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  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 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

**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**

**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

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?
fitting_method vector of one or more methods to be compared: "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 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
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
brnn_neurons positive integer, the number of neurons to be used by the BRNN method
XPSgrowth

\[ x \]

\text{gam}_k \quad \text{numeric, the parameter } k \text{ for General Additive Model (GAM)}

\text{gam}_sp \quad \text{numeric, the parameter } sp \text{ for General Additive Model (GAM)}

\textbf{Value}

\begin{itemize}
  \item a list with the following elements:
  \begin{itemize}
    \item $fitted$ - a data frame with fitted wood formation data
    \item $gompertz\_grid\_search$ - a data frame with selected initial parameter values
    \item $gompertz\_grid\_search\_errors$ - a data frame with unsuccessful cases of gompertz grid search
  \end{itemize}
\end{itemize}

\textbf{Examples}

```r
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)
```

```r

```
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