Point-by-point reply for manuscript gmd-2023-170

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Dear editors,

On behalf of all the coauthors, I thank you for the useful suggestions and for testing the code.
Please find below our point-by-point answers in italic.

Dear Authors,

Thank you for this revised submission addressing the concerns of the reviwers. From a wide perspective, a clear remark form the reviewers is that it is not customary to number versions of a mathematical algorithm. The rules of GMD refer to code versions.
In fact, the Zenodo repository contains the code named "Sword-Code/PythonDA: v1.1.0" not "GHOSH 1.0.0". So my suggestion is to make it clear that the version number refers to code versions. For example:

For Part 1
A novel Gauss-Hermite High-Order Sampling Hybrid ensemble filter for computationally efficient data assimilation in geosciences - Part 1: PythonDA: v1.1.0 (or GHOSH-Lorenz63 1.0.0, or any sutable name for the code)

For Part 2

A novel Gauss-Hermite High-Order Sampling Hybrid ensemble filter for computationally efficient data assimilation in geosciences - Part 2: OGSTM-BFM-GHOSH

Thank you for the comment. We changed the titles as you suggested.

More importantly, the original paper has beed split into 2 differnet parts but the submission is still unique. It think it would be better to keep only part 1 within the current process and initiate a separate sumbission for part 2. In the current state, with only one large pdf file, there is no mechanism within the Copernicus system to send both parts to different reviewers. The skill sets and interests of potential reviewers of both parts are different: on the mathematical underpinnings for Part 1 and on assimilation of satellite chlorophyll for part 2. I the current state, both papers (in one unique pdf file) need to be sent to the same of reviwewers. If you prefer to keep the current state, at least one additional reviewer for the chlorophyll application will be required.

Thank you for considering both options. We would like to keep the present state with one unique submission for both the papers and we understand the need of a new reviewer. We think that having both the manuscripts at hand is important for the reviewers. Moreover,

starting again the procedure with a different editor is something that we would like to avoid if possible.

Minor comments

please check for typos and language again, e.g.:

l82. all the possible second-order samplings correspond to a rotation of this tetrahedron > each possible second-order samplings correspond to a rotation of this tetrahedron or all the possible second-order samplings correspond to rotations of this tetrahedron

we changed: all the possible second-order samplings correspond to a rotation of this tetrahedron -> each possible second-order sampling corresponds to a rotation of this tetrahedron

l97. Gauss-Hermit -> Gauss-Hermite

Thanks for spotting the typo.

l123. "and so on and so forth." please rephrase more clearly/explicitly

We made small changes to the whole paragraph to clarify how system (1) works.

and others I may not have spotted.

We changed the suggested typos and language issue. In case of manuscript acceptance, we will further revise the text by submitting it to a language editing service.

Code documentation

please make explicit the dependencies (scipy, tabulate, etc.) so the user can run without error messages from the first attempt.

We added an "Installation" section in the README file. We divided the dependencies into mandatory (numpy and scipy) and recommended (tabulate and matplotlib). In case of missing recommended dependencies, the code can run, but plot() and table() methods are not available.

Otherwise the models run mostly nicely following the README file.

I only get an error message at the very end of the simple case:

>>> test.plot()
Traceback (most recent call last):
File "", line 1, in
File "/Users/ignacio/dev/PythonDA/DA.py", line 586, in plot
if ivar in obs.indices:
^^^^^^^^^^
AttributeError: 'Observation' object has no attribute 'indices'

Thanks, this happened after one of the final commits improving visualization. Now it works as intended.

also the multi_twin.py file gives the following error

impossible to load (error: [Errno 2] No such file or directory: 'Z.npz'). Starting from scratch.

but exeution finishes. I undrstand that Z needs to be calculated but it would be useful to have a warning message instead of an error.

In the current updated version no error message is shown. Instead, a printed message informs that a new file will be created.

Also an estimate of the remaining calculation time or the progress would be useful. At least you could indicate in the documentation how many times loger multiple takes with respect to simple.

Thanks for the useful suggestion. In the updated version of the code, a shown counter informs the user about the current simulation count and the total simulations needed.