

## ***Interactive comment on “MOMBA 1.1 – a high-resolution Baltic Sea configuration of GFDL’s modular ocean model” by H. Dietze et al.***

**H. Dietze et al.**

hdietze@geomar.de

Received and published: 23 May 2014

We thank reviewer 1 (R1) for his time and effort. Overall, R1 ranks the “topicality” of the paper high and is satisfied with its quality. Even so, R1 requests major revisions because the model fails to reproduce major salt-water inflows. More specifically R1 suggests that a model performance comparable to configurations in Meier (2007), Eilola (2009) and Lehmann et al. (2004) is mandatory for publication.

We agree that MOMBA 1.1 is - as concerns the representation of major inflow events - apparently a step backwards, rather than being a step forward (and we explicitly state and explore this in the manuscript, starting in line 10 of the abstract). However, we disagree with R1, who implies that a model, which fails to represent major inflows, can not be used to make significant Baltic Sea research and that, therefore, the associated

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model description should not be published in its present form.

We have two lines of defense on which we will elaborate in the following. First, we will argue that MOMBA 1.1 provides the means to pursue new and interesting research, even though it fails to reproduce major inflow events. This merits publication because the MOMBA-based research to come needs a reference description. Second, we will argue that MOMBA 1.1 is a substantial improvement compared to Meier 2007 and Eilola 2009 and may, depending on the development of computer architecture, outperform the “Lehmann et al. (2004) kernel” in the future.

(1) MOMBA 1.1 provides the means to pursue new and interesting research: E.g., as a consequence of its high spacial resolution we discovered indications that hitherto unrecognized (or even unaccounted) effects such as the eddy/wind effect (cf. Sec. 3.2) may well be responsible of substantial wind-induced upwelling of nutrient rich and cold waters to the surface. This is an exiting new line of research which could not, due to their coarser resolution, be pursued by the model configurations described in Meier (2007), Eilola (2009) and Lehmann et al. (2004).

(2) MOMBA 1.1 is an improvement compared to Meier 2007, Eilola 2009 and Lehmann et al. 2004: R1 suggests that the models of Meier 2007, Eilola 2009 and Lehmann et al. 2004 feature a resolution higher than 2 nautical miles. This does not apply. Their resolutions are actually all equal, or even coarser than 2 nautical miles. In contrast, MOMBA 1.1 features a higher resolution of 1 nautical mile which resolves more of the mesoscale. To this end MOMBA 1.1 opens up the road for new science.

Two of the authors (Loeptien and Dietze) have been working at the Swedish Meteorological and Hydrological Institute (SMHI), employed to advance the RCO model underlying Meier 2007 and Eilola 2009. Because of “checkerboard” problems (cf. Sec. 3.7) and, in parts associated, severe conservation issues with nutrients, the RCO model is currently replaced at SMHI by newly developed configurations based on the NEMO (Madec, 2010) code such as BaltiX (Hordoir et al. 2013). MOMBA 1.1 has no checker-

board (cf. Sec. 3.7). Further MOMBA 1.1 features a full free surface method and does not have conservation issues like RCO which uses an implementation of the Killworth et al. (1989) “non-rigid lid free surface” which is infamous for its non-conservative behavior “... in shallow seas or in models with very fine vertical grid spacing” (Pacanowski and Griffies, 2000; compare also Griffies et al. 2001). To this end, we think that it is fair to recognize that MOMBA 1.1 is a substantial improvement compared to Meier 2007 and Eilola 2009. As concerns the comparison with the “Lehmann et al. (2004) model kernel” we think that the scalability of Lehmann’s kernel may be limited because it relies on OpenMP parallelization rather than applying MPI. This could cause a problem in a future of ever higher resolutions and increasing number of biogeochemical compartments whose cycles and pathways have to be computed (although advances in computer architecture may well prove us wrong here).

Concerning specific comments and questions:

R1: Additional comparison of modeled transports between different basins against literature values should be made as this could indicate the impact of underestimation of salt water inflows to the general circulation.

A: We agree. In fact, we are currently working on an even more comprehensive analysis than the one already presented in the manuscript (cf. Fig. 15) of simulated inflows which will – eventually – result in a remedy for our retarded inflows. However, we feel that such a comprehensive analysis is, for the sake of brevity (the manuscript is already rather long), beyond the scope of the manuscript at hand. We feel that the issue of “tuning to get the inflows right” deserves a publication on its own because it is so important to rule out the possibility to get the correct inflows for the wrong reason. Note that, getting the “right answer for the wrong reason” would render projections of deep-water renewal and associated changes in biogeochemical cycles questionable or even obsolete.

R1: Is the the tidal forcing in the North Sea used in the model if the model is closed at

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western boundaries? A: There is no tidal forcing in the North Sea. We will clarify this in a revised version of the manuscript.

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Interactive comment on Geosci. Model Dev. Discuss., 7, 2065, 2014.