

Interactive comment on “A coupled pelagic-benthic-sympagic biogeochemical model for the Bering Sea: documentation and validation of the BESTNPZ model (v2019.08.23) within a high-resolution regional ocean model” by Kelly Kearney et al.

Neil Banas (Referee)

neil.banas@strath.ac.uk

Received and published: 19 November 2019

GENERAL COMMENTS

This paper documents and evaluates a biophysical model of the Bering Sea, including not only the present state of the model code but incremental differences among the versions used in published studies. The stated purpose of the paper is to "reveals the model's strengths and weaknesses in reproducing historical patterns" (p.2), motivated

[Printer-friendly version](#)

[Discussion paper](#)



by the fact that “at least a dozen ongoing projects” (p.2) are relying on this model; the assessment also provides a “baseline to which further model improvements can be compared.” Model performance is quite variable, but the analysis and discussion are solid and presented in a pleasingly direct style. I think this paper will serve as useful documentation, and an important reference point as those dozen projects work out how best to use the model in an applied context.

There are a few places where the directness regarding the model’s limitations lapses, and some places where I think the comparison with phytoplankton and zooplankton observations could be, and deserve to be, made more complete—but overall I think the paper well deserves publication after revisions.

SPECIFIC COMMENTS

(1) Description of errors

The paper’s final statement “However, we caution that the use of the biological state variable output should be limited until the model is better able to capture observed characteristics of the Bering Sea phytoplankton and zooplankton communities” is fair and honest. Some equivalent warning belongs in the `_abstract_` as well: “ability. . . remains limited” is euphemistic in a way that most of this clear-eyed paper is not. (However, it would be fair and constructive to state the model limitations in positive form, as a recommendation for how best to make use of the model as it stands: e.g., “near-term application should focus on the use of physical model outputs rather than biological model outputs.”)

(2) Phytoplankton validation

p.17 l.2-7: I think this account of the bloom phenology, along with the phrase “nuances in spatiotemporal variability” in the next paragraph, underplay the complexity and potential importance of these patterns. Ecosystem effects of variation in bloom timing have been at the centre of conceptual pictures of the Eastern Bering Sea ever

[Printer-friendly version](#)[Discussion paper](#)

since Hunt et al. 2002. It would be straightforward and more helpful to the reader to summarise the patterns observed in both satellite data (Brown and Arrigo 2013) and mooring records (Sigler et al. 2014). Most notably, at M2, Sigler et al. show that the bloom date varied by about 70 days, April-June, between 1995-2011. It is fair to separate the mean seasonal cycle from interannual variability to discuss separately, but this history of observational and theoretical attention shouldn't be obscured.

Fig. 10, which shows major differences between modelled and satellite chlorophyll month by month, is well-described in the text. Likewise, the text gives a good account of both biases and agreements between modelled and moored chl at M2 (Fig. 11). I suppose the latter comparison is the support for the statement in the Abstract that the model is “able to capture the mean seasonal cycle of primary production observed on the data-rich eastern middle shelf.” This is not completely unfair, but it is a stretch. I think a more precise statement in terms of timing/magnitude/composition would be better.

It is also worth considering to what extent data limitations and not model limitations are responsible for blurring this picture. How does the mean of the annual-max mooring chl compare with the annual max of the composited mooring chl? Because of the huge variance in bloom timing, they might be quite different. Likewise, it would be interesting to superimpose a satellite time series from M2 on the model and mooring records in Fig 11c: if the observational records disagree on bloom timing, then there is an inherent level of fuzziness that one would expect from a data-model comparison.

(3) Zooplankton biomass

I think there are missed opportunities here for comparison of the model with zooplankton data. The summary of typical biomass numbers by functional group in Sec 3.3 is very helpful, but I notice it doesn't contain any references to the observational work during BEST-BSIERP itself, which might provide more definite points of comparison. For example, Campbell et al. 2016 (Deep-Sea Research 134:157–172) in Table 6 give

[Printer-friendly version](#)[Discussion paper](#)

mesozooplankton biomass by region/season/year, as well as comparisons with integrated phytoplankton biomass and estimated grazing rates in relation to primary productivity—such that the relation of zooplankton to phytoplankton could be assessed in either absolute, relative, or functional terms. Stoecker et al. 2013 (Deep Sea Res 109:134-44) gives similar numbers for microzooplankton.

As best I can tell from a quick comparison, the overall biomass of microzooplankton in the model is on the right order, but the large-zooplankton biomass in reality is orders of magnitude larger than the micro-, not comparable or smaller as in the model. The authors give 10 g C/m^2 as a typical large-zooplankton biomass in Sec 3.3, and from Campbell et al. 2016 Table 6, I would have said $1\text{--}2 \text{ g C/m}^2$ —this difference is not the important one—whereas the model seems to have large zooplankton on the order of 0.01 g C/m^2 , unless I'm misunderstanding Fig. 12. A biomass bias on that scale raises questions about the overall role the zooplankton play in nutrient and phyto-biomass budgets, in the model and in reality. A careful look at the grazing rate parameters might be a good place to start: again, with the BEST/BSIERP observational papers mentioned above, along with others by Stoecker et al. and Sherr et al., as concrete guidance. (I went through this exercise in Banas et al. 2016 (J Geophys Res, 10.1002/2015JC011449) and concluded that microzooplankton max specific grazing was an order of magnitude higher than the value reported in Table A7.) General reviews like Hansen et al. 1997 (Limnol Oceaogr 42:687:704) and Kiorboe and Hirst 2014 (American Naturalist 183, 10.1086/675241) might be a simpler way to get at the same issues.

(4) Design strategies and parameter comparisons

Sec 5 includes a discerning discussion of the design limitations and parameterisation issues that could be degrading the biogeochemical performance of the model. I think the authors have chosen a good set of issues to highlight, such as the approach to ice algae, the photophysiology (p. 24), and the over-resolution of the large zooplankton boxes, especially given the inherent limitations of a stock-flux framework compared

[Printer-friendly version](#)[Discussion paper](#)

with life-stage-resolving models (p. 25). But what are the next steps in model development? Are there design/parameterisation strategies the authors are planning to take, or already taking, or feel are worth mentioning more generally as good possibilities in these sorts of situations?

In this context I think it's worth pointing out that the authors haven't cited any of the other Bering Sea plankton modelling efforts in the literature, but could: not to turn this into a model intercomparison project and certainly not a competition, but to highlight other design, parameterisation, and validation strategies that could have benefits for the future of the BESTNPZ effort. Maybe the Bering Sea modelling literature is too narrow, and it's subpolar/polar plankton modelling in general that deserves some mining. In the Bering Sea, I can think of two recent and one older NPZ models with independent lineages and pretty good agreement with plankton observations: (1) Jin et al., *Geophys Res Lett* 34:L06612, 2007; (2) Zhang et al., *Deep Sea Res* 118:122-135, 2018 (emphasis on Chukchi blooms but unpublished analysis shows it does quite well against against satellite chl in the Bering Sea too); and (3) my own model, Banas et al. 2016 (reference above), further developed by Sloughter et al., *J Mar Sys* 191:64-75, 2019 through photophysiology process data from BEST/BSIERP. Likewise, there are at least two published Calanus life-history models for the Bering Sea with independent lineages: (4) Coyle and Gibson, *J Plankt Res* 39:257-270, 2017, and (5) my own, Banas et al., *Front Mar Res*, 10.3389/fmars.2016.00225, 2016.

I don't mean to push the authors toward intercomparisons or competitions, but the processes we have all concluded we need to attend to are very, very similar. Zhang et al focus on ice algae and under-ice growth conditions, Sloughter et al. focus on photoparameters and bloom timing, and the Calanus IBMs in the Bering Sea focus on (and perhaps disagree on) the constraints on over-winter survival—and these are exactly the issues that the authors of this study highlight as crucial to the performance of BESTNPZ. So I would be surprised if there was nothing to learn or comment on from digging a bit into the similarities and differences among these models and their

[Printer-friendly version](#)[Discussion paper](#)

parameter values.

MINOR COMMENTS

p.3 “of the larger Northeast Pacific (NEP5) domain” -> “of a larger-domain ROMS model of the Northeast Pacific (NEP5)”

p.16, l.14-17: The tidally averaged currents may be much smaller than tidal velocities, but still crucially important to lateral nutrient supply and the distribution of biomass. A more quantitative comparison with the transport patterns synthesized by Stabeno et al. 2016 (e.g. Fig 12 in that study vs fig 9 in this one: Deep-Sea Research 134:13–29) would be helpful.

Table A7: could the feeding preferences be placed in their own table as a matrix? They would be much easier to read that way.

Interactive comment on Geosci. Model Dev. Discuss., <https://doi.org/10.5194/gmd-2019-239>, 2019.

Printer-friendly version

Discussion paper

