Authors' response to anonymous reviewer #1

Jorn Bruggeman on behalf of all authors

The authors addressed my previous comments, and I like the suggested extensions which have been added to the description of the three EAT example applications. The manuscript is easy to follow, and the modified code snippets (Fig. 2, 3, 5) are commented well and easier to interpret. I have only a few minor comments and a bug report related to the first example application.

We much appreciate the reviewer taking the time to reread the ms, rerun the example applications and provide comments. As described below, we have adopted nearly all suggestions verbatim.

bug report

This time around, I tried out all the example applications. Overall, I like the use of Jupyter notebooks, which make it straightforward to run the examples and visualize the output. Perhaps one could reduce the GOTM text output a bit, which takes a lot of scrolling to get through.

Unfortunately, I ran into an early error in the first application "Ensemble" in cell 3 which then lead to a python error in the following cell (No such file or directory: 'result.nc').

Hopefully, this output will help find the bug that may be remaining (I updated eatpy before running the example and hope the problem is not on my end):

```

model(no filter program present)

initialize_gotm

-------------------------------------------------------------------------

Reading configuration from: gotm.yaml

configuring modules ....

init_airsea_yaml

done

[...]

Initializing ice...

model type: surface_constant

initialization succeeded.

ERROR: the following setting(s) were not recognized:

- /instances/phy/coupling/fer

FATAL ERROR: initialize: invalid configuration

STOP 1
```

```

The two other applications ran fine on my machine.

**We suspect that this error was due to EAT being out of date on the reviewer's system, as the error message indicates that a new biogeochemical configuration (fabm.yaml) is being used with a previous version of the PISCES model. The updated PISCES model was included in the 0.9.8 EAT release (https://doi.org/10.5281/zenodo.10934071) that accompanied our revision; moreover, the combination of this 0.9.8 release and the updated applications was extensively tested before we submitted the revised ms. The reviewer does indicate that he/she tried to update EAT before retesting, but we speculate that this may have failed due to a change in the location of EAT packages (they moved from our private bolding-bruggeman channel to the public conda-forge channel).**

**In any case, we have updated both EAT and the example applications again for this new revision, mainly to improve the file and folder organization of the applications. The new release has again been extensively tested (https://github.com/BoldingBruggeman/eat-paper-applications/actions/runs/8939243820/job/24560968244), and we now also include a note in the application description stating which version of EAT is required (https://doi.org/10.5281/zenodo.10307315). This should ensure that such problems do not recur.**

**The update of EAT is reflected by the version increase in the ms title (now: v1.0.0).**

# specific comments (line numbers are based on the "tracked changes" version of the manuscript)

L 57 + 58: In DA lingo, 3D DA is often distinguished from 4D DA, where both use 3D models. Because this part of the manuscript is referring to DA applied to 3D models, no matter if 3D or 4D DA is used, I would recommend using "data assimilation systems based on 3D models", rather than the current "3D data assimilation systems", just to avoid confusion.

**Done**

L 199: Here a double dash "--" accidentally turned into an em dash "–".

**Corrected**

Fig 5: This looks nice and short for implementing something rather complex! Maybe mention that "before_analysis" is run just before each assimilation update (I presume).

**Added**

L 329: Why not mention the strong coupling in the second experiment as a contrast to the first experiment where the weak coupling is emphasized in the text?

**We have added "(strong coupling: assimilation is applied simultaneously to the full system state, with covariances between physical and biogeochemical components allowed to be non-zero)"**

L 335: "which applies log-transformation to all model variables": I presume only the biogeochemical variables are log-transformed, please make this explicit by either adding "biogeochemical", "physical and biogeochemical" or similar.
```

That is correct. As per the preceding sentence, "all *biogeochemical* variables were log-transformed". The subsequent sentence describes generic functionality of the plugin, which could in principle be applied to any selection of physical and/or biogeochemical variables. We now clarify this by stating "which applies log-transformation to a user-specified subset of model variables"

L 346: An early reference to Fig 2 might be useful here.

We have added "This was implemented using EAT's built-in support for ensemble generation (Fig 2)."

Fig 7: It might be confusing for new readers to have the same experiment described in 3 different ways in the same figure: "phys+bgc DA", "remotely sensed temperature and chlorophyll were assimilated", "both SST and chlorophyll were assimilated". I would suggest a more consistent description, which could also reduce the length of the caption.

Changed as suggested

L 569: "This is beyond the scope of EAT; the relevant parameters would need to be added to the depth-explicit model state within the biogeochemical model code.": While true, I would suggest reframing it slightly and simply mentioning that such a change would require modification to the code of the biogeochemical model.

We now write: "This can only be achieved by modifying the (Fortran) source code of the biogeochemical model in order to replace each affected (scalar) parameter by a spatially resolved state variable."