



Interactive comment on “Simulating the growth and distribution of planktic foraminifer using an ecophysiological multi-species model” by F. Lombard et al.

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Received and published: 14 January 2011

This paper presents the results of an attempt to model the growth and abundances of planktonic foraminifera species based on physiological parameters. The aim is to provide a tool to investigate the ecology of species under different boundary conditions, which is essential for the interpretation of proxy signals extracted from fossil foraminifera. The model presented by the authors is the third attempt to date to model planktonic foraminifera and it is by a large margin the most mechanistic one. The previous attempts were either essentially a niche-model (Zaric et al. 2005) or an empirically calibrated species-interaction model (Fraile et al. 2008). The previous attempts have

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already shown how important and useful this exercise is and I congratulate the authors of this study for making a further important step in this quest. Although I have identified a number of issues as detailed below, I am convinced this is an important contribution, which is essentially correct and eminently interesting for the relevant scientific community. I have no hesitation to recommend publication pending the issues outlined below. Importantly, these issues do not relate the formulation of the model itself and are thus unlikely to change the main conclusions.

1) The empirical calibration of individual growth versus population density that is used to “scale” the modeled individual growth to changes in population size ignores the effect of changes in body-size distribution across different populations of a given species. The scaling from individual growth to population growth by itself is already a leap of faith, as it explicitly ignores ecological interactions, but I agree with the authors that it is a legitimate first approximation. However, it only works as long as population density is proportionate to the total biomass of the population in the same way throughout the range of the modeled species. This is, unfortunately, not true in the case of planktonic foraminifera. Here, the distribution of body sizes varies strongly as a function of temperature (and other less well constrained factors). Because volume (and thus mass) is proportional to the cube of size, even small shifts in shell size have a large effect on the change in biomass. Thus, if the size (measured as shell diameter) of a planktonic foraminifera increases by 25%, its biomass will double. This phenomenon is in my opinion responsible for much of the scatter in figure 3. I believe the authors need to take this issue into consideration both when they are calibrating their model but also when they validate it by observations. In both cases, population densities are directly equated by the authors to population biomass, which is not correct. I am aware that Fraile et al. (2008) have not discussed this effect either, but because that model provided explicitly population biomass, the potential error due to changing body size distribution occurred only once, when comparing model results with observations. In this paper, the error is made twice, when the population biomass is estimated and when it is compared with observations. This is why I feel the authors absolutely need to respond to this issue.

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2) The simulated growth rate is limited by nutrition saturation (line 124). This is a reasonable assumption for individuals, but I wonder what exactly the implications of this are for the scaling of individual growth with population growth. Population growth cannot be limited by nutrition saturation in the same way as it is for individuals. Instead, it is limited by the amount of nutrition and ecological interactions.

3) Having seen the entire discussion on the plankton data and the ways in which the comparison is biased by the peculiarities of the validation dataset (as discussed on page 19), I am not sure the data by Bé and Tolderlund (1971) are really useful. I know this is the largest and most consistent survey, but the data itself are no longer available and the "synoptic" representation is fraught with so many assumptions that I almost tend to believe the authors should forget about this comparison and focus on fewer but better constrained surveys.

4) There seems to be several distinct areas where the model underperforms. One such area, as the authors note, represents the marginal seas (Red Sea and the Mediterranean). This is interesting, because these are also the regions where factors other than those considered in the model may be affecting the species distribution. The second area where the model failed is the Western Pacific Warm Pool. Do the authors have any explanation for the low diversity and wrong species dominance in that region as implied by the model?

5) The growth model implies that *G. ruber* is better adapted to oligotrophic conditions than *G. sacculifer*. This is interesting, as it directly contradicts what we have observed in the Red Sea (Siccha et al., 2009). Could the authors comment on this discrepancy?

6) I note that the implied depth of maximum growth for the species used in the model is inconsistent with the observed calcification depths for these species as known from the literature, which are in all cases much deeper. Could the authors comment on this discrepancy?

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Interactive comment on *Biogeosciences Discuss.*, 8, 1, 2011.

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