

We would like to thank the reviewer for their careful review of the manuscript. We have replied to their comments (*italic text*) below.

*My main reservation about this study relates to the fact that it is highly linked to one specific model: ICOM. It is not clear to me if the conclusions drawn from this study would be applicable to other models that use different mesh-adaptation techniques (e.g. r rather h adaptation or different mesh-to-mesh interpolations or different FE/FV discretisations in space).*

Fluidity (previously known as ICOM) uses hr-adaptivity to alter the mesh topology. To the authors knowledge there are no other ocean models that makes use of hr-adaptivity yet published, hence the specificity. P-adaptivity would be an interesting extension to this work and we would encourage researchers to pursue this.

Fluidity has a very flexible discretisation system, including multiple FE discretisations, but also Control Volume (CV), which is similar to FV. We have successfully tested the biology model with a number of discretisations available in Fluidity (linear continuous Galerkin, linear discontinuous Galerkin and CV). All produce result that are satisfactory, including with adaptivity. One of the main points of this work is to show that a fully conservative interpolation scheme is needed for biological tracers in order not to introduce additional, spurious, numerical diffusion via the adaptive mesh process. We are therefore confident that these results should hold for h-, and hr- adaptivity (i.e. adaptive algorithms that change the mesh topology). However, the interpolation scheme is key – only those that are conservative are appear to give reasonable results.

We have edited the text to reflect the above by adding more discussion on the matter.

*Furthermore, this study is purely 1D and hence structured in the vertical. The authors claim that their goal is to later use such an approach in their 3D model to tackle more realistic problems. I am wondering whether that would work out so smoothly as they use a 3D model with a fully unstructured mesh made of tetrahedra. How could they be sure that the method they have assessed in a 1D framework would be applicable in their own 3D model? This is especially worrying since the authors mention in their conclusion that "for this pseudo-1D domain each column of the domain must be identical" (see p. 2019, l. 4-5). I think this is in contradiction with their claim that computational saving will further increase in 3D thanks to vertical adaptation (see p. 2018, l. 14). There are no clear indications that it will actually work in 3D. I would thus advise the authors to "tone down" such claims and provide more details about the extension of their approach to a fully-unstructured 3D framework.*

The reviewer has highlighted an important point here, which we have addressed with additional text in the manuscript. The extension of this work to 3D precludes the use of “fully unstructured” tetrahedral meshes for 3D ocean simulations. However, this was already considered not possible in ocean modelling due to spurious pressure gradient introduced (Piggott et al, 2008. Unstructured adaptive meshes for ocean modeling. Geophysical Monograph). Instead, Fluidity is able to use an unstructured mesh in the horizontal, but columnar in the vertical. Each column may contain different numbers of layers in the vertical and these may be arranged as sigma- or z-layers as the user deems necessary. There are still questions to be answered in terms of how variations in numbers of these layers will affect the biological tracers in such a 3D model. Our pseudo-1D model used large horizontal diffusion and viscosity to ensure each column experienced the same velocity and tracer values. It is an open question as to whether the results presented here hold in a realistic domain where adaptivity is done first in the horizontal and then in the vertical, with realistic values of viscosity and diffusivity in the horizontal. We appreciate the reviewers concern though. We have added a paragraph explaining our 3D approach (as described) above and toned down the the claims in the manuscript.

*Below are some more specific comments:*

*\* Section 4.1: I think it would be useful to see the actual formulation of the metric. I'm sure there are some threshold values on the different terms appearing in the metric that would be useful to the readers. Also, I guess that the authors use the gradients of the density and velocity. That should appear clearly in the text (see p. 2013, l. 9).*

We have added more details of the metric formulation, including details of limits applied and the fact we use the curl of the fields (not the gradient).

*\* Section 4.2: What do the authors mean exactly by "consistent interpolation" (see. p. 2014, l. 12)?*

This is a term used in the options for Fluidity and is linear interpolation. We have changed all occurrences of this term with linear interpolation in the text.

*\* p. 2016, l. 21: "the meshes contains" -> "the meshes contain".*

Corrected.

*\* p. 2021, l.5: I think there is a typo in Eq. (A10).*

The equation is correct.

*\* References: There seems to be a problem with the publication year of each paper. At the end of each citation, 2 or 3 different years appear.*

Noted and will be reported to the publishing team (they are correct in the supplied bibtex file)

*\* References: Note that one third of all the citations come from the ICOM group. I don't think that this is very "healthy" and certainly suggests that this paper is a bit too "ICOM-centered".*

We appreciate that this is indeed the case, but currently, Fluidity is the only model capable of the work presented in this paper. We have added additional references and text for other unstructured mesh models that have embedded or coupled biogeochemical models to show that this work has future utility beyond the Fluidity model.

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