

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

3 Christopher H. Guiterman<sup>\*,a,b</sup>, Ann M. Lynch<sup>a,c</sup>, Jodi N. Axelson<sup>d</sup>

4 <sup>a</sup>*Laboratory of Tree-Ring Research, University of Arizona, 1215 E Lowell St. Box 210045,*  
5 *Tucson, AZ, 85721*

6 <sup>b</sup>*Three Pines Forest Research, LLC, PO Box 225, Etna, NH, 03750*

7 <sup>c</sup>*U.S. Forest Service, Rocky Mountain Research Station, 1215 E Lowell St. Box 210045,*  
8 *Tucson, AZ, 85721*

9 <sup>d</sup>*Dept of Environmental Science, Policy & Management, University of California, Berkeley,*  
10 *130 Mulford Hall #3114, Berkeley, CA 94720*

## 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 **dp1R** 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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\*Corresponding Author

Email addresses: [chguiterman@arizona.edu](mailto:chguiterman@arizona.edu) (Christopher H. Guiterman),  
[ann.m.lynn@usda.gov](mailto:ann.m.lynn@usda.gov) (Ann M. Lynch), [jodi.axelson@berkeley.edu](mailto:jodi.axelson@berkeley.edu) (Jodi N. Axelson)

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

42 (Cook and Krusic, 2004) also suffices. If the host and non-host species respond  
43 similarly to climate (which can and should be tested), the derived series retains  
44 variability that the host and non-host series do not have in common, generally  
45 the insect signal and some unexplained variability (noise). The user defines  
46 a rule base specifying the magnitude and duration that a period of indexed  
47 growth suppression must meet or surpass for a period of suppressed growth to  
48 be inferred as a defoliation event at the tree level.

49 Though powerful, OUTBREAK is outdated and increasingly difficult to use  
50 in modern computing environments. It was written in FORTRAN V with in-  
51 herently severe restrictions, as RAM and disk space were limited at that time  
52 (256 kb and 10 MB, respectively) and FORTRAN conventions imposed very  
53 strict formatting, file naming, and output conventions. The program lacks a  
54 graphical interface or capabilities, forcing users to import generated text files  
55 into spreadsheets or other software to assess results and perform analyses. Fur-  
56 thermore, OUTBREAK can only handle one test at a time, creating barriers  
57 to batch operation and a large burden for researchers with datasets including  
58 multiple sites. We developed **dfoliatR** (Guiterman et al., 2020) as an R- and  
59 **dp1R**-based library to overcome these issues.

60 **dfoliatR** adds to a growing suite of dendrochronology packages in the R  
61 computing environment (R Core Team, 2019). Stemming from the **dp1R** library  
62 (Bunn, 2008) that enables R users to read and write an array of tree-ring data  
63 formats, standardize ring width series, build and evaluate chronologies, and  
64 perform quality control (to name a few), one can now also measure ring widths  
65 from scanned images of prepared samples (Lara et al., 2015; Shi et al., 2019),  
66 conduct and check crossdating (Bunn, 2010), analyze sub-annual anatomical  
67 features (Rathgeber et al., 2011; Campelo et al., 2016), and perform many an-  
68 alytical tests (Zang and Biondi, 2015; Jevšenak and Levanič, 2018). Tools for  
69 assessing stand dynamics and disturbance analyses are under rapid develop-  
70 ment, with new packages for assessing release events (**TRADER**: Altman et al.,  
71 2014), metrics of growth resilience (**pointRes**: van der Maaten-Theunissen et  
72 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”

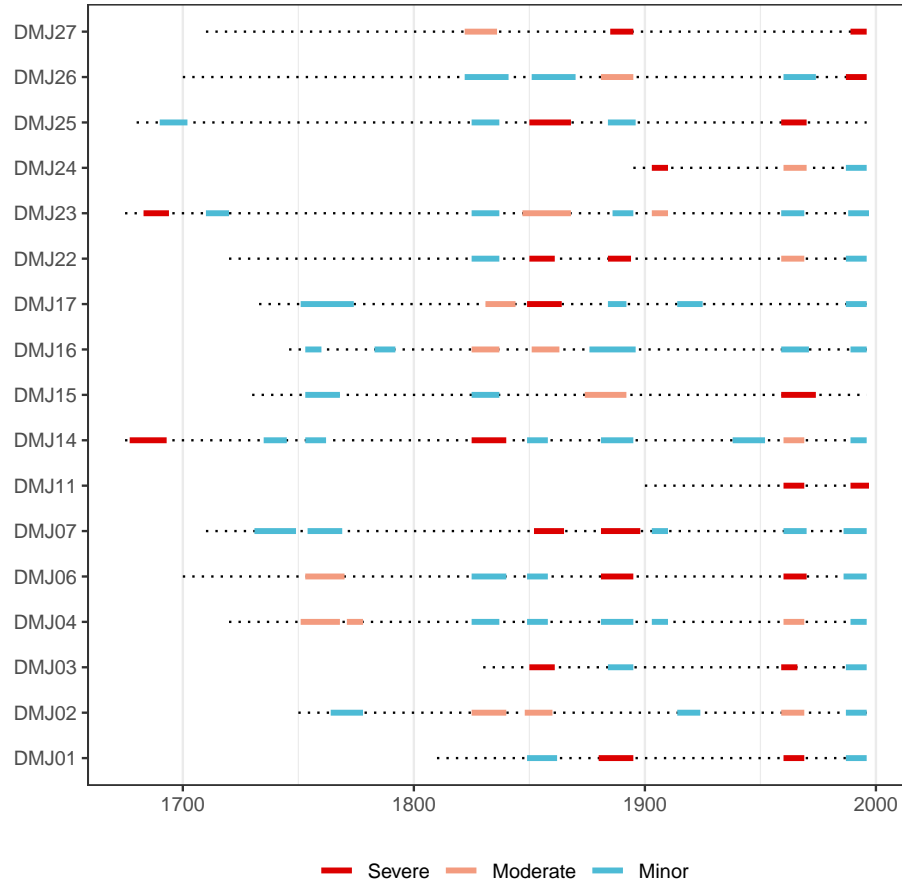


Figure 1: Default `dfoliatR` graphic for individual trees, produced by the `plot_defol()` function. The series names from the DMJ site (Ryerson et al., 2003) are listed on the Y-axis, dotted lines represent the series length for each tree, and colored segments show periods of defoliation. The colors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

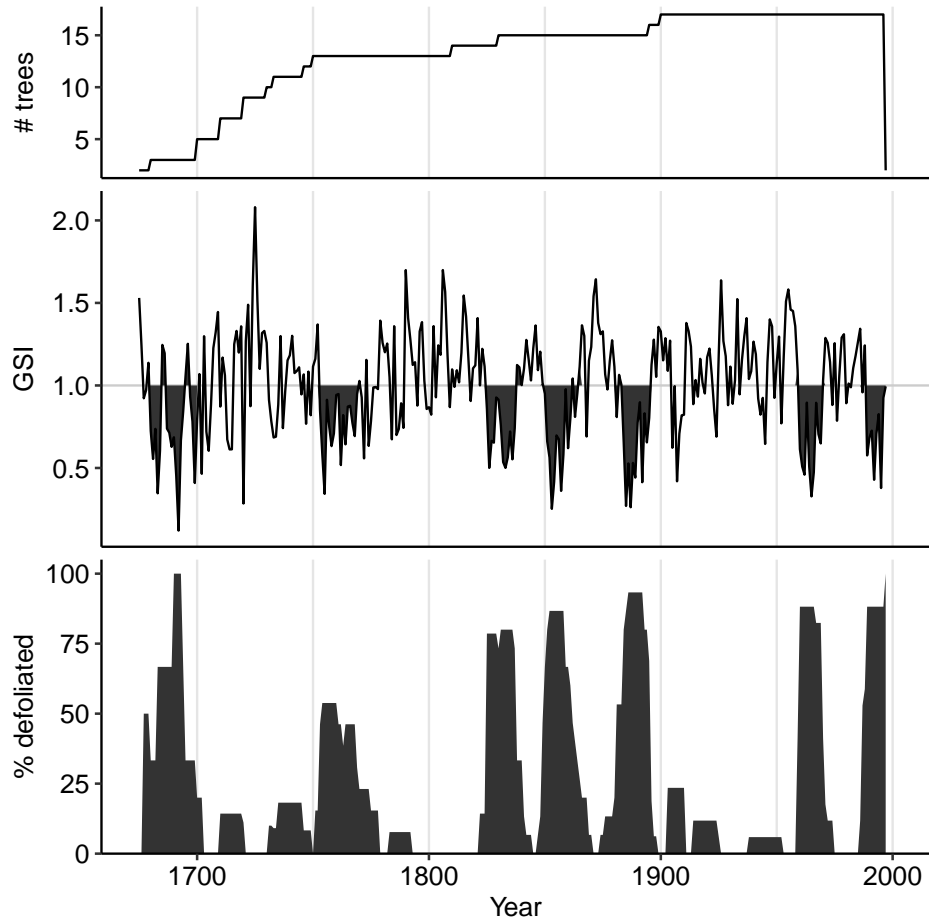


Figure 2: Default `dfoliatR` graphic for site-level outbreak events, produced by the `plot_outbreak()` function. These plots summarize the data in Figure 1 for the DMJ site. Top panel shows the sample depth, the middle panel shows the mean GSI with inferred outbreak events filled, and the bottom panel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

120 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 (for  
125 which one or more values exceeded the magnitude threshold) before and after  
126 the year of maximum departure. Each defoliation event is allowed one single-  
127 year positive excursion on each side of the year of maximum departure. Dura-  
128 tion is computed across the entire sequence that may include these two positive  
129 excursions. As in OUTBREAK, the user specifies a duration threshold (mini-  
130 mum number of years) for a departure sequence to be inferred as a defoliation  
131 event. The default threshold is eight years, as is commonly used in WSBW stud-  
132 ies (Swetnam and Lynch, 1989). If the sequence is shorter than the duration  
133 threshold, the sequence is omitted from the event results (i.e., both thresholds  
134 must be met). Researchers can, and should, adjust the duration and magnitude  
135 parameters accordingly and critically evaluate the results, as insect species vary  
136 in the length of their outbreaks and the degree to which they can suppress tree  
137 growth. OUTBREAK provides two sets of default values, those for WSBW,  
138 which typically has lengthy outbreaks, and ones for Douglas-fir tussock moth  
139 (*Orgyia pseudotsugata* (Lepidoptera: Tortricidae)) of three years duration with  
140 -1.28 departure threshold 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  
144 of defoliation at the site during the sampling campaign. The advantage of  
145 allowing potentially short, series-end events is that it allows a current event to  
146 be 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 2.2. Inferring Outbreak Events

178 Defoliation of one or a few trees does not constitute an outbreak. To de-  
 179 termine when defoliation becomes an *outbreak event*, **dfoliatR** composites the  
 180 individual tree defoliation series into a site-level chronology with the **outbreak()**

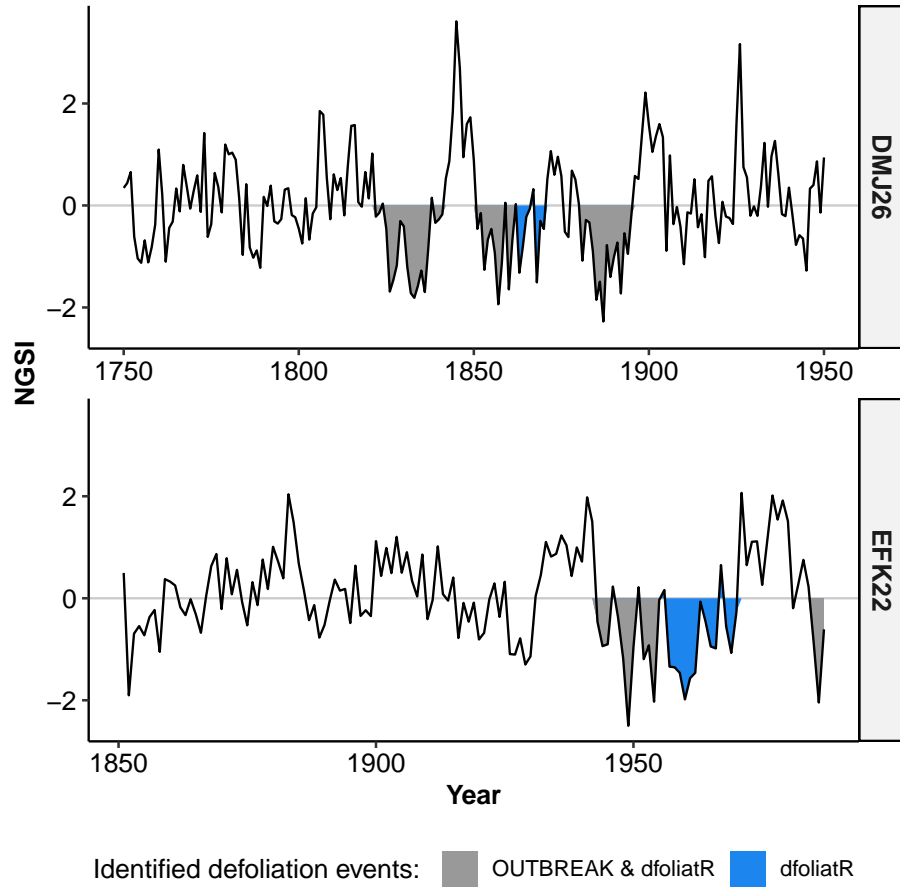


Figure 3: Examples of identified defoliation events on individual trees. For each tree (DMJ26 and EFK22), OUTBREAK and `dfoliatR` identify most of the same events, but there is one added event (in blue) that was omitted by OUTBREAK. These were omitted because they were separated by a single year of positive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

function. Users have options to define the number and/or the proportion of trees required for an event to be considered an outbreak. Three parameters control whether a defoliation event constitutes an outbreak: the minimum number of trees available, the minimum number of trees recording defoliation, and the percent of trees recording defoliation. The first allows the researcher to make a judgment call as to the confidence ascribed to reduced sample depth toward the ends of their chronologies, thus compensating for the “fading record problem” (Swetnam et al., 1999). The second two parameters adjust the scale of defoliation considered to be an outbreak. Absolute numbers of trees and percentages can be applied separately or in conjunction, following filtering conventions in tree-ring fire history studies (Malevich et al., 2018). We urge users to carefully consider the choice of absolute numbers in situations where the number of trees represented in the series varies with time, or the choice of percentages when sample size is small.

### 3. Evaluation

#### 3.1. Approach

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

We detrended host data for both `dfoliatR` and `OUTBREAK` using `ARSTAN` (version 6.1) with cubic smoothing splines (50% frequency response on 100-150 year wavelengths depending on the site). In both `dfoliatR` and `OUT-`

210 BREAK we used event thresholds of -1.28 normalized indices, 8 years duration,  
 211 and allowed for events at the end of series in seven of eight sites that had known  
 212 outbreaks at the time of sampling. We found it necessary to be consistent in  
 213 how we detrended and what software we employed (e.g., ARSTAN vs `dplR`)  
 214 because subtle differences in standardized ring-width indices generated between  
 215 the programs transferred into differences between `dfoliatR` and OUTBREAK.  
 216 In the end, we chose to only use the standardization output files from ARSTAN,  
 217 which are easily read into R (and then `dfoliatR`) using the `dplR` package.

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

### 220 3.2. Findings

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

- 230 • *Series-end events* (40% of the total) in which OUTBREAK included “trun-  
 231 cated outbreaks” (for seven sites) at the end of each series. In `dfoliatR`,  
 232 this option is controlled by the “series\_end\_events” parameter to `defoliate_trees()`.  
 233 In OUTBREAK, the option appears while changing the duration param-  
 234 eter (option 3). When selected, OUTBREAK will include any sequences  
 235 of negative indices at the beginning and the end of each tree series as a  
 236 defoliation event, without consideration of either duration or magnitude  
 237 thresholds. In `dfoliatR`, the duration threshold is omitted and the mag-  
 238 nitude 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.

At the site level, OUTBREAK and `dfoliatR` produce similar time series of percent trees defoliated (Figure 4), which forms the basis for inferring out-

break occurrence, intensity, and duration. In nearly all site-level comparisons, **dfoliatR** included either more events or it inferred a longer duration outbreak. These differences arise from the inclusion of tree-level events by **dfoliatR** that were omitted by OUTBREAK (see note on sequential events above). Thus, in **dfoliatR**, there were a greater number of trees experiencing defoliation during outbreak periods, or outbreaks were represented by a single tree when there was low sample depth.

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

#### 4. Availability and installation

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

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

In each R session, **dfoliatR** can be loaded via

```
library(dfoliatR)
```

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

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

Issues, bug reports, and ideas for improving **dfoliatR** can be posted to <https://github.com/chguiterman/dfoliatR/issues>. As an Open Source library, we welcome and encourage community involvement in future development. The

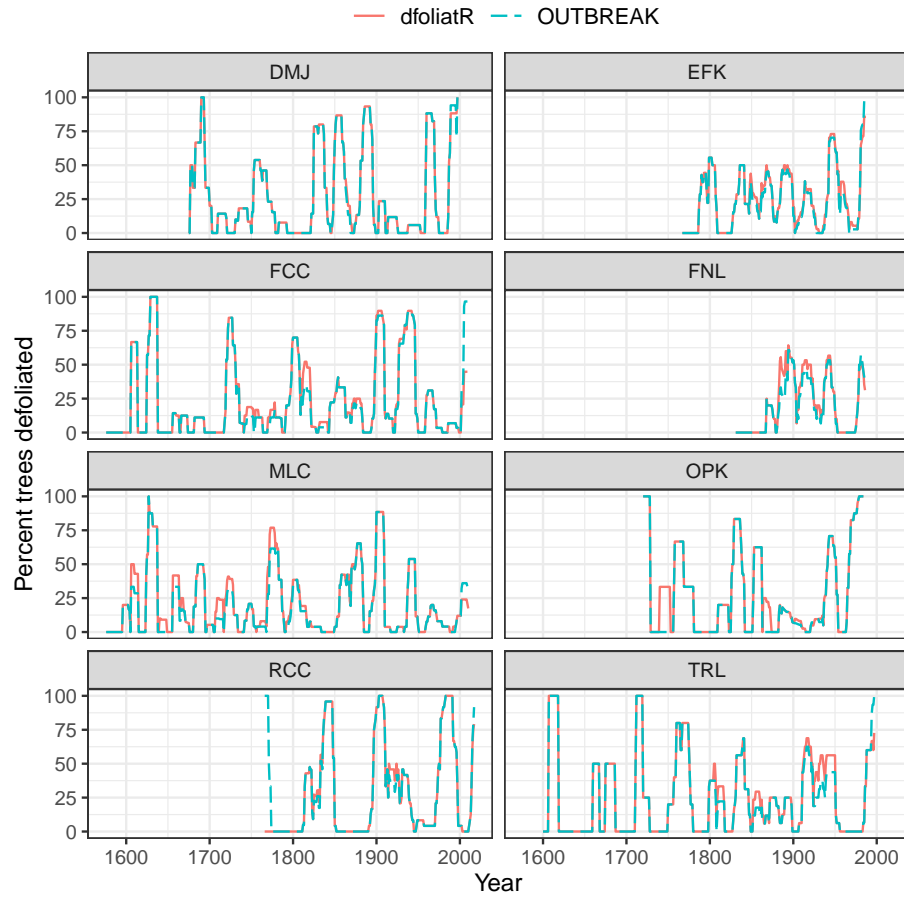


Figure 4: Comparison of reconstructed western spruce budworm outbreaks computed by **dfoliatR** and **OUTBREAK**. Input parameters were identical between programs. Differences arise because **dfoliatR** will identify and record more defoliation events on individual trees.

290 best ways to contribute to `dfoliatR` are through standard GitHub procedures  
291 or by contacting the corresponding author.

## 292 5. Example Usage

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

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

312 In our example scripts below, `##` and `#` denote user comments, per standard  
313 R coding, which are colored in brown. Text in blue denotes functions; black  
314 are loaded objects, and green are quoted variables and links. Values or other  
315 information provided after equal signs are filenames and parameters provided  
316 for this example, and in actual use would be replaced with user-specified infor-  
317 mation. In this example “`dmj_h`” and “`dmj_nh`” are the individual-tree host  
318 series and non-host site chronology files for the Demijohn site, thresholds are set



319 at 8 years and -1.28 standard deviations, bridging is used, series-end events are  
320 included in the interval computations, and comprehensive results information is  
321 not included in the output.

### 322 5.1. Tree-Level Defoliation Events

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

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

331 at DMJ), and “series\_end\_defol” to identify defoliation at the present-end of  
332 the series.

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

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

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

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

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

```
## 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"))

```

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

## 358 5.2. Site-Level Events

359 To infer outbreak events at the site level, the function `outbreak()` compos-  
 360 ites tree-level defoliation series into a single chronology, with input parameters  
 361 that control thresholds in the number and proportions of trees recording a de-  
 362 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)

```

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

373 “outbreak\_status” column shows whether an outbreak event is inferred (“out-  
374 break”) or not (“not\_obr”).

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

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

378 Inferred outbreak events are shown in the middle panel of Figure 2 as  
379 the filled-in spaces. Users can change the time series in this panel with the  
380 “disp\_index” parameter, choosing between the mean NGSI (the default) or  
381 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  
386 event (“n\_df\_start” and “perc\_df\_start”, respectively), the maximum num-  
387 ber of trees recording the outbreak event during a single year (“max\_df\_obr”),  
388 the year corresponding to that peak (“yr\_max\_df”), the year with the lowest  
389 mean NGSI during the event (“yr\_min\_ngsi”), and the minima of mean GSI  
390 and 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  
396 of 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, quan-  
399 tify, analyze, and visualize tree-ring growth suppression events and to recon-  
400 struct forest insect defoliator outbreak regimes. It is built on the long-accepted  
401 host to non-host comparison methodology used in the 1980s FORTRAN pro-  
402 gram OUTBREAK (Swetnam et al., 1985; Swetnam and Lynch, 1989, 1993).  
403 Our evaluation of the two programs revealed that `dfoliatR` excelled in identi-  
404 fying defoliation events on single trees, providing researchers with more consis-  
405 tent and biologically-justifiable results. Other key benefits are that `dfoliatR`  
406 provides easier control of suppression thresholds, additional output tables, high-  
407 quality and customizable graphics, and operates in the open-source R environ-  
408 ment that is stable across computing platforms and is under active development  
409 and maintenance by a large and growing community.

410 Using `dfoliatR` requires standardized ring-width measurements from insect  
411 host trees and either an indexed tree-ring chronology from local non-host trees  
412 or suitable climate chronology. It performs an indexing procedure to remove  
413 the climatic signal represented in the non-host chronology from the host-tree  
414 series. It then infers defoliation events in individual trees. Site-level analyses  
415 identify outbreak events that synchronously affect a user-defined number or

416 proportion of the host trees. Functions are provided for summary statistics and  
417 graphics of tree- and site-level series. The package produces publication-quality  
418 plots, and tabulates growth suppression indices and tree- and site-level outbreak  
419 event statistics for user-defined post-processing needs, including those suitable  
420 for charting and tabulating landscape- and regional-level results.

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

434 **dfoliatR** adds to the on-going open-source software development for den-  
435 drochronological methods (e.g., Bunn, 2008; Brewer, 2014; Brewer and Gui-  
436 terman, 2016). The R environment enables automation of analyses, allowing  
437 input/output processes to become routine, enables efficient sensitivity analy-  
438 ses, and empowers batch processing of large multi-site projects. It also fa-  
439 cilitates additional statistical analyses, such as spectral analyses and super-  
440 posed epoch analyses (e.g., Malevich et al., 2018), with easy transfer from  
441 **dfoliatR** and **dplR** to other libraries in R. Source code for **dfoliatR** is avail-  
442 able in the Comprehensive R Archive Network (CRAN) and GitHub [https:](https://github.com/chguiterman/dfoliatR)  
443 [//github.com/chguiterman/dfoliatR](https://github.com/chguiterman/dfoliatR) with updated descriptions and helpful vi-  
444 gnettes on the package website <https://chguiterman.github.io/dfoliatR/>. Re-  
445 searchers wishing to contribute to the further development of **dfoliatR** are  
446 encouraged to do so via the GitHub repository.



## 447 Acknowledgments

448 We are grateful to late Richard Holmes of the Laboratory of Tree-Ring Re-  
449 search (LTRR) for his achievements in developing OUTBREAK and many other  
450 tree-ring software programs. We also thank Thomas Swetnam for his insights  
451 and encouragement, and David Frank for his support. The `dfoliatR` project is  
452 funded by the Agnes Haury Visiting Scholars Fellowship (to J. Axelson) at the  
453 LTRR, the University of California, Berkeley, and the Western Wildlands Envi-  
454 ronmental Threat Center (WWETAC). Additional support was provided by the  
455 LTRR and the United States Forest Service Rocky Mountain Research Station.  
456 The findings and conclusions in this publication are those of the authors and  
457 should not be construed to represent any official USDA or U.S. Government  
458 determination or policy.

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