

***Interactive comment on “Rapid climatic variability in the west Mediterranean during the last 25 000 years from high resolution pollen data” by N. Combourieu Nebout et al.***

**Anonymous Referee #2**

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Reviewers comments on “Rapid climatic variability in the west Mediterranean during the last 25 000 years from high resolution pollen data”

The authors present a pollen-based climate reconstruction from a marine sediment core in the Alboran Sea (Western Mediterranean) for the period 0–25 kyr BP. The reconstruction includes inferred climate based on a modern-analogue transfer-function (seasonal and annual temperature and precipitation), together with biomes, and standard interpretations based on taxa changes. The authors focus on the high-resolution ‘rapid events’ of the record, and attempt to correlate events in the core with events found elsewhere in the North Atlantic, Greenland and Western Mediterranean.

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Marine pollen records provide a longer and more continuous record of vegetation development than that which is often provided by shorter and more discontinuous continental records, particularly in arid regions such as the Mediterranean. The record provides an important contribution to a growing marine based perspective on Mediterranean vegetation and climate change during the late Quaternary. The article is generally well written, with clear figures.

The main problems with the paper relate to 1) the application of numerical pollen techniques developed on land to the marine environment, and 2) the statistically-robust resolution of the record in determining 'rapid' climate events suggested by the authors. The extent of these problems is sufficiently large that I am unfortunately unable to recommend publication even in a modified form.

The main reasons for this decision are outlined below:

1) The exclusion of *Pinus* from the pollen sum

The authors apply both a modern-analogue pollen-climate transfer function and biomi-  
sation to their pollen record. Both techniques have been widely applied in many previ-  
ous land based studies, but here the authors adapt these techniques for use in a marine  
pollen record by omitting to include *Pinus* in their analysis. The over-representation of  
*Pinus* is a well established problem in marine pollen records, where *Pinus* is routinely  
omitted in calculating the pollen sum. Nevertheless, *Pinus* is a key Mediterranean taxa,  
forming an important component of arid Mediterranean woodlands where it often be-  
comes dominant (even mono-specific) under cooler summer-dry climates (eg classical  
Köppen Csb climates). The omission of *Pinus* as part of the pollen sum therefore  
radically changes the vegetation composition as seen in the pollen diagram, and this  
creates a significant problem in interpretation where-ever *Pinus* occupies an important  
role, as is typical in the Mediterranean region. This presents a difficult problem in itself,  
but when applied to numerical methods such as pollen-climate transfer functions and  
biomisation, a number of further challenges are presented which the authors have not

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fully addressed.

*Pinus* is eurythermic at the genus level, so the omission of *Pinus* could be expected to have little impact on the transfer-function for temperature, but this is a different matter for precipitation. The omission of *Pinus* will mean that forest cover will be underestimated relative to desert/steppe taxa for instance, and therefore where desert/steppe taxa dominate when *Pinus* is not included the transfer-function will significantly underestimate precipitation. Alternatively, *Pinus* is more drought tolerant than temperate deciduous trees for instance, and therefore where these dominate the pollen spectrum when *Pinus* is not included, the transfer-function will over-estimate precipitation. Reconstructing precipitation without *Pinus* would therefore generate large errors in those environments where *Pinus* forms an important part of the vegetation. As an extreme example, a pine forest composed of 95% *Pinus* and 5% *Poaceae* will be viewed as a 100% *Poaceae* steppe, and a pine forest composed of 95% *Pinus* and 5% *Quercus* will be viewed as a 100% *Quercus* oak woodland. The authors do not provide any validation or error assessment for their transfer-function, which ideally should include an evaluation of the inclusion/exclusion of *Pinus* from the sum.

In terms of biomes, *Pinus* has little predictive power to differentiate woodland biomes according to the authors chosen method (Peyron et al 1998). This is because *Pinus* as a pft (eurothermic conifer) is present in virtually all woodland biomes. Its omission would therefore be expected to have little effect in the assignment process between these biomes. However, the omission of *Pinus* would be expected to have a significant effect in the assignment of non-woodland biomes (warm/cold steppe & desert) compared to woodland biomes, since *Pinus* is not included in these non-woodland biomes. Transitions between woodland and non-woodland biomes form an important part of the reconstruction presented and therefore this problem will have a significant impact on the interpretation. The authors do not provide any validation of their revised methodology, and in the absence of this validation it is difficult to see how this new reconstruction method can be accepted. The authors would need to show that the

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omission of *Pinus* does not bias the assignment of woodland to non-woodland biomes, which is somewhat difficult to believe.

## 2) Low pollen count

The authors state that a minimum '100 pollen grains excluding *Pinus*' were counted. Since they exclude *Pinus* from the reconstruction methodology, it means that the reconstruction could be based on as little as 100 grains per sample. This is a very low sample compared to normally acceptable sample sizes of around 500 total grains or 200 tree pollen, and will inevitably lead to large sample-to-sample variability irrespective of the climatic changes interpreted by the authors. A much higher pollen grain count would be needed to limit the extent of commonly experienced sampling errors in the counting procedure. This would be less of a problem if the authors did not attempt to interpret the sample-to-sample variability of the pollen record and only the long-term trends. This problem is also likely to be compounded by the fact that the biomisation and transfer-function use a smaller subset of taxa than provided by the full pollen spectrum, and therefore could be based on an even smaller pollen count.

The implications of this low count should also be obvious given the threshold nature of the biomisation procedure, when the difference between biomes can be decided on the presence or absence of a few pollen grains of a taxa (for instance, from steppe to temperature deciduous forest and back). This problem is partly addressed in the procedure by discounting taxa which contribute 0.5% or less of the sum, but in this case 1 grain will never represent less than 1% of the sum, and so therefore even taxa represented by 1 grain will always be included. Biomes could therefore be defined by the presence or absence of 1 pollen grain. The authors need to have undertaken a higher pollen count to ensure that the variability shown in the pollen data is not simply a statistical artefact of the low pollen count. The essentially arbitrary threshold nature of the biome assignment procedure also makes down-core time-series interpretation of biome changes, as presented here, of limited value.

A key aspect of the paper is the authors attempts to interpret a whole series of wiggles in the temperate deciduous pollen curve (shown in figure 4) as significant climate events. Some of these are represented by single samples, while others are represented by percentage changes of as little as 5-10%. (equivalent to 5-10 grains). Aside from the fact that such wiggles can be caused by any number of non-climatic factors (anthropogenic, fire, disease, ecological), the small count size would caution against too close an interpretation of these events. A simple illustration of this problem would be to consider what would happen if you recounted the pollen slides a second time; how close to the first count would you actually be? Within 5%, 10% or worse? Obviously, the less grains you count in the first place, the less reproducible your results. 100 grains is generally too low to ensure reproducibility at the resolution demanded by the interpretation.

Other comments:

p672, line 20-23: I am not sure why the Mediterranean regions intermediate position would make it 'clearly' more sensitive than other regions. Are there any references that detail this assumption?

p674, Section 2: Need to add more details about the core site (both now and in the past); is sediment focussing/reworking a problem? Is it oxic/anoxic and therefore subject to bioturbation? If so how does possible bioturbation relate to the temporal resolution of the record? How far away was the LGM coastline? Is the pollen deposited by the wind or the result of fluvial input or both? What is the prevailing wind direction?

p675, Section 3: The authors attempt to make correlations between the timing of events in their core with those found at other sites at a sub-millennial resolution. As a result, the chronological control for the core should be discussed in more detail; for instance, the Holocene is constrained by only 4 dates. The age-depth model should be shown as an additional x-y graph figure (this is not shown in the Geology paper to which they refer), and 2-sigma limits on the calibration for each date shown (these will be larger

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than those given for the 14C dates).

p676, Section 3.2: See earlier comments about the amount of pollen grains counted per sample

p676, Section 3.3: The authors need to clearly state the method by which the fossil and modern pollen were matched, including how many taxa were considered. They list a number of studies that have used MAT, but these have differed quite a lot in this part of the methodology. The authors also include seasonal precipitation which is a relatively new parameter to reconstruct using pollen data. They should either refer to a published study which evaluates this new parameter using the transfer-function methodology which they are applying (and not just a MAT study, this should also use the same fossil-modern matching method), or show the results of their own validation. In any case, a validation including/excluding Pinus should be shown for all parameters or reference to such a study be provided. The errors should be discussed (based on leave one out cross-validation etc) and considered when discussing the scale of the events in the core reconstruction. It would also be worth noting that whilst the modern training set may consist of 2000 samples from the Mediterranean, the number of samples that include Cedrus pollen (shown in the fossil assemblages) is likely to be considerably fewer since this is almost exclusive to Morocco.

p677, line 9-10: Just confirm that summer is JJA and winter is DJF.

p678, line 9-11: Clarify what is meant by 'reliability'. For instance, a common question in assessing the reliability of marine pollen records would be to what extent changes in the prevailing wind direction influence the composition of the pollen assemblage at marine sites irrespective of changes in the vegetation? Prevailing wind direction presumably changed a lot between glacial to non-glacial times for instance. Also, to what extent might changes in the level of fluvial input (eg indicated here by isoetes in the pollen spectrum) change the source area?

p678, line 12-18: Clarify what is meant by a 'good correlation'. For instance, the au-

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thors talk about the fact the pollen record includes Cedrus found in Morocco etc, but what is the basis for the 'good correlation' with the Portuguese marine cores?

p680, line 19-24: the authors should be able to explain exactly the reason for the classification 'temperature deciduous forest' by looking at the taxa included in the biomisation for the samples concerned. There should be no mystery here.

p682, line 11-14: Time-series biome reconstructions are notoriously fickle because just a couple of pollen grains in the sum can influence the choice of biome. The defined threshold between biomes is based on a rather arbitrary method ('fuzzy-logic' to put it kindly), and therefore needs to be interpreted with care. I would not consider a change from one biome to another as the basis for defining a real event in the real world unless attributable to more than one sample.

p684, line 14: Which oxygen isotope curve? Greenland?

p684, line 18: In what context are you using the term 'climatic optimum'? This term is usually used to describe mid-Holocene high latitude warming, but evidence here and elsewhere indicates that the Mediterranean region was cooler than present during the mid-Holocene. A wetter, cooler Mediterranean climate may be 'optimum' for the region, but this needs to be defined more clearly.

p684, line 21: The climate reconstruction shows negative temperature anomalies compared to the modern core top sample, so the term 'warm' is rather misleading here.

p684, line 23-24: Precipitation anomalies of 0-100mm are unlikely to be statistically significant. This shows the need for validation of the transfer-function against the modern training set to establish these kinds of limits to the interpretation.

p684, line 27-28: You need to explain how you can suggest a decrease in forest cover when a major tree taxa (Pinus) has been excluded from the sum. How do you exclude the possibility of a pine forest for instance?

p684, line 28: There is an ambiguity here. A late Holocene cooling trend is described,

but at the same time it is stated that this is not clearly expressed in the climate parameters? To what Holocene cooling trend do you therefore refer?

p685, line 4-5: Is there any evidence from terrestrial sites to support the idea that the expansion of *Artemisia* is anthropogenic?

p685, line 8-9: Please see earlier comments about this kind of interpretation

p686, line 3: The authors describe Figure 5 as a 'tentative' correlation, but it looks like the correlations can only occur if we ignore the chronological framework of most of the other events shown at the other sites. This looks like a bit too much wishful thinking unfortunately.

p686, line 6-7: The authors link small changes in alkenone SST and pollen derived TANN over the Holocene, whilst ignoring what appears to be an enormous discrepancy in the amount of early Holocene warming shown by the two records. The SST record shows a warming of 5-6C in the early Holocene, whilst the TANN record shows little change in comparison. One would expect the air temperature and SST to be closely coupled, so this should deserve comment if not an explanation. The TANN for the site is given as around 18C in the site description (Section 2), which appears over 3C warmer than the core top reconstructed TANN, this again should deserve comment. The authors interpret short-term fluctuations in the Holocene alkenone SST curve, but these look smaller than the normal resolution of this proxy ( $\pm 1.5\text{C}$ ), based on its ability to predict modern SST's from core top samples.

Table 2, Table 3, figure 2: Ages should be shown within a reasonable resolution eg to the nearest 100 years for the core events, and the nearest 10-50 years for the Ice Core events and dates.

Table 3: This would be better shown by a figure such as figure 5 rather than a table, with events shown against a time-line.

Figure 1: It might be useful to show the LGM coastline as well as the general

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bathymetry surrounding the core site.

Figure 2: A diagram clearly showing the percentage of arboreal to non-arboreal pollen would be useful, as would the full pollen diagram so that it is clearer what is driving the pollen-climate reconstruction and biomisation. A dotted baseline would help to identify minor occurrences of taxa, as well as a generally larger sized diagram. Families should be shown in non-italicised lower case not capitals.

Figure 3: Diagram needs enlarging, particularly along the vertical axis; it is very difficult to read changes down the core on the vertical axis. The zero anomaly needs to be shown as a line, so that it is clear down the core what is higher and what is lower. Tsum and Twin do not converge at the top sample, why are they offset if they are anomalies?

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