Package ‘rTG’

October 14, 2022

Type Package

Title Methods to Analyse Seasonal Radial Tree Growth Data

Version 1.0.1

Author Jernej Jevsenak [aut, cre]

Maintainer Jernej Jevsenak <jernej.jevsenak@gmail.com>

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 XPScrowth(), while the results can be interpreted using implemented generic S3 methods, such as plot() and summary().

License GPL-3

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), methods

Depends R (>= 3.5)

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

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

NeedsCompilation no

Repository CRAN

RoxygenNote 7.1.2

Config/testthat/edition 3

Date/Publication 2022-05-12 16:30:02 UTC
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**

---

### 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


---

**parameters**

**Description**

data frame with model fitting parameters for different regression methods.

**Usage**

`parameters`
XPSgrowth

**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

---

**Description**

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

**Usage**

```r
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,
  gom_a_range = c(1, 3000, 500),
  gom_b_range = seq(1, 1000, 50),
  gom_k_range = seq(1, 500, 2)
)
```
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

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 TRUE, 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

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

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)

# 1 Example on xylem and phloem 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("brnn"),
fitted_save = FALSE,
search_initial_gom = FALSE,
add_zeros = TRUE,
add_zeros_before = 'min',
post_process = TRUE)

# 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)
Index

* datasets
  data_dendrometers, 2
  data_trees, 3
  parameters, 3

data_dendrometers, 2
data_trees, 3
parameters, 3
XPSgrowth, 4