

Interactive comment on “Scaled biotic disruption during early Eocene global warming events” by S. J. Gibbs et al.

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Response to Anonymous Referee #2, received 17th October 2012.

We are glad that both reviewers have appreciated that we are presenting a novel technique for addressing timely questions. This method directly tackles a long-standing problem of how to objectively and quantitatively compare biotic responses between different climatic events – moving beyond the currently inadequate traditional techniques that rely on simple species diversity comparisons and speculations on the specific paleoecological responses of extinct taxa. One point we would like to highlight is that while we are typically dealing with datasets that may be less than ‘ideal’, this is not a reflection on the inadequacy of our specific record, but rather a common feature of virtually all geological records from the pre-Quaternary. What is important is that

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we find ways in which to maximize the types of data we have available, to address important scientific questions. The fossil record is invaluable as a resource for exploring how biota have responded to past climate change on evolutionary timescales and we continuously strive to improve how we best use this wealth of data, even with its imperfections.

We address the specific concerns of Reviewer 2, as follows:

Comment 1. “how well does genus-level variation in relative abundance of nannofossils represent ‘marine biotic variability through . . . the early Eocene’”.

The genus-level variations in relative abundances does provide a good measure of biotic variability through time as evidenced by intervals of higher biotic variability scaling with higher species turnover. However, while the reviewer appears to argue for a species-level approach, rather confusingly, they then argue that we should use a “counting group approach”. The meaning of this term is unclear to us, but it may equate precisely to what we have done. As the reviewer rightly says, our paleontological species concepts are based on morphology and, as such, genera represent robust morphological groupings of very similar morphology within an assemblage. Arguably, generic classifications in nannofossils are far more stable and unambiguous than species level, which is particularly important for longer-term time series approaches. Furthermore, morphospecies within a genus typically share similar ecologies, i.e., fall within the same broad ecogroup, e.g., all discoasters are thermophilic, *Toweius* are cosmopolitan bloom-formers. There are few exceptions. Therefore, the genera we count, regardless of whether they are monospecific or multi-species genera, are valid morphogroups, internally consistent through time and more reliable than taking a species approach. As a final point on this subject, it should be noted that paleoecological/paleoceanographic studies of calcareous nannofossils have successfully applied the grouped data (i.e. genus-level) approach, across a wide range of time intervals. For example, the principal environmental indicators used in Cretaceous studies are often grouped at generic level, or are species plexi, e.g. see the use of *Biscutum*,

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Watznaueria, Zeughrabdotus, Nannoconus in Gale et al. (2000, J. Geol. Soc., 157: 745) and Erba (2004 Mar. Micropal., 52: 85). However, to address this point we can certainly include more of a discussion on the validity of a morphogroup count approach.

If this comment is also referring to the question of whether one group of organisms can be representative of marine biota in the broader sense, then our answer is threefold: 1) calcareous nannoplankton are ubiquitous and abundant primary producers that form the base of the oceanic food chain as so, yes, disruption in this group may well cascade more widely through the marine ecosystem; 2) we have also provided data from different trophic groups in the paper, including phytoplankton and zooplankton, and similar trends are seen, confirming the broader significance of this approach; and 3) during intervals of significant biotic crisis, where evolutionary rates provide evidence of disruption, e.g. at the K/T boundary (also discussed in our paper), it is clear that the high values in our metric equate to significant disruption throughout the marine ecosystem.

Comment 2. “I contend that the smoothing and binning of time series data should not be used to understand biological responses to events that may occur either abruptly or at rates that are more rapid than bin duration. More time should be devoted to deciphering the biological significance of the changes (which must involve some consideration of flux) and less to interrogation of what I consider to be a questionable analytical approach to the problem”

The objective of our paper is to investigate biotic response across a spectrum of environmental change events and we would contend that this is a key component of deciphering the biological significance. This is why we apply relative abundance data and its variance, which represents a biological response as reflected in assemblage compositions. Such data is not the same as flux, which we have not attempted to document here because it is very difficult to extract, meaningfully, from fossil records that lack sub-milankovitch age control. Yes, flux is another only biological parameter that might be considered, but it was not appropriate in our study material and it is difficult to justify in many deep-time materials.

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Concerning smoothing, we have presented the analysis of smoothed and non-smoothed records and show that we achieve the same results in both. We have applied smoothing in order to facilitate comparisons between datasets, which may contain different levels of noise. We have demonstrated that we are not 'losing signal' in this process.

Similarly, we have applied a range of bin durations to test for sensitivity to duration, and we chose bin durations that are most appropriate to the events we are attempting to compare. Data are carefully binned so that 'peak' event levels can be obtained without influence from background levels and vice versa, taking a holistic approach to quantifying the overall response to an event. We have not smoothed the data within the bins, and so we are not losing the signal of biotic response "to events that may occur either abruptly or at rates that are more rapid than bin duration".

Regarding the comment "surely relative abundance patterns will vary between sites to a similar extent as flux". This is the crux of the matter and the reason for using this kind of data. Relative abundance data is a relatively comparable data type between sites, and less likely to be strongly modified by sedimentation rates.

In response to specific comments, we disagree with the comment that "100 kyr is not long enough for populations to revert to background". Generation times for unicellular nannoplankton are measured in days and recent experimental work has shown that adaptation and evolution occurs in months to a year (Lohbeck et al. 2012, Nat. Geosci.). Biota can respond to very rapid environmental perturbations, e.g. at the onset of the PETM, so why not over longer time periods (e.g. 100 kyrs), after environmental condition have returned to normal? However, we will certainly comment on this point in the revised manuscript. The comment that "A stronger climatic link between paired events?" is an interesting point, and this may be possible, but we are not aware of any evidence for this currently – geochemically or biotically - and we don't think that it would be justified to combine the biotic response for each of these events as that defeats the point of the approach. Finally, yes, we can certainly address any issues

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associated with 'awkward' language.

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