

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

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## 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 and **dplR** computing environments. 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 chronologies, 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.

**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 trees  
16 permits dating and quantification of past forest insect defoliator outbreaks. De-  
17 foliation can be distinguished from climate- and other disturbance-related influ-  
18 ences by comparing ring-width or other annually-resolved features in the wood  
19 of host species to that of non-host species or annually-resolved climate records.  
20 The effect of defoliation on radial growth of trees has been recognized since the  
21 1860s, and used to reconstruct outbreak regimes since the 1950s (Blais, 1954;  
22 Alfaro et al., 1982; Lynch, 2012). It was not until the 1980s, however, that pre-  
23 cise dendrochronological techniques were applied for inferring defoliation events  
24 and reconstructing defoliator outbreak regimes (Swetnam et al., 1985; Speer,  
25 2010; Lynch, 2012). The first studies (Swetnam et al., 1985; Swetnam and  
26 Lynch, 1989, 1993) focused on developing historical outbreak reconstructions of  
27 western spruce budworm (WSBW; *Choristoneura freemani* (Lepidoptera: Tor-  
28 tricidae); 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 characteriz-  
33 ing defoliator outbreaks from tree-ring records has been the software routine  
34 OUTBREAK (Swetnam et al., 1985; Holmes and Swetnam, 1986; Swetnam  
35 and Lynch, 1989). OUTBREAK computes indices (described later in detail) of  
36 suppressed growth by subtracting a detrended and standardized climate series  
37 (a “control” chronology) from individual host-tree detrended and standardized  
38 radial growth series after the host and non-host series have been brought to a  
39 common variance. The non-host chronology usually consists of a site chronol-  
40 ogy developed from non-host tree species growing on a climate-sensitive site,  
41 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.

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 **dplR**-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 **dplR** 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 growth and 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/dfoliatR\\_paper](https://github.com/chguiterman/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 Lynch, 1989) and is commonly used for other species (see Lynch, 2012). The year with the lowest value is termed the “year of maximum departure”

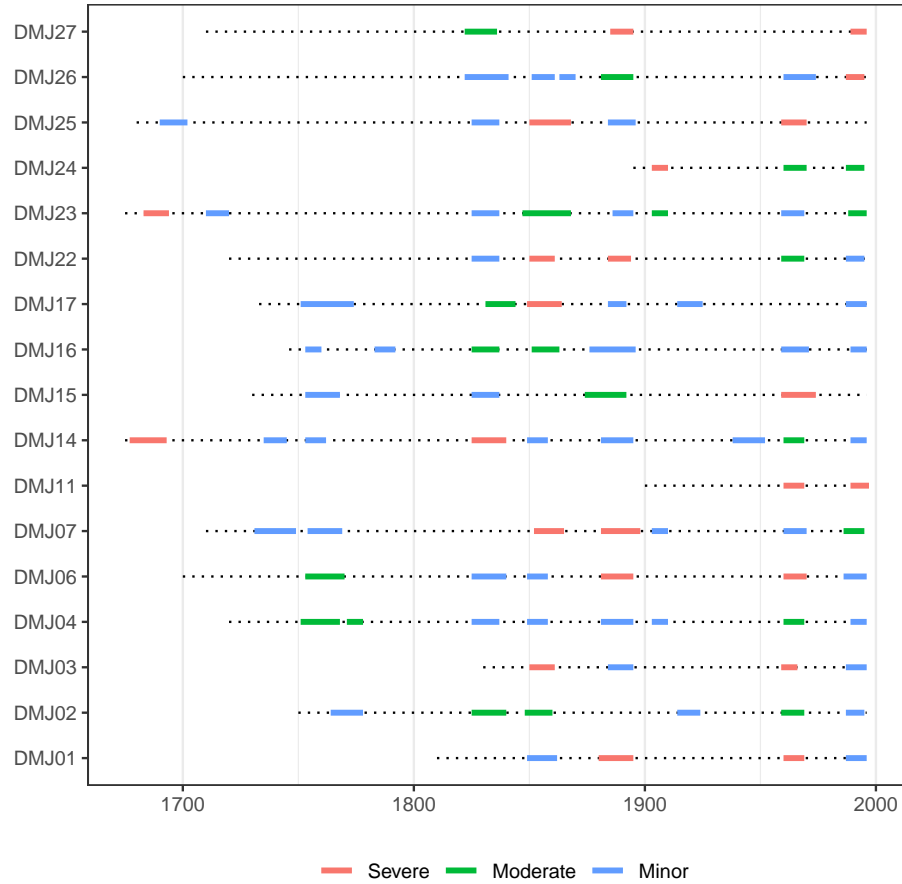


Figure 1: Default **dfoliatR** graphic for individual trees, produced by the `plot_defol()` function. The series names are listed on the Y-axis, dotted lines represent the series length for each tree, and colored segments show periods of defoliation. The colors of defoliation segments represent its severity,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

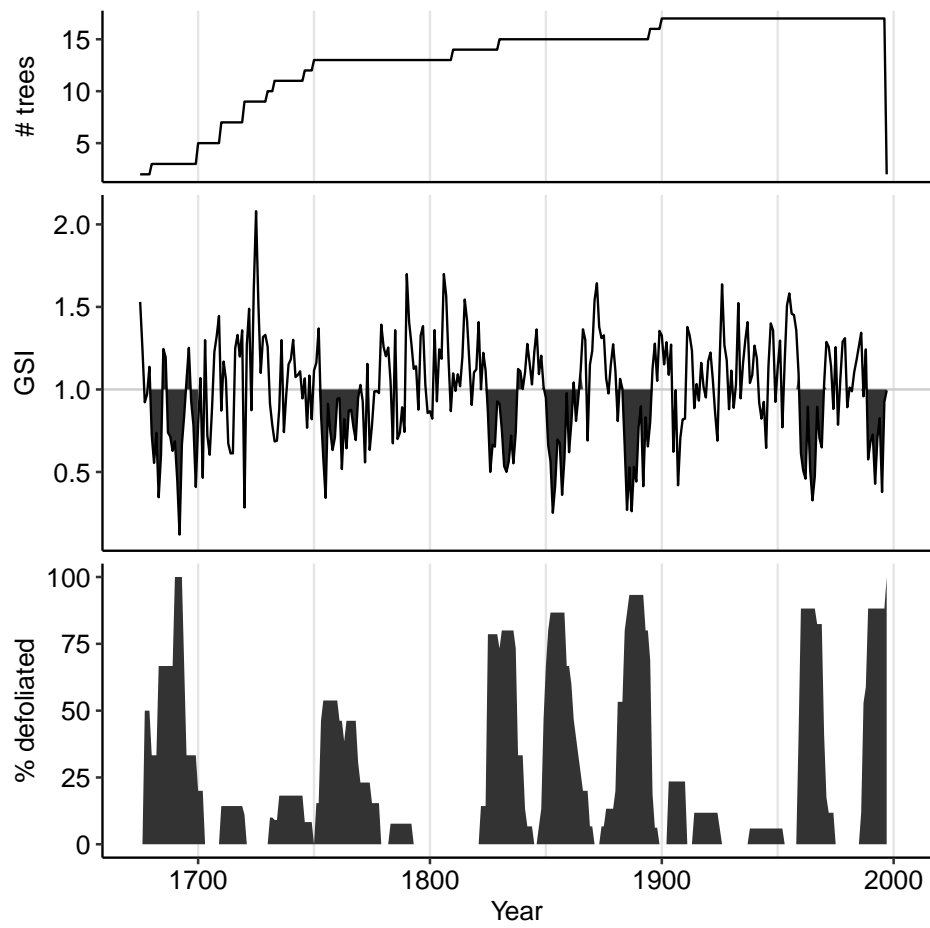


Figure 2: Default graphics showing outbreak events at the DMJ site. Top panel shows the sample depth, the middle panel shows the mean GSI with inferred outbreak events filled, and the bottom panel shows the percent of trees defoliated, used to identify time periods of inferred outbreaks.

120 and becomes a central point in time for assessing other thresholds before being  
121 included as a defoliation event. If the year of maximum departure is higher than  
122 the threshold (i.e.  $\text{NGSI}_{\text{lowest}} > -1.28$ ), the sequence being assessed is omitted  
123 from the event results.

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

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

148 Diverging from OUTBREAK, **dfoliatR** includes an option allowing users  
149 to extend defoliation events on individual trees by bridging between sequential  
150 events (Figure 3). In cases where two defoliation events are separated by a sin-



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

177     Examples of sequential defoliation events (bars), wherein two or three events  
 178 occur separated by single years. In each case OUTBREAK recorded only one  
 179 of the events, omitting those with a higher “max\_defol” year, or the year of the  
 180 lowest NGSI value. **dfoliatR**, by contrast, recorded all of the events, including  
 181 two sequential events on DMJ26 and EFK22, and three on FNL04. Events

182 recorded by both programs have a darker color, while those recorded only by  
183 **dfoliatR** are lighter in color. Adding the bridging option in **dfoliatR** links  
184 these events (“bridge\_defol”) into single longer events that may more accurately  
185 capture the effects of long-term insect herbivory on individual trees.

## 186 2.2. Inferring Outbreak Events

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

## 204 3. Evaluation

### 205 3.1. Approach

206 We tested **dfoliatR** against OUTBREAK by comparing NGSI to OUT-  
207 BREAK’s normalized corrected indices for individual trees and years, defolia-  
208 tion status for individual trees and years, and percentage of trees recording out-  
209 breaks at the site level. Our tests used standardized ring-width data from eight

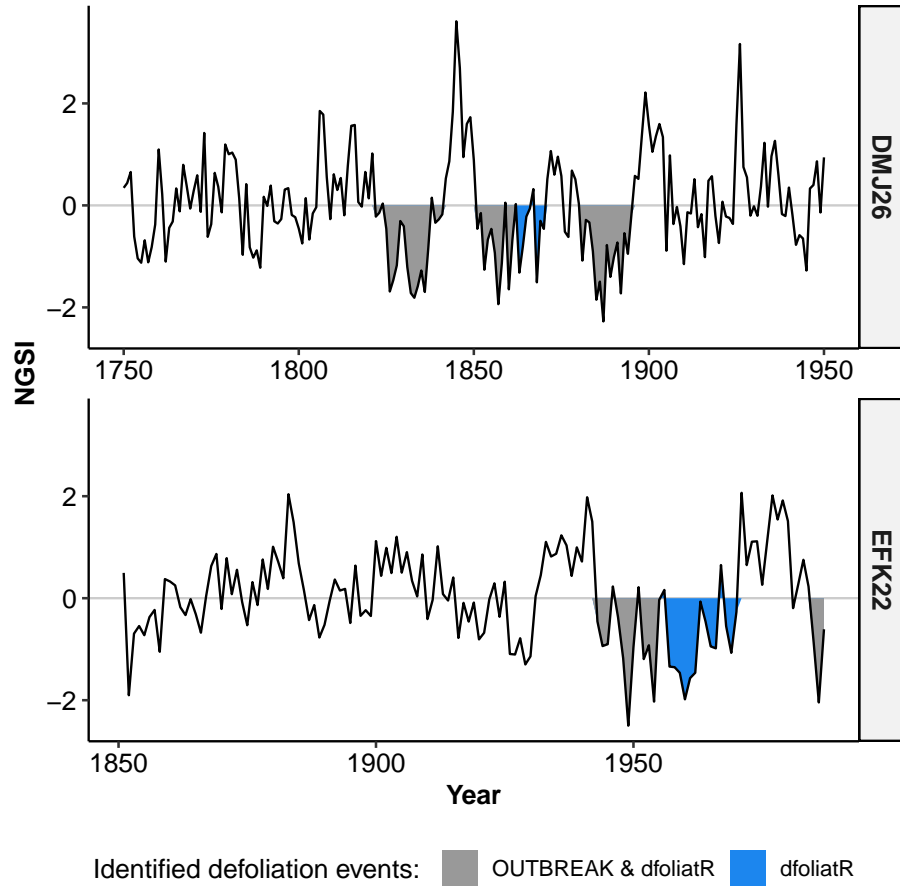


Figure 3: Examples of identified defoliation events on individual trees. For each tree (DMJ26 and EFK22), OUTBREAK and `dfoliatR` identify most of the same events, but there is one added event (blue colored) that was omitted by OUTBREAK. These were omitted because they were sequential, separated by a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

210 host-tree sites spanning the range of WSBW. The sites were sampled in British  
 211 Columbia (Axelson et al., 2015), Wyoming (Axelson et al., 2018), Colorado, and  
 212 New Mexico (Swetnam and Lynch, 1993; Ryerson et al., 2003). These host data  
 213 were compared to non-host chronologies from the original studies, but we made  
 214 no effort here to replicate the reconstructions or analyses of those studies.

215 We detrended host data for both `dfoliatR` and `OUTBREAK` using AR-  
 216 STAN [v6.1] with cubic smoothing splines (50% frequency response on 100-150  
 217 year wavelengths depending on the site). In both `dfoliatR` and `OUTBREAK`  
 218 we used event thresholds of -1.28 normalized indices, 8 years duration, and al-  
 219 lowed for events at the end of series in seven of eight sites that had known  
 220 outbreaks at the time of sampling. We found it necessary to be consistent in  
 221 how we detrended and what software we employed (e.g., ARSTAN vs `dp1R`)  
 222 because subtle differences in standardized ring-width indices generated between  
 223 the programs transferred into differences between `dfoliatR` and `OUTBREAK`.  
 224 In the end, we chose to only use the standardization output files from ARSTAN,  
 225 which are easily read into R (and then `dfoliatR`) using the `dp1R` package.

226 The R code to replicate our comparisons is available from [https://github.](https://github.com/chguiterman/dfoliatR_paper)  
 227 [com/chguiterman/dfoliatR\\_paper](https://github.com/chguiterman/dfoliatR_paper).

### 228 3.2. Findings

229 Across the 43,280 ring-width indices from 222 trees included in our eval-  
 230 uation, we found that `dfoliatR` and `OUTBREAK` compute identical growth  
 231 suppression indices at 0.000 precision. We expected this outcome because both  
 232 programs employ Equation 1. At the tree-level, the programs identified 11,530  
 233 years of defoliation. The programs agreed on 97.9% of the years, leaving 927  
 234 “difference” years in which only one program identified defoliation on an in-  
 235 dividual tree. The differences included 102 events on 85 trees. We carefully  
 236 inspected each of these events in the full context of each tree’s ring-series, and  
 237 categorized the differences as follows

- 238 • *Series-end events* (40% of the total) in which `OUTBREAK` included “trun-  
 239 cated outbreaks” (for seven sites) at the end of each series. In `dfoliatR`,

240 this option is controlled by the “series\_end\_events” parameter to `defoliate_trees()`.

241 In OUTBREAK, the option appears while changing the duration paramete-  
242 ter (option 3). When selected, OUTBREAK will include any sequences of  
243 negative indices at the either the beginning or the end of each tree series  
244 as a defoliation event, without consideration of either duration or magni-  
245 tude thresholds. In `dfoliatR`, the duration threshold is omitted and the  
246 magnitude threshold is retained in series-end-events. Each of the 13 events  
247 included in these differences did not meet the “max\_reduction” parameter  
248 (-1.28 NGSI) in `dfoliatR` and were excluded. In two cases, OUTBREAK  
249 included events at the beginning of the series where `dfoliatR` does not  
250 allow truncated events. In four cases, OUTBREAK omitted only the last  
251 year of the series because the index was positive, but `dfoliatR` allowed this  
252 single positive excursion. Finally, there were two cases in which `dfoliatR`  
253 omitted possible events because it had already included a positive NGSI  
254 excursion after the “max\_reduction” year, and since it will only allow one  
255 excursion on either side of the max year, the events were omitted due to  
256 short duration.

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

270 defoliations.

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

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

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

#### 288 4. Availability and installation

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

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

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

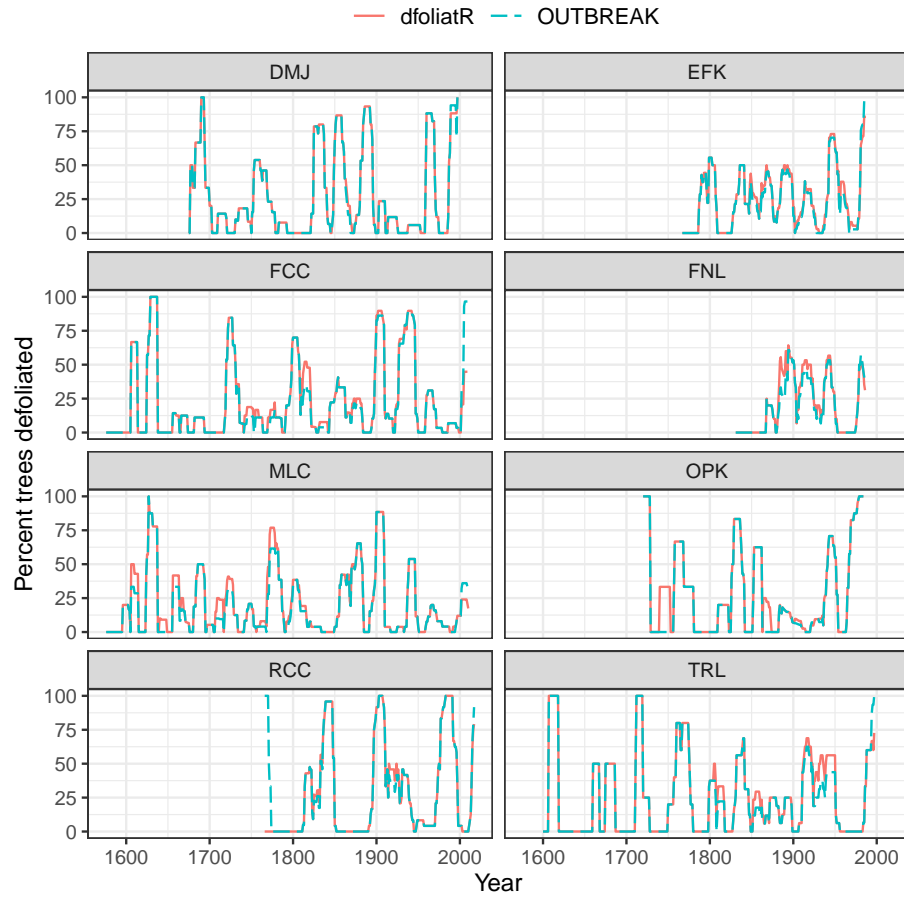


Figure 4: Comparison of reconstructed western spruce budworm outbreaks computed by `dfoliatR` and `OUTBREAK`. Input parameters were identical between programs. Differences arise because `dfoliatR` will identify and record more defoliation events on individual trees.

```
library(dfoliatR)
```

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

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

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

## 300 5. Example Usage

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

314 With **dfoliatR** loaded, the datasets are accessible using the **data()** func-  
315 tion. The data object names are prefixed by their site codes. For instance, the  
316 **dmj\_\*** objects come from the DMJ site and include the host-tree series (**dmj\_h**),  
317 the non-host chronology (**dmj\_nh**), the defoliation series (**dmj\_defol**), and the



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

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

### 330 5.1. Tree-Level Defoliation Events

331 The function `defoliate_trees()` performs the GSI indexing procedure on  
332 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)

```

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

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

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

```

defol_stats(dmj_defol)
View(dmj_defol)

```

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

Table 1: Tree-level tabular output provided by the `defol_stats()` function for the DMJ example site.

| series | first | last | years | num_events | tot_years | mean_duration |
|--------|-------|------|-------|------------|-----------|---------------|
| DMJ01  | 1810  | 1996 | 187   | 4          | 50        | 12            |
| DMJ02  | 1750  | 1996 | 247   | 6          | 75        | 12            |
| DMJ03  | 1830  | 1996 | 167   | 4          | 42        | 10            |
| DMJ04  | 1720  | 1996 | 277   | 8          | 90        | 11            |
| DMJ06  | 1700  | 1996 | 297   | 6          | 81        | 14            |
| DMJ07  | 1710  | 1996 | 287   | 7          | 96        | 14            |
| DMJ11  | 1900  | 1997 | 98    | 2          | 19        | 10            |
| DMJ14  | 1675  | 1996 | 322   | 9          | 112       | 12            |
| DMJ15  | 1730  | 1996 | 267   | 4          | 64        | 16            |
| DMJ16  | 1746  | 1996 | 251   | 7          | 86        | 12            |
| DMJ17  | 1733  | 1996 | 264   | 6          | 85        | 14            |
| DMJ22  | 1720  | 1996 | 277   | 5          | 56        | 11            |
| DMJ23  | 1675  | 1997 | 323   | 8          | 96        | 12            |
| DMJ24  | 1895  | 1996 | 102   | 3          | 28        | 9             |
| DMJ25  | 1680  | 1996 | 317   | 5          | 70        | 14            |
| DMJ26  | 1700  | 1996 | 297   | 6          | 79        | 13            |
| DMJ27  | 1710  | 1996 | 287   | 3          | 34        | 11            |

357 and assign severity based on the mean and first quartile of the averages. “Se-  
 358 vere” events have a mean NGSi above the overall average event-period NGSi.  
 359 “Moderate” events fall between the mean and first quartile. “Minor” events fall  
 360 below the first quartile. Users can re-define the breaks to suit their needs via  
 361 the “breaks” 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 NGS value for each defoliation
## event.
library(ggplot2)
plot_defol(dmj_defol) +
  scale_color_manual(values = c("red", "orange", "purple"))

```

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

## 366 5.2. Site-Level Events

367 To infer outbreak events at the site level, the function `outbreak()` compos-  
 368 ites tree-level defoliation series into a single chronology, with input parameters  
 369 that control thresholds in the number and proportions of trees recording a de-  
 370 foliation 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)

```

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

372 chronology cut-off points with regard to sample depth, “filter\_min\_defol” and  
373 “filter\_perc” to control the minimum number and percent of trees recording a  
374 defoliation event in a given year. `Outbreak()` produces a new data frame with  
375 eight variables: “year”, “num\_defol”, “percent\_defol”, “num\_max\_defol”, “mean\_gsi”,  
376 “mean\_ngsi”, and “outbreak\_status.” All of these variables are populated  
377 regardless of an inferred outbreak event, providing a continuous disturbance  
378 chronology. The “num\_max\_defol” variable counts the number of trees record-  
379 ing their maximum defoliation in a given year. The “mean\_gsi” and “mean\_ngsi”  
380 variables provide averages of these indices across all available trees. Finally, the  
381 “outbreak\_status” column shows whether an outbreak event is inferred (“out-  
382 break”) or not (“not\_obr”).

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

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

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

390 A summary table of the inferred outbreak events is generated by the `outbreak_stats()`  
391 function (Table 2).

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

Table 2: Site-level summary statistics for inferred outbreak events provided with the `outbreak_stats()` function for the DMJ example site.

| start | end  | duration | num_trees_start | perc_trees_start | peak_outbreak_year | num_trees_outbreak | peak_defol_year | min_gsi | mean_ngsi |
|-------|------|----------|-----------------|------------------|--------------------|--------------------|-----------------|---------|-----------|
| 1680  | 1699 | 20       | 1               | 33.3             | 1690               | 3                  | 1692            | 0.121   | -2.407    |
| 1753  | 1769 | 17       | 6               | 46.2             | 1754               | 7                  | 1755            | 0.343   | -1.611    |
| 1825  | 1840 | 16       | 11              | 78.6             | 1831               | 12                 | 1826            | 0.500   | -1.304    |
| 1849  | 1865 | 17       | 7               | 46.7             | 1852               | 13                 | 1853            | 0.252   | -1.994    |
| 1881  | 1895 | 15       | 8               | 53.3             | 1886               | 14                 | 1885            | 0.262   | -1.945    |
| 1959  | 1970 | 12       | 7               | 41.2             | 1960               | 15                 | 1965            | 0.328   | -1.830    |
| 1987  | 1996 | 10       | 9               | 52.9             | 1989               | 15                 | 1995            | 0.378   | -1.640    |

392 The output table from `outbreak_stats()` shows the start and end years of  
 393 each event, along with their corresponding duration, the number and percent of  
 394 trees in defoliation at the start of the event, the the number of trees recording  
 395 the outbreak event (in part or full), the minimums of the mean GSI and NGSI  
 396 indices, and two points of “peak defoliation.” The first, “`peak_outbreak_year`”  
 397 is the year in which the greatest number of trees are recording the outbreak,  
 398 and the second, “`peak_defol_year`” is the year with the lowest average NGSI.

399 Saving the results of `outbreak_stats()` (the `dmj_obr_stats` object above)  
 400 provides an array of options for assessing metrics of the insect defoliation regime.  
 401 Here we use the first year of each outbreak event to calculate the average dura-  
 402 tion of years between outbreaks, via the `diff()` function in R. The average of  
 403 those differences, calculated via `mean()` is the mean return interval.

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

## 404 6. Conclusions

405 The `dfoliatR` package provides dendroecologists with tools to infer, quan-  
 406 tify, analyze, and visualize tree-ring growth suppression events and to recon-  
 407 struct forest insect defoliator outbreak regimes. It is built on the long-accepted  
 408 host to non-host comparison methodology used in the 1980s FORTRAN pro-  
 409 gram OUTBREAK (Swetnam et al., 1985; Swetnam and Lynch, 1989, 1993).  
 410 Our evaluation of the two programs revealed that `dfoliatR` excelled in identi-  
 411 fying defoliation events on single trees, providing researchers with more consis-  
 412 tent and biologically-justifiable results. Other key benefits are that `dfoliatR`  
 413 provides easier control of suppression thresholds, additional output tables, high-  
 414 quality and customizable graphics, and operates in the open-source R environ-  
 415 ment that is stable across computing platforms and under active development  
 416 and maintenance by a large and growing community.

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

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

442 **dfoliatR** adds to the on-going open-source software development for den-  
443 drochronological methods (e.g., Bunn, 2008; Brewer, 2014; Brewer and Gui-  
444 terman, 2016). The R environment enables automation of analyses, allowing  
445 input/output processes to become routine, and empowering batch processing of  
446 large multi-site projects and sensitivity analyses. It also facilitates additional  
447 statistical analyses, such as spectral analyses and superposed epoch analyses



(e.g., Malevich et al., 2018), with easy transfer from `dfoliatR` and `dplR` to other libraries in R. Source code for `dfoliatR` is available in the Comprehensive R Archive Network (CRAN) and GitHub <https://github.com/chguiterman/dfoliatR> with updated descriptions and helpful vignettes on the package website <https://chguiterman.github.io/dfoliatR/>. Researchers wishing to contribute to the further development of `dfoliatR` are encouraged to do so via the GitHub repository.

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