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Interactive comment on "A Meridionally Averaged Model of Eastern Boundary Upwelling Systems (MAMEBUSv1.0)" *by* Jordyn E. Moscoso et al.

Anonymous Referee #1

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Moscoso et al present a newly written ocean circulation biogeochemical model, NAMEBUS, written in C, with Matlab scripts added to set up and visualize the model and its solutions. The model is configured to represent a two dimensional eastern boundary upwelling system. With the idealized set up the computational efficiency is high, which in turn allows to relatively quickly carry out many simulations. An evaluation of the model (set up as the California Current System) against observations indicates that the model reproduces major features of the upwelling system.

The draft is written very well, carefully and clearly. The high model's computational efficiency (it can be run on a laptop/desktop) allows to test physical or biogeochemical parameterizations/model formulations, to run sensitivity studies, or to carry out parameter optimizations. I.e., NAMEBUS promises to be a useful tool that nicely complements

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realistic three dimensional set ups for EBUS. I recommend the draft for publication.

Detailed comments:

- wind stress forcing: I expect the wind stress maximum to be located somewhat offshore, as indicated in your own Fig 1, see also, e.g,. SCOW data in http://www.clivar.org/sites/default/files/EBUS-Prospectus.pdf (Fig 2) or Fennel et al, 2012, https://www.sciencedirect.com/science/article/pii/S0278434312001525 (Fig 3), or also in Castelao and Luo, 2018, that you refer to. This contrasts Fig 5 in your paper which shows maximum wind stress at the coast if I see correctly. Would it be valuable to introduce a parameter that allows to set the offshore distance of the wind stress maximum, similar to the parameter l in Fig 7 of Fennel et al, 2012?
- given that you submitted to GMD and that the computational efficiency of the model is a major point, I suggest to provide in section 4 “Implementation Details” some additional information. What software/Matlab toolboxes/etc are required to run the model, what minimum hardware requirement one needs, if it is platform independent (operating system, laptop/desktop/linux cluster... I presume it is not parallelized?). I.e., if I understand correctly, NAMEBUS’ advantage is that you can simply run it on a laptop (?) and that it is easily transferable. I think it is worth to stress this value. The model could even be used for educational purposes, couldn’t it? Maybe also provide some benchmark number for computation time (to get a sense for, e.g,. how long it will take me if I want to run a parameter optimization).
- P39 L16/17 “This underestimate may be caused by the over-simplification of the ecosystem structure in the NPZD model“: The underestimate could also originate

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in differences due to the circulation, couldn't it (as the pattern of the Chl bias in Fig 5 bottom panel is matched by a bias in temperature, Fig 5 top panel)?

- P39 L27 “5.4 Model Verification (Resolution Tests)”: This title is not entirely clear to me. Also the subsection consists only of a single paragraph and the associated Figure is hardly discussed. I suggest to either delete or add more detail to this subsection.

Grammar:

- P40 L3 “The model is based on solution of a general evolution equations for“: Needs rephrasing
- P40 L8 “we performeda preliminary”: Typo

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