On the example of the North and Baltic Sea, the authors present a very simple way to extend a lower trophic level model (marine biogeochemistry) to an end-to-end model. Two state variables have to be added, both of them two-dimensional (only horizontally resolved). These are the biomasses of fish and macrozoobenthos.

Since these two "upper trophic levels" influence especially the mortality of zooplankton, the result is a spatially heterogenous mortality which replaces the previously uniform closure term of the LTL model. A comparison to a study for the North Sea where fish predation mortality is estimated from observed distributions of planktivorous fish shows, as the authors state, that the correct spatial patterns emerge. In this way, the model outlines a rather simple way to include, to a first order, higher trophic level effects onto the lower trophic food web. Compared to the previous study, this approach has much lower data requirements, which is an advantage not pointed out well enough.

When it comes to overall model performance, the authors could show a slight benefit when adding the two state variables as they compare lower trophic level variables such as nutrient concentrations and oxygen. At least for the North Sea, the authors could also show that fish and macrozoobenthos spatial patterns were similar to observations.

From my point of view, the largest benefit of the model is the opportunity to gain more realistic zooplankton mortality values. I would like this point to be more highlighted. Especially I would like to see the spatial patterns of zooplankton mortality as they emerge from this model compared to those of Maar et al. (2014). Contrary to what the authors state in the caption of Fig. 9, fish production is not a suitable indicator for zooplankton predation mortality, but only the ratio between fish production and zooplankton biomass gives the predation mortality. The comparison should be done to Fig. 10C+D in Maar et al., not to Fig. 4, and it would be very useful if the comparison was shown in this article.

The discussion and conclusions sound reasonable to me, I would support them. The only exception is that I would not present total fish biomass as a model result, since it might be quite sensitive to the feeding efficiency which is poorly confined for the "average fish" I guess? I would rather interpret fish biomass as a tuning parameter which you have to fit to ensure that the ratio between predation mortality and background mortality is reasonable. In this way, quite simple measured quantities like total fish biomass and fishing mortality can be used to confine the zooplankton mortality, which was an arbitrary closure term before your extension.

General remarks:

1.) You say you can interpret the fish functional group as a "fish production potential". In principle it is clear what you mean: Where there is food, there will be fish who eat it. You are not interested in where they will migrate afterwards, but you keep the fish biomass locally as a kind of bookkeeping of what the fish consumed here. However, see a few issues with this interpretation:
   - Zooplankton or macrobenthos will not be consumed if the fish just "potentially" grow. So, the loss terms for these functional groups contradict this interpretation.
   - Consumption of food by fish is limited by local fish biomass in the model. A "fish production potential" in reality could be larger, since fish from remote locations could migrate towards a spot of high prey abundance, which might lead to more efficient food consumption.

   I would like a clearer discussion of why neither of the two interpretations (fish biomass / fish production potential) is entirely correct.

2.) Your extension has a very low computational cost. Not only is it just two state variables that are added, but also these are 2-d only which saves their advection, and the advection of the state variables is the most time consuming step. So your extension is especially suitable for LTL models which are simple by purpose, e.g. because they are used in long-term climate simulations where computational load is critical. You could highlight that even more.

3.) You mix up British and American English, e.g. P1L20: "analysed", P1L24: "summarizes". Please be consistent.

4.) Also, please be consistent with "3d" vs. "3-d" / "end-to-end" vs. "End-to-End".

5.) Please capitalise "Figure 4" etc.

6.) Commas are often missing in sentences which do not start with the subject, please add them.

Specific comments:

P1L20: "the observed pattern" -> "the observed patterns"?

P1L26: "pattern agree" -> "patterns agree"?

P2L10: "The differentiation of trophic levels" -> hard to understand what exactly you mean, can you rephrase?

P2L11: Citation missing in reference list.

P2L26: Please explain "foodweb models" as opposed to end-2-end models

P2L31: "based on environmental condition" -> "based on environmental conditions"?

P2L31: "excluded" -> "excludes"?

P3L25: "relative low" -> "relatively low"?

P4L16-17: This is not a complete sentence.

P4L21-22: Please cite Neumann and Schernewski (2008) who invented this approach in the model world.

P5L2-3: "with additional restriction as" -> "with the additional restriction that"?

P5L8,10: Please use different symbols for the velocity vector and its vertical component.

P5L10: A_v needs italics here. Actually, italics are missing a few times in this section when variables appear in the text. Please check.

P5L15: "RC" needs formatting.

P5L25: "the MB menu" -> "the MB diet"?

P6L2: I suggest the use of X' instead of X to make clear it has nothing to do with the X in line 1.

P6L29: To be precise, the vertical integral of equation 1 reduces to the equation given in the text. Equation 1 itself would still keep a vertical migration term $(C w_m(z))_z$, even if the vertical migration velocity $w_m(z)$ is only known implicitly.

P7L13: Does this consumption even occur in anoxic layers?

P7L14: There is no respiration of fish in the model? You rather treat fish respiration as an excretion and subsequent detritus mineralisation? Could you state this explicitly?

P7L20: In your formulation, TK is always equal to 1/273.15 because T/T cancels out. This is certainly not correct.

P7L28-29: Which food web did the study consider? I assume this value differs a lot between different seas/regions.

P7L31: "is considerable higher" -> "is considerably higher with"?

P7L31: Please state more explicitly that intraguild predation in zooplankton does not need to be represented in the model since it is not stage-resolving.

P8L21-27: Could you add a reference to the hydrodynamic model you used and the atmospheric forcing dataset?

P9L2: "at each of the location" -> "at each location" / "at each of the locations"?

P9L9: "on" -> "onto"

P10L6: "equals" -> "equals to"

P13L9: "concrete" -> "actual"?

P13L12: "relative small" -> "relatively small"?

P13L11-13: Could you give relative values (in % of average mass)?

P13L15: A minimum never falls, does it? A function of time falls until it reaches the minimum.

P13L30-31: Macrozoobenthos and fish can feed on their own excretions, since the energy contained in the carbon is not considered, correct? Also, there is no MB or fish respiration in the model which would convert the organic carbon to DIC. So, there can be an infinite loop in the model where MB feeds and excretes, feeds and excretes, with no need to add energy from primary production. In Section 4 where you discuss future model improvements, could you comment on how to prevent this? I see, besides the way of explicitly defining "nutritional value classes" in detritus, the possibility to limit detritus consumption to ensure that at least a specific percentage of the total diet is fresh (non-detrital) material.

P13L33: This is because the North Sea is a tidal sea, correct? I would consider it as helpful for the non-European readers to state this difference here.

P13L33: "Zooplankton and Phytoplankton is included" -> "Zooplankton and phytoplankton are included"?

P15L5: "zooplankton form" -> "zooplankton forms"?

P16L6-9: I would consider this as the main benefit of your model: You can obtain reasonable spatial patterns in zooplankton mortality without requiring data on planktivorous fish abundance. I would point this out already in the abstract and see it as the main point why your approach should be used.

P16L12-16: Couldn't you split your model fish into pelagic and demersal "feeding groups" based on their diet-dependent vertical distribution and then compare the spatial patterns?

P16L25: What is zero at which boundary?

P17L8: "fish and MB is resolved" -> "are resolved"?

P17L12: "for e.g." -> "e.g.", P18L31: the same