

# 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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13 budworm, defoliator regimes, insect outbreak reconstruction

## 14 1. Introduction

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

32 The main dendrochronological tool for inferring, dating, and characterizing  
33 defoliator outbreaks from tree-ring records has been the software routine OUT-  
34 BREAK (Swetnam et al., 1985; Holmes and Swetnam, 1986; Swetnam and Lynch,  
35 1989). OUTBREAK computes indices (described later in detail) of suppressed  
36 growth by subtracting a detrended and standardized climate series (a “control”  
37 chronology) from individual host-tree detrended and standardized radial growth  
38 series after the host and non-host series have been brought to a common variance.  
39 The non-host chronology usually consists of a site chronology developed from  
40 non-host tree species growing on a climate-sensitive site, but a gridded climate  
41 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), conduct and check crossdating (Bunn, 2010), analyze sub-annual anatomical features (Rathgeber et al., 2011; Campelo et al., 2016), and perform many analytical tests (Zang and Biondi, 2015; Jevšenak and Levanič, 2018). Tools for assessing stand dynamics and disturbance analyses are under rapid development, with new packages for assessing release events (**TRADER**: Altman et al., 2014),

metrics of growth resilience (`pointRes`: van der Maaten-Theunissen et al., 2015),  
 and fire history (`burnr`: Malevich et al., 2018). The key objective of `dfoliatR` is  
 to provide tools to identify and analyze insect defoliation and outbreak events by  
 building on the methods employed by OUTBREAK. It capitalizes on the robust  
 software already available in R by using `dplR` data formats for incoming tree-ring  
 series and providing output data formats embodied by the `tidyverse` (Wickham  
 et al., 2019) that include efficient data manipulation (`dplyr`: Wickham et al.,  
 2020) and graphics (`ggplot2`: Wickham, 2016).

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

## 2. Overview of the software

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

- 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  $\text{NH}$  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.

Negative departures in the normalized GSI (NGSI, or GSI converted to z-scores) that surpass user-specified thresholds in duration and magnitude are defined as *defoliation events*. As in OUTBREAK, the lowest NGSI value in the particular sequence being assessed must reach the magnitude threshold. The default setting is -1.28 (NGSI is in units of standard deviation), which was previously determined to be representative of WSBW effects (Swetnam and

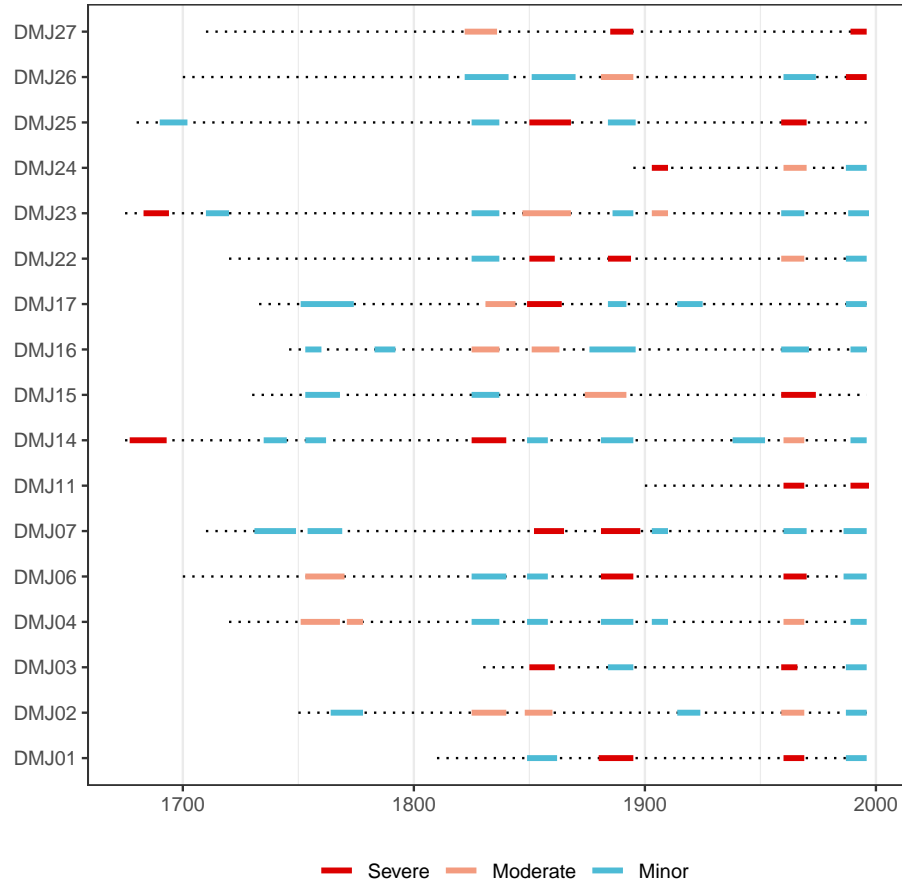


Figure 1: Default `dfoliatR` graphic for individual trees, produced by the `plot_defol()` function. The series names from the DMJ site (Ryerson et al., 2003) are listed on the Y-axis, dotted lines represent the series length for each tree, and colored segments show periods of defoliation. The colors 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.

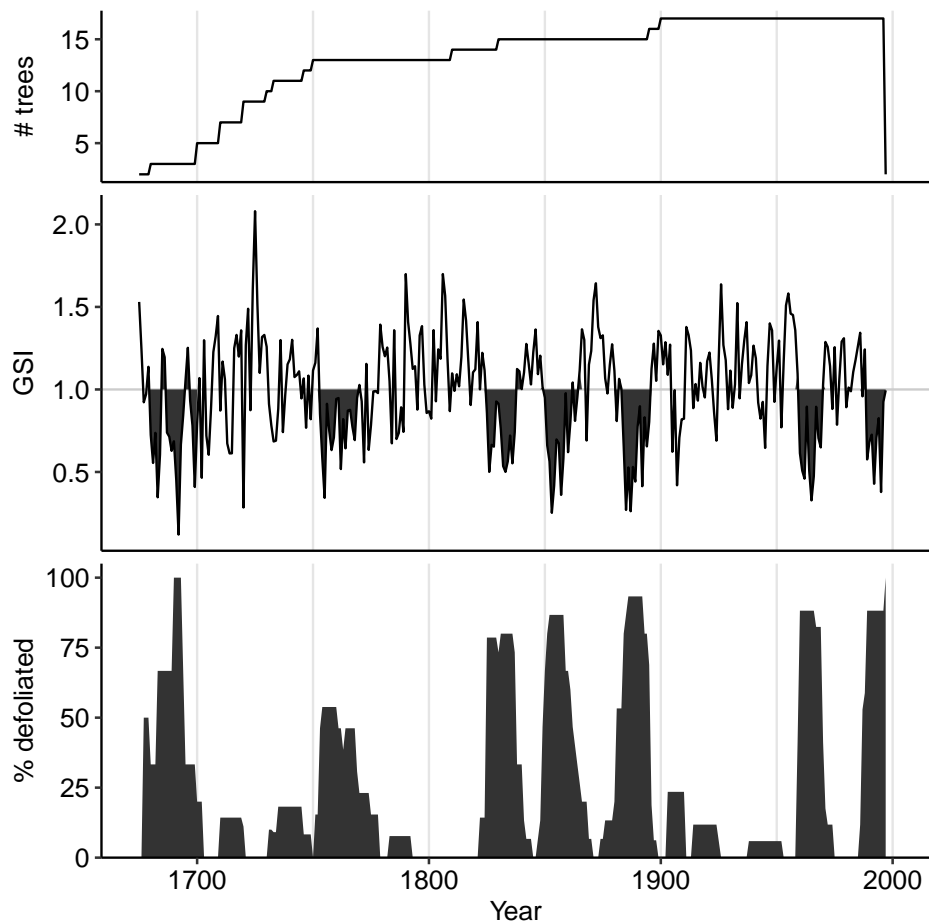


Figure 2: Default `dfoliatR` graphic for site-level outbreak events, produced by the `plot_outbreak()` function. These plots summarize the data in Figure 1 for the DMJ site. Top panel shows the sample depth, the middle panel shows the mean GSI with inferred outbreak events filled, and the bottom panel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

120 Lynch, 1989) and is commonly used for other species (see Lynch, 2012). The year  
 121 with the lowest value is termed the “year of maximum departure” and becomes  
 122 a central point in time for assessing other thresholds before being included as a  
 123 defoliation event. If the year of maximum departure is higher than the threshold  
 124 (i.e.  $\text{NGSI}_{\text{lowest}} > -1.28$ ), the sequence being assessed is omitted from the event  
 125 results.

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

143 Like OUTBREAK, users are provided an option to suspend the duration  
 144 threshold at the recent end of the series in cases where an outbreak event is  
 145 known to be ongoing. This should be used if the user has direct knowledge of  
 146 defoliation at the site during the sampling campaign. The advantage of allowing  
 147 potentially short, series-end events is that it allows a current event to be included  
 148 in return-interval estimates, and can aid in identifying the start-year for the  
 149 current defoliation event or outbreak.

150 Diverging from OUTBREAK, `dfoliatR` includes an option allowing users to



151 extend defoliation events on individual trees by bridging between sequential events  
 152 (Figure 3). In cases where two defoliation events are separated by a single year,  
 153 bridging will link them into a single event. This option was added to `dfoliatR`  
 154 during the testing phase of development, when we realized that OUTBREAK  
 155 deliberately omits sequential, or back-to-back events, even when both events  
 156 surpass the magnitude and duration thresholds. Instead, OUTBREAK will  
 157 select the one sequential event with the lowest negative departure year. In  
 158 every case we assessed (described below) we felt that the OUTBREAK-omitted  
 159 defoliation events should have been maintained and recorded. Due in large part  
 160 to reconstructions using OUTBREAK (see papers cited by Lynch, 2012), we  
 161 now know considerably more about forest defoliator outbreak regimes than we  
 162 did in the 1980s when OUTBREAK was under development. We think that two  
 163 or more prolonged events separated by a single year should in some situations  
 164 be considered a single event. This is particularly relevant to WSBW and spruce  
 165 budworm (*C. fumiferana*), for which multiple outbreak regime reconstruction,  
 166 as well as other research and forest health observations, show that outbreaks  
 167 can be very long (Schmitt et al., 1984; Sanders et al., 1985; Brookes et al., 1987,  
 168 and many later publications). Often the greatest growth suppression occurs late  
 169 in the outbreak due to lag effects between defoliation and radial growth, and  
 170 to cumulative effects accrued on a tree’s resources (Brubaker, 1978; Alfaro et  
 171 al., 1982; Wickman, 1986; Swetnam and Lynch, 1989, 1993; Mason et al., 1997;  
 172 Axelson et al., 2014). We urge caution in using the bridging option, however,  
 173 because it may not be appropriate for all studied insects, such as in situations  
 174 where impacted stands barely recover from one outbreak before another begins,  
 175 as with pine processionary caterpillars (*Thaumetopoea pityocampa* (Lepidoptera:  
 176 Thaumetopoeidae)) (Carus, 2004, 2009) or where outbreaks are known to be  
 177 very short, such as larch budmoth (*Zeiraphera diniana* Gn.) in the European  
 178 Alps (Esper et al., 2007).

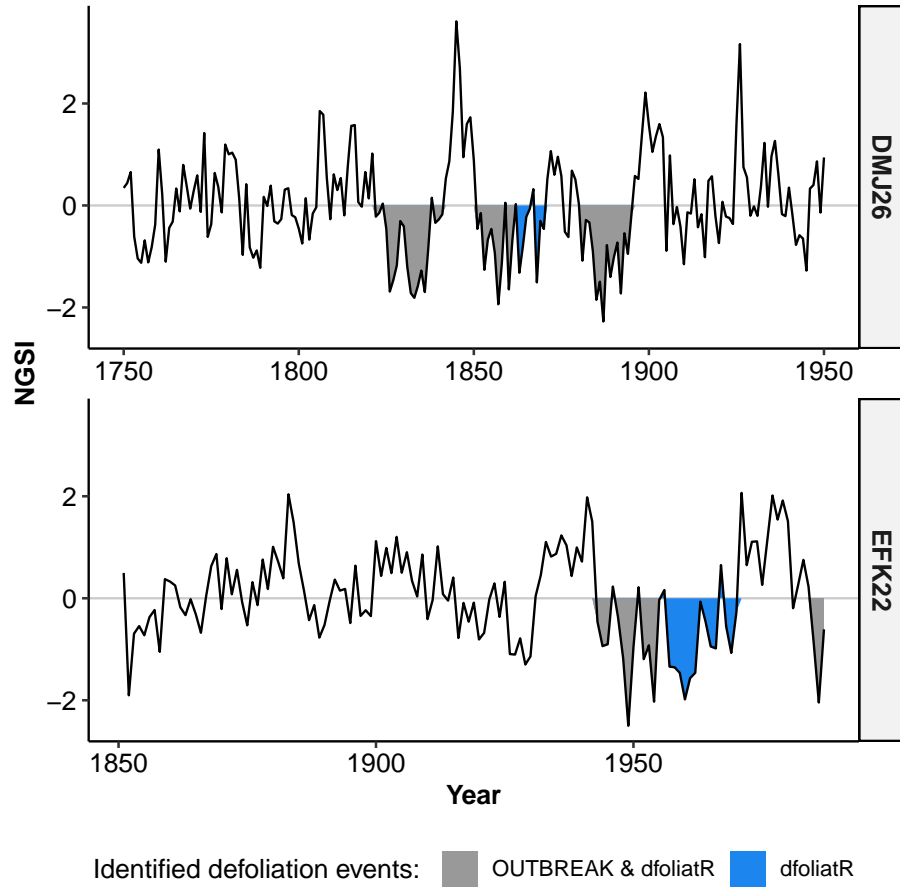


Figure 3: Examples of identified defoliation events on individual trees. For each tree (DMJ26 and EFK22), OUTBREAK and `dfoliatR` identify most of the same events, but there is one added event (in blue) that was omitted by OUTBREAK. These were omitted because they were separated by a single year of positive 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.

## 179 2.2. Inferring Outbreak Events

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

## 197 3. Evaluation

### 198 3.1. Approach

199 We tested `dfoliatR` against OUTBREAK by comparing NGSI to OUT-  
200 BREAK’s normalized corrected indices for individual trees and years, defoliation  
201 status for individual trees and years, and percentage of trees recording outbreaks  
202 at the site level. Our tests used standardized ring-width data from eight host-tree  
203 sites spanning the range of WSBW. The sites were sampled in British Columbia  
204 (Axelson et al., 2015), Wyoming (Axelson et al., 2018), Colorado (Ryerson et  
205 al., 2003), and New Mexico (Swetnam and Lynch, 1993). These host data were  
206 compared to non-host chronologies from the original studies, but we made no  
207 effort here to replicate the reconstructions or analyses of those studies.

208 We detrended host data for both `dfoliatR` and OUTBREAK using ARSTAN  
 209 (version 6.1) with cubic smoothing splines (50% frequency response on 100-150  
 210 year wavelengths depending on the site). In both `dfoliatR` and OUTBREAK  
 211 we used event thresholds of -1.28 normalized indices, 8 years duration, and  
 212 allowed for events at the end of series in seven of eight sites that had known  
 213 outbreaks at the time of sampling. We found it necessary to be consistent in  
 214 how we detrended and what software we employed (e.g., ARSTAN vs `dplR`)  
 215 because subtle differences in standardized ring-width indices generated between  
 216 the programs transferred into differences between `dfoliatR` and OUTBREAK.  
 217 In the end, we chose to only use the standardization output files from ARSTAN,  
 218 which are easily read into R (and then `dfoliatR`) using the `dplR` package.  
 219 The R code to replicate our comparisons is available from [https://github.com/chguiterman/dfoliatR\\_paper](https://github.com/chguiterman/dfoliatR_paper).  
 220

### 221 3.2. Findings

222 Across the 43,280 ring-width indices from 222 trees included in our evaluation,  
 223 we found that `dfoliatR` and OUTBREAK compute identical growth suppression  
 224 indices at 0.00 precision. We expected this outcome because both programs  
 225 apply Equation 1 to calculate disturbance indices. At the tree-level, the programs  
 226 identified 11,530 total index years with defoliation. The programs agreed on  
 227 97.9% of the years, leaving 927 “difference” years in which only one program  
 228 identified defoliation on an individual tree. The differences included 102 events  
 229 on 85 trees. We carefully inspected each of these events in the full context of  
 230 each tree’s ring-series, and categorized the differences as follows

- 231 • *Series-end events* (40% of the total) in which OUTBREAK included  
 232 “truncated outbreaks” (for seven sites) at the end of each series. In  
 233 `dfoliatR`, this option is controlled by the “series\_end\_events” parameter  
 234 to `defoliate_trees()`. In OUTBREAK, the option appears while chang-  
 235 ing the duration parameter (option 3). When selected, OUTBREAK will  
 236 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 defoliations.
- *Rounding differences* (2%) in the indices either omitted or cut short events on two trees. In both cases the indices were very close to zero, and the difference was less than the precision of the raw data measurement.

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

276 This comparison revealed what we believe are shortcomings in how OUT-  
277 BREAK identifies defoliation events on individual trees. In every one of the  
278 102 cases we inspected, we felt that `dfoliatR` provided a more biologically and  
279 statistically appropriate assessment of defoliation, translating to more robust  
280 inferences of outbreak events and associated statistics at the site level.

#### 281 4. Availability and installation

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

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

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

```
library(dfoliatR)
```

286 Development versions of `dfoliatR` are available on GitHub and installed  
287 using the `devtools` library,

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

288 Issues, bug reports, and ideas for improving `dfoliatR` can be posted to  
289 <https://github.com/chguiterman/dfoliatR/issues>. As an Open Source library,

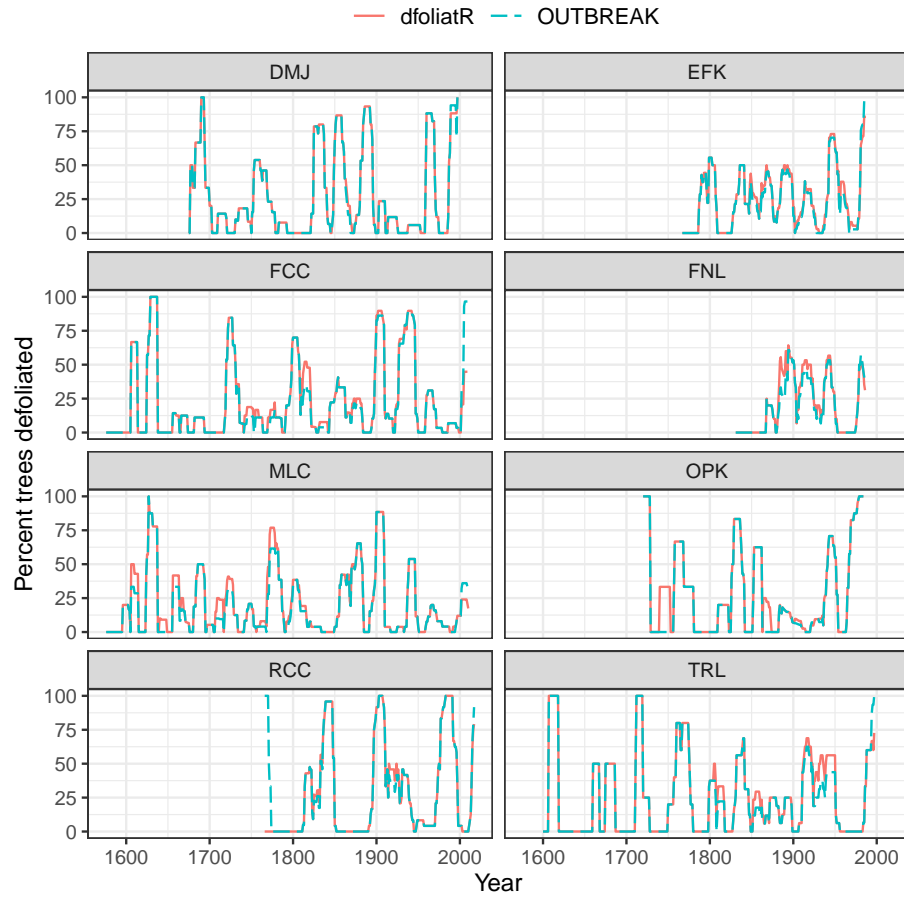


Figure 4: Comparison of reconstructed western spruce budworm outbreaks computed by `dfoliatR` and `OUTBREAK`. Input parameters were identical between programs. Differences arise because `dfoliatR` will identify and record more defoliation events on individual trees.

we welcome and encourage community involvement in future development. The best ways to contribute to **dfoliatR** are through standard GitHub procedures or by contacting the corresponding author.

## 5. Example Usage

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

With **dfoliatR** loaded, the datasets are accessible using the `data()` function. The data object names are prefixed by their site codes. For instance, the `dmj_*` objects come from the DMJ site and include the host-tree series (`dmj_h`), the non-host chronology (`dmj_nh`), the defoliation series (`dmj_defol`), and the outbreak series (`dmj_obr`). The same suite of data are available for EFK using the `efk_*` prefix.

In our example scripts below, `##` and `#` denote user comments, per standard R coding, which are colored in brown. Text in blue denotes functions; black are loaded objects, and green are quoted variables and links. Values or other information provided after equal signs are filenames and parameters provided for this example, and in actual use would be replaced with user-specified information. In this example “`dmj_h`” and “`dmj_nh`” are the individual-tree host series and



319 non-host site chronology files for the Demijohn site, thresholds are set at 8 years  
320 and -1.28 standard deviations, bridging is used, series-end events are included in  
321 the interval computations, and comprehensive results information is not included  
322 in the output.

### 323 5.1. Tree-Level Defoliation Events

324 The function `defoliate_trees()` performs the GSI indexing procedure on  
325 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)
```

326 The result is long-format (stacked) data frame with five variables: “year”,  
327 “series”, “gsi”, “ngsi”, and “defol\_status.” The “defol\_status” column indicates  
328 whether that year has defoliation or not, with a set of factors that include  
329 “nd” for non-defoliation year, “defol” for a defoliation year, “max\_defol” for  
330 the year of maximum suppression (that acts as the basis for individual events),

331 “bridge\_defol” to identify years that link subsequent events (only one is present  
332 at DMJ), and “series\_end\_defol” to identify defoliation at the present-end of  
333 the series.

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

340     The results of running `defoliate_trees()` can be assessed through graphical  
341 and table outputs. The function `get_defol_events()` will provide a list of every  
342 defoliation event for every tree, with the corresponding mean “ngsi” value. A  
343 summary table of the results for each tree is produced by `defol_stats()` (Table  
344 1).

```
dmj_defol_stats <- defol_stats(dmj_defol)
View(dmj_defol_stats)
```

345     The `plot_defol()` function produces a “ggplot” graphics object with line  
346 segments showing the measured sequence of each series and a filled segment  
347 for each identified defoliation event (Figure 1). The defoliation segments are  
348 colored by their relative severity based on their average NGSI value. By default,  
349 `plot_defol()` will calculate the average NGSI for all identified events, and assign  
350 severity based on the mean and first quartile of the averages. “Severe” events  
351 have a mean NGSI above the overall average event-period NGSI. “Moderate”  
352 events fall between the mean and first quartile. “Minor” events fall below the  
353 first quartile. Users can re-define the breaks to suit their needs via the “breaks”  
354 parameter in `plot_defol()`.

```
plot_defol(dmj_defol)
## This creates a ggplot object. Additions can
## be made to adjust plotting themes and
```

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

```
## 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 NGSI value for each defoliation
```

```
## event.
library(ggplot2)
plot_defol(dmj_defol) +
  scale_color_manual(values = c("red", "orange", "purple"))
```

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

## 5.2. Site-Level Events

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

Input parameters to `outbreak()` include “`filter_min_series`” to control the chronology cut-off points with regard to sample depth, “`filter_min_defol`” and “`filter_perc`” to control the minimum number and percent of trees recording a defoliation event in a given year. `outbreak()` produces a new data frame with eight variables: “`year`”, “`num_defol`”, “`percent_defol`”, “`num_max_defol`”, “`mean_gsi`”, “`mean_ngsi`”, and “`outbreak_status`.” All of these variables are populated regardless of an inferred outbreak event, providing a continuous outbreak reconstruction. The “`num_max_defol`” variable counts the number of trees recording their maximum defoliation in a given year. The “`mean_gsi`” and “`mean_ngsi`” variables provide averages of these indices across all available

374 trees. Finally, the “outbreak\_status” column shows whether an outbreak event  
375 is inferred (“outbreak”) or not (“not\_obr”).

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

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

379 Inferred outbreak events are shown in the middle panel of Figure 2 as the filled-  
380 in spaces. Users can change the time series in this panel with the “disp\_index”  
381 parameter, choosing between the mean NGSI (the default) or GSI.

382 A summary table of the inferred outbreak events is generated by the `outbreak_stats()`  
383 function (Table 2). The table provides a range of summary statistics, including  
384 the start and end years of each outbreak event, along with the corresponding  
385 duration, the number and percent of trees in defoliation at the start of the event  
386 (“n\_df\_start” and “perc\_df\_start”, respectively), the maximum number of  
387 trees recording the outbreak event during a single year (“max\_df\_obr”), the  
388 year corresponding to that peak (“yr\_max\_df”), the year with the lowest mean  
389 NGSI during the event (“yr\_min\_ngsi”), and the minima of mean GSI and  
390 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

391 Saving the results of `outbreak_stats()` (the `dmj_obr_stats` object above)  
392 provides an array of options for assessing metrics of the insect outbreak regime.  
393 For example, taking the first year of each outbreak event, we can calculate  
394 the duration of years between outbreaks, via the `diff()` function in R. The  
395 average of those differences, calculated via `mean()` is the mean return interval of  
396 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
```

## 397 6. Conclusions

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

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

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

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

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



447 with updated descriptions and helpful vignettes on the package website <https://chguiterman.github.io/dfoliatR/>. Researchers wishing to contribute to the  
448 further development of **dfoliatR** are encouraged to do so via the GitHub  
449 repository.  
450

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## 463 References

- 464 Alfaro, R., Sickle, G. van, Thomson, A., Wegwitz, E., 1982. Tree mortality  
465 and radial growth losses caused by the western spruce budworm in a Douglas-fir  
466 stand in British Columbia. *Canadian Journal of Forest Research* 12, 780–87.
- 467 Altman, J., Fibich, P., Dolezal, J., Aakala, T., 2014. **TRADER**: A package for  
468 Tree Ring Analysis of Disturbance Events in R. *Dendrochronologia* 32, 107–12,  
469 doi:10.1016/j.dendro.2014.01.004.
- 470 Axelson, J., Bast, A., Alfaro, R., Smith, D., Gärtner, H., 2014. Variation  
471 in wood anatomical structure of Douglas-fir defoliated by the western spruce  
472 budworm: a case study in the coastal-transitional zone of British Columbia,  
473 Canada. *Trees* 28, 1837–46, doi:10.1007/s00468-014-1091-1.

474 Axelson, J., Csank, A., Lee, R., McGee, J., McNiel, K., 2018. Reconstructing  
 475 historical *Choristoneura freemani* outbreaks using *Pseudotsuga menziesii* in the  
 476 greater Yellowstone region, Wyoming, U.S.A. Final Report of the 20th Annual  
 477 North American Dendroecological Fieldweek (NADEF).  
 478 Axelson, J.N., Smith, D.J., Daniels, L.D., Alfaro, R.I., 2015. Multicentury  
 479 reconstruction of western spruce budworm outbreaks in central British Columbia,  
 480 Canada. Forest Ecology and Management 335, 235–48, doi:10.1016/j.foreco.2014.10.002.  
 481 Blais, J., 1954. The recurrence of spruce budworm infestations in the past  
 482 century in the lac seul area of northwestern ontario. Ecology 35, 62–71.  
 483 Brewer, P.W., 2014. Data management in dendroarchaeology using tellervo.  
 484 Radiocarbon Cambridge University Press 56, S79–S83, doi:10.2458/azu\_rc.56.18320.  
 485 Brewer, P.W., Guiterman, C.H., 2016. A new digital field data collection sys-  
 486 tem for dendrochronology. Dendrochronologia 38, 131–35, doi:10.1016/j.dendro.2016.04.005.  
 487 Brookes, M.H., Campbell, R.W., Colbert, J.J., Mitchell, R.G., Stark, R.W.,  
 488 1987. Western spruce budworm. USDA Forest Service, Cooperative State  
 489 Research Service, Technical Bulletin No. 1694. 198 p., Washington D.C.  
 490 Brubaker, L.B., 1978. Effects of defoliation by douglas-fir tussock moth on  
 491 ring sequences of douglas-fir and grand fir. Tree-Ring Bulletin 38, 49–60.  
 492 Bunn, A.G., 2008. A dendrochronology program library in R (**dp1R**). Den-  
 493 drochronologia 26, 115–24, doi:10.1016/j.dendro.2008.01.002.  
 494 Bunn, A.G., 2010. Statistical and visual crossdating in R using the **dp1R**  
 495 library. Dendrochronologia 28, 251–58, doi:10.1016/j.dendro.2009.12.001.  
 496 Campelo, F., Nabais, C., Carvalho, A., Vieira, J., 2016. **tracheideR**–  
 497 An R package to standardize tracheidograms. Dendrochronologia 37, 64–68,  
 498 doi:10.1016/j.dendro.2015.12.006.  
 499 Carus, S., 2004. Impact of defoliation by the pine processionary moth  
 500 (*Thaumetopoea pityocampa*) on radial, height and volume growth of Calabrian  
 501 pine (*Pinus brutia*) trees in Turkey. Phytoparasitica 32, 459–69.  
 502 Carus, S., 2009. Effects of defoliation caused by the processionary moth on  
 503 growth of Crimean pines in western Turkey. Phytoparasitica 37, 105–14.  
 504 Cook, E.R., Holmes, R.L., 1996. Guide for computer program ARSTAN.

505 The international tree-ring data bank program library version 2 75–87.

506 Cook, E.R., Krusic, P.J., 2004. The North American Drought Atlas. (Lamont-  
507 Doherty Earth Observatory; the National Science Foundation: New York) Avail-  
508 able at [https://www.ncdc.noaa.gov/data-access/paleoclimatology-data/datasets/tree-](https://www.ncdc.noaa.gov/data-access/paleoclimatology-data/datasets/tree-ring/drought-variability)  
509 [ring/drought-variability](https://www.ncdc.noaa.gov/data-access/paleoclimatology-data/datasets/tree-ring/drought-variability) [Last accessed May 2020].

510 Esper, J., Büntgen, U., Frank, D.C., Nievergelt, D., Liebhold, A., 2007. 1200  
511 years of regular outbreaks in alpine insects. *Proceedings of the Royal Society B:*  
512 *Biological Sciences* 274, 671–79, doi:10.1098/rspb.2006.0191.

513 Guiterman, C., Lynch, A., Axelson, J., 2020. **dfoliatR**: Detection and  
514 Analysis of Insect Defoliation Signals in Tree Rings. R package version 0.2.0.,  
515 <https://chguiterman.github.io/dfoliatR/>, doi:10.5281/zenodo.3626135.

516 Holmes, R.L., Swetnam, T.W., 1986. Dendroecology program library: pro-  
517 gram OUTBREAK user’s manual. Laboratory of Tree-Ring Research, University  
518 of Arizona, Tucson.

519 Jevšenak, J., Levanič, T., 2018. **dendroTools**: R package for studying  
520 linear and nonlinear responses between tree-rings and daily environmental data.  
521 *Dendrochronologia* 48, 32–39, doi:10.1016/j.dendro.2018.01.005.

522 Lara, W., Bravo, F., Sierra, C.A., 2015. **MeasuRing**: An R package to  
523 measure tree-ring widths from scanned images. *Dendrochronologia* 34, 43–50,  
524 doi:10.1016/j.dendro.2015.04.002.

525 Lynch, A.M., 2012. What Tree-Ring Reconstruction Tells Us about Conifer  
526 Defoliator Outbreaks, in: Barbosa, P., Letourneau, D.K., Agrawal, A.A. (Eds.),  
527 *Insect outbreaks revisited*. Blackwell Publishing Ltd, pp. 126–54, doi:10.1002/9781118295205.ch7.

528 Malevich, S.B., Guiterman, C.H., Margolis, E.Q., 2018. **burnr**: Fire history  
529 analysis and graphics in R. *Dendrochronologia* 49, 9–15, doi:10.1016/j.dendro.2018.02.005.

530 Mason, R.R., Wickman, B.E., Paul, H.G., 1997. Radial growth response of  
531 douglas-fir and grand fir to larval densities of the douglas-fir tussock moth and  
532 the western spruce budworm. *Forest Science* 43, 194–205.

533 Rathgeber, C.B.K., Longuetaud, F., Mothe, F., Cuny, H., Le Mognédec, G.,  
534 2011. Phenology of wood formation: Data processing, analysis and visualisation  
535 using R (package **CAVIAR**). *Dendrochronologia* 29, 139–49, doi:10.1016/j.dendro.2011.01.004.

536 R Core Team, 2019. R: A language and environment for statistical comput-  
537 ing. R Foundation for Statistical Computing, Vienna, Austria, [https://www.R-](https://www.R-project.org/)  
538 [project.org/](https://www.R-project.org/).

539 Ryerson, D.E., Swetnam, T.W., Lynch, A.M., 2003. A tree-ring reconstruc-  
540 tion of western spruce budworm outbreaks in the San Juan Mountains, Colorado,  
541 U.S.A. Canadian Journal of Forest Research 33, 1010–28, doi:10.1139/X03-026.

542 Sanders, C.J., Stark, R.W., Mullins, E.J., Murphy, J. (eds), 1985. Recent Ad-  
543 vances in Spruce Budworms Research, *Proceedings of the CANUSA Spruce Bud-*  
544 *worms Research Symposium*, 16-20 September, Bangor, ME. Canadian Forestry  
545 Service, Ottawa, Ontario. 527p.

546 Schmitt, D.M., Grimble, D.G., Searcy, J., 1984. Managing the spruce  
547 budworm in eastern North America. USDA Forest Service, Cooperative State  
548 Research Service, Agriculture Handbook No. 620. 192p., Washington D.C.

549 Shi, J., Xiang, W., Liu, Q., Shah, S., 2019. **MtreeRing**: An R package with  
550 graphical user interface for automatic measurement of tree ring widths using im-  
551 age processing techniques. Dendrochronologia 58, 125644, doi:10.1016/j.dendro.2019.125644.

552 Speer, J.H., 2010. Fundamentals of Tree-Ring Research. The University of  
553 Arizona Press, 333 pp.

554 Swetnam, T., Allen, C., Betancourt, J., 1999. Applied historical ecology:  
555 using the past to manage for the future. Ecological applications 9, 1189–1206,  
556 doi:10.1890/1051-0761(1999)009[1189:AHEUTP]2.0.CO;2.

557 Swetnam, T.W., Lynch, A.M., 1989. A tree-ring reconstruction of western  
558 spruce budworm history in the southern Rocky Mountains. Forest Science 35,  
559 962–86, doi:10.1093/forestscience/35.4.962.

560 Swetnam, T.W., Lynch, A.M., 1993. Multicentury, Regional-Scale Patterns  
561 of Western Spruce Budworm Outbreaks. Ecological Monographs 63, 399–424,  
562 doi:10.2307/2937153.

563 Swetnam, T.W., Thompson, M.A., Sutherland, E.K., 1985. Using den-  
564 drochronology to measure radial growth of defoliated trees. United States  
565 Department of Agriculture handbook No. 639. 38 p., Washington D.C, 38p. pp,  
566 [www.fs.usda.gov/treesearch/pubs/40898](http://www.fs.usda.gov/treesearch/pubs/40898).

567 van der Maaten-Theunissen, M., van der Maaten, E., Bouriaud, O., 2015.  
 568 **PointRes**: An R package to analyze pointer years and components of resilience.  
 569 *Dendrochronologia* 35, 34–38, <http://dx.doi.org/10.1016/j.dendro.2015.05.006>,  
 570 doi:10.1016/j.dendro.2015.05.006.

571 Wickham, H., 2016. **ggplot2**: Elegant Graphics for Data Analysis. Springer-  
 572 Verlag, New York, <https://ggplot2-book.org/>.

573 Wickham, H., Averick, M., Bryan, J., Chang, W., McGowan, L., François,  
 574 R., Golemund, G., Hayes, A., Henry, L., Hester, J., Kuhn, M., Pedersen, T.,  
 575 Miller, E., Bache, S., Müller, K., Ooms, J., Robinson, D., Seidel, D., Spinu, V.,  
 576 Takahashi, K., Vaughan, D., Wilke, C., Woo, K., Yutani, H., 2019. Welcome  
 577 to the **Tidyverse**. *Journal of Open Source Software The Open Journal* 4, 1686,  
 578 <https://doi.org/10.21105/joss.01686>, doi:10.21105/joss.01686.

579 Wickham, H., François, R., Henry, L., Müller, K., 2020. **dplyr**: A Grammar  
 580 of Data Manipulation., <https://CRAN.R-project.org/package=dplyr>.

581 Wickman, B.E., 1986. Radial growth of grand fir and douglas-fir 10 years  
 582 after defoliation by the douglas-fir tussock moth in the blue mountains outbreak.  
 583 USDA Forest Service, Pacific Northwest Research Station, Research Paper  
 584 PNW-367. Portland, Oregon.

585 Zang, C., Biondi, F., 2015. **treeclim**: An R package for the numerical calibra-  
 586 tion of proxy-climate relationships. *Ecography* 38, 431–36, doi:10.1111/ecog.01335.