Technical Note

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

Christopher H. Guiterman\textsuperscript{a,b,*}, Ann M. Lynch\textsuperscript{a,c}, Jodi N. Axelson\textsuperscript{d}

\textsuperscript{a} Laboratory of Tree-Ring Research, University of Arizona, 1215 E Lowell St., Box 210045, Tucson, AZ 85721, United States
\textsuperscript{b} Three Pines Forest Research, LLC, PO Box 225, Ena, NH 03750, United States
\textsuperscript{c} U.S. Forest Service, Rocky Mountain Research Station, 1215 E Lowell St., Box 210045, Tucson, AZ 85721, United States
\textsuperscript{d} Dept of Environmental Science, Policy \& Management, University of California, Berkeley, 130 Mulford Hall \#3144, Berkeley, CA 94720, United States

Keywords:
Dendroecology
Dendroentomology
OUTBREAK
Western spruce budworm
Defoliator regimes
Insect outbreak reconstruction

A B S T R A C T

We present a new \textit{R} package to provide dendroecologists with tools to infer, quantify, analyze, and visualize growth suppression events in tree rings. \textit{dfoliatR} is based on the OUTBREAK program and builds on existing resources in the \textit{R} computing environment and the well-used \textit{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. \textit{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 graphs of tree- and site-level series. We evaluated \textit{dfoliatR} against OUTBREAK, using eight datasets including 222 host-trees, and found that \textit{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 \textit{R} Archive Network (CRAN) and on GitHub.

1. Introduction

Variation in the width and morphology of annual radial growth rings in trees permits dating and quantification of past forest insect defoliator outbreaks. Defoliation can be distinguished from climate- and other disturbance-related influences by comparing ring-width or other annually-resolved features in the wood of host species to that of non-host species or annually-resolved climate records. The effect of defoliation on radial growth of trees has been recognized since the 1860s, and used to reconstruct outbreak regimes since the 1950s \citep{Blais1954, Alfaro2010, Lynch2012}. The first studies \citep{Swetnam1985, Speer2010, Lynch2012} focused on developing historical outbreak reconstructions of western spruce budworm (WSBW; \textit{Choristoneura freemani} \textit{(Lepidoptera: Tortricidae)}; previously known as \textit{C. occidentalis}). The methodology has since been successfully applied to a wide range of defoliator species, most of which are conifer herbivores, and has evolved in sophistication for a wide range of ecosystem situations \citep{Lynch2012}.

The main dendrochronological tool for inferring, dating, and characterizing defoliator outbreaks from tree-ring records has been the software routine OUTBREAK \citep{Swetnam1985, Holmes1986, Swetnam1989}. OUTBREAK computes indices (described later in detail) of suppressed growth by subtracting a detrended and standardized climate series (a “control” chronology) from individual host-tree detrended and standardized radial growth series after the host and non-host series have been brought to a common variance. The non-host chronology usually consists of a site chronology developed from non-host tree species growing on a climate-sensitive site, but a gridded climate data point series, like the North American Drought Atlas \citep{Cook2004} 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 dplyr-based library to overcome these issues.

dfoliatR adds to a growing suite of dendrochronology packages in the R computing environment (Core Team, 2019). Stemming from the dplyr 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 cross-dating (Bunn, 2010), analyze sub-animal anatomical features (Rathgeber et al., 2011; Campelo et al., 2016), and perform many analytical tests (Zang and Biondi, 2015; Jevssenak and Levanic, 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 dplyr 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://github.com/chguiterman/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.

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 dplyr or ARSTAN (Cook and Holmes, 1996). It is important that the host-tree data include only one tree-ring series per tree. dplyr (via the dplyr::treeMean() function) and dplyr 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 (Fig. 1) and then composite across multiple trees to infer stand or site level outbreak events (Fig. 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

$$GSI = NH - \left( NH - \frac{NH}{\sigma} \right) \frac{NH}{\sigma}$$

where $H$ and $NH$ are the host-tree series and the non-host chronology, in year $i$, respectively. Only the common period between the host-tree series and the non-host chronology are used in Eq. (1). The host and non-host chronologies are brought to common variance by scaling the non-host chronology by its mean (NH) and multiplying by the ratio of host and non-host standard deviations ($\frac{NH}{\sigma}$), 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” and becomes a central point in time for assessing other thresholds before being included as a defoliation event. If the year of maximum departure is higher than the threshold (i.e., NGSI$_{\text{lower}} > -1.28$), the sequence being assessed is omitted from the event results.

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

Like OUTBREAK, users are provided an option to suspend the duration threshold at the recent end of the series in cases where an
Defoliation of one or a few trees does not constitute an outbreak. To determine when defoliation becomes an outbreak event, dfoliatR composites the individual tree defoliation series into a site-level chronology with the outbreak() 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.
We detrended host data for both dfoliatR and OUTBREAK using ARSTAN (version 6.1) with cubic smoothing splines (50% frequency response on 100–150 year wavelengths depending on the site). In both dfoliatR and OUTBREAK we used event thresholds of −1.28 normalized indices, 8 years duration, and allowed for events at the beginning of the series 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., Fig. 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 (Fig. 4), which forms the basis for inferring outbreak occurrence, intensity, and duration.

3.2. Findings

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

- Series-end events (40% of the total) in which OUTBREAK included “truncated outbreaks” (for seven sites) at the end of each series. In dfoliatR, this option is controlled by the “series-end_events” parameter to defoliate_trees(). In OUTBREAK, the option appears while changing the duration parameter (option 3). When selected, OUTBREAK will include any sequences of negative indices at the beginning and the end of each tree series as a defoliation event, without consideration of either duration or magnitude thresholds. In dfoliatR, the duration threshold is omitted and the magnitude threshold is retained in series-end-events. Each of the 13 events included in these differences did not meet the “max_reduction” parameter (−1.28 NGSI) in dfoliatR and were excluded. In two cases, OUTBREAK included events at the beginning of the series where dfoliatR does not allow truncated events. In four cases, OUTBREAK omitted only the last year of the series because the index was positive, but dfoliatR allowed this single positive excursion. Finally, there were two cases in which dfoliatR omitted possible events because it had already included a positive NGSI excursion after the “max_reduction” year, and since it will only allow one excursion on either side of the max year, the events were omitted due to short duration.

- Sequential events (36%) in which OUTBREAK omitted back-to-back events that occur one year prior to, or one year following an identified event. When this occurs, OUTBREAK selects the one event sequence with the lowest negative index year (e.g., Fig. 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.

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
In each R session, dfoliatR can be loaded via 

```r
library(dfoliatR)
```

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

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

5.1. Tree-level defoliation events

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

![Fig. 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.](image)
## 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.

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

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 trees. Finally, the “outbreak_status” column shows if an
outbreak event is inferred (“outbreak”) or not (“not obr”), and whether it represents an ongoing series-end event (“se outbreak”).

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

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

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

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

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

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

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

### 6. Conclusions

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

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

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

`dfoliatR` adds to the on-going open source software development for dendrochronological methods (e.g., Bunn, 2008; Brewer, 2014; Brewer and Guiterman, 2016). The R environment enables automation of analyses, allowing input/output processes to become routine, enables efficient sensitivity analyses, and empowers batch processing of large multi-site projects. It also facilitates additional 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.

### Conflict of interest

The authors have no conflicts of interest or competing interests to declare.
Declaration of Competing Interest

The authors report no declarations of interest.

Acknowledgments

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

References

Alfaro, R., Sickle, G., Thomson, A., Wegwitz, E., 1982. Tree mortality and radial growth losses caused by the western spruce budworm in a Douglas-fir stand in British Columbia. Can. J. Forest Res. 12, 780–787.

Altmann, J., Frich, P., Dolezal, J., Aakula, T., 2014. TRADER: a package for tree ring analysis of disturbance events in R. Dendrochronologia 32, 107–172. https://doi.org/10.1016/j.dendo.2014.01.004.

Axelson, J., Bast, A., Alfaro, R., Smith, D., Gartner, H., 2014. Variation in wood anatomical structure of Douglas-fir defoliated by the western spruce budworm: a case study in the coastal-transitional zone of British Columbia, Canada. Trees 28, 1837–1846. https://doi.org/10.1016/j.tree.2014.10.002.

Blais, J., 1954. The recurrence of spruce budworm infestations in the past century in the Loe Seal area of northwestern Ontario. Ecology 35, 62–71.

Brewer, P.W., 2014. Data Management in Dendroarchaeology Using Tellervo, vol. 56. Radiocarbon Cambridge University Press, pp. S79–S83. https://doi.org/10.2458/azu_rc.56.18320.

Brewer, P.W., Guiterman, C.H., 2016. A new digital field data collection system for dendrochronology. Dendrochronologia 38, 131–135. https://doi.org/10.1016/j.dendo.2016.04.005.

Brookes, M.H., Campbell, R.W., Colbert, J.J., Mitchell, R.G., Stark, R.W., 1987. Western spruce budworm. In: USDA Forest Service, Cooperative State Research Service, Technical Bulletin No. 1694. Washington D.C., 198 p.

Brubaker, L.B., 1978. Effects of defoliation by douglas-fir tussock moth on ring sequences in Pseudotsuga menziesii. Dendrochronologia 26, 115–124. https://doi.org/10.1016/j.dendo.2008.01.002.

Bunn, A.G., 2010. Statistical and visual crossdating in R. Dendrochronologia 28, 251–258. https://doi.org/10.1016/j.dendo.2009.12.001.

Campelo, F., Nabbais, C., Carvalho, A., Vieira, J., 2016. trachWilds+ an R package to standardize tracheidograms. Dendrochronologia 37, 64-68. https://doi.org/10.1016/j.dendo.2015.12.006.

Carus, S., 2004. Impact of defoliation by the pine processionary moth (Thaumetopoea pityocampa) on radial, height and volume growth of Calabrian pine (Pinus nigra) trees in Turkey. Phytosanitica 32, 459–469.

Carus, S., 2009. Effects of defoliation caused by the processoiny moth on growth of Crimean pines in western Turkey. Phytosanitica 37, 105–114.

Cook, E.R., 1990. Guide for computer program ARSTAN. In: Grissino-Mayer, H., D., Holmes, R., L., Fritts, H., C., Fritts, H., Cal., Eds. (Eds.). The international tree-ring data bank program library version 2.0 user’s manual. University of Arizona, Tucson, Arizona, USA, pp. 75–87.

Esper, J., Büntgen, U., Frank, D.C., Niegrelger, D., Liebhold, A., 2007. 1200 years of regular outbreaks in alpine insects. Proc. R. Soc. B: Biol. Sci. 274, 671–679. https://doi.org/10.1098/rspb.2006.0191.