

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 identify, quantify, analyze, and visualize growth suppression events in tree rings produced by insect defoliation. The ‘dfoliatR’ library is based on the Fortran V program OUTBREAK, and builds on existing resources in the R computing environment. ‘dfoliatR’ expands on OUTBREAK to provide greater control of suppression thresholds, additional output tables, and high-quality graphics. To use ‘dfoliatR’ requires standardized ring-width measurements from insect host trees and an indexed tree-ring chronology from local non-host trees. 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 available for summary statistics and graphics of tree- and site-level series.

Key words: Dendroecology, spruce budworm, Choristoneura, pandora moth, Coloradia pandora Blake, larch-bud-moth

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27 Introduction

28 The **dfoliatR** library is unique among a growing suite R packages designed
29 for dendrochronology. Stemming from the **dplR** library (Bunn 2008) that pro-
30 vides R the ability to read and write an array of tree-ring data formats, stan-
31 daridize ring widths, build and evaluate chronologies, perform quality control
32 (to name a few), one can now also measure, perform and check crossdating,
33 and perform many analytical tests (Bunn 2010, Lara et al. 2015, Zang and
34 Biondi 2015, Jevšenak and Levanič 2018). Tools for assessing stand dynamics
35 and disturbance analyses are under rapid development, with new packages for
36 assessing growth and release events (**TRADER**: Altman et al. 2014), metrics of
37 growth resilience (**pointRes**: Maaten-Theunissen et al. 2015), and fire history
38 (**burnr**: Malevich et al. 2018). The key objective of **dfoliatR** is to provide
39 tools to identify and analyse insect defoliation and outbreak events by build-
40 ing on the methods employed the FORTRAN program OUTBREAK (Swetnam
41 and Lynch 1989). What sets **dfoliatR** apart from packages such as **TRADER** is
42 that it explicitly performs an indexing procedure on host-tree series to remove
43 climatic and other non-defoliation related signals represented by non-host tree
44 species. Insect defoliation signals are identified in the disturbance index by the
45 duration and magnitude of negative departures.

46 **dfoliatR** draws upon data formats in **dplR** that are commonly employed
47 by other tree-ring libraries. It uses and outputs a data formats that facilitate
48 the use packages embodied by **tidyverse** (Wickham et al. 2019) that include
49 efficient data wrangling (**dplyr**: Wickham et al. 2020) and graphics (**ggplot2**:
50 Wickham 2016).

51 In this paper, we describe the statistical methods employed by **dfoliatR**,
52 its availability, and run through analyses for a single site in New Mexico. Users
53 need not have much experience in R to replicate the analyses and graphics
54 below. All R code presented below is executable in an R session once the
55 required libraries are installed and loaded. Support documentation in addi-
56 tion to this paper is provided within the package via standard help menus

(accessed by typing ? before a function name) and on the package website (https://chguiterman.github.io/dfoliatR/), which includes up-to-date vignettes that describe in detail the functionality of the software. Code to create a preprint of this manuscript including the R scripts is available from https://github.com/chguiterman/dfoliatR_paper.

Overview of the software

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

- Standardized ring-width series for individual trees of the host species
- Standardized tree-ring chronology from a local non-host species

Users can develop these data sets in software of their choosing, such as in `dp1R` or `ARSTAN`. It is important that the host-tree data include only one tree-ring series per tree. Both `dp1R` and `ARSTAN` have options for averaging multiple sample series into a tree-level series. The tree-ring series and chronology can be read into R via several available `dp1R` functions.

`dfoliatR` begins to identify defoliation events in individual trees by removing the climatic signal as represented by the non-host chronology from the host tree series. This indexing procedure creates a series – the “growth suppression index” (GSI) – in which disturbance is the predominant signal. The GSI is calculated as

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

where H and NH are the host tree series and the non-host chronology, in year i , respectively (Swetnam et al. 1985, Swetnam and Lynch 1989). Only years in which the individual host-tree series and the non-host chronology overlap are used in Equation 1. The non-host chronology is scaled by its mean ($\overline{\text{NH}} \approx 1.0$) and multiplied 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. This “corrected” non-host chronology is subtracted from the host-tree series.

79 Negative departures in the normalized growth suppression index that surpass
80 user-defined thresholds in duration and magnitude will be defined as *defoliation*
81 *events*.

82 The individual tree defoliation series are composited in an additional step
83 to identify *outbreak events* that synchronously affect multiple trees. Users have
84 options to define the number and/or the proportion of trees required for a
85 defoliation event to be considered an outbreak.

86 Note that these methods of separating tree- vs site-level disturbance cate-
87 gories is a major departure from the OUTBREAK program. In OUTBREAK
88 the two levels of analysis are combined and users have more limited control of
89 thresholds to define defoliation events versus outbreaks.

90 Availability and installation

91 The `dfoliatR` is provided free and open source (Guiterman 2020). It is
92 provided to R users via the Comprehensive R Archive Network (CRAN; <https://cran.r-project.org/>). To install `dfoliatR` from CRAN use

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

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

```
library(dfoliatR)
```

95 Development versions of `dfoliatR` are available on Github and installed
96 using the `devtools` library,

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

97 Issues, bug reports, and ideas for improving `dfoliatR` can be posted to
98 <https://github.com/chguiterman/dfoliatR/issues>. As an Open Source library,
99 we welcome and encourage community involvement in future development. The
100 best ways to contribute to `dfoliatR` are through standard Github procedures
101 or by contacting the first author.

102 **Usage**

103 *Tree-level defoliation events*

104 `##Site-level events`

105 **Evaluation**

106 **Extensions**

107 **References**

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