Package 'dfoliatR'

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Type Package

Title Detection and Analysis of Insect Defoliation Signals in Tree
Rings

Version 0.2.0

Description Tools to identify, quantify, analyze, and visualize growth
suppression events in tree rings that are often produced by insect
defoliation. Described in Guiterman et al. (2020) <doi:10.1016/j.dendro.2020.125750>.

URL https://chguiterman.github.io/dfoliatR/

BugReports https://github.com/chguiterman/dfoliatR/issues

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License GPL (>= 3)

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R topics documented:

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as.defol   *Alias to* `as_defol()`

Description

Alias to `as_defol()`

Usage

```
as.defol(x)
```

Arguments

x   A data frame or list-like object to cast. Must have named elements for "year", "series", "gsi", "ngsi", and "defol_status".

Value

x cast to a `defol` object

Examples

```
data(dmj_defol)
example_data <- as.data.frame(dmj_defol)
is.defol(example_data)
back_to_defol <- as_defol(example_data)
is.defol(back_to_defol)
```

---

as.obr   *Alias to* as_obr()

Description

Alias to as_obr()

Usage

```
as.obr(x)
```

Arguments

x   A data frame or list-like object to cast. Must have named elements for "year", "samp_depth", "num_defol", "perc_defol", "num_max_defol", "perc_max_defol", "mean_gsi", "mean_ngsi", "outbreak_status".

Value

x cast to an `obr` object

Examples

```
data(dmj_obr)
example_data <- as.data.frame(dmj_obr)
is.obr(example_data)
back_to_obr <- as_obr(example_data)
is.obr(back_to_obr)
```

---

as_defol   *Cast data frame to list-like* defol *object*

Description

Cast data frame to list-like defol object

Usage

```
as_defol(x)
```

Arguments

x   A data frame or list-like object to cast. Must have named elements for "year",
                "series", "gsi", "ngsi", and "defol_status".

Value

x cast to a defol object

Examples

```
data(dmj_defol)
example_data <- as.data.frame(dmj_defol)
is.defol(example_data)
back_to_defol <- as_defol(example_data)
is.defol(back_to_defol)
```

---

as_obr   *Cast data frame to list-like* obr *object*

Description

Cast data frame to list-like obr object

Usage

```
as_obr(x)
```

Arguments

x   A data frame or list-like object to cast. Must have named elements for "year",
                "samp_depth", "num_defol", "perc_defol", "num_max_defol", "perc_max_defol",
                "mean_gsi", "mean_ngsi", "outbreak_status".

Value

x cast to an obr object

Examples

```
data(dmj_obr)
example_data <- as.data.frame(dmj_obr)
is.obr(example_data)
back_to_obr <- as_obr(example_data)
is.obr(back_to_obr)
```

---

defol   *Constructor for S3 defol class*

Description

Constructor for S3 defol class

Usage

```
defol(year, series, gsi, ngsi, defol_status)
```

Arguments

year	An n-length integer vector of observation years
series	An n-length factor or character vector of series names
gsi	An n-length numeric vector of growth suppression index, such as calculated by gsi()
ngsi	An n-length numeric vector of normalized gsi, such as calculated by gsi().
defol_status	An n-length factor or character vector denoting the defoliation event status of each year. This uses a controlled vocabulary, see dfoliatR:::make_defol_status for possible values.

Value

a tree-level defol object

---

defoliate_trees *Identify defoliation events in host trees*

Description

[defoliate_trees()](#) is the starting point for most analyses of insect defoliation signals preserved in the growth patterns of trees. It requires individual-tree standardized measurements from potential host trees and a tree-ring chronology from a nearby non-host species. First, [defoliate_trees()](#) combines these tree-ring indices by calling [gsi()](#) to perform a "correction" of the host-tree indices to remove the climatic influences on tree growth as represented by the non-host chronology. This should isolate a disturbance-related signal. Second, [defoliate_trees()](#), runs [id_defoliation()](#), which completes a runs analyses to evaluate sequences of negative departures in the host tree growth series (ngsi) for potential defoliation events.

Usage

```
defoliate_trees(
  host_tree,
  nonhost_chron,
  duration_years = 8,
  max_reduction = -1.28,
  bridge_events = FALSE,
  series_end_event = FALSE,
  list_output = FALSE
)
```

Arguments

host_tree   A dplR::rwl object containing the tree-level growth series for all host trees to be compared to the non-host chronology.

nonhost_chron   A dplR::rwl object containing a single non-host chronology.

duration_years   The minimum length of time in which the tree is considered to be in defoliation.

max_reduction   The minimum value of ngsi required to be considered a defoliation event. If a sequence of negative ngsi values does not reach this threshold, the potential event is rejected. Defaults to -1.28.

bridge_events   Binary, defaults to FALSE. This option allows for successive events that are separated by a single year to be bridged and become one event. It should be used cautiously and closely evaluated to ensure the likelihood that the two (or more) events are actually one long event.

series_end_event
                 Binary, defaults to FALSE. This option allows the user to identify an event occurring at the time of sampling as a defoliation event, regardless of duration. Including it will help to quantify periodicity and extent of an outbreak. This should only be used if the user has direct knowledge of an ongoing defoliation event when the trees were sampled.

list_output Defaults to FALSE. This option is to output a long list object containing a separate data.frame for each series in host_tree that includes the input series and the nonhost_chron, the corrected series, and the character string identifying the defoliation events.

Value

By default this returns a long-form data frame of tree-level growth suppression indices and identified defoliation events. If list_output = TRUE, it returns a list object with each element containing a data.frame rwl object of the host and non-host series, plus the outputs from gsi(). The list object is useful for assessing the effects of running gsi() on the host and nonhost data.

Note

Other functions in dfoliatR, like outbreak() and plot_defol(), require a long-form data frame identifiable as a defol() object. Selecting list_output = TRUE will trigger errors in running other functions.

Examples

```
# Load host and non-host data
data("dmj_h") # Host trees
data("dmj_nh") # Non-host chronology

dmj_defol <- defoliate_trees(dmj_h, dmj_nh)
```

---

defol_stats   *Descriptive statistics for defoliation trees*

Description

Descriptive statistics for defoliation trees

Usage

```
defol_stats(x)
```

Arguments

x   A defol object after running defoliate_trees().

Value

A data frame containing tree/series-level statistics.

Note

If series-end-events are present, they are omitted from calculations of total event years and mean duration.

Examples

```
data("dmj_defol")
defol_stats(dmj_defol)
```

---

dmj_defol   *Demi John dfol object*

Description

Produced by running `defoliate_trees(dmj_h,dmj_nh,series_end_events=TRUE)`

Usage

```
dmj_defol
```

Format

A `defol` object with 4267 rows and 5 columns

---

dmj_h   *Demi John Douglas-fir*

Description

Western spruce budworm host series

Usage

```
dmj_h
```

Format

An `rwl` object with 17 tree-level series, standardized in ARSTAN. Dates range from 1620-1997.

---

dmj_nh   *Demi John area ponderosa pine*

Description

Non-host pair to Demi John Douglas-fir `dmj_h`

Usage

    dmj_nh

Format

An `rwl` object with 1 series, 1675-1997.

---

dmj_obr   *Demi John outbreak object*

Description

Produced by running `outbreak(dmj_defol)`

Usage

    dmj_obr

Format

An object of class obr (inherits from `data.frame`) with 323 rows and 9 columns.

Details

@format An `outbreak` object with 323 rows and 9 columns

---

efk_defol   *East Fork defol object*

Description

Produced by running `defoliate_trees(efk_h,efk_nh,series_end_event = TRUE)`

Usage

`efk_defol`

Format

A `defol` object with 5142 rows and 5 columns

---

efk_h   *East Fork Jemez River Douglas-fir*

Description

Western spruce budworm host series

Usage

`efk_h`

Format

An `rwl` object with 37 tree-level series, standardized in ARSTAN. Dates range from 1776-1987.

Source

https://esajournals.onlinelibrary.wiley.com/doi/10.2307/2937153

---

efk_nh   *Baca ponderosa pine chronology*

Description

Non-host pair chronology for East Fork Douglas-fir efk_h

Usage

```
efk_nh
```

Format

An `rwl` chronology object with 1 series, 1612-1987. Standardized in ARSTAN.

Source

https://esajournals.onlinelibrary.wiley.com/doi/10.2307/2937153

---

efk_obr   *East Fork outbreak object*

Description

Produced by running outbreak(efk_defol)

Usage

```
efk_obr
```

Format

An `outbreak` object with 221 rows and 9 columns

---

ef_defol   *East Fork defol object*

Description

Produced by running `defoliate_trees(ef_h,ef_nh,series_end_event = TRUE)`

Usage

    ef_defol

Format

A `defol` object with 2500 rows and 5 columns

---

ef_h   *East Fork Jemez River Douglas-fir*

Description

Western spruce budworm host series

Usage

    ef_h

Format

An `rwl` object with 15 tree-level series, standardized in ARSTAN. Dates range from 1776-1987.

---

ef_nh   *East Fork Jemez area ponderosa pine*

Description

Non-host pair chronology for East Fork Douglas-fir `ef_h`

Usage

    ef_nh

Format

An `rwl` chronology object with 1 series, 1612-1987. Standardized in ARSTAN.

---

ef_obr   *East Fork outbreak object*

Description

Produced by running outbreak(`ef_defol`)

Usage

```
ef_obr
```

Format

An outbreak object with 221 rows and 9 columns

---

get_defol_events   *Defoliation event list*

Description

Defoliation event list

Usage

```
get_defol_events(x)
```

Arguments

x   a defol object

---

gsi   *Calculate the growth suppression index*

Description

This function removes the nonhost growth signal from a host tree-ring series.

Usage

```
gsi(input_series)
```

Arguments

input_series   A dplr::rwl object with the host tree series as the first column and the non-host
chronology as the second. Years should be the row names. This is specifically
created by defoliate_trees() and passed to gsi().

Details

The growth suppression index (GSI) is referred to as the "corrected" series in OUTBREAK. It is
calculated as:

$$GSI(i) = H(i) - (NH(i) - mean(NH))sd(H)/sd(NH)$$

where H and NH are the host and nonhost tree-ring series as standardized index values; i is the year,
and the functions mean() and sd() are applied to the common period.

gsi() will rarely be run directly by a user. It is called from defoliate_trees().

Value

A data frame with the two input columns (host and nonhost series) and 3 added columns:

1. The mean/sd adjusted non-host chronology,
2. The growth suppression index ("gsi") of the host series after subtraction of the adjusted non-host chronology,
3. The normalized growth suppression index ("ngsi") generated by applying scale() to the gsi.

---

id_defoliation   *Identify defoliation events in a host series*

Description

After calculating the growth suppression index in gsi(), id_defoliation() performs a runs
analysis on the normalized growth suppression index, or ngsi, in which sequences of negative
departures are assessed as possible defoliation events. id_defoliation() is the workhorse for
defoliate_trees(), performing much of the necessary criteria evaluation used in OUTBREAK.
The defaults for most parameters originate from OUTBREAK. Two new features distinguish the
dfoliatR version: bridging events that occur in close sequence and allowing for the recent end of
a series to be evaluated for defoliation regardless of the event duration. See parameter specifics for
details.

Usage

```
id_defoliation(
  input_series,
  duration_years = 8,
  max_reduction = -1.28,
  bridge_events = FALSE,
  series_end_event = FALSE
)
```

Arguments

input_series	A data frame with 5 columns, as generated by gsi().
duration_years	The minimum length of time in which the tree is considered to be in defoliation.
max_reduction	The minimum value of ngsi required to be considered a defoliation event. If a sequence of negative ngsi values does not reach this threshold, the potential event is rejected. Defaults to -1.28.
bridge_events	Binary, defaults to FALSE. This option allows for successive events that are separated by a single year to be bridged and become one event. It should be used cautiously and closely evaluated to ensure the likelihood that the two (or more) events are actually one long event.
series_end_event	
	Binary, defaults to FALSE. This option allows the user to identify an event occurring at the time of sampling as a defoliation event, regardless of duration. Including it will help to quantify periodicity and extent of an outbreak. This should only be used if the user has direct knowledge of an ongoing defoliation event when the trees were sampled.

Value

After performing runs analyses, the function adds a column to the input data frame that distinguishes years of defoliation and the maximum defoliation year (ie. the year the greatest negative growth departure within the event).

Note

id_defoliation() is called by defoliate_trees(). It might only be used by the user for troubleshooting.

---

is.defol	*Check if object is tree-level defoliation object:* defol

---

Description

Check if object is tree-level defoliation object: defol

Usage

```
is.defol(x)
```

Arguments

x	Any R object.

Value

Boolean indicating whether x is a defol object.

---

is.obr   *Check if object is outbreak, meaning site-level outbreak object*

Description

Check if object is outbreak, meaning site-level outbreak object

Usage

```
is.obr(x)
```

Arguments

x   Any R object.

Value

Boolean indicating whether x is an outbreak object.

---

obr   *Constructor for an* obr *object.*

Description

Constructor for an obr object.

Usage

```
obr(
  year,
  samp_depth,
  num_defol,
  perc_defol,
  num_max_defol,
  perc_max_defol,
  mean_gsi,
  mean_ngsi,
  outbreak_status
)
```

Arguments

year	An n-length numeric vector of observed years.
samp_depth	An n-length numeric vector of the number of trees.
num_defol	An n-length numeric vector of the number of trees experiencing defoliation.
perc_defol	An n-length numeric vector of the percent of trees experiencing defoliation.
num_max_defol	An n-length numeric vector of the number of trees experiencing their maximum level of defoliation (i.e., their most extreme negative growth departure).
perc_max_defol	An n-length numeric vector of the percent of trees experiencing their maximum level of defoliation (i.e., their most extreme negative growth departure).
mean_gsi	An n-length numeric vector of the average growth suppression index across all observed trees.
mean_ngsi	An n-length numeric vector of the average normalized (scaled) growth suppression index.
outbreak_status	
	An n-length factor or character vector that identified whether that year surpasses the designated thresholds for an "outbreak event". Threshold criteria are provided in [outbreak()]().

Value

An obr object with columns matching the input variables.

---

outbreak	*Composite defoliation series to determine outbreak events*

Description

[outbreak()]() takes a defol object from [defoliate_trees()]() and composites it into a site-level object. Function parameters allow the user to filter the tree-level series in various ways to optimize thresholds of what constitutes an "outbreak" level event recorded by the host trees.

Usage

```
outbreak(x, filter_perc = 25, filter_min_series = 3, filter_min_defol = 1)
```

Arguments

x	a defol object
filter_perc	the minimum percentage of defoliated trees to be considered an outbreak. Default is 25 percent.
filter_min_series	
	The minimum number of trees required for an outbreak event. Default is 3 trees.
filter_min_defol	
	The minimum number of trees recording a defoliation event. Default is 1 tree.

Value

A data.frame obr object for the site that includes all trees in the host defol object. Columns in the obr include:

1. year for every year in the set of host trees,
2. num_defol the number of trees recording a defoliation event,
3. percent_defol the percent of trees recording a defoliation,
4. num_max_defol the number of trees recording a maximum growth suppression (or peak of that event on that tree),
5. perc_max_defol the percent of trees at maximum defoliation,
6. mean_gsi the average of all trees growth suppression index (gsi),
7. mean_ngsi the average of all trees normalized growth suppression index (ngsi),
8. outbreak_status whether that year constitutes an outbreak based on the filters applied to the function.

Examples

```
data("dmj_defol")
head(outbreak(dmj_defol))
```

---

outbreak_stats   *Outbreak statistics*

Description

Summary statistics for inferred outbreaks

Usage

```
outbreak_stats(x)
```

Arguments

x   An obr object after running outbreak()

Value

A data frame with descriptive statistics for each outbreak event determined by outbreak(), including:

- "start" – first year of outbreak
- "end" – last year of outbreak
- "duration" – length of outbreak (in years)
- "n_df_start" – number of trees defoliated at the start

- "perc_df_start" – percent of trees defoliated at the start

- "max_df_obr" – maximum number of trees in the outbreak during a single year

- "yr_max_df" – year with the maximum number of trees defoliated

- "yr_min_ngsi" – year with the lowest mean normalized growth suppression index (NGSI)

- "min_gsi" – minimum growth suppression index

- "min_ngsi" – minimum normalized gsi

Note

Certain statistics will be set to NA for the final outbreak event if there was an ongoing defoliation event (in which series_end_event = TRUE in `defoliate_trees()`). This is because the end of the outbreak remains unknown, so statistics such as duration cannot be calculated. Statistics pertaining to the start of the event are provided.

Examples

```
data("dmj_obr")
outbreak_stats(dmj_obr)
```

---

plot.defol   *Plot a* defol *object*

Description

Plot a `defol` object

Usage

```
## S3 method for class 'defol'
plot(...)
```

Arguments

...   arguments passed to `plot_defol()`

---

plot_defol	*Produce a Gantt plot of individual tree-ring series to show defoliation events in time*

Description

Produce a Gantt plot of individual tree-ring series to show defoliation events in time

Usage

```
plot_defol(x, breaks)
```

Arguments

x   a defol object produced by [defoliate_trees()](#).

breaks   a vector length two providing threshold (negative) ngsi values to separate minor, moderate, and severe defoliation events. If blank, the mean and 1st quartile are used.

Examples

```
data("dmj_defol")
plot_defol(dmj_defol)

## Change the values severity classes
plot_defol(dmj_defol, breaks = c(-1.0, -0.5))
```

---

plot_outbreak	*Produce a stacked plot to present composited, site-level insect outbreak chronologies*

Description

Produce a stacked plot to present composited, site-level insect outbreak chronologies

Usage

```
plot_outbreak(x, disp_index = c("GSI", "NGSI"))
```

Arguments

x   an 'obr' object produced by [outbreak()](#)

disp_index   Identify the timeseries index to plot. Defaults to NGSI, the average normalized growth suppression index for the site. The only other option is GSI, the average growth suppression index.

Examples

```
data(dmj_obr)
plot_outbreak(dmj_obr)

# Change middle panel display from the default "NGSI" to "GSI"
plot_outbreak(dmj_obr, disp_index = "GSI")
```

---

sample_depth	*Calculate the sample depth of a defol object*

Description

Calculate the sample depth of a defol object

Usage

```
sample_depth(x)
```

Arguments

x   A `defol` object.

Value

A data.frame containing the years and number of trees

Examples

```
data("dmj_defol")
head(sample_depth(dmj_defol))
```

---

series_names	*Extract series names from a defol object*

Description

Extract series names from a defol object

Usage

```
series_names(x)
```

Arguments

x   a defol object

stack_defoliation   *Stack a defoliation list*

Description

Stack a defoliation list

Usage

```
stack_defoliation(x)
```

Arguments

x   a list object created by [defoliate_trees()](#)

Value

a defol object (long-format data frame)

Index