following elements:

1. `$fitted` - a data frame with fitted wood formation data
2. `$gompertz_grid_search` - a data frame with selected initial parameter values
3. `$gompertz_grid_search_errors` - a data frame with unsuccessful cases of gompertz grid search

Examples

```
library(rTG)

# Load data
data(parameters)
data(data_trees)
simulation_1 <- XPSgrowth(data_trees = data_trees,
  parameters = parameters,
  ID_vars = c("Species", "Tissue", "Site", "Year", "Tree"),
  fitting_method = c("gompertz", "gam", "brnn"),
  fitted_save = FALSE,
  search_initial_gom = TRUE,
  add_zeros = TRUE,
  add_zeros_before = 'min',
  post_process = TRUE)
```

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