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Rate-of-change analysis in palaeoecology revisited: a new approach

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Abstract

Dynamics in the rate of compositional change beyond the time of human observation are uniquely preserved in palaeoecological sequences of terrestrial and marine origin. Periods with a high rate-of-change (RoC) have been assigned to reflect changes due to external factors such as climate and human forcing. However, changes in sedimentation rates and sampling strategies can result in an uneven distribution of time intervals within a stratigraphic sequence, which are known to affect RoC estimates and thus derived conclusions. Several approaches have been used to account for these issues (e.g. binning of levels, data smoothing, etc.) but despite the importance and frequency of these, there has been relatively little exploration of the implications of these challenges into quantifying RoC in palaeoecology.

Here, we introduce R-Ratepol – an easy-to-use R package – that provides a new, robust numerical technique for detecting and summarising RoC patterns in complex multivariate time-ordered stratigraphical sequences. First, we compare the performance of common methods of estimating RoC and detection of periods of high RoC (peak-point) using simulated pollen-stratigraphical data with known patterns of compositional change and temporal resolution. Then, we apply our new

methodology to four representative European pollen sequences to detect potential drivers of compositional change.

We show that the successful detection of known shifts in compositional changes identified by RoC depends heavily on the smoothing methods and dissimilarity coefficients used, and the density of stratigraphical levels. Identifying the need for an improved numerical approach, we propose a new method of binning with a moving window in combination with a generalised additive model for peak-point detection. Our method shows a 68% increase in the correct detection of peak-points compared to the more traditional way of peak selection by individual levels, as well as achieving a reasonable compromise between Type I and Type II errors. Likewise, by using the four pollen sequences from Europe, we show that our approach also performs well in detecting periods of significant compositional change during known onsets of human activity, early land-use transformation, and changes in fire frequency.

Expanding the approach using R-Ratepol to the increasing number of open access paleoecological datasets in global databases, such as Neotoma, will allow future palaeoecological and macroecological studies to quantify major changes in biotic composition or in sets of abiotic variables across broad spatio-temporal scale.

KEYWORDS: Compositional change; peak-point detection; stratigraphic sequences; pollen analysis; rate-of-change; simulated data

1. INTRODUCTION

Quantifying spatio-temporal changes in biological composition or diversity is essential for monitoring the current biodiversity crisis and for disentangling underlying drivers such as climate, land-use change, pollution, or introduction of invasive species, as well as intrinsic population dynamics driven by biotic interactions (e.g. Dodd et al., 1994; Dornelas et al., 2013; Gotelli et al., 2010; Magurran et al., 2010; Monchamp et al., 2018; Morecroft et al., 2009; Richardson et al., 2006; Silvertown et al., 2006; Steinbauer et al., 2018; Wolfe et al., 1987). Therefore, the importance of such ecological long-term observational studies (50-100 years) is increasingly recognised (Dornelas et al., 2013; Hillebrand et al., 2018; Magurran et al., 2019). Substantial compositional change has been observed during recent decades (e.g. Feeley et al., 2020; Steinbauer et al., 2018), the last centuries ("The Great Acceleration"; Steffen et al., 2015), and during the Holocene as a result of human impact (Stephens et al., 2019) or in response to regional climate change (Seddon et al., 2015; Shuman et al., 2005). However, similar rates of substantial change in composition have also been detected on longer time scales (Kemp et

al., 2015). To understand the impacts of humans, for instance, on ecosystems it is essential to compare temporal changes in species composition and diversity through human history and to investigate whether such changes are unique to the epoch of human impact ("Anthropocene") or whether they precede human-dominated systems (Birks, 1997; Birks et al., 2016).

Assemblage data of palaeoecological sequences of terrestrial and marine proxies (pollen, diatoms, chironomids, cladocerans, corals, molluscs, sediment chemical variables, etc.) are a unique resource for quantifying spatio-temporal changes in biotic or abiotic composition and diversity beyond the time period of human observations. Rate-of-change (RoC) analysis was introduced into palaeoecology by Jacobson and Grimm (1986) to quantify the rate and the magnitude of compositional change within a Holocene pollen sequence. It was extended by Jacobson et al. (1987) to quantify and compare rates of change within and between sequences (see also Grimm and Jacobson, 1992) in an attempt to identify regional-scale and local-scale patterns in rates of change. RoC analysis estimates compositional change or temporal beta-diversity between adjacent stratigraphical levels and hence between times. Unlike other estimates of beta-diversity, RoC analysis specifically estimates the magnitude of compositional change per *unit time*. Therefore, an essential requirement in RoC analysis is a robust age-depth model for the stratigraphical sequence of interest to estimate the precise age of levels within the sequence.

Despite the wide use of RoC analysis in palaeoecology (e.g. Birks and Ammann, 2000; Birks, 1997; Birks and Birks, 2008; Correa-Metrio et al., 2012; Grindean et al., 2019; Laird et al., 1998; Solovieva et al., 2008; Urrego et al., 2009), there has been relatively little exploration of the underlying methodology of RoC analysis and how the various methodologies and sequence properties influence RoC estimates (but see Bennett and Humphry, 1995; Birks, 2012; Lotter et al., 1992). Different approaches to estimate RoC (Bennett and Humphry, 1995; Birks, 2012) involve choices in terms of approach and technique, such as transforming the stratigraphical levels and associated assemblage data (using binning or interpolation to constant time intervals), smoothing the data, and the metric used to estimate the amount of compositional dissimilarity between adjacent levels (Birks, 2012).

The variety of approaches available to RoC analysis can, however, create problems. First, Anderson et al. (2020) stress the sensitivity of RoC to temporal sampling variation within and between records, consequently hampering conclusive comparisons. Second, there has been a lack of standardisation between studies (i.e. incorporating different dissimilarity metrics, different temporal procedures) which means RoC outcomes cannot be directly compared between sequences or studies (Birks, 2012). Third, intrinsic properties of an individual sequence, such as its taxonomic richness and the density and distribution of levels within the sequence, can influence the estimated RoC. The end result is that,

since the expected patterns of RoC in a sequence are unknown, the most appropriate choices or methods to undertake RoC analysis are also unknown (Bennett and Humphry, 1995; Birks, 2012).

Here, we present and evaluate the performance of R-Ratepol, a new R package (R Core Team, 2018), for RoC analysis introducing a standardised and robust method, which incorporates age uncertainties from age-depth modelling as well as standardisation of taxa richness, and hence current best practice, for estimating and comparing RoC estimates within and between stratigraphical sequences. First, we present the R-Ratepol and its capacities for data commonly used in palaeoecological studies. Second, we compare the performance of various methods of estimating RoC using simulated pollen-stratigraphical data (Blaauw et al., 2010) with known patterns of compositional change and resolution. In addition, we introduce a method for detecting 'peak-points', defined as a rapid change in composition or relative abundances of variables within the sequence, which provides an intuitive, much-needed means to compare directly RoC between sequences and thus facilitates the interpretation of potential drivers of assemblage change on a regional scale. We compare the effectiveness of our new method for the successful detection of peak-points with commonly used methodologies which are also provided in R-Ratepol. Finally, we illustrate our findings by estimating RoC values for four pollen palynological sequences with different densities of stratigraphical levels and pollen richness and link the observed patterns to known anthropogenic activities. Our approach can provide important information for future palaeoecological and macroecological studies attempting to quantify, and then attribute, major changes in biotic or abiotic composition across broad spatial areas, and to compare the observed changes in recent decades with changes that occurred within the Holocene (e.g. Gibson-Reinemer et al., 2015).

The term 'assemblage' is used through the text to refer to sets of biotic (pollen, macrofossils, etc.) or abiotic (sediment chemistry, isotope ratios, etc.) variables studied in levels within a stratigraphical sediment sequence.

2. Materials and Methods

2.1. R-Ratepol

R-Ratepol is written as an R package and includes a range of possible settings including a novel method to evaluate RoC in a single stratigraphical sequence using assemblage data and age uncertainties for each level. There are multiple built-in dissimilarity coefficients (DC) for different types of data, and various levels of data smoothing that can be applied depending on the type and variance of the data. In addition, R-Ratepol can use randomisation, accompanied by use of age uncertainties of each level

and taxon standardisation to detect RoC patterns in datasets with high data noise or variability (i.e. numerous rapid changes in composition or sedimentation rates).

The computation of RoC in R-Ratepol is performed using the following steps (Fig. 1) and detailed descriptions of the underlying methods and formulae are given in the Supplementary Material:

1. Assemblage and age-model data are extracted from the original source and should be compiled together, i.e. depth, age, taxon 1, taxon 2, etc.
2. (optional) Smoothing of assemblage data: Each variable within the assemblage data is smoothed using one of five in-built smoothing methods: none, Shepard's 5-term filter (Davis, 1986; Wilkinson, 2005), moving average, age-weighted average, Grimm's smoothing (Grimm and Jacobson, 1992).
3. Creation of time bins: A template for all time bins in all window movements is created.
4. A single run (an individual loop) is computed:
    a. (optional) Selection of one time series from age uncertainties (see section 2.1.1.2. on randomisation)
    b. Subsetting levels in each bin: Here the working units are created (WUs; see section 2.1.1.1.)
    c. (optional) Standardisation of assemblage data in each WU (see section 2.1.1.2. on randomisation)
    d. Calculation of RoC between adjacent WUs: RoC is calculated as the dissimilarity coefficient (DC) standardised by age differences between WUs. Five in-built dissimilarity coefficients are available: *Euclidean distance*, *standardised Euclidean distance*, *Chord distance*, *Chi-squared coefficient* (Prentice, 1980), *Gower's distance* (Gower, 1971). The choice of DC depends on the type of data (see Supplementary Material).
    e. Summary of a single run is produced based on all moving windows
5. Step 4 is repeated multiple times (e.g. 10,000 times).
6. Validation and summary of results from all runs of RoC calculation are produced.
7. (Optional) Data beyond a certain age can be excluded (e.g. 8000 cal yr BP for the pollen sequences in this study)
8. Detection and validation of significant peak-points. There are five in-built methods to detect significant peak-points: *Threshold*, *Linear trend*, *Non-linear trend*, *first derivative* of a generalised additive model (f-deriv GAM; Simpson, 2018), and *Signal-to-Noise Index* (SNI; Kelly et al., 2011).

2.1.1. Specific methodological considerations

2.1.1.1. Selection of working units (WU; Step 3)

RoC is calculated between consecutive Working Units (WU). Traditionally, these WUs represent individual stratigraphical levels. However, changes in sedimentation rates and sampling strategies can result in an uneven temporal distribution of levels within a time sequence, which in turn makes the comparison of RoC between sequences problematic. There are various methods that attempt to minimise such problems. The first is *interpolation of levels* to evenly spaced time intervals, and the use of the interpolated data as WUs. This can lead to a loss of information when the density of levels is high. Second is *binning of levels*: assemblage data are pooled into age brackets of various size (bins) and these serve as WUs. Here, the issue is a lower resolution of WUs and their uneven size in terms of total assemblage count (bins with more levels have higher assemblage counts). Third is *selective binning*: like classical binning, bins of selected size are created, but instead of pooling assemblage data together, only one level is selected as representative of each bin. This results in an even number of WUs in bins with a similar count size in the assemblage. However, the issue of low resolution remains.

Therefore, we propose a new method of *binning with a moving window*, which is a compromise between using individual levels and selective binning. This method follows a simple sequence: bins are created, levels are selected as in selective binning, and RoC between bins is calculated. However, the brackets of the time bin (window) are then moved forward by a selected amount of time (Z), levels are selected again, and RoC calculated for the new set of WUs. This is repeated X times (where X is the bin size divided by Z) while retaining all the results. R-Ratepol currently provides several options for selecting WU, namely as individual levels, binning of levels, selective binning, and our new method of binning with a moving window.

2.1.1.2. Randomisations

Due to the inherent statistical errors in uncertainties in the age estimates from age-depth and the assemblage datasets (e.g. pollen counts in each level; Birks and Gordon, 1985), R-Ratepol can be run several times and the results summarised (Steps 5-6). Therefore, two optional settings are available by using age uncertainties and assemblage data standardisation.

Age uncertainties (Step 4a)

For each run, a single age sequence from the age uncertainties is randomly selected. The calculation between two consecutive WUs (i.e. one working-unit combination) results in a *RoC score* and a *time position* (which is calculated as the mean age position of the two WUs). However, due to random sampling of the age sequence, each WU combination will result in multiple RoC values and age positions. R-Ratepol assigns the age position of each WU combination as the median time position from all calculations (Step 6).

The final RoC value for a single WU combination is calculated as the median of the scores from all randomisations. In addition, the 95th quantile from all randomisations is calculated as an error estimate.

Data standardisation (Step 4b)

Taxa in the assemblage dataset can be standardised to a certain count (e.g. number of pollen grains in each WU) by rarefaction. Random sampling without replacement is used to draw a selected number of individuals from each WU (e.g. 150 pollen grains).

2.1.2. Detection of peak-points in RoC sequence (Step 8)

A rapid change in composition or relative abundances of taxa within the sequence can provide a means of comparing RoC between sequences and interpreting the potential drivers of assemblage change. To detect such significant peak-points of RoC scores in each sequence, each point is tested to see if it represents a significant increase in RoC values. There are various ways to detect peak-points in a time series and R-Ratepol is able detect peak-points using five methods:

1) Threshold: Each point in the RoC sequence is compared to a median of all RoC scores from the whole sequence (i.e. *threshold value*). The point is considered significant if the 95th quantile of the RoC scores from all calculations is higher than the *threshold value*.
2) Linear trend: linear model is fitted between the RoC values and their ages. Differences between the model and each point are calculated (residuals). The standard deviation (SD) is calculated from all the residuals. A peak is considered significant if it is 1.5 SD higher than the model.
3) Non-linear trend: A conservative generalised additive model (GAM) is fitted through the RoC scores and their ages ($\mathrm{GAM} = \mathrm{RoC} \sim \mathrm{s}(\mathrm{age}, k = 3)$) using the *mgcv* package (Wood, 2011). The distance between each point and the fitted value is calculated (residuals). The standard deviation (SD) is calculated from all the residuals. A peak is considered significant if it is 1.5 SD higher than the model.
4) F-deriv GAM: smooth GAM model is fitted to the RoC scores and their ages ($\mathrm{GAM} = \mathrm{RoC} \sim \mathrm{s}(\mathrm{age})$). The first derivative as well as continuous confidence intervals are calculated from the model using the *gratia* package (Simpson, 2019). A peak is considered significant if the confidence intervals of the first derivative differ from 0 (for more information see Simpson, 2018).
5) Signal-to-noise (SNI) method: We adapted SNI from Kelly et al. (2011), which was developed to detect changes in charcoal stratigraphical records. SNI is calculated for the whole RoC sequence and a peak-point is considered significant if it has an SNI value higher than 3.

2.2. Testing the successful detection of peak-points using simulated data

In order to compare the performance of various methods of estimating RoC, we used simulated pollen-stratigraphical data (Blaauw et al., 2010) with known patterns of compositional change and temporal resolution to test the success of peak-point detection in the expected time period of compositional change. In addition, we used a generalised linear mixed modelling approach to evaluate the effects of the different R-Ratepol parameters.

2.2.1. Data simulation

We simulated pollen datasets following Blaauw *et al.* (2010) based on generating pollen-assemblage data in response to known changes in environmental conditions and compositional properties (Fig. S1). We used the following process of data generation: (i) we used the density of levels from a European pollen sequence, Glendalough (Sequence A) as a template for the number of levels and the corresponding ages for each level. (ii) Pollen data were created as abundance data with a total of 300 pollen grains in each level. (iii) We then adjusted the total values of each simulated taxon so that the pollen assemblage resembled a log-scale rank distribution. (iv) We added jitter to each of the pollen taxa (function *jitter*, factor = 1.5). All changes were made in order to make the simulated data more similar to data from a real-life study.

Two additional settings were altered during the simulation of datasets: (i) richness – *low richness* (LR) datasets contain 5 pollen taxa, *high richness* (HR) datasets contain 50 pollen taxa; and (ii) position of change in external environmental properties – *recent* (R) has a sudden increase of environmental properties at 2000 calibrated years before present (1950 CE: cal yr BP) and a decrease at 3000 cal yr BP, *late* (L) has a sudden increase at 5500 and a decrease at 6500 cal yr BP (Fig. S1). This results in two abrupt changes in pollen composition in each dataset. Note that the different timings of the change in environmental properties (hereafter called 'focal area') were selected to illustrate the effects of level density (datasets with the *later* change have a low density of levels within the focal area and datasets with a *recent* change have a high density). The combination of these two settings results in four types of simulated datasets: *low richness – recent change* (LR-R)*, low richness – late change* (LR-L)*, high richness – recent change* (HR-R), and *high richness – late change* (HR-L).

2.2.2. Using the simulated datasets to test analytical performance of RoC methods with different settings

To investigate the differences between the various settings in RoC methods, we simulated 100 datasets for each dataset type (LR-R, LR-L, HR-R, HR-L; see previous section), and compared the success rate of detecting peak-points in the expected time period for all combinations of (i) WU selection, (ii) smoothing method, (iii) dissimilarity coefficient, and (iii) peak-point detection.

We tested three types of WU selection (individual stratigraphical levels, selective binning, and binning with moving window), five types of smoothing methods (none, Shepard's 5-term filter, moving average, age-weighted average, Grimm's smoothing), two types of dissimilarity coefficients appropriate for compositional data (Chord distance, Chi-squared coefficient), and five types of peak-point detection (Threshold, Linear trend, Non-linear trend, f-deriv GAM, SNI).

For each simulated dataset we calculated RoC using combinations of all WU selections, data smoothing, dissimilarity coefficient, and peak-point detection method (150 different settings in total). R-Ratepol has been set up with standardisation of pollen assemblage data to 150 pollen grains in each WU and 100 randomisations per calculation. The number of randomisations is not higher due to high computational demands (60,000 RoC calculations, each with 100 randomisations). Randomisations are in place only for taxa standardisation as no age uncertainties have been used in this example. We then extracted (i) the number of WUs where R-Ratepol detected a significant peak-point during the focal area (± 500 yr), and (ii) the number of samples, where R-Ratepol detected a peak-point during a time of no expected change ('false positives'). We transformed these numbers of peak-points into ratios of points detected to total points in the area (inside or outside focal area; see Fig. S2 for example of peak-point detection).

Statistical tests to evaluate RoC options

First, we tested if the various WU selection methods affect the successful detection of peak-points within the focal area. We pooled all RoC calculations from all dataset types and created generalised linear mixed models using the Template Model Builder (Brooks et al., 2017) $\mathrm{glmmTMB}_{success-method}$ with the ratio of WU marked as peak-points to all WUs in the focal area ($R_{success-method}$) as the dependent variable with a beta error distribution. Independent variables are: WU (3 level factor), peak-point detection method (5 level factor), dataset type (4 level factor), and all their interactions. Individual dataset ID and RoC setting (factor combining smoothing method and DC; 10 levels) were selected as the random factors. We then used the *dredge* function from the *MuMIn* package (Barton, 2020) to fit models with all possible combinations of predictors (with a constraint that dataset type must be present), and ordered the models by parsimony (assessed by corrected Akaike information criterion; AIC_C). We only selected the best model if ΔAIC_C (i.e. $delta$ in the *MuMIn* package) < 2. In the case where multiple models had similar parsimony, we selected the best model using the *compare_performance* function from the *performance* package (Ludecke et al., 2020). We then used the *emmens* package (Russell, 2020) to obtain estimated marginal means and the 95th quantile of the independent variables from the final model. Similarly, we built $\mathrm{glmmTMB}_{FalsePositive-method}$ using the ratio of WUs marked as peak-points to all WUs outside the focal area ($R_{FalsePositives-method}$).

295 Next, for a more detailed exploration of different settings in R-Ratepol, we divided the data to only
296 include the best performing WU selection and peak-point detection combination (i.e. binning with
297 moving window and non-linear trend peak-point detection, see Results) and created
298 $\mathrm{glmmTMB}_{success-detail}$ and $\mathrm{glmmTMB}_{FalsePositive-detail}$ with $R_{success-detail}$ and
299 $R_{FalsePositives-detail}$ as the dependent variables, respectively. Both models were fitted with a beta
300 error distribution and the independent variables are data-smoothing type (5 level factor), dissimilarity
301 coefficient (2 level factor), position of environmental change (i.e. density of levels; 2 level factor),
302 richness of dataset (2 level factor), and all their interactions. Individual dataset ID was selected as a
303 random factor. As before, the *dredge* and *compare_performance* functions were used to select the
304 best model and reduce unnecessary predictors.

305 ### 2.3. Examples of rate-of-change results using empirical palynological data

306 After assessing the differences between the individual settings of R-Ratepol based on the results from
307 the simulated datasets, we examined the RoC estimates for real palynological data representing
308 different pollen richness and composition, and different density of levels. We obtained pollen data
309 from the Neotoma database (Williams et al., 2018) using the *Neotoma R package* (Goring et al., 2015).
310 We chose four European sequences (A–D; Fig 2).

311 In each sequence, taxa were harmonised to the taxonomically highest pollen morphotype (Level =
312 MHVar2) using the pollen harmonisation table in Giesecke et al. (2019). To develop age-depth models,
313 we used the pre-selected radiometric control points provided in Giesecke et al. (2014) and calibrated
314 the radiocarbon dates using the IntCal13 Northern Hemisphere calibration curve (Reimer et al., 2013).
315 For each sequence, we constructed an age-depth model using the *Bchron* R package (Haslett and
316 Parnell, 2008) to generate 1000 possible age estimates for all sample levels at the sampling resolution
317 of the original pollen sequences. We used these 1000 draws to build posterior estimates of age
318 uncertainty. We calculated the median age estimate for each sample level to obtain the default age
319 used in subsequent analyses.

320 In each sequence, we excluded all levels that contained less than 150 pollen counts of terrestrial taxa,
321 and all levels beyond a 3000-year extrapolation of the oldest chronological control point. In addition,
322 we excluded all levels with an age older than 8500 cal yr BP to ensure a focus on the period with
323 detectable human impact.

324 **Sequence A** is from Glendalough, Ireland (53°00’10.0"N 6°22’09.0"W; Neotoma dataset id = 17334;
325 Haslett et al., 2006). It has a very uneven distribution of levels (N = 102) with the highest density
326 around 2000 cal yr BP (Fig. 2A). The sequence contains 80 pollen taxa with abundant *Corylus*, *Quercus,*
327 *Alnus, Betula*, and Poaceae. Cyperaceae, Poaceae, and Ericales all increase in the last 1000 cal yr BP,

preceded by a period with high values of *Quercus*, *Betula*, and *Alnus* until ~ 5000 cal yr BP. Before 5000 cal yr BP the sequence has large variations in *Pinus*, an increase of *Alnus*, and a large decrease in *Corylus*. **Sequence B** is from Dallican Water, Scotland (60°23'14.5"N 1°05'47.3"W; Neotoma dataset id = 4012; Bennett et al., 1992). It has a relatively even distribution of levels (N = 63; Fig. 2B) and contains 50 pollen taxa with Ericales, *Betula*, and Poaceae being the most abundant. The pollen record shows sudden increases of Ericales after 4000 cal yr BP. **Sequence C** is from Steerenmoos, Germany (47°48'20.0"N 8°12'01.6"E; Neotoma dataset id = 40951; Rösch, 2000). It is an example of a very detailed sequence, but with an uneven distribution of levels (N = 273; Fig. 2C). The sequence contains 103 pollen taxa with *Abies*, *Fagus*, *Corylus, Betula*, and *Quercus* being the most abundant. As with Sequence A, the pollen stratigraphy can be separated into three major parts: i) a recent period until 1000 cal yr BP typified by high values of *Pinus*; ii) 2000–6000 cal yr BP typified by *Abies* and *Fagus*; and iii) 6000 cal yr BP to the base with abundant *Betula*, *Corylus*, and *Quercus*. **Sequence D** is from Alanen Laanijärvi, a boreal-forest lake in Swedish Lapland (67°58'N 20°29'W; Neotoma dataset id = 45314; Heinrichs et al., 2005). It is an example of a sequence with 54 levels across the time of interest, containing 44 pollen taxa with high abundance of *Pinus* and *Betula* throughout the whole sequence (Fig. 2D).

We calculated RoC scores for the four selected European sequences (A-D) using all three methods of WU selection with Shepard's 5-term filter smoothing and Chi-squared coefficient as the dissimilarity coefficient. A non-linear trend peak-point detection was used in each sequence, the number of randomisations was set to 10,000, and the size of time bin was selected as 500 yr (see Fig. S3 for an example of changes of RoC values with size of time bin). In addition, to provide examples of the differences between different settings of R-Ratepol, we explored data from sequence A using binning with the moving window method of WU selection and calculated RoC scores for all combinations of five smoothing methods and two dissimilarity coefficients (Chi-squared, Chord distance).

3. Results

3.1. Comparison of success rates in peak-point detection for simulated datasets

Successful detection of peak-points ($R_{success-method}$) and the number of incorrectly (false positives) detected peak-points ($R_{FalsePositives-method}$) are both significantly affected by WU selection and the method of peak-point detection (Fig. 3; see Table S1 and Table S2 for the AIC_C of all models). For detecting peak-points successfully within the focal area, our approach of binning with a moving window results in an overall better performance in successful peak-point detection than the use of individual levels or binning (effect of successful detection increases by 68% and 20%, respectively; Fig.

3A). Simulations show that the non-linear trend method performs best in detecting peak-points within the focal area (14% higher than the second-best, the linear trend method; Fig. 3B), and detects a similar amount of false positives compared to the other peak-point detection methods (with the exception of SNI, which detects 10-fold less false positives).

While using only the binning with the moving-window approach and the non-linear trend method for peak-point detection, the successful detection of peak-points ($R_{success-detail}$) and the number of false positives ($R_{FalsePositives-detail}$) are both influenced by the density of levels, type of dissimilarity coefficient, and data-smoothing type (Fig. 4; see Tables S3, S4, S5, and S6 for the best selected models). Using Chi-squared coefficient as the dissimilarity measure results in a 10% increase in the estimated correctly detected peak-points than Chord distance on average (Fig. 4) but the coefficient intervals of their estimates overlap (Fig. S4A). The level of smoothing has, on average, a decreasing effect on the successful detection of peak-points, with data without smoothing being the most successful (10% higher effect than the second-best Shepard's 5-term filter smoothing; Fig. S4B). The number of false positives is affected in a similar way, with no smoothing and Shepard's 5-term filter having the lowest number of false positives. The datasets with an assemblage change which occurred during a time period characterised by a high density of levels (i.e. recent environmental change) show, on average, a 14-fold higher success of peak-point detection and a 7-fold higher false positive detection than datasets with change at the time of a low density of levels (i.e. environmental change later in the sequence; Fig. S4C). Richness of pollen does not show a significant effect on the detection of peak-points (note that the assemblage data standardisation was used for all computation).

3.2. Examples of rate-of-change results using real palynological data

The selection of WUs affects not only the overall shape of the RoC curve in all sequences but also the timing of the period of significant increase in RoC (Fig. 2). Binning with a moving window detects significant periods of increased RoC scores at sequence A (Glendalough) from 4900–4200 cal yr BP; sequence B (Dallican Water) from 3500–3000 cal yr BP; sequence C (Steerenmoos) from 6400–5800 cal yr BP; and sequence D (Alanen Laanijärvi) from 550–350 cal yr BP (Fig. 2). The binning method shows relatively similar patterns and position of peak-points (except for sequence D). However, the error intervals (95th quantile of RoC scores) are much wider. Using individual levels as WUs (Fig. 2. 'RoC-levels') results in very different positions of peak-points and a different shape of the RoC curve with wide error intervals.

4. Discussion

Based on the results of our simulations, the choice of methods and parameters is critical in the analysis of rate-of-change. Comparison of methods using simulated datasets shows that selection of WUs, peak-point detection method, dissimilarity coefficient, smoothing of the data, and the density of the levels in the period of environmental change significantly influence the detection of sudden changes in stratigraphical sequences. Our proposed method of binning with a moving window in combination with a non-linear trend peak-point detection method improves such detection of an increased RoC. The method shows a 68% increase in the effect of correct detection of peak-points compared to the more traditional approach of selection by individual levels. Peak-point detection using a non-linear trend provides a reasonable compromise between statistical error Type I (linear trend and threshold method) and Type II (SNI method).

There is little difference between using Chi-squared coefficient or Chord's distance as the dissimilarity coefficient for pollen compositional data, and we therefore recommend using both for palaeoecological data sequences that are expressed as percentages or proportions and that contain many zero values. However, R-Ratepol is created as modular tool and can be used for many different paleo-proxies present in sedimentary sequences. Euclidean distance (see Supplementary Material) is appropriate for absolute assemblage data such as pollen concentrations or pollen accumulation rates (e.g. Peglar, 1993; Peglar and Birks, 1993). Such data may require a log-transformation prior to calculating the Euclidean distance between levels or WUs. Standardised Euclidean distance (see Supplementary Material) is appropriate when the variables in an assemblage are expressed in different units, such as geochemical, isotope, and sediment variables (e.g. Bakke et al., 2009; Birks and Birks, 2006; Nesje et al., 2014)). Gower's (1971) distance is appropriate for assemblage data consisting of different numerical types (continuous quantitative, qualitive, binary) such as plant macrofossil data (e.g. Birks, 2014).

Recommendation of a specific smoothing technique of data is less straightforward. There is a trade-off between the potential loss of information by smoothing the data and the incorrect attribution of noise (for example from sampling error) as signal. In our simple simulation experiment, data with a relatively low amount of smoothing (Shepard's 5-term filter and data without smoothing) perform relatively well, independently of the density of samples (Fig. 3). All the other smoothing methods perform worse, especially if environmental change occurred during a period characterised by a low density of levels. However, detailed exploration of the RoC pattern in a real pollen sequence (sequence A; Fig. 5) shows that all smoothing methods result in a similar RoC curve and position. Therefore, there is a need for critical evaluation in future studies to assess the risks of using data smoothing, depending on the density of samples and research questions of interest.

A multitude of appropriate data-smoothing approaches (Wilkinson, 2005), dissimilarity coefficients (e.g. Legendre and Legendre, 2012; Prentice, 1980), techniques for creating WUs, and methods of peak-point detection (e.g. Simpson, 2018) are potentially available. Of the two selected dissimilarity methods and five smoothing algorithms, all commonly used in palaeoecology, we conclude that datasets with a high density of levels tend to have a higher chance of successfully detecting peak-points. Anderson et al. (2020) reached similar conclusions in a regional-scale synthesis of fossil pollen data from California. Here the authors suggest maintaining a consistent temporal spacing within records, and the use of probabilistic models explicitly incorporating age-model uncertainties to increase the precision of age estimates of each level. We show that our method of binning with a moving window yields even better results than the traditional use of individual levels or binning, and has an advantage here, as age-model uncertainties can be incorporated.

RoC analysis has several applications in palaeoecological research. It is a useful numerical tool to detect patterns in stratigraphical data that cannot readily be seen by visual inspection (see Jacobson et al., 1987 for an example at Gould Pond, Maine). It is also useful to compare the rates of change in different proxies (pollen, diatoms, chironomids, etc.) studied in the same stratigraphical sequence (e.g. Birks and Ammann, 2000; Szabó et al., 2020). Moreover, it is most useful when RoC results are compared from several sequences (e.g. Grimm and Jacobson, 1992; Jacobson et al., 1987). Consistent patterns in RoC peaks in several sequences may potentially indicate responses to extrinsic drivers such as regional climate change, pathogenic attacks, or widespread human activity. Ecologists are recognising the importance of quantifying RoC of extrinsic environmental drivers such as temperature, toxins, and salinity on ecosystems (Pinek et al., 2020) and are developing new and powerful numerical tools for space–time analysis of community compositional data over time intervals of decades (e.g. Legendre and Gauthier, 2014). RoC peaks unique to individual sequences may, in contrast, reflect local factors such as sequence hiatuses, sediment reworking, or spatially restricted human impact or natural disturbance.

A connection between RoC and local factors can be seen in the sequences used in this study (Fig. 2). Sequence A (Glendalough) shows significant peak-points at the time of the onset of human activity and the expansion of grassland and heath (Haslett et al., 2006). Sequence B (Dallican Water) has significant peak-points at times when major changes in land-use occurred as the island was abandoned by humans and then reinhabited 800 years later (Bennett et al., 1992). Sequence C (Steerenmoos) has several significant peak-points at the time of the expansion of *Abies* pollen in the late Neolithic period and with frequent fires (Rösch, 2000). Sequence D (Alanen Laanijärvi) has significant peak-points in the very recent period, possibly associated with changes in organic deposition, fertilisation, and timber harvesting (Heinrichs et al., 2005). Here we can assume that our approach of binning with a moving

window is closest to the expected pattern, further supported by the relatively high, successful detection of peak-points in the simulated datasets (Fig. 3). In contrast, the traditional use of individual levels fails to detect the periods of significant change, or falsely assigns peak-points to other, non-relevant periods, or a combination of both (Fig 2). Some of these errors occur, as expected, with a low density of sample levels. These sequences and the RoC outcomes exemplify the usefulness of quantifying rates of compositional change estimated through time.

In summary, we have developed a framework for the robust estimation of rate-of-change in stratigraphical time-ordered sequences of terrestrial and marine palaeoecological datasets. Our overall framework consists of four major parts:

1. Establishing a robust age-depth model for the stratigraphical sequence of interest with age uncertainties for all individual levels.
2. Selecting consecutive working units prior to RoC estimation to allow for uneven temporal distribution of the analysed levels within the sequence using selective binning with a moving window.
3. Estimating compositional dissimilarity between working units.
4. Detecting statistically significant peak-points in the RoC estimates within the sequence.

Given the various choices of coefficients, methods, and evaluations in RoC analysis, it is essential when presenting RoC results for stratigraphical assemblage data to document what choices were made. There are, as we have shown, many decisions in RoC analysis. Publishing plots of 'Rate of Change' with no explanation about what choices were made in the RoC analysis is to be strongly discouraged (cf. Abrook et al., 2019).

Our RoC analysis approach as implemented in R-Ratepol is a significant improvement over existing methods for RoC analysis that do not incorporate methods to detect statistically significant peak-points (Birks, 2012). R-Ratepol is, we believe, a powerful and much needed addition to the toolkit of robust numerical techniques available to palaeoecologists and palaeolimnologists for detecting and summarising patterns in complex multivariate time-ordered stratigraphical sequences (Birks, 2010, 1997).

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6. Authors' contribution

OM and HJBB conceived the ideas and designed the study. OM led the manuscript writing, data analyses, and interpretation of the results. OM, AWRS, KPB, VAF, and SGAF designed the methodology for extracting and processing palaeoecological sequences from Neotoma. OM, JAG, AWRS, MJS, and HJBB contributed to methodology development. HJBB acquired the funding. All authors contributed to the writing of the text and interpretation of the results and gave final approval for publication.

7. Data availability

R-Ratepol is available as an R package at GITHUB (https://github.com/HOPE-UIB-BIO/R-Ratepol-package), including all the data used in this study. Scripts for all analyses used in this study can be found at GITHUB repository (https://github.com/HOPE-UIB-BIO/RateOfChange).

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9. Figures and tables

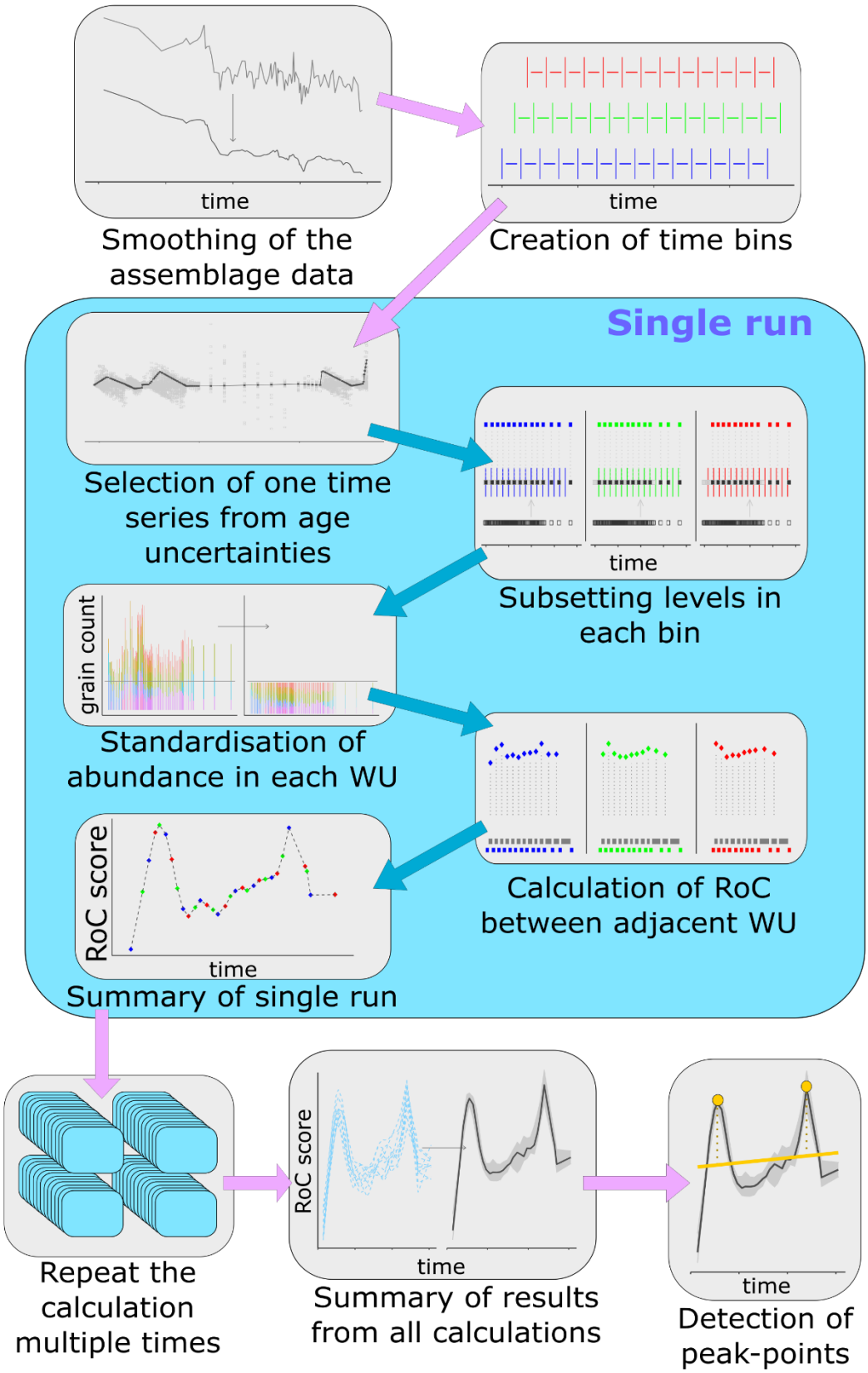

Figure 1. Schematic visualisation of RoC calculation in R-Ratepol with binning with a moving window. Methodological retails are provided in section 2.1 and Supplementary Material.

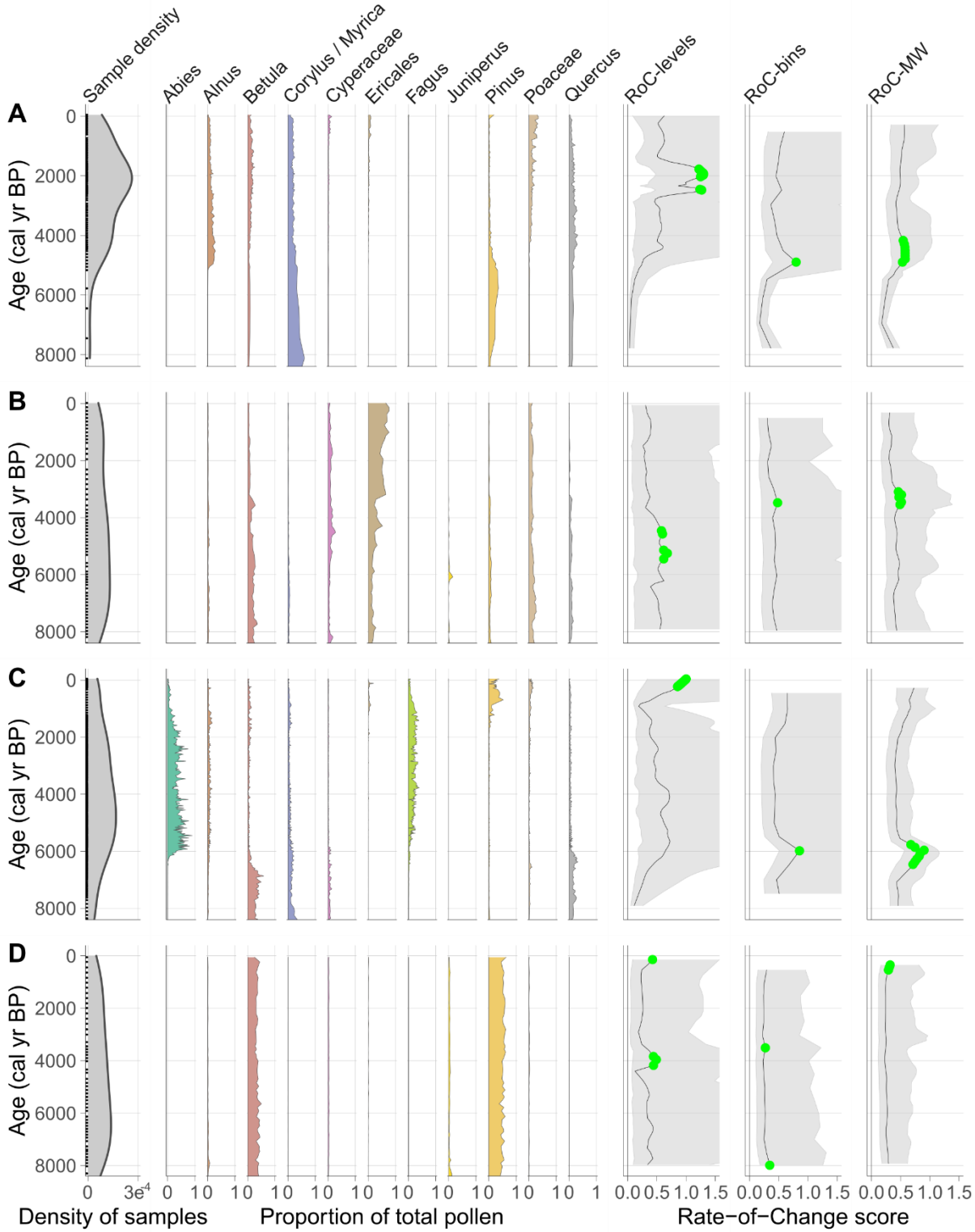

Figure 2. Summary of four sequences used in this study. Glendalough (A), Dallican Water (B), Steerenmoos (C), and Alanen Laanijärvi (D). For each sequence, three different plots are shown. First plot (left) shows the density of levels within each sequence for the last 8000 cal yr BP. Second

plot (middle) shows pollen stratigraphies for the most common taxa in the sequences. Values are presented as proportions of pollen grains in each level. Last plot (right) shows the rate-of-change score calculated with R-Ratepol for three different methods for WU selection: RoC-levels = use of individual levels, RoC-binning = binning, RoC-MW = binning with moving window. Shepard's 5-term filter smoothing and Chi-squared coefficient were selected for smoothing and dissimilarity measure, respectively. Green points indicate significant peak-points detected using the non-linear trend method. For a detailed explanation of the methods, see Materials and Methods, and Supplementary Material.

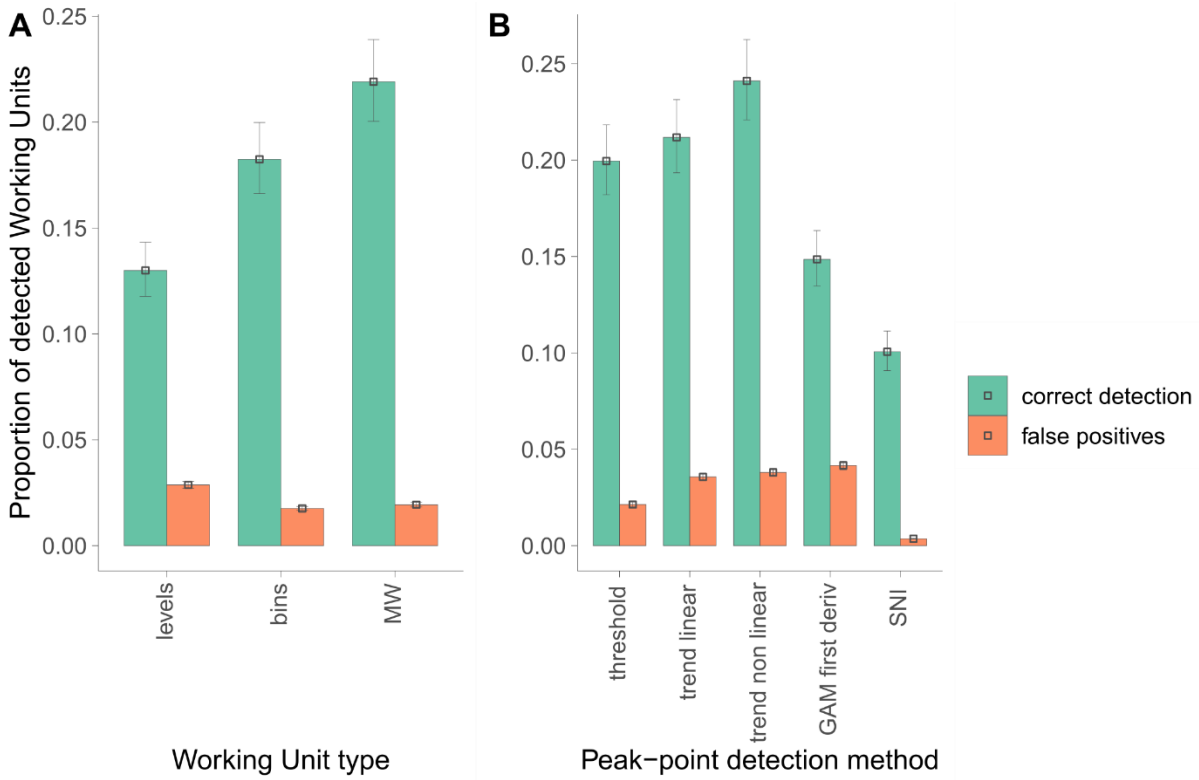

Figure 3. Comparison of the correct detection of peak-points in simulated datasets. A) Comparison of estimated marginal means of peak-point detection rates between different WU selections. Working unit selection: levels = use of subsequent levels, bins = selective binning, MW = binning with moving window. B) Comparison of estimated marginal means of peak-point detection rates between different peak-point detection methods. GAM first deriv = first derivative of a GAM; SNI = signal-to-noise index.

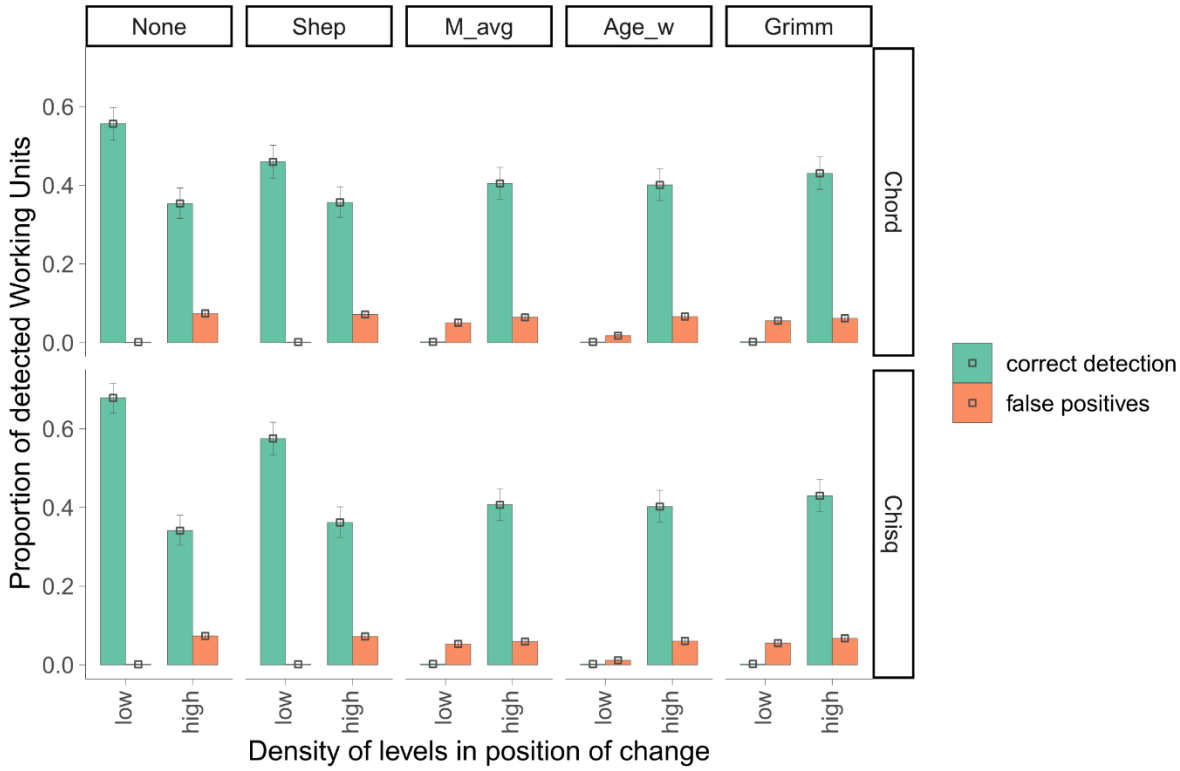

Figure 4. Comparison of peak-point detection rates using binning with the moving window and non-linear peak detection method. Smoothing methods: None = data without smoothing, Shep = Shepard's 5-term filter, M_avg = moving average, Age_w = age-weighted average, Grimm = Grimm's smoothing. Dissimilarity coefficients: Chord = Chord distance, Chisq = Chi-squared coefficient. For a detailed explanation of the methods, see Supplementary Material.

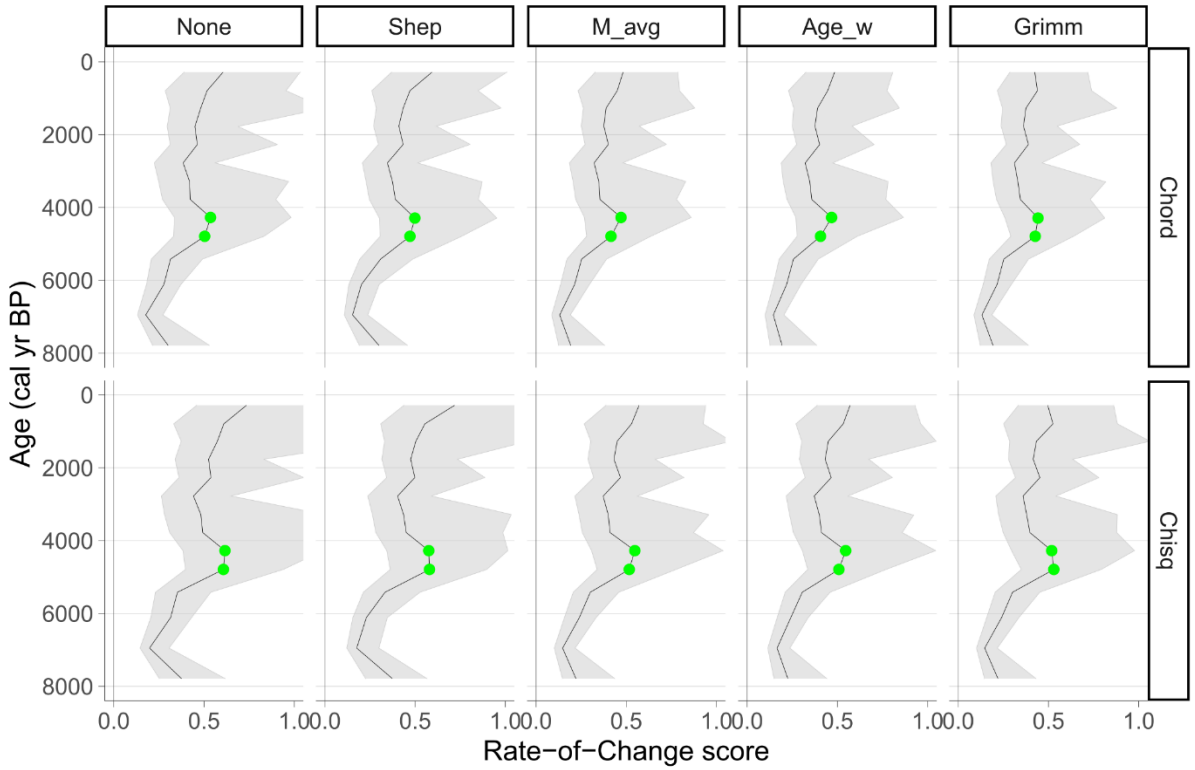

Figure 5. Rate-of-change (RoC) and peak-points detected in Sequence A (Glendalough) for five categories of data smoothing (columns) on two dissimilarity coefficients (rows). The binning with moving window was selected as Working Units, with 500 yr bin and 5 window shifts. Green points indicate significant peak-points detected using the non-linear trend method. Smoothing methods: None = data without smoothing, Shep = Shepard's 5-term filter, M_avg = moving average, Age_w = age-weighted average, Grimm = Grimm's smoothing. Dissimilarity coefficients: Chord = Chord distance, Chisq = Chi-squared coefficient. For a detailed explanation of the methods, see Supplementary Material.