

Response to Reviewer #2 (RC2, egusphere-2026-711)

We thank Reviewer #2 for the review and comments. Its scrutiny of the optimizer and of the model equations shaped the revision directly, and in one case it led us to reconsider the optimization method itself, as explained below. We are also glad that the study's motivation and its four-part structure came across clearly.

This reviewer asked why the search was stopped before the parameters stagnated (a point also raised in the technical corrections below), and following that question we ran systematic convergence tests. They showed that our genetic algorithm gave results that depended on the random seed: the best cost and the recovered parameters differed substantially from one run to the next. We therefore replaced it with CMA-ES (covariance matrix adaptation evolution strategy, Hansen and Ostermeier 2001), which reaches a lower cost with fewer model evaluations. CMA-ES stops on its own convergence criterion rather than a fixed iteration count (Fig. 7), and it reduces the dependence on the random seed. This lowers the risk that our identifiability conclusions reflect an instability of the optimizer rather than the information carried by the data, and it is the methodological basis of the revised manuscript.

Beyond this change of method, we have taken all of the reviewer's comments into account. The two main revisions are a rewritten Appendix A built around the McKendrick-Von Foerster aging equation, and a single consistent description of the CMA-ES optimizer that removes the ambiguous genetic-algorithm terminology (tournament, NSGA-II, evolutionary algorithm). Following the reviewer's request, we also state explicitly the variable the model computes, the zooplankton biomass, and its units. We reply to each comment below, grouping closely related ones. Section, figure, equation and table numbers refer to the revised manuscript.

General comments

I find the paper interesting and well written and found the motivation very clear to understand. Moreover, I appreciate the usage of several state-of-the-art python libraries, and also the clear structure of (i) numerical model evaluation, (ii) studying the influence of transport (or its missing), (iii) sensitivity analysis and (iv) parameter optimization.

Author response. We thank the reviewer for this positive assessment. The four-part structure is retained in the revision, now within fuller sections and a clearer narrative.

Specific comments

I miss a clear statement what quantity the model actually computes.

Author response. Section 2.2 now states that the model computes one variable, the zooplankton biomass B , and follows its time evolution in carbon mass per unit area (g C m^{-2}). The rewritten Appendix A defines the units of every state variable and flux, the biomass B in g C m^{-2} , the production field p and the recruitment flux R in $\text{g C m}^{-2} \text{d}^{-1}$.

Changes in the manuscript. Sect. 2.2 names the output variable, the zooplankton biomass, and its units. Units given for all state variables and fluxes in Appendix A.

There are symbols in the Appendices, I suggest to refer to them also earlier in the paper.

Author response. The main text now introduces the model's key quantities before the appendix. The new Sect. 2.1 describes the three biological processes of the mesozooplankton group, the energy intake as a fraction E of primary production, the aging of that production, its recruitment at a temperature-dependent recruitment age τ_r , and the mortality rate λ , with the steady-state relation $B_{eq} = R/\lambda$, each pointing forward to Appendix A. Table 1 lists the five parameters with their symbols and units and an "Eq." column giving the Appendix A equation in which each appears.

Changes in the manuscript. Sect. 2.1 introduces the key symbols with forward references to Appendix A. Table 1 gains an "Eq." column linking each parameter to its equation.

I would appreciate a little bit more details on the GA realization in Section 2.2. GAs are used by many people in quite different configurations, an explanation (e.g. of the term "tournament") would help. At some points the authors also use the term evolutionary algorithm, and in the discussion (line 295) they refer to CMAES, an evolutionary strategy, which works different. Specifically for readers not aware of these differences or relations I would prefer clarity here.

Author response. The optimization now uses CMA-ES throughout, so the genetic-algorithm machinery that prompted the question, tournament selection, NSGA-II settings and crossover, has been removed, and the manuscript no longer mixes the terms genetic algorithm, evolutionary algorithm and evolution strategy. Section 2.6 now describes CMA-ES in plain terms, a derivative-free method that adapts a multivariate normal search distribution to the local shape of the cost, with its standard settings (population size, initial step size, box-bound handling and convergence criteria). The framework still provides a genetic algorithm as one interchangeable optimizer, but it is not used in this study and is no longer described in detail.

Changes in the manuscript. Optimization rewritten around CMA-ES (Sect. 2.6). Genetic-algorithm terminology (tournament, NSGA-II, evolutionary algorithm) removed and replaced by a single consistent description of the CMA-ES optimizer.

The explanation of the model parts in Appendices 2 and 3 was difficult to understand to me. I would appreciate more details on the dependence on the age τ .

Author response. Appendix A has been rewritten with the age dependence made explicit. The production is the zooplankton produced from primary production before its recruitment into the biomass pool B . It is represented by the field $p(t, \tau)$, the production of age τ present at time t , which describes how the age structure of the production changes with time. Production enters at age zero as a fraction E of net primary production (the source, Eq. A5), ages at unit velocity while conserved, following the loss-free McKendrick-Von Foerster equation (Eq. A4), and is recruited into the biomass pool when it reaches the temperature-dependent recruitment age $\tau_r(t)$ (the absorbing boundary, Eqs. A6-A7). In the numerical solution, the age axis is discretized into daily classes. The production entering on a given day forms a cohort that advances by one class per day, so that at any time step an age class holds one cohort, the production of that age (Eqs. A8-A9).

Changes in the manuscript. Appendix A rewritten around the production field $p(t, \tau)$, with the age-zero source (Eq. A5), the McKendrick-Von Foerster aging equation (Eq. A4) and the recruitment boundary (Eqs. A6-A7) stated explicitly before the discrete scheme (Eqs. A8-A9).

To me it was not clear if the forcing was temperature and NPP only or additionally the euphotic layer depth. If the first is the case, I wonder why the authors use the spatial domain for computations. To me it would be also or even more reasonable to take the 2-D domain of occurring temperature and NPP values as computational domain, since the pure spatial location itself does not seem to have any influence then.

Author response. The forcing of SeapoPym is temperature and NPP only. The euphotic depth appears in two places that are not model forcings: in the description of the SEAPODYM-LMTL vertical layers (Sect. 2.1) and in the definition of the epipelagic layer over which the temperature is vertically averaged within the CMEMS product (Sect. 2.3). SeapoPym itself takes the layer-averaged temperature and NPP as its forcings.

On the computational domain, the reviewer is right that pure spatial location has no direct effect, since the output depends only on the local temperature and NPP forcing. That forcing is a time series, not a pair of values, and because the dynamics are time-dependent and age-structured, two cells with the same mean temperature and NPP produce different biomass. Sect. 2.2 now states this, and the model is therefore run at each grid point, which carries the full forcing time series, rather than over the reduced two-dimensional temperature-NPP space the reviewer suggests.

Changes in the manuscript. Sects. 2.2 and 2.3 clarify that SeapoPym is forced by temperature and NPP only and that the euphotic depth only sets the averaging layer. Sect. 2.2 states that the local forcing cannot be reduced to its mean, so the model is run at each grid point rather than over a reduced temperature-NPP space.

I wonder why the GA optimization was stopped before a stagnation in the parameters was reached.

Author response. With CMA-ES the search is no longer stopped at a fixed iteration count. It stops on the standard CMA-ES convergence criteria, when the step size and the spread of the cost fall below fixed tolerances, and a generation cap is kept only as a backstop that does not bind (Sect. 2.6). The convergence of each experiment is shown in Fig. 7 as the best-so-far cost against the number of model evaluations, so the reader can see the search running to stagnation.

Changes in the manuscript. Sect. 2.6 states the CMA-ES convergence criteria and that the generation cap does not bind. Fig. 7 shows the convergence of each experiment.

Technical corrections

line 11 abstract: at this point it might be not clear to what kind of "machine learning emulators" the authors are referring

Author response. The abstract no longer uses the terminology "machine learning emulators." The concept is introduced in the Discussion (Sect. 4), where a learned emulator is proposed as one route to reintroduce transport, a computationally expensive process, into the otherwise local model.

Changes in the manuscript. Phrase removed from the abstract. The learned-emulator idea is explained in the Discussion (Sect. 4).

line 65: "all data management (including I/O and intermediate states)" it is not clear what the authors mean by "intermediate states" here

Author response. The parenthetical has been removed, since it added no clarity.

Changes in the manuscript. "(including input/output and intermediate states)" removed (Sect. 2.2).

line 79: "traditional methods": I assume gradient methods are meant, but it is not clear at this point, to many people also GAs are "traditional", too

Author response. The ambiguous phrase "traditional methods" no longer appears. The motivation for a derivative-free global search is now made concrete in Sect. 2.6, where CMA-ES is described as a derivative-free method and the multiple restarts are said to guard against a single search stalling in a starting-point-dependent local optimum.

Changes in the manuscript. "traditional methods" removed. Motivation for the derivative-free optimizer stated concretely in Sect. 2.6.

*line 92: here the authors use the term "evolutionary algorithm" (EA). I suggest to stick to one term.
line 92: what do the authors mean by "orchestration"?*

Author response. Both terms are removed. The manuscript now uses a single, consistent description of the CMA-ES optimizer (Sect. 2.6) and no longer speaks of an "evolutionary algorithm." The vague "orchestration" has been removed, the framework being described plainly as independent, interchangeable components (model, observations, cost function, optimizer) coupled by a driver.

Changes in the manuscript. "evolutionary algorithm" and "orchestration" removed (Sects. 2.2 and 2.6).

line 95: here the authors state the forcings are temperature and NPP, in line 61 there also euphotic layer depth was mentioned.

Author response. The euphotic depth belongs to the SEAPODYM-LMTL layer description and to the averaging of the temperature within the product, not to the SeapoPym forcing, which is temperature and NPP.

Changes in the manuscript. See the forcing clarification above (Sects. 2.2 and 2.3).

line 124: typo: SI units are not to be written in italics

Author response. Corrected.

Changes in the manuscript. SI Units are not italics now.

line 151: "synthetic plot" please explain

Author response. We meant a summary figure. The phrase has been removed, and the Sobol sensitivity indices are now presented in Fig. 6.

Changes in the manuscript. The phrase "synthetic plot" has been removed and the sensitivity indices are shown in Fig. 6.

line 158: "stopping criterion": the authors are using a maximal number of iterations/generations of 20 [...] why not [use no-improvement stopping]? computational effort?

Author response. Same change as the parameter-stagnation comment above: CMA-ES stops on its convergence criteria, not a fixed generation count (Sect. 2.6, Fig. 7).

Changes in the manuscript. See Sect. 2.6 and Fig. 7 above.

line 345: I assume that the values T_{env} are the given forcing data here?

Author response. Yes. In the rewritten Appendix A, T_{env} is defined as the temperature forcing (Eq. A3), with the temperature entering the metabolic terms floored at the reference temperature, $T = \max(T_{\text{env}}, T_{\text{ref}})$.

Changes in the manuscript. T_{env} defined as the temperature forcing in Appendix A (Eq. A3).

Appendix A2 in general: this section is a bit difficult to understand: for somebody not familiar with the model the appearance and importance of τ is not explained, on the other hand: for people not familiar with the maths the derivation of the analytic solution in (A.7) is not clear. I did not consult the mentioned references, but I suggest to include some more explanations in here. (A.4) is not quite a standard PDE, so I think a little bit of discussion would help. line 365: "Assuming μ is integrable": μ is a step function depending on τ which depends on T_{env} . It may have many jumps, but will it ever become not integrable? line 365: "characteristic lines": in the meaning of characteristics of partial differential equations?

Author response. These appendix comments are addressed together by the rewrite of Appendix A. The aging of production is now stated directly as the loss-free McKendrick-Von Foerster transport equation (Eq. A4), named and cited, with its meaning explained in words, so the role of the age τ is explicit. The previous derivation along characteristic lines, together with the survival exponential $\exp(-\int_0^\tau \mu ds)$ and its integrability caveat, has been removed. Mortality acts only on the biomass pool B (Eqs. A1-A2), while the production field is loss-free until recruitment, so no integral of μ over age remains, and the question of its integrability no longer arises. For completeness, the reviewer is right that on the finite age interval $[0, \tau_r]$ the mortality is a bounded step function, and therefore always integrable however many jumps it has. Finally, the dependence of the recruitment flux on the production field is now explicit in the continuous equations, the recruitment being the production reaching the recruitment age, $R(t) = p(t, \tau_r(t))$ (Eq. A7), which feeds the biomass balance (Eq. A1). This is the continuous counterpart of the discrete recruitment sum in the numerical part.

Changes in the manuscript. Appendix A rewritten. Production aging stated as the McKendrick-Von Foerster equation (Eq. A4) with age dependence explained. Characteristic-line derivation, survival exponential and integrability caveat removed. Recruitment flux $R(t) = p(t, \tau_r(t))$ made explicit (Eq. A7) and linked to the biomass balance (Eq. A1) and to the discrete scheme (Eqs. A8-A9).

code availability: I appreciate the availability of the code. It might be usable as it is, but it is very difficult to understand, and it lacks comments, at least in the github version.

Author response. We are improving the code's inline documentation, its docstrings and comments, for the next release, which directly addresses the reviewer's point. The model repository includes installation instructions and a user manual, and the separate reproducibility repository accompanying the paper provides the notebooks, scripts and pinned software environment needed to reproduce every experiment and figure, which also serve as usage examples (both are listed in the Code Availability statement, with the versions archived on Zenodo). This reproducibility deposit was not available at the time of the first review.

Changes in the manuscript. None required in the text. The Code Availability statement already points to the installation instructions, the user manual and the reproducibility deposit. The code's inline documentation (docstrings and comments) is being improved in the next release.