

1 **dfoliatR**: An R package for detection and analysis of 2 insect defoliation signals in tree rings

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11 **Abstract**

We present a new R package to provide dendroecologists with tools to infer, quantify, analyze, and visualize growth suppression events in tree rings. **dfoliatR** is based on the OUTBREAK program and builds on existing resources in the R computing environment and the well-used **dplR** package. It is designed to aid research in the ecology of insect defoliation events and to reconstruct defoliator outbreak chronologies, but can be applied to other studies where host–non-host comparisons are useful. **dfoliatR** performs an indexing procedure to remove climatic signals in the host-tree series that are represented in the non-host chronology, or other annually-resolved climate series. It then infers defoliation events in individual trees based on user-specified thresholds. Site-level analyses identify outbreak events that synchronously affect user-defined numbers or proportions of involved host trees. Functions are provided for summary statistics and graphics of tree- and site-level series. We evaluated **dfoliatR** against OUTBREAK, using eight datasets including 222 host-trees, and found that **dfoliatR** improves on OUTBREAK with greater user control, identification of defoliation events, computing capacity, and both the statistical summary and graphical outputs. We provide two example data sets and script to enable users to gain familiarity with the package and its capabilities. The source code is available in the Comprehensive R Archive Network (CRAN) and on GitHub.

12 **Key words:** Dendroecology, dendroentomology, OUTBREAK, western spruce

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19 1. Introduction

20 Variation in the width and morphology of annual radial growth rings in
21 trees permits dating and quantification of past forest insect defoliator outbreaks.
22 Defoliation can be distinguished from climate- and other disturbance-related
23 influences by comparing ring-width or other annually-resolved features in the
24 wood of host species to that of non-host species or annually-resolved climate
25 records. The effect of defoliation on radial growth of trees has been recognized
26 since the 1860s, and used to reconstruct outbreak regimes since the 1950s (Blais,
27 1954; Alfaro et al., 1982; Lynch, 2012). It was not until the 1980s, however,
28 that precise dendrochronological techniques were applied for inferring defoliation
29 events and reconstructing defoliator outbreak regimes (Swetnam et al., 1985;
30 Speer, 2010; Lynch, 2012). The first studies (Swetnam et al., 1985; Swetnam and
31 Lynch, 1989, 1993) focused on developing historical outbreak reconstructions
32 of western spruce budworm (WSBW; *Choristoneura freemani* (Lepidoptera:
33 Tortricidae); previously known as *C. occidentalis*). The methodology has since
34 been successfully applied to a wide range of defoliator species, most of which
35 are conifer herbivores, and has evolved in sophistication for a wide range of
36 ecosystem situations (Lynch, 2012).

37 The main dendrochronological tool for inferring, dating, and characterizing
38 defoliator outbreaks from tree-ring records has been the software routine OUT-
39 BREAK (Swetnam et al., 1985; Holmes and Swetnam, 1986; Swetnam and Lynch,
40 1989). OUTBREAK computes indices (described later in detail) of suppressed
41 growth by subtracting a detrended and standardized climate series (a “control”

chronology) from individual host-tree detrended and standardized radial growth series after the host and non-host series have been brought to a common variance. The non-host chronology usually consists of a site chronology developed from non-host tree species growing on a climate-sensitive site, but a gridded climate data point series, like the North American Drought Atlas (Cook and Krusic, 2004) also suffices. If the host and non-host species respond similarly to climate (which can and should be tested), the derived series retains variability that the host and non-host series do not have in common, generally the insect signal and some unexplained variability (noise). The user defines a rule base specifying the magnitude and duration that a period of indexed growth suppression must meet or surpass for a period of suppressed growth to be inferred as a defoliation event at the tree level. Rule bases are derived from the user’s knowledge of insect and host ecologies, and from consideration of the likelihood and relative importance of Type I and II errors.

Though powerful, OUTBREAK is outdated and increasingly difficult to use in modern computing environments. It was written in FORTRAN V with inherently severe restrictions, as RAM and disk space were limited at that time (256 kb and 10 MB, respectively) and FORTRAN conventions imposed very strict formatting, file naming, and output conventions. The program lacks a graphical interface or capabilities, forcing users to import generated text files into spreadsheets or other software to assess results and perform analyses. Furthermore, OUTBREAK can only handle one test at a time, creating barriers to batch operation and a large burden for researchers with datasets including multiple sites. We developed **dfoliatR** (Guiterman et al., 2020) as an R- and **dp1R**-based library to overcome these issues.

dfoliatR adds to a growing suite of dendrochronology packages in the R computing environment (R Core Team, 2019). Stemming from the **dp1R** library (Bunn, 2008) that enables R users to read and write an array of tree-ring data formats, standardize ring width series, build and evaluate chronologies, and perform quality control (to name a few), one can now also measure ring widths from scanned images of prepared samples (Lara et al., 2015; Shi et al., 2019),

73 conduct and check crossdating (Bunn, 2010), analyze sub-annual anatomical
 74 features (Rathgeber et al., 2011; Campelo et al., 2016), and perform many
 75 analytical tests (Zang and Biondi, 2015; Jevšenak and Levanič, 2018). Tools for
 76 assessing stand dynamics and disturbance analyses are under rapid development,
 77 with new packages for assessing release events (**TRADER**: Altman et al., 2014),
 78 metrics of growth resilience (**pointRes**: van der Maaten-Theunissen et al., 2015),
 79 and fire history (**burnr**: Malevich et al., 2018). The key objective of **dfoliatR** is
 80 to provide tools to identify and analyze insect defoliation and outbreak events by
 81 building on the methods employed by **OUTBREAK**. It capitalizes on the robust
 82 software already available in **R** by using **dplR** data formats for incoming tree-ring
 83 series and providing output data formats embodied by the **tidyverse** (Wickham
 84 et al., 2019) that include efficient data manipulation (**dplyr**: Wickham et al.,
 85 2020) and graphics (**ggplot2**: Wickham, 2016).

86 In this paper, we describe the statistical methods employed by **dfoliatR**,
 87 compare results to those produced by **OUTBREAK**, and present an example
 88 analysis including test data sets and script. Users need not have much experience
 89 in **R** to replicate the analyses and graphics as presented. The **R** code below is
 90 executable in an **R** session once the required libraries are installed and loaded.
 91 Support documentation in addition to this paper is provided within the package
 92 via standard help menus and on the package website (<https://chguiterman.github.io/dfoliatR/>), which includes up-to-date vignettes that describe various routines.
 93 Code to generate a preprint of this manuscript, including the **R** scripts and
 94 tabular and graphical output is available from [https://github.com/chguiterman/](https://github.com/chguiterman/dfoliatR_paper)
 95 [dfoliatR_paper](https://github.com/chguiterman/dfoliatR_paper).
 96

97 **2. Overview of the software**

98 The **dfoliatR** library requires two sets of tree-ring data to infer defoliation
 99 and outbreak events:

- 100 • Standardized ring-width series for individual trees of the host species

- A standardized tree-ring chronology from a local non-host species, or a climate reconstruction

Users can develop these data sets in the software of their choosing, such as `dplR` or ARSTAN (Cook and Holmes, 1996). It is important that the host-tree data include only one tree-ring series per tree. `dplR` (via the `dplR::treeMean()` function) and `dpl` versions of ARSTAN have options for averaging multiple sample series into a tree-level series.

At the heart of `dfoliatR` lies two functions: `defoliate_trees()` and `outbreak()`. These identify defoliation events on individual trees (Figure 1) and then composite across multiple trees to infer stand or site level outbreak events (Figure 2).

2.1. Identifying Defoliation of Trees

The `defoliate_trees()` function is the point of entry to the `dfoliatR` library. It performs two processes, removing climate-related growth signals from the host-tree series and identifying tree-level defoliation events. The climatic or non-defoliation signals in each host-tree series are characterized by a non-host chronology or climate reconstruction. `dfoliatR` removes the non-defoliation signal by subtracting the non-host series from each host-tree series, which generates a residual index. In OUTBREAK, this residual index was termed the “corrected index.” We call it the “growth suppression index” (GSI). The GSI is calculated the same as in OUTBREAK for each host tree as

$$\text{GSI}_i = H_i - (\text{NH}_i - \overline{\text{NH}}) \frac{\sigma_H}{\sigma_{\text{NH}}} \quad (1)$$

where H and NH are the host-tree series and the non-host chronology, in year i , respectively. Only the common period between the host-tree series and the non-host chronology are used in Equation 1. The host and non-host chronologies are brought to common variance by scaling the non-host chronology by its mean ($\overline{\text{NH}}$) and multiplying by the ratio of host and non-host standard deviations ($\frac{\sigma_H}{\sigma_{\text{NH}}}$), which approximates the variance of the host tree series.

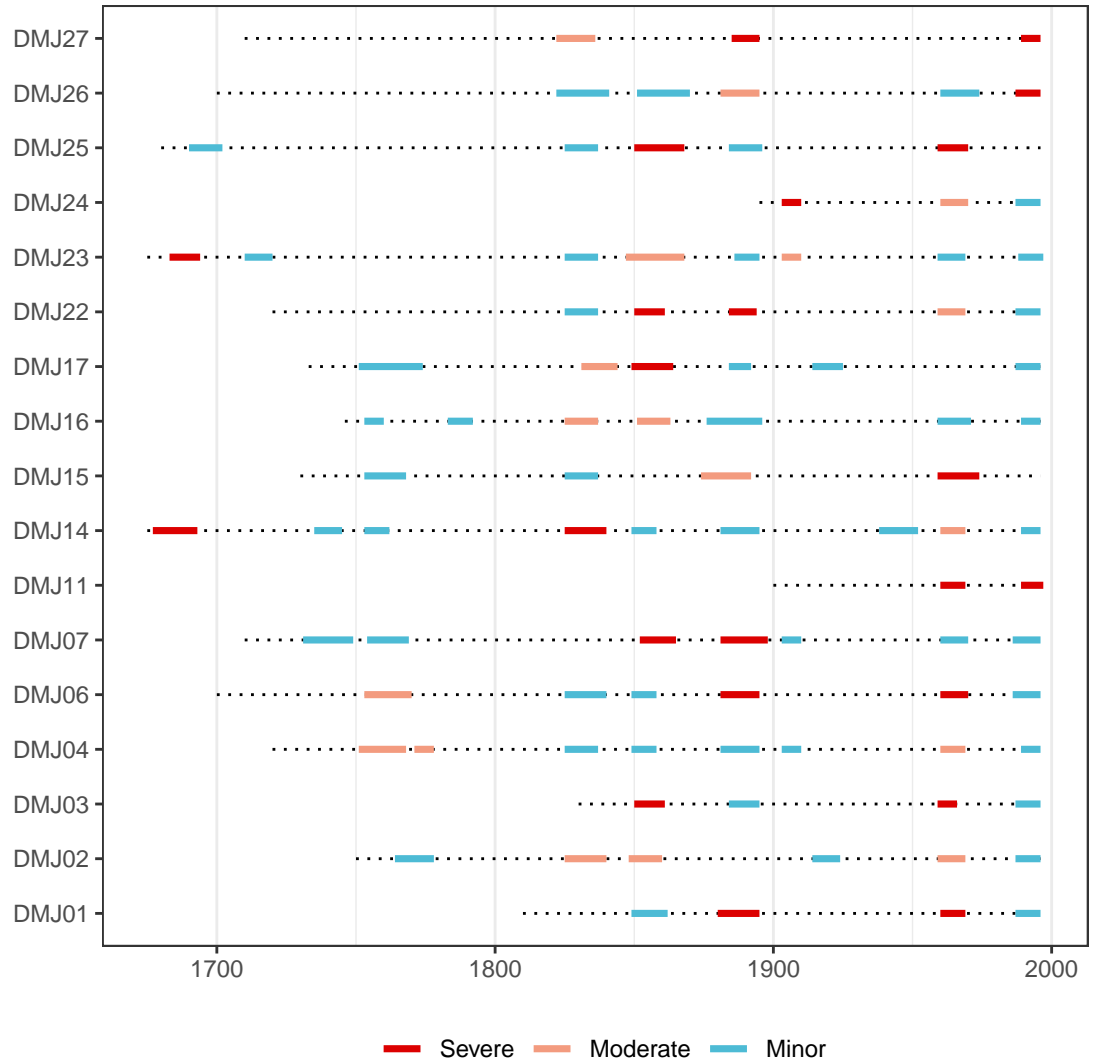


Figure 1: Default `dfoliatR` graphic for individual trees, produced by the `plot_defol()` function. The series names from the DMJ site (Ryerson et al., 2003) are listed on the Y-axis, dotted lines represent the series length for each tree, and colored segments show periods of defoliation. The colors of defoliation segments represent its severity, for which users can define cut-off values to determine severe–moderate–minor defoliation intensities. The default break points for severity classes are the mean and first quartile for event NGSI values. Colors and other features of the graphic can be adjusted using `ggplot2` parameters, as shown below.

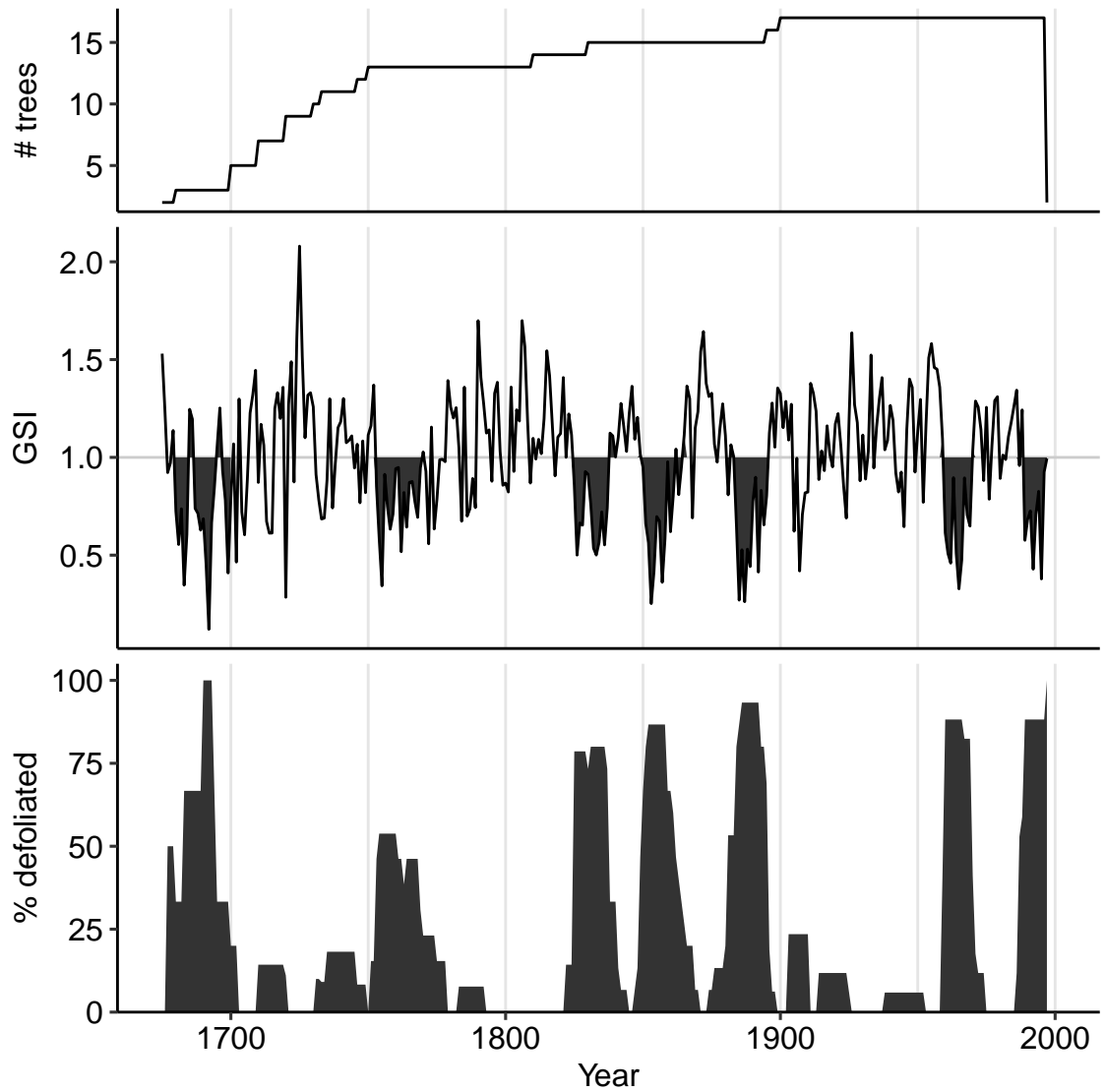


Figure 2: Default `dfoliatR` graphic for site-level outbreak events, produced by the `plot_outbreak()` function. These plots summarize the data in Figure 1 for the DMJ site. Top panel shows the sample depth, the middle panel shows the mean GSI with inferred outbreak events filled, and the bottom panel shows the percent of trees defoliated, used to identify time periods of inferred outbreaks.

119 Negative departures in the normalized GSI (NGSI, or GSI converted to
 120 z-scores) that surpass user-specified thresholds in duration and magnitude are
 121 defined as *defoliation events*. As in OUTBREAK, the lowest NGSI value in the
 122 particular sequence being assessed must reach the magnitude threshold. The
 123 default setting is -1.28 (NGSI is in units of standard deviation), which was
 124 previously determined to be representative of WSBW effects (Swetnam and
 125 Lynch, 1989) and is commonly used for other species (see Lynch, 2012). The year
 126 with the lowest value is termed the “year of maximum departure” and becomes
 127 a central point in time for assessing other thresholds before being included as a
 128 defoliation event. If the year of maximum departure is higher than the threshold
 129 (i.e. $\text{NGSI}_{\text{lowest}} > -1.28$), the sequence being assessed is omitted from the event
 130 results.

131 Event duration is assessed by examining sequences of negative NGSI (for
 132 which one or more values exceeded the magnitude threshold) before and after the
 133 year of maximum departure. Each defoliation event is allowed one single-year
 134 positive excursion on each side of the year of maximum departure. Duration
 135 is computed across the entire sequence that may include these two positive
 136 excursions. As in OUTBREAK, the user specifies a duration threshold (minimum
 137 number of years) for a departure sequence to be inferred as a defoliation event.
 138 The default threshold is eight years, as is commonly used in WSBW studies
 139 (Swetnam and Lynch, 1989). If the sequence is shorter than the duration
 140 threshold, the sequence is omitted from the event results (i.e., both thresholds
 141 must be met). Researchers can, and should, adjust the duration and magnitude
 142 parameters accordingly and critically evaluate the results, as insect species vary
 143 in the length of their outbreaks and the degree to which they can suppress tree
 144 growth. OUTBREAK provides two sets of default values, those for WSBW,
 145 which typically has lengthy outbreaks, and ones for Douglas-fir tussock moth
 146 (*Orgyia pseudotsugata* (Lepidoptera: Tortricidae)) of three years duration with
 147 -1.28 departure threshold that may be suitable for more eruptive species.

148 Like OUTBREAK, users are provided an option to suspend the duration
 149 threshold at the recent end of the series in cases where an outbreak event is

known to be ongoing. This should be used if the user has direct knowledge of defoliation at the site during the sampling campaign. The advantage of allowing potentially short, series-end events is that it allows a current event to be included in return-interval estimates, and can aid in identifying the start-year for the current defoliation event or outbreak.

Diverging from OUTBREAK, **dfoliatR** includes an option allowing users to extend defoliation events on individual trees by bridging between sequential events (Figure 3). In cases where two defoliation events are separated by a single year, bridging will link them into a single event. This option was added to **dfoliatR** during the testing phase of development, when we realized that OUTBREAK deliberately omits sequential, or back-to-back events, even when both events surpass the magnitude and duration thresholds. Instead, OUTBREAK will select the one sequential event with the lowest negative departure year. In every case we assessed (described below) we felt that the OUTBREAK-omitted defoliation events should have been maintained and recorded. Due in large part to reconstructions using OUTBREAK (see papers cited by Lynch, 2012), we now know considerably more about forest defoliator outbreak regimes than we did in the 1980s when OUTBREAK was under development. We think that two or more prolonged events separated by a single year should in some situations be considered a single event. This is particularly relevant to WSBW and spruce budworm (*C. fumiferana*), for which multiple outbreak regime reconstruction, as well as other research and forest health observations, show that outbreaks can be very long (Schmitt et al., 1984; Sanders et al., 1985; Brookes et al., 1987, and many later publications). Often the greatest growth suppression occurs late in the outbreak due to lag effects between defoliation and radial growth, and to cumulative effects accrued on a tree's resources (Brubaker, 1978; Alfaro et al., 1982; Wickman, 1986; Swetnam and Lynch, 1989, 1993; Mason et al., 1997; Axelson et al., 2014). We urge caution in using the bridging option, however, because it may not be appropriate for all studied insects, such as in situations where impacted stands barely recover from one outbreak before another begins, as with pine processionary caterpillars (*Thaumetopoea pityocampa* (Lepidoptera:

181 Thaumetopoeidae)) (Carus, 2004, 2009) or where outbreaks are known to be
182 very short, such as larch budmoth (*Zeiraphera diniana* Gn.) in the European
183 Alps (Esper et al., 2007).

184 2.2. Inferring Outbreak Events

185 Defoliation of one or a few trees does not constitute an outbreak. To determine
186 when defoliation becomes an *outbreak event*, **dfoliatR** composites the individual
187 tree defoliation series into a site-level chronology with the **outbreak()** function.
188 Users have options to define the number and/or the proportion of trees required
189 for an event to be considered an outbreak. Three parameters control whether a
190 defoliation event constitutes an outbreak: the minimum number of trees available,
191 the minimum number of trees recording defoliation, and the percent of trees
192 recording defoliation. The first allows the researcher to make a judgment call
193 as to the confidence ascribed to reduced sample depth toward the ends of their
194 chronologies, thus compensating for the “fading record problem” (Swetnam et
195 al., 1999). The second two parameters adjust the scale of defoliation considered
196 to be an outbreak. Absolute numbers of trees and percentages can be applied
197 separately or in conjunction, following filtering conventions in tree-ring fire
198 history studies (Malevich et al., 2018). We urge users to carefully consider the
199 choice of absolute numbers in situations where the number of trees represented
200 in the series varies with time, or the choice of percentages when sample size is
201 small.

202 3. Evaluation

203 3.1. Approach

204 We tested **dfoliatR** against OUTBREAK by comparing NGSI to OUT-
205 BREAK’s normalized corrected indices for individual trees and years, defoliation
206 status for individual trees and years, and percentage of trees recording outbreaks
207 at the site level. Our tests used standardized ring-width data from eight host-tree
208 sites spanning the range of WSBW. The sites were sampled in British Columbia

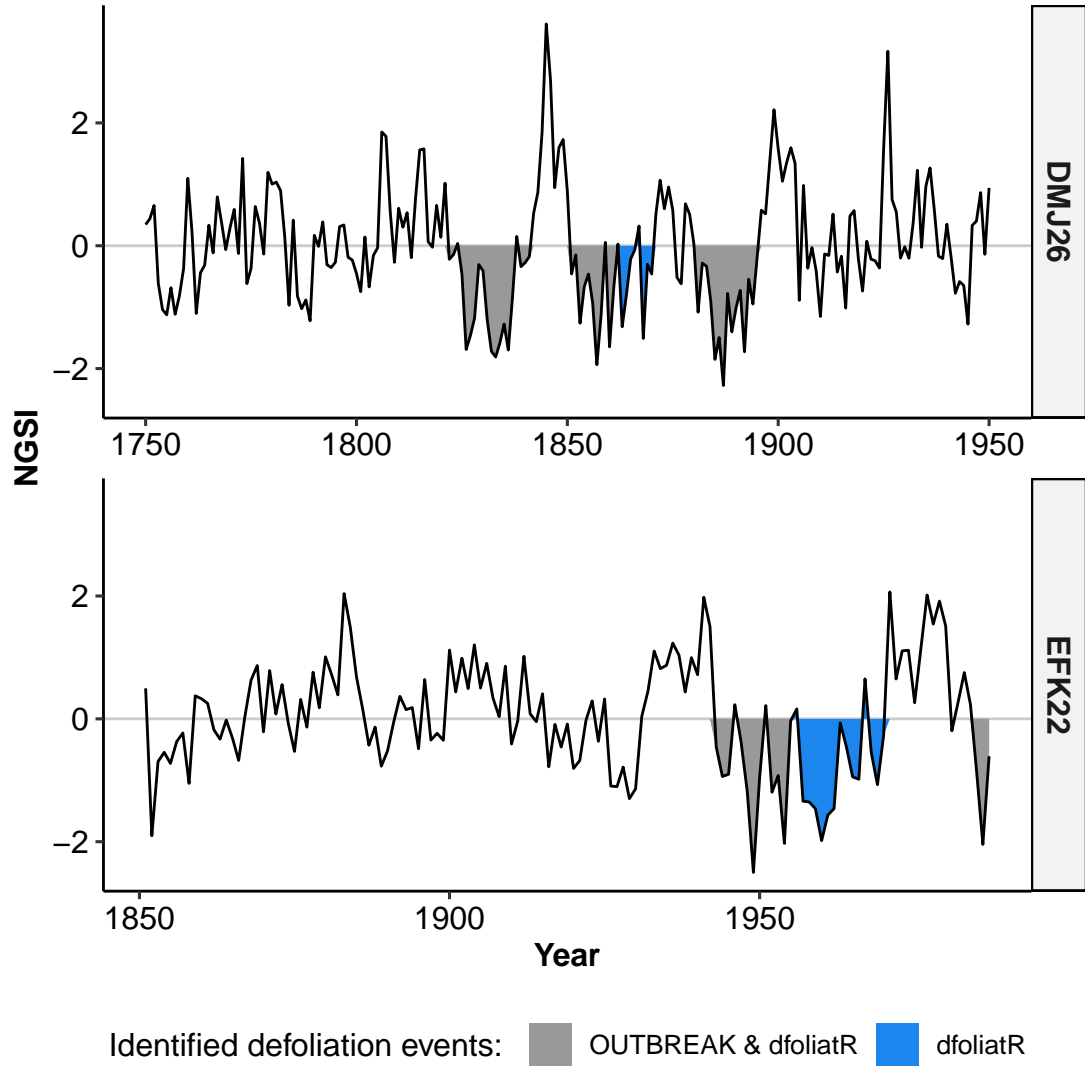


Figure 3: Examples of identified defoliation events on individual trees. For each tree (DMJ26 and EFK22), OUTBREAK and `dfoliatR` identify most of the same events, but there is one added event (in blue) that was omitted by OUTBREAK. These were omitted because they were separated by a single year of positive normalized growth suppression index (NGSI) and OUTBREAK selected the one event with the lowest maximum departure value. `dfoliatR` provides an option to bridge these sequential events into single long events that may better represent the duration of defoliation given the insect and sites under consideration.

(Axelson et al., 2015), Wyoming (Axelson et al., 2018), Colorado (Ryerson et al., 2003), and New Mexico (Swetnam and Lynch, 1993). These host data were compared to non-host chronologies from the original studies, but we made no effort here to replicate the reconstructions or analyses of those studies.

We detrended host data for both `dfoliatR` and OUTBREAK using ARSTAN (version 6.1) with cubic smoothing splines (50% frequency response on 100-150 year wavelengths depending on the site). In both `dfoliatR` and OUTBREAK we used event thresholds of -1.28 normalized indices, 8 years duration, and allowed for events at the end of series in seven of eight sites that had known outbreaks at the time of sampling. We found it necessary to be consistent in how we detrended and what software we employed (e.g., ARSTAN vs `dplR`) because subtle differences in standardized ring-width indices generated between the programs transferred into differences between `dfoliatR` and OUTBREAK. In the end, we chose to only use the standardization output files from ARSTAN, which are easily read into R (and then `dfoliatR`) using the `dplR` package.

The R code to replicate our comparisons is available from https://github.com/chguiterman/dfoliatR_paper.

3.2. Findings

Across the 43,280 ring-width indices from 222 trees included in our evaluation, we found that `dfoliatR` and OUTBREAK compute identical growth suppression indices at 0.00 precision. We expected this outcome because both programs apply Equation 1 to calculate disturbance indices. At the tree-level, the programs identified 11,530 total index years with defoliation. The programs agreed on 97.9% of the years, leaving 927 “difference” years in which only one program identified defoliation on an individual tree. The differences included 102 events on 85 trees. We carefully inspected each of these events in the full context of each tree’s ring-series, and categorized the differences as follows

- *Series-end events* (40% of the total) in which OUTBREAK included “truncated outbreaks” (for seven sites) at the end of each series. In

`dfoliatR`, this option is controlled by the “series_end_events” parameter to `defoliate_trees()`. In OUTBREAK, the option appears while changing the duration parameter (option 3). When selected, OUTBREAK will include any sequences of negative indices at the beginning and the end of each tree series as a defoliation event, without consideration of either duration or magnitude thresholds. In `dfoliatR`, the duration threshold is omitted and the magnitude threshold is retained in series-end-events. Each of the 13 events included in these differences did not meet the “max_reduction” parameter (-1.28 NGSI) in `dfoliatR` and were excluded. In two cases, OUTBREAK included events at the beginning of the series where `dfoliatR` does not allow truncated events. In four cases, OUTBREAK omitted only the last year of the series because the index was positive, but `dfoliatR` allowed this single positive excursion. Finally, there were two cases in which `dfoliatR` omitted possible events because it had already included a positive NGSI excursion after the “max_reduction” year, and since it will only allow one excursion on either side of the max year, the events were omitted due to short duration.

- *Sequential events* (36%) in which OUTBREAK omitted back-to-back events that occur one year prior to, or one year following an identified event. When this occurs, OUTBREAK selects the one event sequence with the lowest negative index year (e.g., Figure 3). On two trees, OUTBREAK omitted two of three sequential events. While inspecting these differences, we added an option to `defoliate_trees()` that would “bridge” between sequential events (that each surpass the magnitude and duration thresholds) into single, long events. We felt that this was ecologically justified, especially for studies of WSBW, because outbreaks are known to be of long duration and tree-ring reconstructions have shown that outbreaks may persist for as long as 30-50 years at the site level.
- *Undetermined differences* (22%) occurred in cases where OUTBREAK omitted events without clear cause that `dfoliatR` correctly identified as

268 defoliations.

- 269 • *Rounding differences* (2%) in the indices either omitted or cut short events
270 on two trees. In both cases the indices were very close to zero, and the
271 difference was less than the precision of the raw data measurement.

272 At the site level, OUTBREAK and `dfoliatR` produce similar time series of
273 percent trees defoliated (Figure 4), which forms the basis for inferring outbreak
274 occurrence, intensity, and duration. In nearly all site-level comparisons, `dfoliatR`
275 included either more events or it inferred a longer duration outbreak. These
276 differences arise from the inclusion of tree-level events by `dfoliatR` that were
277 omitted by OUTBREAK (see note on sequential events above). Thus, in
278 `dfoliatR`, there were a greater number of trees experiencing defoliation during
279 outbreak periods, or outbreaks were represented by a single tree when there was
280 low sample depth.

281 This comparison revealed what we believe are shortcomings in how OUT-
282 BREAK identifies defoliation events on individual trees. In every one of the
283 102 cases we inspected, we felt that `dfoliatR` provided a more biologically and
284 statistically appropriate assessment of defoliation, translating to more robust
285 inferences of outbreak events and associated statistics at the site level.

286 4. Availability and installation

287 The `dfoliatR` library is provided free and open source from the Compre-
288 hensive R Archive Network (CRAN; <https://cran.r-project.org/>). To install
289 `dfoliatR` from CRAN use

```
install.packages("dfoliatR")
```

290 In each R session, `dfoliatR` can be loaded via

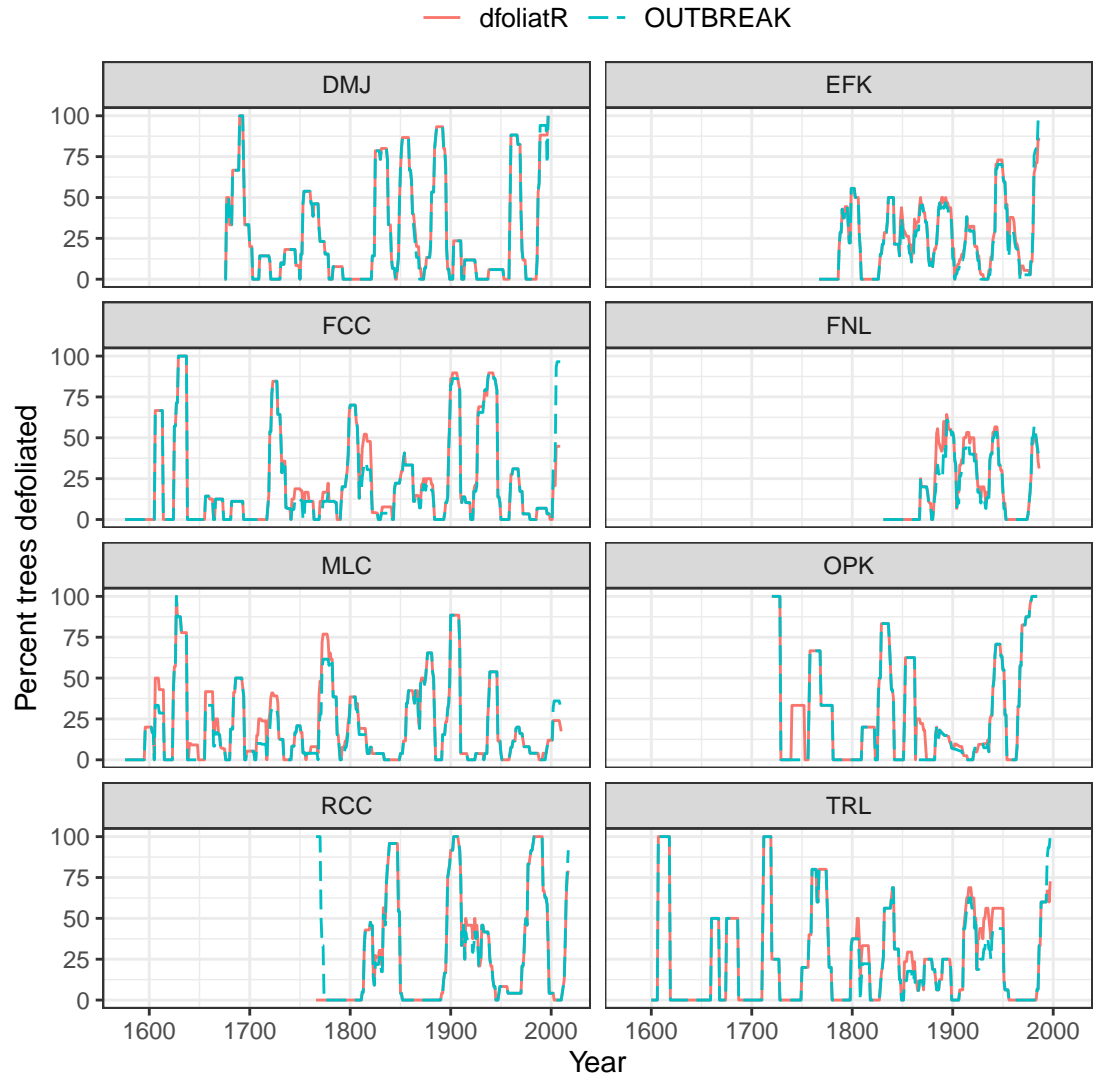


Figure 4: Comparison of reconstructed western spruce budworm outbreaks computed by **dfoliatR** and **OUTBREAK**. Input parameters were identical between programs. Differences arise because **dfoliatR** will identify and record more defoliation events on individual trees.

```
library(dfoliatR)
```

291 Development versions of **dfoliatR** are available on GitHub and installed
292 using the **devtools** library,

```
devtools::install_github("chguiterman/dfoliatR")
```

293 Issues, bug reports, and ideas for improving **dfoliatR** can be posted to
294 <https://github.com/chguiterman/dfoliatR/issues>. As an Open Source library,
295 we welcome and encourage community involvement in future development. The
296 best ways to contribute to **dfoliatR** are through standard GitHub procedures
297 or by contacting the corresponding author.

298 5. Example Usage

299 Once **dfoliatR** is loaded into an R session (via `library(dfoliatR)`) users
300 can access two sets of tree-ring data to aid in exploring the functions, graphics,
301 and outputs. Each data set consists of individual host-tree series and a local
302 non-host chronology. The host-tree series were standardized using 128-year
303 splines with a 50% frequency response, while the non-host ring-width data
304 were standardized using 150-year splines with a 50% frequency response and
305 then averaged via Tukey's biweight robust mean procedure. Host trees from
306 Demijohn Peak (DMJ; 2902 m asl) in the San Juan Mountains of southern
307 Colorado include Douglas-fir (*Pseudotsuga menziesii*) compared against a local
308 non-host ponderosa pine (*Pinus ponderosa*) chronology (Ryerson et al., 2003).
309 The East Fork site (EFK; 2580 m asl) in the Jemez Mountains of north-central
310 New Mexico includes Douglas-fir and white fir (*Abies concolor*) host trees and a
311 ponderosa pine non-host chronology (Swetnam and Lynch, 1993).

312 With **dfoliatR** loaded, the datasets are accessible using the `data()` function.
313 The data object names are prefixed by their site codes. For instance, the `dmj_*`
314 objects come from the DMJ site and include the host-tree series (`dmj_h`), the non-
315 host chronology (`dmj_nh`), the defoliation series (`dmj_defol`), and the outbreak

316 series (`dmj_obr`). The same suite of data are available for EFK using the `efk_*`
317 prefix.

318 In our example scripts below, `##` and `#` denote user comments, per standard
319 R coding, which are colored in brown. Text in blue denotes functions; black
320 are loaded objects, and green are quoted variables and links. Values or other
321 information provided after equal signs are filenames and parameters provided for
322 this example, and in actual use would be replaced with user-specified information.
323 In this example “`dmj_h`” and “`dmj_nh`” are the individual-tree host series and
324 non-host site chronology files for the Demijohn site, thresholds are set at 8 years
325 and -1.28 standard deviations, bridging is used, series-end events are included in
326 the interval computations, and comprehensive results information is not included
327 in the output.

328 5.1. Tree-Level Defoliation Events

329 The function `defoliate_trees()` performs the GSI indexing procedure on
330 each host-tree series and then identifies defoliation events.

```
## Load the package
library(dfoliatR)

## Load data
data("dmj_h") # host tree series
data("dmj_nh") # non-host chronology
# View data structure for any data object via
# "View(dmj_h)" or "head(dmj_h)"

## Calculate indices, identify defoliation events
dmj_defol <- defoliate_trees(host_tree = dmj_h,
                             nonhost_chron = dmj_nh,
                             duration_years = 8,
                             max_reduction = -1.28,
```

```

bridge_events = TRUE,
series_end_event = TRUE,
list_output = FALSE)

```

331 The result is long-format (stacked) data frame with five variables: “year”,
 332 “series”, “gsi”, “ngsi”, and “defol_status.” The “defol_status” column indicates
 333 whether that year has defoliation or not, with a set of factors that include
 334 “nd” for non-defoliation year, “defol” for a defoliation year, “max_defol” for
 335 the year of maximum suppression (that acts as the basis for individual events),
 336 “bridge_defol” to identify years that link subsequent events (only one is present
 337 at DMJ), and “series_end_defol” to identify defoliation at the present-end of
 338 the series.

339 Selecting `list_output = TRUE` in `defoliate_trees()` provides a list-object
 340 of data frames, each with an `rw1` object that combines the host tree and non-host
 341 series and the other columns created by `defoliate_trees()`. This option is not
 342 used by subsequent functions in `dfoliatR`, but researchers can examine it to
 343 check the results of the GSI calculation (Equation 1), such as the non-host series
 344 after scaling to a common variance with a particular host-tree series.

345 The results of running `defoliate_trees()` can be assessed through graphical
 346 and table outputs. The function `get_defol_events()` will provide a list of every
 347 defoliation event for every tree, with the corresponding mean “ngsi” value. A
 348 summary table of the results for each tree is produced by `defol_stats()` (Table
 349 1).

```

dmj_defol_stats <- defol_stats(dmj_defol)
View(dmj_defol_stats)

```

350 The `plot_defol()` function produces a “ggplot” graphics object with line
 351 segments showing the measured sequence of each series and a filled segment
 352 for each identified defoliation event (Figure 1). The defoliation segments are
 353 colored by their relative severity based on their average NGSi value. By default,
 354 `plot_defol()` will calculate the average NGSi for all identified events, and assign

Table 1: Tree-level tabular output provided by the `defol_stats()` function for the DMJ example site. Note that these calculations exclude the ongoing “series-end” events as selected in `defoliate_trees()`.

series	first	last	years	n_events	tot_years	mean_duration
DMJ01	1810	1996	187	4	40	13
DMJ02	1750	1996	247	6	66	13
DMJ03	1830	1996	167	4	32	11
DMJ04	1720	1996	277	8	82	12
DMJ06	1700	1996	297	6	70	14
DMJ07	1710	1996	287	7	86	14
DMJ11	1900	1997	98	2	10	10
DMJ14	1675	1996	322	9	104	13
DMJ15	1730	1996	267	4	64	16
DMJ16	1746	1996	251	7	78	13
DMJ17	1733	1996	264	6	75	15
DMJ22	1720	1996	277	5	47	12
DMJ23	1675	1997	323	8	87	12
DMJ24	1895	1996	102	3	19	10
DMJ25	1680	1996	317	5	70	14
DMJ26	1700	1996	297	6	70	14
DMJ27	1710	1996	287	3	26	13

355 severity based on the mean and first quartile of the averages. “Severe” events
356 have a mean NGSI above the overall average event-period NGSI. “Moderate”
357 events fall between the mean and first quartile. “Minor” events fall below the
358 first quartile. Users can re-define the breaks to suit their needs via the “breaks”
359 parameter in `plot_defol()`.

```

plot_defol(dmj_defol)
## This creates a ggplot object. Additions can
## be made to adjust plotting themes and
## aesthetics, like color.
## For more on the features of ggplot see
## https://ggplot2.tidyverse.org/
## Adding 'scale_color_manual()' will
## change the colors that denote
## the average NGSF value for each defoliation
## event.
library(ggplot2)
plot_defol(dmj_defol) +
  scale_color_manual(values = c("red", "orange", "purple"))

```

360 These output functions aid in assessing the sensitivity of input parameters to
 361 `defoliate_trees()`, including the duration and magnitude thresholds for iden-
 362 tifying defoliation events. Using `plot_defol()` also provides a direct assessment
 363 of the between-tree variability in defoliation.

364 5.2. Site-Level Events

365 To infer outbreak events at the site level, the function `outbreak()` composites
 366 tree-level defoliation series into a single chronology, with input parameters that
 367 control thresholds in the number and proportions of trees recording a defoliation
 368 event.

```

## Use the defol object "dmj_defol" created above
dmj_obr <- outbreak(dmj_defol,
  filter_min_series = 3,
  filter_min_defol = 1,
  filter_perc = 25)

```

369 Input parameters to `outbreak()` include “`filter_min_series`” to control the

370 chronology cut-off points with regard to sample depth, “filter_min_defol” and
 371 “filter_perc” to control the minimum number and percent of trees recording
 372 a defoliation event in a given year. `outbreak()` produces a new data frame
 373 with eight variables: “year”, “num_defol”, “percent_defol”, “num_max_defol”,
 374 “mean_gsi”, “mean_ngsi”, and “outbreak_status.” All of these variables are
 375 populated regardless of an inferred outbreak event, providing a continuous
 376 outbreak reconstruction. The “num_max_defol” variable counts the number
 377 of trees recording their maximum defoliation in a given year. The “mean_gsi”
 378 and “mean_ngsi” variables provide averages of these indices across all available
 379 trees. Finally, the “outbreak_status” column shows whether an outbreak event
 380 is inferred (“outbreak”) or not (“not_obr”).

381 The default plotting function to visualize results from `outbreak()` is `plot_outbreak()`.
 382 It creates a three-panel graph showing the sample depth, mean site-level chronol-
 383 ogy, and percent of trees recording a defoliation over time (Figure 2).

```
plot_outbreak(dmj_obr, disp_index = "GSI")
```

384 Inferred outbreak events are shown in the middle panel of Figure 2 as the filled-
 385 in spaces. Users can change the time series in this panel with the “disp_index”
 386 parameter, choosing between the mean NGSI (the default) or GSI.

387 A summary table of the inferred outbreak events is generated by the `outbreak_stats()`
 388 function (Table 2). The table provides a range of summary statistics, including
 389 the start and end years of each outbreak event, along with the corresponding
 390 duration, the number and percent of trees in defoliation at the start of the event
 391 (“n_df_start” and “perc_df_start”, respectively), the maximum number of
 392 trees recording the outbreak event during a single year (“max_df_obr”), the
 393 year corresponding to that peak (“yr_max_df”), the year with the lowest mean
 394 NGSI during the event (“yr_min_ngsi”), and the minima of mean GSI and
 395 mean NGSI indices during the event.

```
dmj_obr_stats <- outbreak_stats(dmj_obr)
View(dmj_obr_stats)
```

Table 2: Site-level summary statistics for inferred outbreak events as generated by the `outbreak_stats()` function for the DMJ example site. Note that missing (“NA”) values occur for certain statistics because the last outbreak event was defined earlier as ongoing (i.e. we set `series_end_event = TRUE` in the call to `defoliate_trees()`).

start	end	duration	n_df_start	perc_df_start	max_df_obr	yr_max_df	yr_min_ngsi	min_gsi	min_ngsi
1680	1699	20	1	33.3	3	1690	1692	0.121	-2.407
1753	1769	17	6	46.2	7	1754	1755	0.343	-1.611
1825	1840	16	11	78.6	12	1831	1826	0.500	-1.304
1849	1865	17	7	46.7	13	1852	1853	0.252	-1.994
1881	1895	15	8	53.3	14	1886	1885	0.262	-1.945
1959	1970	12	7	41.2	15	1960	1965	0.328	-1.830
1987	NA	NA	9	52.9	15	NA	NA	0.378	-1.640

396 Saving the results of `outbreak_stats()` (the `dmj_obr_stats` object above)
397 provides an array of options for assessing metrics of the insect outbreak regime.
398 For example, taking the first year of each outbreak event, we can calculate
399 the duration of years between outbreaks, via the `diff()` function in R. The
400 average of those differences, calculated via `mean()` is the mean return interval of
401 reconstructed outbreak events at the DMJ site.

```
## calculate mean return interval for outbreak start years  
intervals <- diff(dmj_obr_stats$start)  
mean(intervals) ## 51.2 year mean return interval
```

402 6. Conclusions

403 The `dfoliatR` package provides dendroecologists with tools to infer, quantify,
404 analyze, and visualize tree-ring growth suppression events and to reconstruct
405 forest insect defoliator outbreak regimes. It is built on the long-accepted host
406 to non-host comparison methodology used in the 1980s FORTRAN program
407 OUTBREAK (Swetnam et al., 1985; Swetnam and Lynch, 1989, 1993). Our
408 evaluation of the two programs revealed that `dfoliatR` excels in identifying
409 defoliation events on single trees, providing researchers with more consistent
410 and biologically-justifiable results. `dfoliatR` provides easier control of the rule
411 base for suppression thresholds, additional output tables, and high-quality and
412 customizable graphics. These features allow users to compare insect outbreak
413 regimes of different tree species or geographic regions, evaluate sample-size
414 considerations, examine a multitude of relevant insect disturbance questions,
415 and more readily evaluate the potential for Type I and II errors in their results.
416 Finally, `dfoliatR` operates in the open-source R environment that is stable across
417 computing platforms and is under active development and maintenance by a
418 large and growing community.

419 Using `dfoliatR` requires standardized ring-width measurements from insect
420 host trees and either an indexed tree-ring chronology from local non-host trees

421 or suitable climate chronology. It performs an indexing procedure to remove
422 the climatic signal represented in the non-host chronology from the host-tree
423 series. It then infers defoliation events in individual trees. Site-level analyses
424 identify outbreak events that synchronously affect a user-defined number or
425 proportion of the host trees. Functions are provided for summary statistics and
426 graphics of tree- and site-level series. The package produces publication-quality
427 plots, and tabulates growth suppression indices and tree- and site-level outbreak
428 event statistics for user-defined post-processing needs, including those suitable
429 for charting and tabulating landscape- and regional-level results.

430 **dfoliatR** adds a new option for dendroentomology to combine, or “bridge,”
431 sequential tree-level defoliation events into single events. In practice, we suggest
432 that researchers carefully evaluate if bridging is ecologically applicable to study
433 situations and insect ecology, and to carefully explore the data before deciding
434 whether or not to use this option. It is probably not appropriate for insects
435 with high-frequency, high-severity outbreaks, such as processionary caterpillars.
436 Outbreak reconstructions of insects for which the interval is notably longer than
437 typical outbreak duration, such as Douglas-fir tussock moth, are unlikely to be
438 significantly affected. Species for which outbreak duration or individual tree
439 resilience to defoliation varies considerably, or which may chronically infest trees
440 or sites, or alternate between chronic, outbreak, and minimal activity states such
441 as conifer-feeding *Choristoneura*, present more complicated challenges, and the
442 researcher should use discretion with the bridge option.

443 **dfoliatR** adds to the on-going open-source software development for den-
444 drochronological methods (e.g., Bunn, 2008; Brewer, 2014; Brewer and Gui-
445 terman, 2016). The R environment enables automation of analyses, allowing
446 input/output processes to become routine, enables efficient sensitivity analyses,
447 and empowers batch processing of large multi-site projects. It also facilitates ad-
448 ditional statistical analyses, such as spectral analyses and superposed epoch anal-
449 yses (e.g., Malevich et al., 2018), with easy transfer from **dfoliatR** and **dp1R** to
450 other libraries in R. Source code for **dfoliatR** is available in the Comprehensive R
451 Archive Network (CRAN) and GitHub <https://github.com/chguiterman/dfoliatR>

452 with updated descriptions and helpful vignettes on the package website <https://chguiterman.github.io/dfoliatR/>. Researchers wishing to contribute to the
453 further development of **dfoliatR** are encouraged to do so via the GitHub
454 repository.

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