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 supression 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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Introduction

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 `dplR` or ARSTAN. It is important that the host-tree data include only one tree-ring series per tree. Both `dplR` and ARSTAN have options for averaging mutliple sample series into a tree-level series. The tree-ring series and chronology can be read into R via several available `dplR` 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" – in which disturbance is the predominant signal. Negative departures in the growth suppression index that surpass user-defined thresholds in duration, and magnitude will be defined as *defoliation events*. The individual tree defoliation series are composited in an additional step to identify *outbreak events* that synchronously affect mutliple trees. Users have options to define the number and/or the proportion of trees required for a defoliation event to be considered an outbreak.

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

Availability and installation

The `dfoliatR` is provided free and open source (Guiterman, 2020). It is provided to R users via the Comprehensive R Archive Network (CRAN; https:

//cran.r-project.org/). To install `dfoliatR` into R 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 in R,

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

Support documentation is provided within the package via help menus (accessed by typing `?` before a function name), this paper, and on the package website (https://chguiterman.github.io/dfoliatR/) which includes updated vignettes. Code to execute a preprint of this manuscript and the code included below is available at (*insert later*).

Tree-level defoliation events

Site-level events

Evaluation

Extensions

References

Guiterman, C., 2020. Chguiterman/dfoliatR: First release. Zenodo. doi:10.5281/zenodo.3626136