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DendroSync: An R package to unravel synchrony patterns in tree-ring networks

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ABSTRACT

Spatial synchrony refers to the presence of a common signal for a time-varying characteristic that, in dendrosciences, is shared among tree-ring chronologies from a particular area. Analysis and interpretation of synchrony patterns in tree-ring networks is currently limited by: (i) the requirement for flexible modelling of complex correlations and heteroscedastic errors and (ii) the availability of ready-to-use open software to fulfil this task. We present an R package (DendroSync) that facilitates estimating and plotting synchrony patterns for pre-defined groups. The package has been devised to work with traits derived from tree rings (e.g. ring-width), but other data types are also suitable. It combines variance-covariance mixed modelling with functions that quantify the degree to which tree-ring chronologies contain a common signal over a fixed time period. It also estimates temporal changes in synchrony using a moving window algorithm. The functionality and usage of DendroSync are illustrated using a simple example.

1. Introduction

Dendrochronological archives provide long-term records of tree performance at varying spatial scales. The rising interest on the spatiotemporal dependence of forest dynamics on environmental cues has resulted in an increase of tree-ring networks worldwide (e.g. Barber et al., 2000; Briffa et al., 2002, 2008; Babst et al., 2013; St. George, 2014). These networks may contain complex patterns of coordinated (i.e. synchronous) temporal fluctuations in tree-ring signals. For instance, it has been reported that there is a common variation in regional tree-ring patterns engendered by correlated climatic forces and that the strength of this common variation diminishes with increasing distance. This phenomenon has received ample attention over the last decades (e.g. Fritts, 1976; Feliksik, 1993; Rolland, 2002; Frank and Esper 2005; Macias et al., 2006; Shestakova et al., 2016) and has been shown to be species- and region-specific (Di Filippo et al., 2007; Trouet et al., 2012; St. George, 2014; Shestakova et al., 2014, 2016). Hence, a natural question arises as to how such coordinated responses are structured across spatially disjunct stands (Rolland, 2002). Indeed, detailed analyses of coordinated patterns of tree-ring variability across geographical scales is likely to provide further insights into the influence of local and regional processes on the structure and function of forests. On the other hand, the available methodological approaches to unravel the complexities of tree-ring signals are still scarce.

In this context, spatial synchrony can be defined as the presence of a relevant common signal for a time-varying trait (e.g. ring-width) in a collection of tree-ring chronologies covering a particular area. Traditionally, the strength of the common signal shared by tree-ring series has been estimated through classical analysis of variance (ANOVA) (i.e. fixed effects model; Fritts, 1976). The seminal paper by Wigley et al. (1984) broadened the application of ANOVA in dendrosciences by establishing the theoretical background for estimating the uncertainty in the average common signal of a set of correlated series. Time series of indexed ring widths were described in terms of variance components of several random effects (Wigley et al., 1984). Indeed, tree-ring data are often better defined through a mixed model setting because of the associated random sources of variation, e.g. those associated with measurements repeated in time (Jennrich and Schluchter, 1986). Once the time (year) factor is taken as a random variable, inferences about the entire population of years can be derived from the estimation of the inter-annual variance common to a set of chronologies for a trait of interest. Hence, the proportion of common variance, or intra-class correlation, estimates the extent of coordinated (or synchronous) fluctuations among chronologies (Shestakova et al., 2014).

Synchrony patterns across geographical scales (i.e. from plots to continents) can be better disentangled and interpreted by grouping chronologies into potentially homogeneous subsets (e.g., Babst et al.,

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2013; Shestakova et al., 2014). For instance, contrasting physiological responses between species or across regions may cause differential forest reactions to environmental conditions that remain registered in tree rings (de Luis et al., 2013; Galván et al., 2014). Factors such as phylogeny, geographical proximity or functional similarity may underlie different patterns of synchrony in a particular area. Shestakova et al. (2014) presented a mixed model framework to disentangle spatial patterns of tree-ring signals that was applied using proprietary software. This methodology allows assessing to what extent temporal responses are spatially structured by partitioning the variability associated to the time effect at intra- and inter-group levels. By applying different grouping criteria, temporal signals of different strength, shared within and between the subsets, can be quantified by variance-covariance mixed modelling. This framework has proved to be well suited to interpret synchrony patterns in tree-ring networks ranging from local (Shestakova et al., 2017) to sub-continental scales (Shestakova et al., 2016). However, broad analyses of such synchrony patterns are currently limited because of lack of non-proprietary software tools.

Despite their potential ecological applications, mixed models to study spatially structured tree-ring records are not yet broadly in use. Here, we present ‘DendroSync’ (Alday et al., 2017, CRAN: DendroSync), a package for the open-source R statistical environment (R Development Core Team, 2016) that facilitates the analysis and interpretation of synchrony patterns existing in tree-ring networks. DendroSync is based upon previously described methods (Shestakova et al., 2014). The package contains a suite of customizable functions that allow (i) evaluating and plotting complex patterns of synchrony for tree-ring traits over a given time period at within- and between-group levels that are pre-defined by the user and (ii) assessing temporal changes in those patterns using a moving window algorithm that divides the whole period of study into shorter sub-periods. We begin by describing the package functionality. We then provide an illustrative example and indicate where the package is available for download. Finally, we conclude by providing a general outlook of the package.

2. Package functionality

The package DendroSync quantifies synchrony across ring-width chronologies (or other tree-ring traits) for (i) a fixed time period defined by the user (i.e. at sub-centennial or centennial scales) and (ii) a moving time window that pre-defines intervals within the study period for which synchrony estimates are obtained independently (e.g. 30-year window). We note that this package can accommodate various time series datasets apart from tree rings, but it was originally devised to be used in a dendrochronological framework.

The package workflow is illustrated in Fig. 1. Following Shestakova et al. (2014, 2016), the package contains three function types: (i) functions to fit and, afterwards, select variance-covariance (VCOV) models based on goodness-of-fit statistics using a user-defined grouping criterion for any given tree-ring dataset; (ii) functions to calculate synchrony at within- and between-group levels from the selected VCOV models for the whole study period and (iii) functions to calculate temporal changes in synchrony using moving-window intervals across the time series. Appropriate plotting functions of synchrony patterns at within- and between-group levels for the whole period and of temporal changes in synchrony across sub-periods are also available. In total, 15 different functions are implemented, but nine are mainly for internal use (Fig. 1).

2.1. Data handling

The package DendroSync has been designed to work with residual indices of tree-ring width (TRW) chronologies that may partly overlap, hence covering a given period. To obtain indexed chronologies we recommend the use of high-pass filter algorithms. In this way, biological growth trends are eliminated while a common variance at inter-annual time scales is potentially preserved across chronologies (i.e. high-frequency variability related to climate or other external drivers of tree performance). The package can also handle other ecological data in which long-term trends and temporal autocorrelation have been previously removed (e.g. tree-ring traits such as isotopic series or density measurements, climatic time series, remote sensing derived data, etc.). The input data must be formatted as a data frame with TRW (response variable), time and grouping variables as columns. The time variable is used to specify the years to be included in the analyses, and the grouping variable defines the grouping criterion applied to stratify the dataset of chronologies into subsets for analysis of synchrony patterns at both within- and between-group levels. A variable coding for a chronology factor (Code) should also be included to account for the effect of series (fixed) in the model. However, if time series vary around the same mean (as in the case of indexed ring-width chronologies), the variable Code becomes redundant and can be saved. In this case, the model turns into a random effects model. Missing values can be reported as NA.

2.2. Variance-covariance model selection

The first step to calculate synchrony values of indexed TRW chronologies for a grouping variable over a fixed time period (Fig. 1) is the selection of the best VCOV model. The function dendro.varcov fits seven VCOV models relating TRW against specific names of tree-ring width chronologies (TRW ~ Code) or, alternatively, the VCOV models can be fitted without code identification of chronologies if they are centred on the same mean value (TRW ~ 1). Whatever the choice, time and grouping variables are modelled using positive-definite matrices (?pdClasses) to characterize synchrony for each level of the grouping variable and also across pairwise combinations of levels (i.e. within- and between-group synchrony). The function returns the following VCOV model outputs (Shestakova et al., 2014): a null positive-definite matrix structure (mBE; *broad evaluation*), and the homoscedastic and heteroscedastic (homoscedastic = TRUE or FALSE) versions of a diagonal positive-definite matrix structure (mNE, mHeNE; *narrow evaluation*), a positive-definite matrix with compound symmetry structure (mCS, mHeCS; *compound symmetry*) and a general positive-definite matrix structure (mUN, mHeUN; *unstructured*). Briefly, *broad evaluation* ignores the existence of groups so the year variance is constant at the within- and between-group levels; *narrow evaluation* tests for lack of common signals between chronologies belonging to different groups (i.e. covariances are set to zero); *compound symmetry* fits homogeneous year variances across groups and homogeneous covariances across pairwise combinations of groups; finally, *unstructured* allows for heterogeneous variances and covariances. The heteroscedastic variants of these VCOV models arise from allowing the residual variance to vary among groups. Afterwards, the function mod.table provides a table comparing VCOV models by Akaike’s Information Criterion (AIC), corrected AIC (AICc) and Bayesian Information Criterion (BIC) in the smaller-is-better form (Burnham and Anderson, 2002). Based on these criteria the best fitting VCOV model can be selected from this table.

2.3. Synchrony estimation

The function sync estimates synchrony from a previously selected VCOV model, amongst those produced by dendro.varcov. A modname argument is included in sync function to select one among the seven models of interest (mBE, mNE, mHeNE, mCS, mHeCS, mUN, mHeUN). The output lists synchrony estimates at the within- and between-grouping variable levels, quantifying the degree to which the values of chronologies contain a common signal. A standard error (SE) of each synchrony estimate is also included. This output can be directly used as input for the sync.plot function where dot plots of within- and between-grouping variable synchrony are produced. These dot plots are used to