Dear Prof. Bartlein,

Thank you very much for your input on my manuscript. I think the suggestions were really 'on-point' and I do feel that my manuscript has become clearer, better-organised and more engaging thanks to your inputs.

The comments of Reviewer 2 are in black, and my responses in blue. Italicised texts are quotes from the revised manuscript.

General comments:

This paper introduces an R package, crestr, for implementing a probability-density- function (PDF) variant of the Mutual Climatic Range (MCR) approach for making climate reconstructions from, for example, fossil-pollen data. The paper is not simply a user manual or vignette, but also discusses some of the conceptual underpinnings of the whole approach, and the philosophy behind some of the methodological choices that necessarily have to be made.

I generally prefer to see the pdf methods and MCR as both variants of a broader family of 'Indicator species' approaches. The pdf methods and MCR rely on distinct data modelling hypotheses, and the pdf methods are not a more complex version of MCR. However, I agree that the two types of methods are closer to each other than to other existing techniques, such as WA-PLS, MAT or Inverse modelling. I appreciate that Reviewer 2 appreciated the extra efforts put into re-explaining the different aspects of the method in the light of the package – even if some of these parts were a bit imprecise.

There are a few reorganization or further-explanation issues that need to be sorted out. For example, the motivation for producing the R package in the first place doesn't appear until Section 5 of the paper, and the particular reconstruction approach that is implemented here should be mentioned first among the list of various approaches mentioned in the introductory paragraph. Otherwise, the basic approach, and its implementation using the package is laid out nicely.

This comment is similar to a suggestion made by Reviewer 1. The introduction has been reworked to make it more package oriented. And all the types of data used by the package are also described at the beginning of section 2 (i.e. before describing the mathematics of the method) to avoid any misunderstanding. Overall, many more details have been added everywhere across the manuscript.

One important contribution of the paper is the release of the global data sets, both taxonomic and climatic, that can be used to apply the approach generally. However, there is a tension between attempting to reconstruct as many environmental variables as one can get into a database and reconstructing only those that can be mechanistically related to, say, terrestrial vegetation, which typically are simply growing season warmth, winter cold, and moisture stress. Those that argue for the former approach argue that the environmental variables are all related one way or another, so if you can reconstruct one, you can reconstruct all, while those that argue for the latter approach point out that assumption is nonsense. Likewise, there are

probably taxa included in the data base that are completely insensitive to the macroclimatic variables provided, but may wind up contributing to the reconstructions when they provide little real information. From a purely statistical perspective, overfitting is the issue here. I know users don't necessarily have to attempt to reconstruct all of the environmental variables in Tables 1 or 2, and that they can use their own data, and manage the particular variables or taxa that are used, but I think that providing so many variables creates an "attractive nuisance". So, I think it would be good to caution the users about these issues. No good deed goes unpunished.

This is something that I have also thought a lot about. I agree that plants respond to growing season warmth, winter cold, and moisture stress, especially in the mid to high latitudes. However, important climate drivers are different in tropical and subtropical regions, where the seasonality of precipitation and associated seasonal temperatures are key in defining vegetation. I can easily envision a climate zone and vegetation type where most of the variables included in the package could be important to look at. In my opinion, the only ones that are probably not decisive factors relate to diurnal or annual temperature variability (e.g. Bio2, bio3, bio4 or bio7). However, I think it is suitable for users to have access to more variables than could/should be reconstructed to understand their study area's climate regime better. In addition, the package is not designed for vegetation only, and these variables could be of importance for the other proxies that are part of the calibration dataset (rodents, beetles, insects). The list of marine variables in coordination with an oceanographer with experience in proxy-based reconstructions and the decision was made to use similar variables to those released with modern sample databases (de Vernal et al., 2020). In summary; I do not think there is a need to restrict the list of available terrestrial or marine variables. Still, I agree that it is important to add an explicit warning that variable selection should be made carefully and that running serial reconstruction is a generally bad idea.

In section 3 when introducing the calibration dataset as a whole: "*In the _gbif4crest_ database, all the QDGC grid cells were associated with a collection of terrestrial and oceanic environmental variables that can be reconstructed (@Fick_Hijmans_2017, @Zomer2008, @WOA_2018_temp, @WOA_2018_salinity, @WOA_2018_oxy, @WOA_2018_nutrients, @Reynolds2007, see details in Tables \ref{table:variables-terr} and \ref{table:variables-mari}). **Despite the diversity of variables available, it is recommended to avoid serial reconstructions and, on the contrary, to identify the few important variables for the studied palaeoecological datasets a priori.** "*
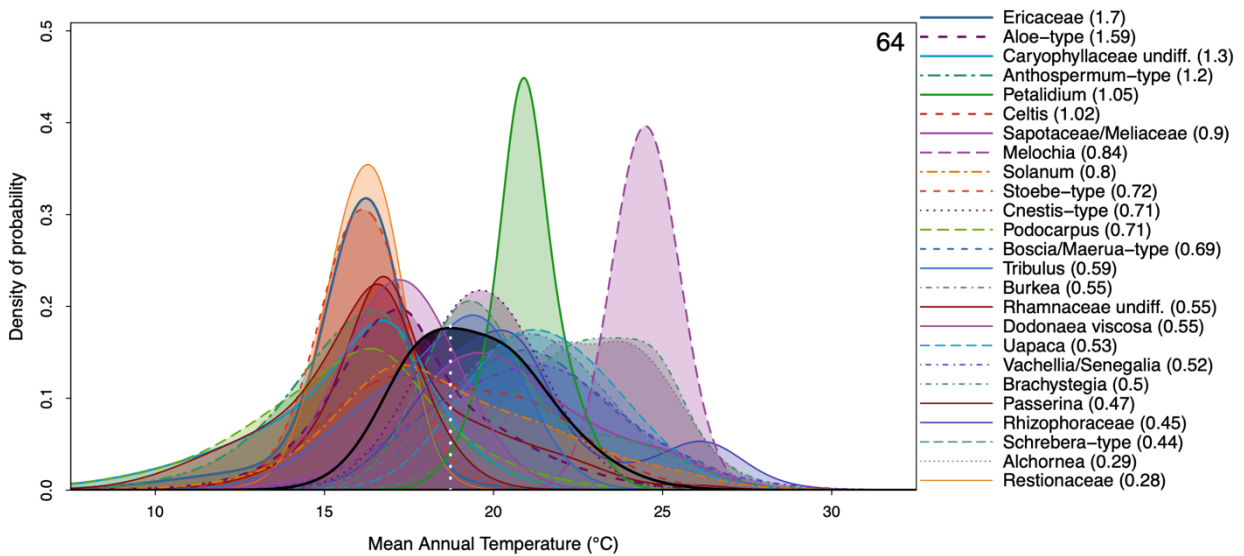
In section 5 when introducing the variable selection in the package: "*However, serial reconstructions should be avoided, even if many variables are provided with this package. Careful interpretations of the fossil data should be done before selecting variables.*"

Similarly, I cannot curate the database to exclude all the species that might not be responsive to the selected variables. This is unrealistic and subject to personal interpretations anyway. The package contains explicit tools to determine which taxa should be used to reconstruct which variables (fully explained in section 5), and I believe this to be the optimal way of dealing with the problem.

Another issue that might be discussed a little is the "no analogue" one. Although usually raised in the context of modern analogue technique (MAT) approaches, it applies here too, as illustrated by Fig. 10, where the reconstruction lies in sort of trough of individual PDFs, and it's also probably the case that some PDFs don't overlap at all. If I understand this correctly, all of taxa with PDFs that appear in the figure co-occurred in the sample, but they don't today (otherwise their PDFs would overlap). This deserves a sentence or two of discussion, perhaps by handing it off to other papers.

I both agree and disagree with this comment. One reason the no-analogue situation is mainly associated with MAT is that MAT works with entire pollen assemblages and includes the relative percentages in the estimation of analogues. Techniques that rely on the individual responses of the pollen taxa are, on the contrary, a lot more resilient to the problem because they do not require the fossil assemblage to exist in the modern landscape. They only require the individual climate responses to do so. In the example represented in Fig. 10, 25 of the observed taxa were used in the reconstruction. 24 of the pdfs overlap between roughly 17 and 20 degrees (see the modified version of Fig. 10 below). Only one taxon (*Melochia,* in purple) stands on the side. This is a very mild no analogue case, especially considering the size of the catchment of the studied record (the catchment of the Limpopo River). And technically, all the pdfs are defined for any possible climate value, as opposed to MCR for instance, where the minimum and maximum climate values must be estimated. As such, the pdfs always overlap, although with a very low probability in this case for *Melochia*.

In addition, one might argue that all the samples from this core do not have modern vegetation analogues since they are derived from a marine core – there is nowhere across the Limpopo Basin where such vegetation composition can be observed, either today or in the past The strength of the approach is to consider each taxon independently of the others and to return an estimate of what climate values are the most likely considering the presence of a range of taxa. It does not require the taxa to be found in the same location in modern environments. However, I think it might be a nice idea to include something along the line of 'limited overlapping between pdfs' in future versions of the package and the generation of the figure itself. But this would be threshold dependent (*e.g.* do the 99% ranges of the pdfs overlap?), and the next question would immediately be what is a good threshold to define a no analogue situation? And if two pdfs do not overlap for temperature, can we still use them for precipitation or moisture? All these questions highlight that the nature of the problem is very different in the context of indicator species methods [no analogue defined from modelled climate responses] than it is from MAT [no analogue directly defined from the vegetation data themselves].

Density of probability

Mean Annual Temperature (°C)

64

Ericaceae (1.7)
Aloe-type (1.59)
Caryophyllaceae undiff. (1.3)
Anthospermum-type (1.2)
Petalidium (1.05)
Celtis (1.02)
Sapotaceae/Meliaceae (0.9)
Melochia (0.84)
Solanum (0.8)
Stoebe-type (0.72)
Cnestis-type (0.71)
Podocarpus (0.71)
Boscia/Maerua-type (0.69)
Tribulus (0.59)
Burkea (0.55)
Rhamnaceae undiff. (0.55)
Dodonaea viscosa (0.55)
Uapaca (0.53)
Vachellia/Senegalia (0.52)
Brachystegia (0.5)
Passerina (0.47)
Rhizophoraceae (0.45)
Schrebera-type (0.44)
Alchornea (0.29)
Restionaceae (0.28)

One stylistic thing about the paper is the sometimes jarring transitions between text and code blocks. Starting out, there are transitions like "...similar results would be obtained using the following command: (followed by the code block)", but that format gets abandoned later in the manuscript. I know from experience that Copernicus journals' choice of a type face for code makes it appear pretty clunky, and sometimes unreadable, which makes setting it off more important for readability in the two-column paper format.

I have homogenised these transitions from text to code and from text to equations, and I have made sure that the width of each text block is not larger than one column in a two-column formatted paper format.

Specific and technical comments:

line 2: "the methods ... are powerful at producing robust results..." I'm not sure that robustness in the usual statistical sense is either evaluated or demonstrated in this paper.

The use of the word 'robust' seems to have bothered Reviewer 2 (this comment and about three more later). I am struggling a bit to understand where this resistance to the term comes from. But being pragmatic with this issue, I am assuming that if it bothered Reviewer 2, it is likely that it will also bother other readers. I have therefore removed all the mentions of robust and robustness from the manuscript.

line 3: Not parallel: accessing/curating/the complexity" (action/action/characteristic). The sentence could be made parallel by rewording: "The problem of accessing and curating the necessary calibration data and the complexity of interpretation..."

I have reworked the abstract and it is now phrased as follows: "*However, the difficulty of accessing and curating these calibration data and the complexity of interpreting probabilistic results often limit their use in palaeoclimatological studies.*"

line 17: "climate drivers" Meaning the climatic controls of the variations in the fossil data, or the controls of the climatic variations themselves?

Rephrased as 'The drivers of climate change'.

Line 19: "climate reconstructions"?

Text amended.

line 23: "robust" Again, I don't think this is the right word. I think that "robustness" is a property of a statistic (e.g. the median) that signals that it will perform well at estimating, in this case, location, no matter what the underlying distribution of the data looks like. I don't think this notion really applies to a dataset. Maybe "extensive datasets"?

I think it does apply, but see my generic response above. Now rephrased as: "However, the limited availability of the necessary calibration datasets beyond the Northern Hemisphere extratropics has often hindered their application in many environments and regions where quantified climate records are needed, despite the existence of suitable fossil records."

line 25: Before going further, it would be good to alert the reader as to which particular approach this paper implements (i.e. as in Section 5.1.2 of Chevalier et al. 2020), and a little about how it works. (It seems it's NOT WA, WA-PLS, MAT, etc., but what is it?). I don't think it would inappropriate at all (in terms of self-citation padding) to use Chevalier et al. 2020 a little more for background.

I agree that the introduction needed to be boosted by a bit more context and clarity in terms of what this paper presents. I have reworked large parts of it, and I hope things are now clearer. The second paragraph introduces CREST and broadly speaking how it works. And then I introduce why a new R package was needed.

line 26: By "un-quantified fossil pollen records" do you mean that the data are "qualitative" as opposed to "quantitative" or simply that quantitative reconstructions have yet be made? Same issue on line 35.

This sentence has been removed from the reworked introduction.

line 27: "built upon the"

Text amended.

line 28: "modern proxy geolocalised occurrence data". I don't know what that means.

Now defined as follow: *"the 'Indicator species' family of reconstruction techniques uses modern proxy occurrences (_i.e._ **collections of locations where the studied proxy species can be observed in modern environments).**"*

line 39: "estimates, weights and propagates…" I'm confused by the "propagates" idea.

The sentence has been simplified to: *"While techniques such as MAT or WA-PLS are primarily designed to associate modern proxy observations with their 'most likely' or 'mean' climate values only,* **CREST estimates and weighs all the climate values that are compatible with the observed fossil data**. *As such, the climate reconstructions obtained from CREST can be understood as an ensemble of all data-compatible climate values and not a simpler, less informative 'most likely' or 'best' climate estimate with statistical errors"*

line 40: "posterior climate reconstructions" I'm not exactly sure what's Bayesian about this.

Nothing, indeed. The word posterior was improperly used in this manuscript and has been removed.

line 41: "weighted ensemble" An ensemble in this context is a collection or a group of something. Do you mean a "weighted average of an ensemble of estimates" or "an ensemble average"?

The sentence has been simplified to: *"While techniques such as MAT or WA-PLS are primarily designed to associate modern proxy observations with their 'most likely' or 'mean' climate values only*, **CREST estimates and weighs all the climate values that are compatible with the observed fossil data. As such, the climate reconstructions obtained from CREST can be understood as an ensemble of all data-compatible climate values** *and not a simpler, less informative 'most likely' or 'best' climate estimate with statistical errors"*

line 46: "can model" Does this mean "can represent"?

I used 'can estimate' instead.

line 55: "embedded" Replace with "accompanying"?

Accompanying suggests two distinct elements, e.g. 'the dataset accompanying the package'. In the present case, the package and the dataset are only one thing, and I think 'embedded' is more adapted based on definition 2 from https://www.dictionary.com/browse/embedded).

Figure 1 caption: Describe the Full (or "true") distribution first.

Done.

line 61-70. Repeated material.

Corrected.

line 72: "PDFs are used to transform the information". Transform how? Doesn't the PDF (or histogram) of a particular taxon just represent the frequency of occurrence of a taxon along a climatic gradient?

The PDFs do not transform the information; they are the result of the transformation. Now clarified: "The transformation of the information contained in the modern observations of the biological climate proxies into probabilistic climate responses can be done in one or two steps depending on the nature and taxonomic resolution of the studied proxy.".

line 73: "weighted ensemble" again.

Removed.

line 77: It might be good to remind the reader that, for example, some pollen taxa represent individual species while other only genera (or indistinguishable types, e.g. Larix and Pseudotsuga). You could refer to section 3.3.2 for a discussion of how the species-to- taxon translation is made.

I have added a bit more explanation on that at the beginning of section 2.

> CREST takes into account that some fossil taxa can be identified at the species level (_e.g._ plant macrofossils), while others can only be identified at a lower taxonomic resolution (_e.g._ fossil pollen are commonly identified at the genus, sub-family, or family level; @Chevalier_etal_2020). The transformation of the information contained in the modern observations of the biological climate proxies into probabilistic climate responses is thus done in one or two steps depending on the taxonomic resolution of the studied proxy. When the observed fossil taxa are identified at the species level, determining a list of species that could have produced that fossil is, however, necessary (see Section 3.3.2 to know how to format this information for _crestr_).

Line 78: "empirical mean and associated variance" Isn't this step in fact adopting the approach you reject in panel (a) in Fig. 1, especially when a taxon might have a nonsymmetric distribution?

In Fig. 1, I present climate reconstructions, which can (and should) be multimodal and irregular if dictated by the data. On the contrary, species responses to climate are much more regular. If a species response along a climate gradient is irregular, it is most likely because they do not respond to the specified variable (and shouldn't be considered) or because another confounding variable is excluding its presence in places. It is unreasonable to assume that a plant species (not a pollen taxon!) might like living under 15degrees, not like it at 20, and like it again at 25. If a species is excluded from regions with 20degree it is either because another

factor is excluding it (e.g. different rainfall patterns or humidity) or because 20degrees is largely absent from the study area due to, for instance, incomplete data sampling. In both cases, it is not reasonable to assume it cannot grow under 20 degrees. In addition, CREST allows for asymmetry (right-skew) with the lognormal shape. It simply does not allow multimodality for monospecific responses, which is based on ecological considerations. When the monospecific responses are combined, multimodality and all sorts of irregularities become possible and be propagated to the climate reconstruction. I have made this more evident in Section 2.1.1.

"Contrary to the previous step, no additional constraints are added here. The distribution of the PDFtx(t,c) can thus be asymmetrical and even multimodal if different (groups of) composing species exhibit distinct climate requirements."

line 85: Right. And see also Liu et al., 2020, Proceedings of the Royal Society A https://doi.org/10.1098/rspa.2020.0346 and the fxTWAPLS package.

This is an interesting study that I had missed. However, I do not see what it would add here, since it is a study fully focused on WA-PLS.

page 5: Some things missing here. What exactly is k()? What does i index? N vs N-sub- s?

All these terms have now been properly defined in the text in a more logical order (see page 5 of the revised manuscript).

line 100: I think this combination-of-PDFs needs to be better explained. Would one want to ever lump all of the species of, say, Pinus, into one taxon? Some paleoecological data sources (e.g. pollen) are pretty "blunt" taxonomically, whereas others (e.g. plant macrofossils) are usually identified at the species level.

Users determine the type of combination based on their fossil identification. Only the first step is used if the fossil is identified at the species level. If it is identified at any higher taxonomic level, then species pdfs are fitted for each composing species, and these species pdfs are subsequently combined into a taxon pdf. If the fossil pollen is identified as Pinus, then yes, all the Pinus species found in the user-designed study area should be lumped together because they are all considered are likely to have produced the observed pollen grain. I think the miscomprehension here is linked to the remark made about line 77 above. I have clarified the distinction at the beginning of the section and hopefully, this clarifies the two steps.

line 105: "grid cells" This is the first mention of grids/gridding. Does that have something to do with "geolocalized occurrence data"?

Replaced with 'occurrences'.

lines 105-107: Again, I'm worried about "robustness" which I think is being used more to denote some notion of reliability than in its usual sense. If robustness of the location and scale parameters (eqn. 1 and 2) is really a concern, why not use robust estimators of them?

See above.

line 117: "These definitions of sensitive taxa are always specific to a specific region…". Too many specifics. Maybe "the definitions are specific to particular regions"?

The sentence was removed.

line 119: So the estimate is basically a weighted geometric mean of the individual taxon PDFs?

Absolutely.

line 135: "own design"?

Corrected. *"[…] users can also design their own weights to better account for the specificity of their data."*

line 139: It might be good to cite to some of the discussions on fitting SDMs with presence-only data. (See Valavi et al., 2022, Ecol. Mono. https://doi.org/10.1002/ecm.1486)

I have now clarified why I do not use these more complex models. CREST is designed to be usable in data-sparse regions, and usually, the most complex models require a lot more data than is commonly available. As such, the model that was designed is simpler in its assumptions and might lead to suboptimal results in regions with high data density, but its strength is its capability to produce reliable results <u>everywhere</u>.

"Because CREST aims to be applicable even in data-sparse environments, the estimation of these responses is based on simple assumptions that exclude using complex algorithms, such as those described in, for instance, the recent review of @Valavi2021."

line 148: "upscaled at a spatial 150 resolution"?

This was a typo. '150' has been removed.

Figure 4: Increase the spacing between the bottom two panels to match the others?

The last two panels are actually the same table, hence the different spacing. I have clarified it in the caption.

Figure 5: Nice figure. The resolution of the image in the discussion .pdf obscures the double-framed boxes, however.

I have increased the spacing a bit to avoid this type of issue in the final version.

Section 3.2: In a "real-world" example, how large might a crestObj become?

For example, the crestObj created by the application presented in the paper is 28.5Mb once exported as an RData file. This object includes all the calibration data, modelling steps and results. The size will vary with the diversity of the calibration data and I would expect the object to grow up to 100-200Mb for pollen studies in Europe or North America.

line 236: Hyphenate "species-to-proxy".

Corrected.

line 256: Are the weights completely arbitrary, or should the lie within some particular ranges (e.g. 0-1 or 0-100)?

Thank you for noticing this important omission. The weights must be between 0 and 100, and this is now clarified in the manuscript.

Section 3.3.4: Describe how the points in the climate-space data frame are associated with the taxon distribution data? Should there be a one-to-one correspondence between the rows?

The table is a standard XYZ matrix. Each row corresponds to a location, and a location is characterised with a longitude, a latitude and one or more climate values. This table is never connected with the distribution table presented in section 3.3.3. These data are used 1/ to make plots such as figures 6 and 7, and 2/ to weigh the climate space through equation 3. This is now clarified.

line 285: "the original CREST software" This raises the question "Why not just use the original CREST software?" which is answered on lines 578-579. I think that the motivation for the development of the R package should be moved up to the introduction.

This element of 'discussion' has now been moved to the introduction.

line 303: "the three input files" Are these files available anywhere? I don't see them in the GitHub repository.

These files were provided as supplementary material to the paper. This is now clarified in the manuscript.

line 320: Should there be some kind of transition between the text and code block? (As on line 349).

As mentioned at the beginning, the text-to-equation and text-to-code transitions have been smoothed and homogenised across the manuscript.

line 364: "different parameters" -- "different parameters that control the reconstruction"?

Corrected.

line 374: Again, some kind of transition is needed.

Corrected.

line 387: "the climate values to reconstruct are likely to be in the study area" Does this mean that the range(s) of climate values in the calibration data set should have the same (or larger) amplitude?

Only values present in the calibration dataset can be reconstructed. This is true for CREST and for any statistical reconstruction technique. Since all methods tend to shrink the reconstructed ranges, a modern range larger than the (unknown) range of past climate change will lead to better results. Rephased as follow: "*In every study involving estimating relationships between biological entities and environmental parameters, the first step is always to ensure that the defined study area and associated calibration dataset are as coherent as possible.* **This includes ensuring that** *1) all the essential taxa are present in the study area, and their distribution is not truncated, 2)* **the climate values to reconstruct are likely to be covered by present-day climate values (the reconstructions are bounded by the lowest and highest values observed in the modern climate space)** *and 3) there is no large sampling or representativity bias (_e.g._ along country borders due to different sampling efforts). The 'climateSpace' graphical diagnostic tool (Fig. \ref{fig:climatespace}) was designed for a rapid assessment of all these characteristics.*"

line 390: "homogeneous" In geographical space? Climate space? Both would be good I guess.

Rephrased as: "*Ideally, the climate sampling should be as homogeneous as possible to ensure proper sampling of all the possible climate values, even if the extreme climate values will always be under-represented compared to the median ones.* ".

line 428: "violin plots" Violin plots are cool looking, but they are affected by our tendency to misinterpret/misjudge areas (i.e. Cleveland, W.S., 1993, Visualizing Data). I think viewers tend to notice the blobs as opposed to the profile, which is the important information. I think simply plotting the PDFs as in Fig. 6 of Quick et al. (2021) is more effective.

I generally agree that violin plots can induce interpretation biases; However, I would imagine that is only a problem if the figure cannot be looked at thoroughly for an extended period of time (e.g. during a talk). On the contrary, I would imagine that users who make the plot are actually interested in spending a bit of time on it to better understand their data. And the areas of all the violins are the same in this plot. Therefore, what remains is the shape of the violins, which I what people should be looking at.

I must also confess certain laziness to dive back into the code of the figures to make the necessary changes. Writing scripts that are <u>robust</u> (;-)) to a wide range of data is really difficult. I think the figure already does a good job and I am not convinced that the suggested benefits are worth the additional coding work. I am nevertheless taking note of this suggestion and will re-evaluate it down the road if I decide to update the diagnostic tools.

line 435: "to have objective" -- "to make objective"?

Corrected.

line 460: "to reduce the noise" One pollen type's noise may be another's signal. Pollen types have long-tailed distributions, and so an alternative approach might be to transform the data, with the square-root transformation in particular having some desirable properties.

I generally agree with this statement. I am personally not a user of these hard presence/absence thresholds. I prefer using my weighting function that will automatically consider 2% as important if the average percentage is relatively low and not important for taxa like Poaceae or Pinus that usually have much larger percentages. I have this option because I know it has been used in the past. The square-root transformation is very useful to compare assemblages to one another (such as in MAT). I think its usefulness would be more limited for indicator species. The option is not included in the package, but as now mentioned in the manuscript, users can square root transform their data and feed these data to the algorithm.

*"The data can be directly weighted by the values provided in `df`, which implies that users can define their own specific weighting strategy (**e.g. using the square-root transformation of the pollen percentages**)."*

Figure 10: "the thickness of the lines" I don't see much differentiation in line thickness.

I have tried different options and I am now assigning a thickness based on 1.5*sqrt(weight). It gives a reasonable thickness range without overfilling the graphics. Considering that the taxon name information is also colour coded and included in the type of dashed line, I think the results are satisfying. See some examples below:
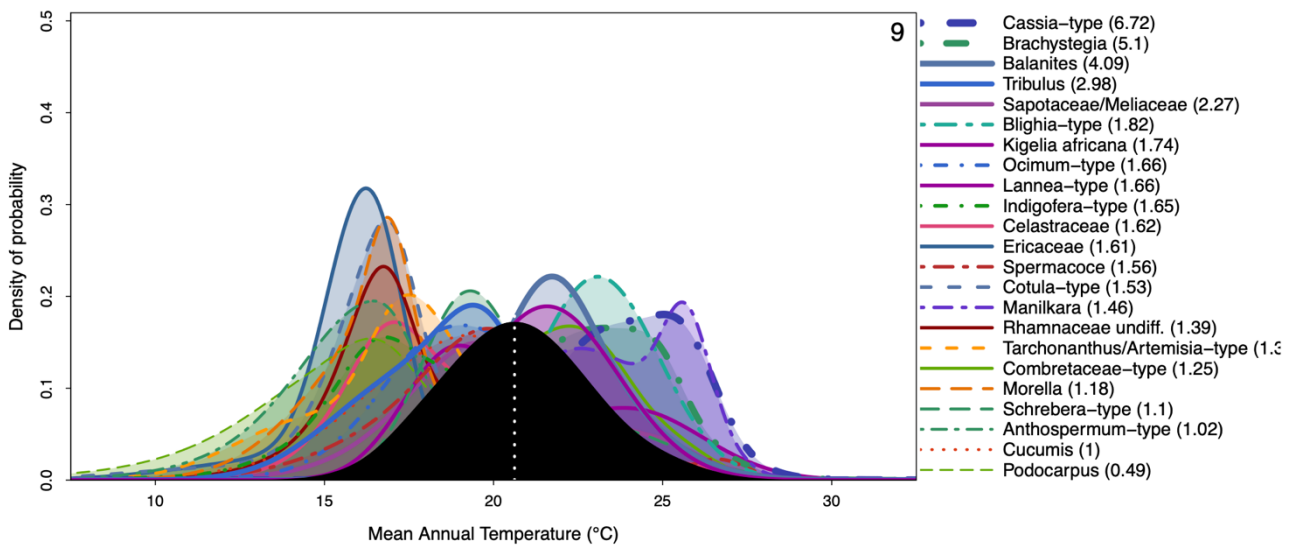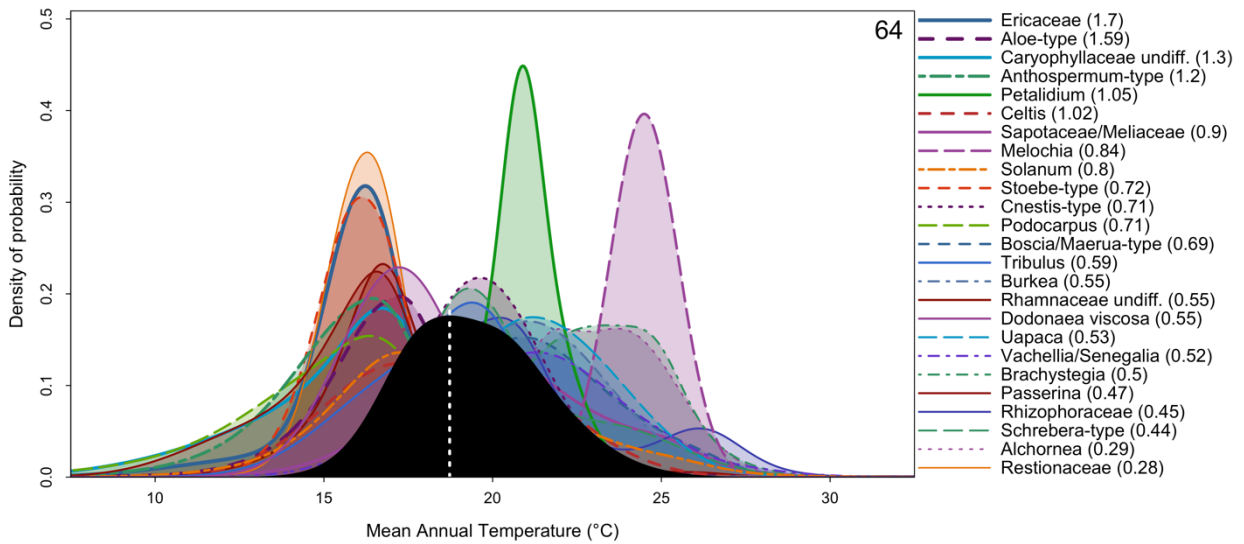
line 505: "full uncertainties" Could a second panel be added to Fig. 9 to show that?

This is what is represented. The alternative is to plot, for instance, only the 90% range instead of the coloured background. I am not sure adding this to the paper would add much. In addition, this type of plot is illustrated in the get-started vignette that Reviewer2 extracted and played with (see below).

Figure 11: Why are all the values positive? What is the "net effect"?

The absolute value is plotted (what I inappropriately called the 'net' effect), and the sign of the difference is colour coded. This was designed to save vertical space on the figure. I have now modified the figure with a legend that specifies what the colour means. I have also rephrased it as follows to increase clarity:

Leave-one-out (LOO) graphical diagnostic tool to illustrate the influence of different taxa on the reconstructions. Here, the results are only shown for a subset of the taxa observed in marine core MD96-2048 (only 20 out of the 171 available taxa are represented). The height of each bar represents the absolute effect (in °C) of removing the taxon from the reconstruction, and the sign of this effect (increase or decrease of the reconstructed temperature) is colour-coded. Here, blue (cf. Ericaceae) and red (cf. Combretaceae-type) taxa are cold and warm indicators, respectively.

Code:

I was able to install the package and run the example with only a few issues. The code in the get-started.html vignette and the GitHub README.md is a little different. I was able to "purl" the get-started.Rmd R Markdown file without an issue to reproduce the example. It wouldn't hurt to also provide a pure get-started.R file.

This is an excellent suggestion. The file is now available on the webpage.

The results of the example wound up in an obscure temporary file. Adding "file.path(tempdir())" to the example would help the user to find that folder.

This is a requirement of CRAN – all files created in the vignettes must be saved in tempdir(). Users can however specify where they want to save their files. I added a note.

Pat Bartlein

References cited:

de Vernal, A., Radi, T., Zaragosi, S., Van Nieuwenhove, N., Rochon, A., Allan, E., De Schepper, S., Eynaud, F., Head, M. J., Limoges, A., Londeix, L., Marret, F., Matthiessen, J., Penaud, A., Pospelova, V., Price, A. and Richerol, T.: Distribution of common modern dinoflagellate cyst taxa in surface sediments of the Northern Hemisphere in relation to environmental parameters: The new n=1968 database, Marine Micropaleontology, 159(November 2019), 101796, doi:10.1016/j.marmicro.2019.101796, 2020.