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Interactive comment on “Patterns in recent and Holocene pollen influxes across Europe; the Pollen Monitoring Programme Database as a tool for vegetation reconstruction” *by* Vojtěch Abraham et al.

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We are pleased that both reviewers see the value of the database that we aim to make publically available with this publication. We also appreciate the comments on the manuscript that will certainly help to improve it. We like to take this opportunity to respond to some of the comments, each response is introduced by ### and finished by $$$

Anonymous Referee #1 The manuscript presents a new and valuable dataset that is made publicly available on a well-established database (NeotomaDB) that adheres to the World Data System and FAIR principles. The dataset consists of pollen counts from traps located in various European regions (and associated metadata). It is potentially extremely useful to explore pollen-vegetation relationships, as has already been shown in a number of previous, regionally-focussed, studies. In comparison to these prior studies, the present manuscript explores this modern-pollen dataset at a scale that spans across much wider geographical (latitudinal and altitudinal) gradients. The manuscript focuses on pollen abundances of 14 pollen taxa (12 trees and shrubs genera, 2 herb families) and explores the relationships between the sum of the pollen-accumulation rates (PAR) of the 14 taxa ("total PAR") and selected environmental parameters (mean annual temperature, annual precipitation, forest cover). It also explores the relationship between tree PAR and forest cover, and the relationship between pollen deposition as a function of increasing distance to the nearest range boundary of the parent plant species. A long-distance transport threshold (LDT) is obtained that may be used to infer range-size changes based on fossil PAR values. Further a comparison between modern and fossil PAR is presented that shows PAR-inferred population-size changes for selected taxa through time at different sites located across the latitudinal gradient.

The manuscript is at times very confusing. For instance, as far as I was able to understand, the results indicate that total PAR is strongly related with forest biomass within a 10km radius around the traps (Table S4). The text instead reports that forest cover explains 72% of the variance of total PAR.

We realize that due to the many analyses conducted and co-authors contributions some arguments were unresolved and miscommunications occurred. Unfortunately, we were not able to obtain biomass data for European vegetation cover and used "forest cover" instead. We will work to streamline the manuscript correctly indicating the usage of "forest cover" throughout. $$$

Further, Figure 3 shows how total PAR is related to latitude (besides, this relationship seems to be strongly determined by one datapoint),

We tested the influence of the data point on Spitsbergen, which of cause has a strong pull, but removing it is not changing our observations and conclusions as the following table with that point removed will show: PAR adjusted_PAR latitude 0.09 0.37 MAT 0.19 0.34 Forest cover 10 km 0.69 0.79 latitude+MAT+Forest cover 10 km 0.74 0.78 latitude+MAT+Forest cover 10 km+elevation 0.70 0.80

We would add this table with and without the point on Spitsbergen to the supplementary information of the manuscript. $$$

but does not show how total PAR are related to forest cover. Instead, the Figure shows how tree PAR is related to forest cover. -> It is striking to see that you explored the relationship between the sum of the pollen-accumulation rates (PAR) of the 14 taxa ("total PAR") and forest cover (text on P8L24-30 and Table S4). On which grounds would one expect a relationship between the PAR of herbs (Poaceae and of Cyperaceae) and forest cover?

We cannot expect a strong relationship between total PAR and forest cover as there may be 100% cover in a forest with very low productivity in northern Finland or a high productivity in southern Europe. By broadly accounting for differences in pollen productivity between trees and also grasses we are able to investigate a relationship between adjusted PAR and latitude and mean annual temperature. In a multiple regression model forest cover is however contributing to explain the variance in PAR and adjusted PAR. We illustrate in Fig. 3B that there is however a relationship between the minimum PAR values and the amount of forest cover. This relationship is important for interpretations as we are often interested to provide conservative interpretations on this "minimum" side of the spectrum e.g. during the initial spread of forest after the ice age. $$$

In my opinion, one of the main weaknesses of the manuscript is that the Introduction does not convey which knowledge gaps and hypotheses are being addressed. The

Introduction is strongly disconnected from the Abstract, the Results, the Discussion, and the Conclusions. It dwells on how and why the Pollen Monitoring Programme was established and lists prior, regional, studies. Some concepts that are mentioned both in the Abstract and the Discussion (CO2 fertilization, land use) are not found in the Introduction. Another concept (the importance of comparisons between modern and fossil pollen data, and of past and modern plant distributions and abundances) is only marginally mentioned in the Introduction, although it is important in the Discussion.

We acknowledge that that the introduction need to be improved addressing open questions. However, this manuscript also aims to introduce the database itself, which is a result of decades of research with its own history and like to find room for this aspect as well. $$$

(besides, I was surprised when I noticed that the taxa specific linkage is placed as supplementary material for some of the taxa. Maybe it was mentioned earlier in the Mat & Methods section?).

We selected the 8 most important taxa to be included in the main text. The remaining taxa including Cyperaceae and Poaceae, for which we assume the trapping data to be potentially biased are placed in the supplementary. We inform the reader about this in the Methods section. $$$

- the statement “A signal of regional forest cover can be detected [...], while local tree cover seems more important” suggests that forest cover is substantially different from tree cover. I might have missed this difference when reading the text and suggest to better point this difference out.

We use only data from 10 km radius. We use forest cover in whole manuscript. Sentence merged with previous sentence. $$$

- the statement “Comparisons to fossil data from the same areas show comparable values” is unclear. What is meant exactly with the term “the same area”? Figures 6-13 show that the geographical distance between similar modern and fossil PAR values is often quite high.

Yes, this was unclear, because in Figures 6-13 we link individual traps or trap areas. In this sentence, we mean the comparison at level of same trap region (Fig. 5). $$$

-> A regression model for tree PAR vs forest cover is presented. The regression is based on selected tree PAR values for 3% wide forest-cover bins (Figure 3b). The regression model suggests that an 80% forest cover within 10 km radius results in tree PAR values > 3200 (Conclusions, P23 L 15). I might miss an important point, but it seems to me that the deduction is not supported by the data presented in Figure3b. The Figure shows that values greater than 3200 tree PAR can be found even for 0% forest cover. It seems to me, instead, that tree PAR are > 20,000 for forest cover >20% (though strikingly the two sites with highest forest cover show rather low tree PAR values).

We believe that there is value in looking at the minimum values as clarified above. So yes it is well possible to obtain much higher PAR values at 80% forest cover, but values lower than 3200 grains per cm2 are unlikely. This relationship is important for interpretations as we are often interested to provide conservative interpretations on this “minimum” side of the spectrum e.g. during the initial spread of forest after the ice age. $$$

-> the manuscript shows decreasing pollen deposition as a function of increasing distance to the nearest distribution limit of the parent plant species (Figure 4). Based on this evidence, a long-distance transport threshold (LDT) for a distance of 200 km beyond the distribution limit is calculated. The thresholds could be used to infer range-size changes based on fossil PAR values, the manuscript reports. - While these are interesting results and a potentially useful approach, some critical discussion of this may be useful. The distribution limits were extracted from GIS shapefiles published by Caudullo et al. (2017), which are publicly available on the figshare website with associated DataCite link (Caudullo, Giovanni; Welk, Erik; San-Miguel-Ayanz, Jesús (2017): Chorological maps and data for the main European woody species. figshare. Collection. https://doi.org/10.6084/m9.figshare.c.2918528.v5).

We cite the version we used - v2. $$$

In the original manuscript where Caudullo et al. present the maps, they specifically mention that “Since the maps aim at representing the species general chorology at continental scale, providing a synthetic overview of distribution range, the mapped boundaries should not be considered as precise and sharp limits where the species is definitely present or absent, particularly at local level. Indeed, the first version of this dataset was created for the European Atlas of Forest Tree Species [16] to concisely outline the distribution ranges of described species, complementing information on the species biology and ecology. Errors and imprecision are partly inevitable, due to various causes, such as the quality of the original source, the geo-referencing procedure, the interpretation and the comparison of the sources in the same area and finally due to the limited precision of the manual digitalization process of the range borders (Fig. 1).”

We are aware that these distribution maps have uncertainties. However, PARs are unlikely to be much effected by the occurrence of parent trees at very low abundance. Due to plantations we did not look at the western distribution limits, but only explore latitudinal limits of tree distributions. We agree that additional critical discussion of these maps will be useful. $$$

- It is therefore highly questionable as to whether the distances to the distribution limits measured by Abraham et al. truly represent the actual distances to the species distribution limits. Thus, the precision and accuracy of the LDT values may be strongly overestimated and misleading. Instead of using one single distribution limit, a range of distribution limits may better represent the uncertainty of the mapped limits. Question is therefore: what LDT values would be obtained if the distribution limits of Caudullo et al. (2017) had an uncertainty? Say ca. +100km or even +200km?

Since we focus in these comparisons on the northern distribution limits we believe that rare occurrences of trees will be less and less likely as further north we go. So a given uncertainty in the maps would not change the relative differences between taxa nor the order of magnitude of the absolute values, which in any case are gross estimates. Still these numbers are useful as modern analogues and represent guidelines rather than hard thresholds. $$$

Moreover, it would be useful to show the complete data in the plots of figure 4, including the PAR values within the distribution range (thus extend the x-axes of the plots to include negative x-axis values). In theory at least, these PAR values should be greater than PAR values around the distribution limit and beyond the limits.

We included the data for all traps in Fig. 4a). Within the area of distribution area the data is represented as boxplots outside as a dots. $$$

-> The comparison between modern and fossil PARs is interesting (paragraphs 3.3 and3.4). - Paragraph 3.3. should be deeply revised and could be shortened. It could focus more on PAR-inferred presence/absence based on LDT limits that were presented previously (Figure 5), and on the identification of the closest modern counterparts of populations sizes and forest cover. Currently, some statements are descriptive and their relevance could be made clearer (for instance, on P13 L31 “Modern and fossil values agree for the sites in central Sweden at PARs between 1900-5600 grains...”). Some phrases could be removed (e.g. P13 L27 “As discussed in the main manuscript, ”), other ones are unclear (e.g. P13 L25 “ignoring traps from the Caucasus and Turkey”), and several statements should be supported with references to the literature (e.g. P16 L12“Picea abies is planted in many European regions outside its natural distribution”, or“ Fagus pollen occurs at fossil sites that were assumed to have never been within the distribution of the tree”), to name few examples.

Paragraph 3.3 will be shortened to the first and two last sentences. The rest of summarizing sentences we removed. $$$

- Paragraph 3.4 is enlightening. However, the term “analogue” (and “modern analogue”, which is used later in the Discussion) is not appropriate. With pollen records, modern analogues are generally referred to pollen assemblages (thus to vegetation composition). Here instead you refer to “comparable, similar, population size of one taxon”. Using the term “modern analogue” without clarifying that you are using it with a different meaning creates confusion, particularly in the Discussion where reference is made to the early-Holocene hazel maximum.

We agree that the term “modern analogue” evokes comparison of assemblages of pollen percentages (sensu Overpeck et al., 1985), however we, similarly to Overpeck et al. (1985), think that “modern analogue” should not be reduced to comparisons of modern pollen assemblages, but describes any link between a modern situation and its resemblance of a fossil find, including PAR. Also in geology and macro-ecology the term “modern analogue” is used in a broader context as exemplified by these publications: Sidder, A. (2020), Ancient sea levels in South Africa may offer modern analogues, Eos, 101, https://doi.org/10.1029/2020EO147001. ; Horsák, M., ChytrÃ¡, M., Hájková, P., Hájek, M., Danihelka, J., Horsáková, V., Ermakov, N., German, D. A., Kočí, M., Lustyk, P., Nekola, J. C., Preislerová, Z. and Valachovič, M.: European glacial relict snails and plants: environmental context of their modern refugial occurrence in southern Siberia, Boreas, 44(4), 638–657, doi:10.1111/bor.12133, 2015. We did look for a different terminology but could not find a better term for what we are comparing and are happy to clarify this in the introduction. $$$

-> There are other proxies that may be useful to determine presence of trees in fossil records (plant macrofossils and stomata). This could be mentioned in the text. Moreover, using fossil sites where such data is available could be useful to actually test the LDT limits, at least for some of the taxa. -> Further, how do the inferences based on the LDT limits compare with inferences made previously based on pollen percentages (or on plant macrofossils and stomata)? For instance, in a prior study (Giesecke et al., 2017 in JBiogeogr) a good agreement between the estimates of overall spread (Fig. 5a) based on different pollen percentage abundance classes was found. Some of the fossil sites were actually analysed for pollen, stomata, and plant macrofossils (e.g. Sägistalsee, Bachalpsee), but these results are not mentioned in this manuscript.

This is an interesting aspect, which indeed we did not address in this manuscript. In making the database accessible we hope that questions like these will lead to additional usages of the database. We would be interested to explore it but feel it would add too much extra analysis and text and to the current manuscript. $$$

Detailed comments: - P7 L8: why 271 modern samples? The abstract mentions 2742 annual samples.

While the database contains all data that was submitted, we only considered trap record with at least 3 years and thus obtained 271 traps that we base the analysis on. $$$

- P11 L13: am having trouble to understand why 92 pairs were obtained. please clarify.

We have 15 taxa in 7 regions, which make 105 cases that we investigate, however some regions lack species in the fossil and/or trap record and thus it is only possible to perform the t-test for 92 pairs of trap and fossil sites. $$$

- P11 L14: cannot find t-test and p-values on figure 6. Neither were “t-test” and “p-values” mentioned in the Material and Methods section. Please clarify why and what has been done.

We are sorry for this omission and will add it to the Methods section and add a table with p-values to the Supplementary. $$$

-> Figures 6-13: - the a) and b) frames could be merged by using horizontal boxplots (instead of barplots) in a), and adding b) as an overlay;

I have tried to use horizontal boxplots (Fig. R1), but the highest values enlarge the x-axis while the lowest classes are not visible. The way of our presentation allows to appreciate the general pattern of mean values for trap areas (a) and we make the full variability of individual traps visible within the trap areas by coloured squares (b). - font sizes are too small; Font was enlarged to 2.5 for names of the fossil sites/trap areas and 2 for rest of the text. $$$

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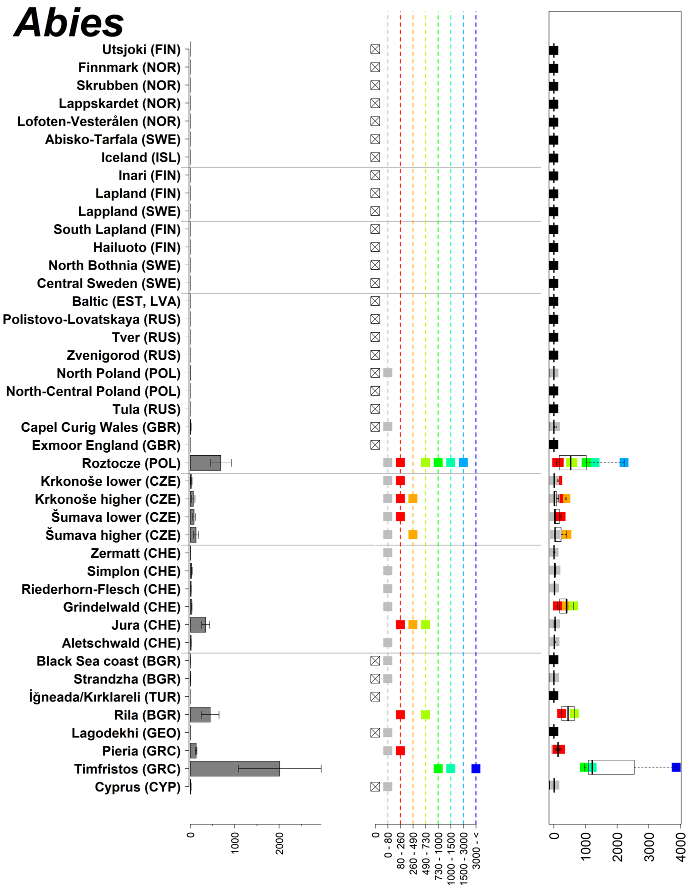

Fig. 1. Fig. R1: Figure 6 - current version (first two panels) and proposed version (third panel, boxplot).