Responses to Reviewer 3

We thank Reviewer 3 for his/her comments and provide our detailed responses below (in bold)

General Comment

An NPZD-type ecosystem model is used to examine seasonal and interannual variability of the MAB shelfbreak front. This is a nice example of using a model to better understand observed processes. The manuscript appears to be appropriate for publications in Biogeosciences, but would be improved by addressing the comments below.

We thank the reviewer for his/her kind comments and encouragement.

Specific Comments

1) Abstract: It would be helpful to have some more detailed (perhaps more quantitative) results/conclusion included in this abstract.

We have revised the abstract accordingly.

2) The one specific thing I learned from reading the abstract is that the phytoplankton bloom starts 1-2 mouths after the nutrient peak. How sensitive is this result to the parameter choices made in the model?

We used the same biological model and model parameters as used in Lehmann et al., 2009 (Biogeosicences, 6, 1961-1974). Our model experiments show the basic temporal patterns are not sensitive to the parameters chosen.

3) The authors call this model a "size-structured" ecosystem model, but in fact this model is not structured according to size. The author should take "size-structured" out of the model description (and the title).

Following the reviewer's suggestion, we revised the text and title accordingly.

4) I didn't really see the "shelfbreak biomass enhancement" in the satellite data, which seems to me to be a problem since a large portion of the manuscript discusses this feature.

The existence of shelfbreak enhancement has been confirmed by synoptic observations (e.g., Marra et al., 1982; Ryan et al., 1999). We agree with the reviewer that such a shelfbreak biomass enhancement is difficult to detect in both satellite and modeled mean fields (Figure 8, upper panel) because it is not a permanent feature in the MAB region. That's why we invoked EOF analysis to highlight this variability. The first mode (Figure 8, middle panel, also re-plotted below) show the shelfbreak enhancement in N, P and Z fields much more clearly.



5) End of section 1: the names of the sections here don't really match the names of the section in the paper.

We have revised the names to the sections so they are consistent with the latter sections of manuscript.

6) The text makes it sounds like the Lehmann model differs from Lima and Doney. The difference between these models should be provided. Are there simply parameter differences, or structural differences? Line 25, P. 1559- are the biological equations and parameterizations different in Lehmann? If not, the reader should simply be referred here to Lima and Doney.

We have revised the text as follows: "In *Lehmann et al.* (2009) implementation, silicate was not included and hence the diatom group was interpreted more generally as large phytoplankton. Interested reader is referred to *Lima and Doney* (2004) and *Lehmann et al.* (2009) for more detailed biological equations and parameterizations as well as differences between two implementations."

7) The authors should talk a little more about spin-up issues, and why they think there short spin-up time is adequate. In Figure 6, it looks to me a lot of the difference between 2004 and 2007 could be due to inadequate spin-up time.

Our shelfbreak biophysical model is nested inside a shelf-wide "parent" model that has the same dynamics and model parameterizations (Lehmann et al., 2009, Biogeosicences, 6, 1961-1974). Because the shelfbreak model simulation is initialized and driven at the boundaries by dynamically balanced solutions from the "parent", the model fields can spin up rather quickly (within a month). Indeed, other sensitivity experiments we have done show that if the biological fields are initialized using spatially uniformed constants or some kind of climatology (like most of biological modeling studies do), it will take longer spin-up time (on the order of years) to establish equilibrium conditions.

8) The model is compared almost exclusively to remote sensed surface observations. Some comparisons to in-situ and subsurface data is required.

Chen and He (2010, JPO) validated the shelfbreak physical simulation using both satellite and in-situ subsurface observations. While we very much agree with the reviewer on the limitation of remote sense surface data, we were unable to find and get hold of subsurface nutrient and biological observations in this area for model validations.

9) Is the MABGOM model nested with a North Atlantic simulation? More details here would be appreciated.

Yes, the MABGOM model is nested inside global HyCOM/NCODA model. We have added this information in the revision.

10) Units should be double-checked in many figures. In figures 5 and 6 it looks like phytoplankton is shown in mmols of phytoplankton. Unites aren't given in many figures, such as Figure 7... also, why is N in log units in Figure 7?

We have doubled check and added the unit for all the figures. In Figures 5 and 6, the phytoplankton shown should have a unit mmol N/m3. We used the log scale for the upper panel of Figure 7 to highlight the spatial distribution in the mean field.

11) Figure 4- the comparison in winter is really not very good, which is hidden in the color log scale. It is customary and easier to read if the actual units on the color bar 0.5, 1.0, 1.5, etc as opposed to -0.4, 0, 0.4.

We have revised figure and colorbar as the reviewer suggested, and also acknowledged in the revision the deficiency of model skill in resolving the winter seasonal surface chlorophyll distribution.

12) Figure 10- the normalization factors need to be explained a bit more thoroughly. Why are these needed? Why is the dashed line constant? The text talks about not being able to see the time lag in figure 10, which makes me wonder why the authors didn't simply zoom in on a certain time period and show us the time lag, if it exists (maybe it doesn't)?

The variables are normalized so that we can see their temporal relationship more clearly. We have revised the caption of Figure 10 as follows to make it clear:

"Monthly means of domain-averaged upper 50m nutrient concentration (black line), the upstream nutrient influx (blue line), and the surface mixed layer depth (red line) from 2004 to 2007. Also shown in the dashed red line is 50 m as a reference depth for MLD. Both N-influx and local N time series are normalized, whereas the domain- averaged, monthly mean MLD is not and has unit of meter"

The analysis on Figure 10 is based on monthly output, and thus not able to resolve the time lag. We have clarified this as follows:

"Because monthly values were used in Figure 10, such a time lag between local upper water-column N content and N-influx from the shelfbreak jet is not discernable."

13) Figure 13- Why is VADV blue in the deepest waters in 2004 and red in 2007? Is this spin-up issue? This seems like a big different between these two years. Also the author should comment on the fact that it is the physics that is varying between years, the biology (SmS) is almost identical in both year. I think it's an interesting point that should be discussed.

As mentioned before, our shelfbreak biophysical model is nested inside a shelf-wide "parent" model that has the same dynamics and model parameterizations (Lehmann et al., 2009, Biogeosicences, 6, 1961-1974). Because the shelfbreak model simulation is initialized and driven at the boundaries by dynamically balanced solutions from the "parent", the model fields can spin up rather quickly (within a month). So we believe the differences between 2004 and 2007 are reflecting realistic interannual variability rather than a model spin up issue.

We very much thank the reviewer for pointing out SmS term is almost identical in both years. This suggests advection and diffusion processes play the major role in determining the local rate of change of shelfbreak nutrient content. We have included this discussion in the revision.