Geoscientific
Model Development
Discussions

Interactive comment on "ERSEM 15.06: a generic model for marine biogeochemistry and the ecosystem dynamics of the lower trophic levels" by M. Butenschön et al.

A. Yool

axy@noc.ac.uk

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Comment prepared by **Andrew Yool** (axy@noc.ac.uk), **Tom Anderson** (tra@noc.ac.uk) and **Katya Popova** (ekp@noc.ac.uk).

In the first instance, we are very pleased to see ERSEM get a thorough and updated description, and the authors are to be commended. As a long-standing and much-used staple of many marine biogeochemistry studies, particularly in the shelf seas region, it is crucial that ERSEM is transparent and accessible to interested researchers. Especially since recent work (e.g. Kwiatkowski et al., 2014) has shown ERSEM now running at the largest possible scales.

However, while welcoming this manuscript, there are a number of weaknesses in it that we feel do not allow ERSEM to be shown in its best light. In our opinion, addressing these would make the resulting manuscript a much more valuable resource, both for existing ERSEM users and as an advert to potential new users of ERSEM.

We have divided our comments into general, overarching points and shorter remarks on specific facets of the manuscript.

General points:

1. While the model equations are doubtless mathematically correct, they are expressed throughout in an overly nested and quite repetitive style that makes following and interpreting them unnecessarily difficult. We would suggest that the authors examine descriptions of comparable models (e.g. PISCES was very recently published; Aumont et al., 2015) and adopt some of the style conventions there.

2. More broadly, while the model equations are scrupulously documented, their origins are not explained. As such, it is difficult for readers to chase up particular functions to understand the rationale for framing them or their underlying assumptions and limitations. Where possible, we suggest that the authors either make reference to their sources and / or identify where they have used "standard" functions (e.g. type-II or type-III responses).

3. Oddly, the model description includes a number of additional optional functionalities for particular processes, but it offers no information on how these perform (functionally and computationally), how they impact model performance, or under which circumstances they should be preferred. We would suggest that an obvious inclusion on these occasions would be to perform a simple sensitivity analysis that illuminates on these points. Alternatively, if these options have formed part of a preceding publication, a pointer to this would help.

4. The paper is exceptionally long, even by GMD standards, and we appreciate that our suggestions are unlikely to shorten it. One possible avenue might be to separate the manuscript into two shorter manuscripts in which the pelagic and benthic submodels are (semi-)separately described and explored. At present, the manuscript does not do the benthic submodel justice.

5. The extensive use of idealised 0D and 1D configurations followed by just two paragraphs on a 3D configuration does something of an injustice to ERSEM's long record in 3D work. While the former configurations have particular uses, as the authors note, they are a poor representation of what ERSEM is capable of. We would suggest that that manuscript would be much improved if the focus was on the 3D model (either in shelf seas or global mode) with passing mention made of these useful, cut-down modes.

6. On a related point, the demonstration of ERSEM's range and utility is very weak. The ways chosen to illustrate this are limited and do not provide any context for the model-observation comparisons (i.e. is ERSEM doing well / badly relative to other models?). This is compounded by some weak figures and analysis, but is principally hampered by the focus on idealised cases rather than ERSEM's work in 3D (which, as already noted, is given seriously short shrift in this draft of the manuscript). Again, we would strongly suggest that the authors examine recent model descriptions in GMD, of which the PISCES model provides (in our opinion) a good example.

7. ERSEM's treatment of alkalinity appears to have several confusing elements. Calcifiers are included, but alkalinity is effectively implicit ... while also being open to modification – it's not at all clear how the model can "remember" this modification in the absence of an explicit TA tracer. It is also unclear what this does to carbonate chemistry and air-sea CO2 exchange. On a related point, if TA is a function of T S, what happens to it at depth where these relationships com-

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pletely breakdown because of the biological pump? More broadly, either ERSEM or the manuscript (or both?) are not self-consistent when it comes to alkalinity – even simple nutrient-restoring models manage this more straightforwardly.

8. The concluding statement "The ERSEM 15.06 model is the only model currently available that provides the structure for simulating in one coherent system the bio-geochemical cycles of carbon, the major macronutrients and iron, the carbonate system and calciﬁcation, the microbial food-web and the benthic biogeochem-istry" is over-reaching in the extreme. That this description is not backed up in this manuscript by any strong evidence that it does a good job on any of these components makes it difficult to sustain. The manuscript needs to demonstrate ERSEM's skill (e.g. comparison with a range of other models) to justify as strong a statement as this.

Specific points:

- Why is this version "15.06" of ERSEM?; why not version 15?; like many mod-els, ERSEM is documented sporadically so does it really need a ".06" desig-nation in its version number?; this especially seems odd given that previous manuscripts do not routinely report a specific model revision, and also because this manuscript will presumably be the go-to description for the model for years to come; in the language of modern marketing, Apple promotes iOS 9, not iOS 9.06 ...

- An explanation of the differences between BFM and ERSEM might be helpful; they are introduced as cousins but one is shelf seas while the other is (at least ostensibly) open ocean

- Lots of examples of diverse use are given in the introduction, but it's used in a very narrow way in this manuscript; arguably, the 1D uses are rather passé when

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we know that it's more routinely used in 3D and even at the global scale (of which, the manuscript is rather coy about its performance)

- A "model of intermediate complexity" is an odd way to hear ERSEM described; relative to most other plankton models, it's more a "kitchen sink" model in which complexity has been successively extended to include functional groups for which there is arguably still only limited knowledge about; perhaps some examples of other models would make this intermediate status clearer?

- What does "a particularity of ERSEM" actually mean?; this is not unique to ERSEM by a long chalk

- Figure 1 does not do a good job of describing something as complex as ERSEM; it would be far better to separate out the pelagic and benthic components and do a better job separately for each; for instance, the diagram makes it look like all phytoplankton use all nutrients, that all zooplankton have access to all phytoplankton, and that there's only a single size class of detritus (which the text later makes clear is not the case); also, the diagram has no need of including the carbonate system in this way – one assumes pH and omega; the arrows on the diagram, in particular, for this part are unhelpful since they imply that alkalinity is consumed by not just the phytoplankton (and possibly the "microbes" and zooplankton; which P and Z, incidentally, is left to the imagination of the reader) but also the DIC system, which in turn is consumed by pCO2

- Stating "small scale and high resolution applications" would benefit from having scales attributed to them; among other things, the continuity assumption is only ever an approximation

- Table 3, which describes the predator-prey relationships in the model, would surely have been better off as a diagram; Figure 1's job should have been this

- From the get-go the equations, while doubtless mathematically correct, are fairly impenetrable to read; it would be a lot of work to understand and follow them enough to reproduce them in another model; and why is the format of a vertical line followed by a shorthand description used?; wouldn't underbraces, or just well-chosen names, be better?

- In section 2.3, how sensitive is the model to the size of this number?; while it's small, it's a value that the model could reach relatively easily; also, does this mean that the ocean has an enormous standing stock of biological material when integrated everywhere?

- We presume that "hetero nanoflagellates" are "heterotrophic nanoflagellates"?

- The equations contain a large number of diverse functional forms, but these are neither sourced to particular work, nor are the functional responses of them illustrated diagrammatically – this might help in the more complex cases; for instance, how is the rather complex nitrification equation derived?; is there empirical support for such a multi-factorial form, or is it a composite function based on separate studies for each factor?

- Is there any exploration in the manuscript of the different bacterial degradation schemes?; if not, why not?; the text makes a point of describing both at length

- Where does this calcification form originate?; it is not sourced; also, extra functionality is described for CaCO3 dissolution but again appears unexplored; ordinarily one would expect a sensitivity analysis section in the manuscript, not least to help users of ERSEM decide which of the optional functions (here and elsewhere) they should use; of course, it may be obvious from the sources of the functional responses, but – as noted – these are not made clear

- Nice light modelling, but, again, what's the difference in the schemes presented?; is either functionally superior, and does it come at extra cost?

- The second benthic scheme is a bucket; would it be better to present this as tier 1, with the more advanced one as its successor (which is doubtless how the model actually evolved)

- On benthic schemes, again, is there any sensitivity analysis on the choice?; also, the "complex" scheme is simplified from a model that is 20 years old – why not include the full scheme it's derived from as an option?; one would expect it to be more computationally tractable now than before

- In passing, it is difficult to ascertain the total number of tracers (and parameters) in the model; a table could help

- The information in Section 6 seems oddly placed; should this not have appeared when these terms were first introduced?

- Section 6.2's stoichiometric adjustments are presented as if they are a simple fudge rather than being derived from an existing formulation; is this correct?

- ERSEM-Aquarium seems to be a perfect system that could be used to examine the model's sensitivity to the extra functionality that's loaded onto it; but that hasn't been done here

- The manuscript's imbalance towards idealised frameworks (0D, 1D) is difficult to understand given that ERSEM is largely used in 3D simulations

- Section 8 is an anomaly; ostensibly about the "Development and Testing Framework", it wraps up on a discussion of diatoms and chlorophyll which should really appear during the model description

- Section 8's concluding paragraph on not having to write visualisation for the model in a second language is unnecessary; most users would almost certainly run the model and visualise the output alongside in a separate program anyway

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- Table 2 – this has got to be among the most arcane naming convention we've seen

- Table 3 (and other locations in the text) – "preys" is grammatically incorrect; "prey" is both plural and singular, like "sheep"

- Table 4 – "particulate" spelt wrong

- Figure 1 – inadequate; would benefit from being split into pelagic and benthic components, and from a focus on the core nutrient cycles rather than including peripheral (in a diagrammatic sense) processes; arrow heads are also missing in places, and sometimes convey implausible pathways (e.g. TA -> DIC -> pCO2)

- Figure 2 – the use of line thickness does not make this diagram clear; it's also missing what would be interesting detail re: differing phytoplankton and zooplankton fluxes between functional types; the diagram also makes it look like different model structures were used rather than just different pathways being favoured; that these different foodwebs are derived from idealised simulations makes the inclusion of this diagram questionable

- Figure 3 – are the modelled cycles really out of phase in places?; that's not good; also, these target diagrams would be much more useful if they compared the model to another model (or different versions of the same model; like, for instance, versions using different options); as it stands, all the reader can see is that the model performs differently well for different properties (which, to be fair, is all that showed in our MEDUSA-1 paper, but in MEDUSA-2 we also included model intercomparisons); that the model shows that the relative fit for different properties varies between sites (Figures 3-5) makes it difficult to judge how ERSEM is actually performing

- Figure 4 – seems to show the model including a bloom that doesn't occur in the real world at all

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- Figure 5 – this figure has a number of issues; these include: 1. Including the model spin-up period in the plot when it should be perfectly possible not to do this; 2. Showing the model for a period when there's no data; 3. Not having data on a plot when the data is widely known to exist (this looks suspicious); 4. Showing the same data twice for no good reason

- Figure 6 – any observations here?; for instance, Hirata et al. (2011) and Ward (2015) present absolute and fractional chlorophyll data that would provide a good comparison; as it happens, it looks like ERSEM is going a good job here

- Figure 7 – while eyeballing model vs. observations is considered bad form these days, would it really hurt here to show the spatial map of observed chlorophyll?; we know it exists because the model has been compared to it

- Figure 8 – is this comparing the model to a dataset that was used to parameterise it?; that seems to undercut the rationale for this figure

- Figure 9 – is there any observational data to add to this plot?; and why is this plot not in colour?; it is difficult to discern the different lines easily

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