1 Mayor comments

Reviewer Comment

1) While I recognize that this is a complex model and study design, the manuscript is on the long end, and there may be opportunities to streamline the text (particularly in 2.2-2.7) to avoid repetition and allow the core messages to come through more clearly. The authors could consider using a Supplemental Information Section to present some details of the model assumptions and parameterization, as well as for some supporting figures (e.g., Figure 12). In addition, the manuscript would benefit from additional review for typos and readability. Some have been flagged below in minor comments.

Author Response

Thank you for your insights. I suggest that I move the model specifics such as the exact parameterization to the supplementary section. I suggest that I move Table 2 and Table 3 to the supplement. It is essential to show the exact parameterization used, but the large tables distract from the core message of the paper. Lastly, I suggest moving Figures 4, 5, and 6 to the supplement. I think it is good to show the seasonal progression of the bioaccumulation in all setups, but moving it to the supplement would allow an interested reader to verify the seasonal progression of the bioaccumulation while not distracting from the core message of the paper, especially since we have no seasonal data to verify against. Additionally, as you suggested, I would move Fig. 12 to the supplement. The results shown in Fig. 12 are interesting and help contextualize the air-sea exchange, but they are indeed not a core part of the message. Putting that in the supplement will mean it does not distract and bloat the paper. The tables and figures below I would suggest moving to the supplement:

Table 2. Dimensions, shape, and maximum growth and mortality rates of most common phytoplankton species in the North and Baltic Seas, to resemble ECOSMO E2E functional groups and the conversion ratio of mg C to cm^2 cell membrane and dm^3 cell volume. The dimensions and shapes are based on Olenina et al. (2003). For the Cylinder they are radius and height, for the sphere and hemisphere - the radius. The maximum growth rate and the mortality are based on Daewel et al. (2019).

Group	Species	Shape	Dimensions (μm)	μ_{max} (d^{-1})	Mortality (d^{-1})
Diatoms	*T. baltica*	Cylinder	12.5 x 25	1.4	0.04
Flagellate	*P. Catanata*	Hemisphere	6	1.2	0.04
Cyanobacteria	*A. flos-aquae*	Sphere	4	1.0	0.08

Table 3. The parameterization of consumers. The preference and consumption rate (r_{cons}) determine how much of each prey is consumed, the assimilation efficiency (AE) how much of the consumed carbon is assimilated into the predator; the mortality (r_{mort}) and respiration (r_{resp}) rate determine the total loss. Adjustments were made for higher trophic levels compared to Daewel et al. (2019) to enhance the model's suitability for bioaccumulation. Specifically, the AE and grazing rate were lowered. Additionally, fish 2 was introduced as a top predator with modified parameters. It has a higher preference for macrobenthos and consumes fish 1 rather than microzooplankton. As a top predator, fish 2 has a lower AE and consumption rate compared to fish 1. All other rates and equations remain consistent with the ECOSMO E2E model (Daewel et al., 2019).

Group	Prey	Preference (1)	r_{cons} (d^{-1})	AE (1)	r_{mort} (d^{-1})	r_{resp} (d^{-1})
Microzooplankton	Diatom	0.25	0.8	0.75	0.05	0.02
	Flagellates	0.70	0.8	0.75		
	Cyanobacteria	0.30	0.3	0.75		
	Detritus	0.10	0.8	0.8		
Mesozooplankton	Diatom	0.85	0.7	0.6	0.025	0.015
	Flagellates	0.10	0.7	0.6		
	Cyanobacteria	0.30	0.3	0.6		
	Microzooplankton	0.15	0.8	0.6		
	Detritus	0.10	0.7	0.6		
Macrobenthos	Phytoplankton	0.2	0.1	0.6	0.01	0.001
	Zooplankton	0.2	0.2	0.6		
	Sediment	0.15	0.15	0.6		
	Detritus	0.15	0.15	0.6		
	DOM	0.15	0.1	0.6		
Fish 1	Microzooplankton	0.45	0.015	0.5	0.001	0.002
	Mesozooplankton	0.45	0.015	0.5		
	Macrobenthos	0.05	0.015	0.5		
	Detritus	0.05	0.0125	0.5		
Fish 2	Mesozooplankton	0.25	0.012	0.45	0.001	0.002
	Fish 1	0.25	0.012	0.45		
	Macrobenthos	0.45	0.013	0.45		
	Detritus	0.05	0.001	0.45		

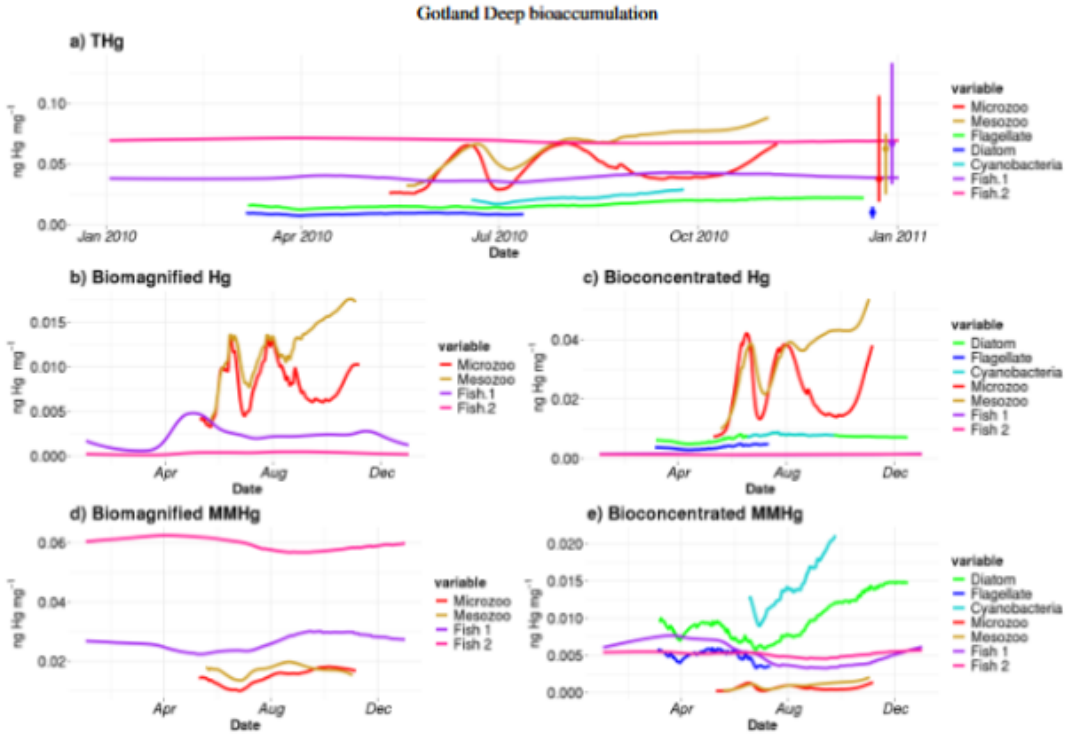


Figure 4. Hg accumulation in the Gotland Deep during the last simulation year (Jan 2010-Jan 2011). Plot 4a shows tHg bioaccumulation with mean and range of observations from Nfon et al. (2009) represented by the point and vertical bar on the right side of the plot. Bioaccumulation is displayed when biomass of the respecitive funtional group exceeds 0.1 gC m^{-2}. tHg bioaccumulation is highest in fish 2, followed by fish 1, microzooplankton, mesozooplankton, cyanobacteria, flagellates, and diatoms with tHg concentrations in observed ranges. The consecutive Fig. show the bioamagnification (4b, 4d) and bioconcentration (4c, 4e) of Hg^{2+} (4b, 4c) and $MMHg^{+}$ (4d, 4e). Biomagnified Hg^{2+} is highest in microzooplankton, followed by mesozooplankton and fish, while biomagnified $MMHg^{+}$ increases notable in fish 1 and fish 2. Bioconcentrated Hg^{2+} is very low in fish and highest in zooplankton. Bioconcentrated $MMHg^{+}$ is notable higher in cyanobacteria than in all biota and lowest zooplankton.

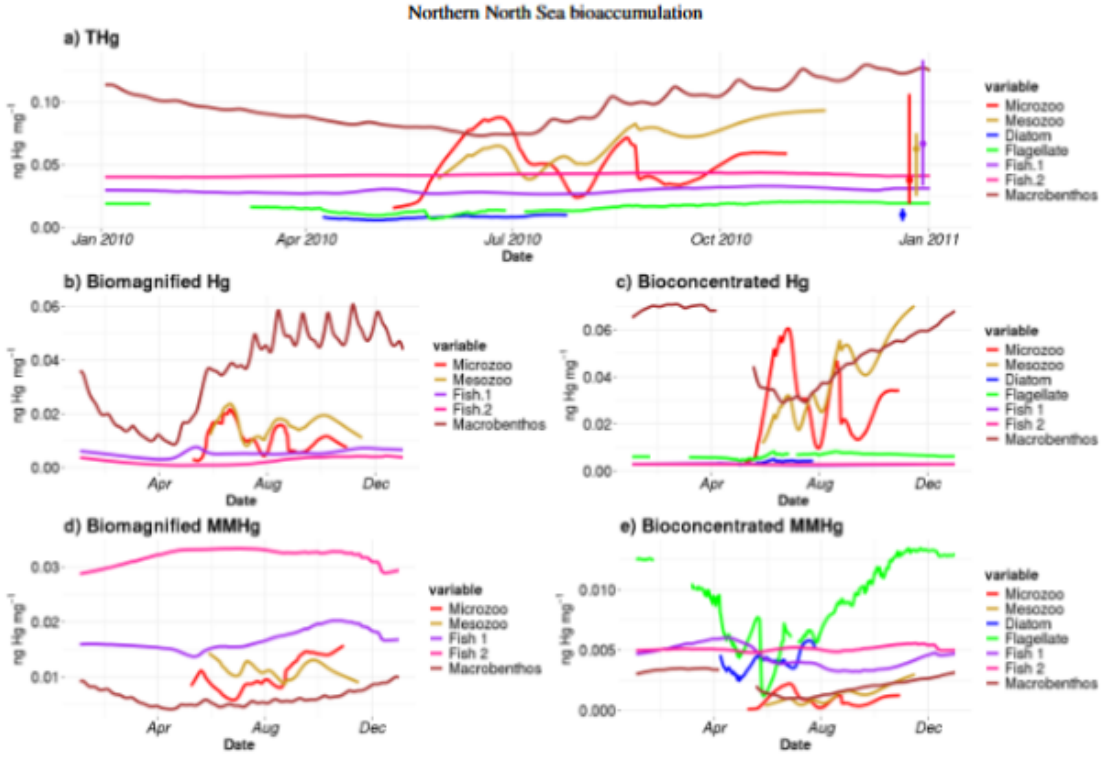
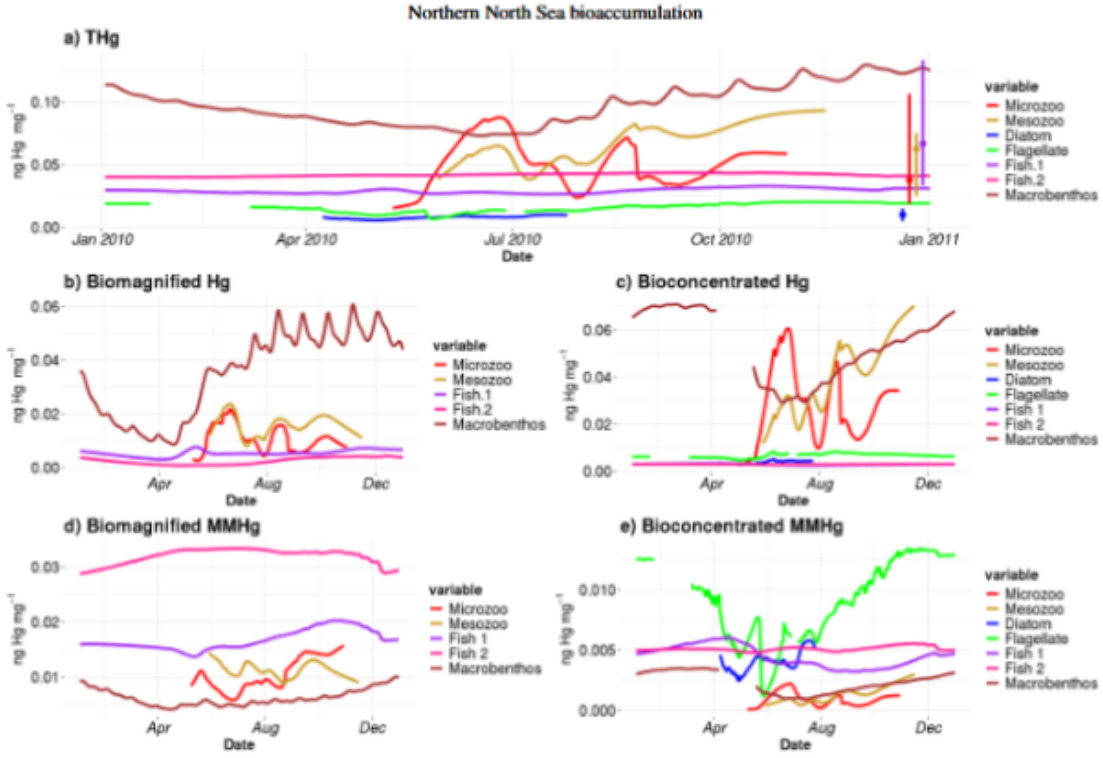


Figure 5. Hg bioaccumulation in the Northern North Sea. Plot 5a shows the tHg bioaccumulation in the Northern North Sea. Phytoplankton and zooplankton are shown if their average biomass is more than 0.1 gC m^{-2}. Phytoplankton has the lowest tHg, which is followed by fish 1, fish 2, mesozooplankton and macrobenthos. Plots 5 b-e show the origin (Biomagnification or Bioconcentration) and species (Hg^{2+} or $MMHg^{+}$) of the bioaccumulated tHg. Figure 5b and 5c show that the high tHg in microzooplankton, mesozooplankton and macrobenthos is due to high levels of Hg^{2+} bioconcentration and biomagnification. $MMHg^{+}$ Biomagnification follows a pattern in which it is lower in zooplankton and macrobenthos, higher in fish 1, and highest in fish 2. This means that while fish 2 has a lower Hg content than macrobenthos and zooplankton for part of the year, $MMHg^{+}$ is higher in fish than in zooplankton and macrobenthos. Figure 5e shows the bioconcentration of $MMHg^{+}$ and shows that this is highest in phytoplankton, followed by fish 1 and 2, macrobenthos, and zooplankton.



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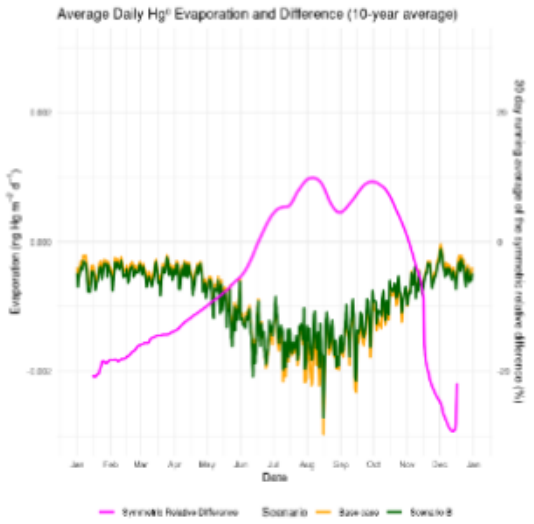

Figure 12. The 10-year average daily atmospheric exchange of Hg0 between the atmosphere and the sea surface in the base case and scenario c (no bioaccumulation nor biogenic reduction).

Reviewer Comment

2) It could be helpful to provide a brief summary of the drivers of spatial and temporal variation in the results, as some of these details may be contained in the cited original model papers and therefore less clear to a reader. For example, for seasonality: to what extent is temperature dependence also considered in the bioaccumulation and toxicokinetic modeling, in addition to biomass modeling? For spatial variation: What determines the spatial distribution of higher trophic levels? Is migration relevant and, if so, how is it considered? If not, what additional implications could this have for the spatial dynamics?

Author Response

Thank you for your comment. I will expand on this in several ways. I will first discuss in the Mercy and Ecosmo sections respectively what spatial and temperaol drivers control biomass and Hg speciation and then add a segment to the discussion. In section 2.2.3 I would suggest to add:

Suggested edit

In the MERCY V2.0 model, several drivers are incorporated to model the spatial temporal variability of Hg speciation. All Hg species are treated as tracer variables and thus moved with the movement of water. Light is used to estimate the photolytic reduction rate (Hg^0 + photon $\rightarrow$ Hg^{2+}), the photolytic oxidation rate (Hg^{2+} + photon $\rightarrow$ Hg^0), and photolythic demethylation ($MMHg^+$ + photon $\rightarrow$ Hg^{2+}, DMHg + photon $\rightarrow$ Hg^{2+}, and DMHg + photon $\rightarrow$ $MMHg^+$). Temperature is used to estimate the temperature dependent dark reduction of Hg^{2+} ($Hg^{2+} \rightarrow Hg^0$). Furthermore, the air-sea exchange of Hg in the MERCY V2.0 model is based on the approach used in Kuss (2014) and Kuss et al. (2009), which uses the temperature and salinity dependent Henry's law to estimate the equilibrium between atmospheric and marine Hg^0 concentrations and a wind-speed-dependent transfer rate.

Author Response

In the ECOSMO E2E section, I would suggest to add:

Suggested edit

The ECOSMO E2E and the MERCY V2.0 model interact in multiple ways. First, light absorption by phytoplankton, detritus, and DOM decreases available light, affecting light-dependent Hg speciation and photosynthesis in deeper water. Ecosystem variables are treated as tracers and move with water flow, with the exception of fish 1 and fish 2, which both have no movement. Thus, if water currents carry biological variables, they also transport bioaccumulated Hg. Detritus is the only biological component with intrinsic movement, sinking at 5 m d^{-1}.

Author Response

In the discussion section I would add:

Suggested edit

Model limitations

Movement of higher trophic level

In our model, phytoplankton and zooplankton are treated as tracers without implicit movement, while fish has no movement at all. This means that, plankton and its bioaccumulated Hg^{2+} and $MMHg^{+}$, is transported by currents but do not move themselves while fish remains stationary. For most biological variables, this implementation is a reasonable simplification. However, in the case of fish, it might influence the model results. Moving fish could transport Hg; if fish move around, they could accumulate Hg in areas with high Hg while releasing it in areas with lower Hg, thus spreading the Hg around. Implementing migration for fish provides an interesting direction for further model development, but in the current implementation it would likely not cause major differences. This is because migration would only be relevant to implement in the 3D setup, but this setup is focussed on plankton and only includes mid trophic levels of fish, which are less migratory than larger higher trophic level species.

Reduced complexity in detritus-Hg interactions

Another limitation in the model is the limited complexity of the detritus-Hg interactions. In our model, there is only one functional group for detritus. When biota die, they instantly release all bioaccumulated Hg^{2+} and $MMHg^{+}$, which is then in constant equilibrium with the detritus. The sinking rate of detritus bound Hg is estimated based on how much Hg is bound to detritus on a given time step. This approach is a reasonable simplification for small biota, such as phytoplankton and microzooplankton. But it introduces two limitations in higher trophic levels. First of all, if a larger animal such as fish dies and sinks, it might transport some of its bioaccumulated Hg with the carcass. That is not accounted for in the model. Additionally, the equilibrium between detritus bound and dissolved Hg is based on small particulate organic carbon, as this is the most common form of detritus in marine water. But in the model, predators consumes detritus, and the detritus consumed by higher trophic level predators would mostly be larger particles that could have different Hg binding characteristics.

Limitations in the modeled ecosystem complexity

As discussed when analyzing the modeled and observed trophic levels, the ecosystem model uses a functional group approach to constrain the complexity of the ecosystem. This does, however, introduce limitations in the model's ability to model bioaccumulation. Several animals might be classified under the same functional group while affecting Hg dynamics in different ways. An example is the observations that some Baltic Sea zooplankton can have *in vivo* Hg speciation (Gorokhova et al., 2020). Increasing the modeled ecosystem complexity could improve the model performance by accounting for these differences.

Physical drivers of bioaccumulation

In the current paramatizaterion physical drivers such as temperature and light influence the biomass and the Hg speciation, but the bioaccumulation is purely based on the concentration of bioaccumulative Hg species, a biota functional group specific bioaccumulation rate, and the biomass of the biotic functional group. The only temperature dependent driver direclty influencing bioaccumulation is the temperature dependent respiration rate

of fish. As the temperature increases, so does the respiration rate of fish and consequently they release Hg faster, as this is coupled to their respiration rate. As shown by Garcia-Arevalo et al. (2024) the bioaccumulation of $MMHg^+$ in phytoplankton is also dependent on cell dependent drivers, such as the availability of membrane transport channels. These cell dependent drivers might be different during different stages of the phytoplankton bloom due to altering species composition or the physiological state of phytoplankton. While these changes could not be incorporated in our current model due to lack of our understanding of nuanced drivers of bioaccumultion, seasonal changes could influence bioaccumulation at every trophic level.

Reviewer Comment

3) See below for some places where clarification of some methodological details could be beneficial, potentially in supporting material (e.g., in model-obs comparison for 1D, initial conditions).

Reviewer Comment

4) The authors may have the opportunity to deepen the reflection on next steps and future directions, given the importance of the call to better represent ecosystem effects in models. Some questions I am particularly curious to get their thoughts on are: a) is model coupling the only way to do this, is it reasonable to do a back-of-the-envelope adjustment factor that is regionally specific; b) how much trophodynamic complexity is needed — does capturing the base of the food web get most of the effect or do fish 1 and 2 shift the patterns; if so, what might be missing in this current simplified representation of the ecosystem

Author Response

I would suggest that I add the following part to the discussion segment:

Suggested edit

The required ecosystem complexity to capture Hg dynamics

As discussed, a main conclusion of this paper is showing that the ecosystem is an integral part of Hg cycling, and that this should not be overlooked. However, there is nuance in how the ecosystem should be implemented in Hg cycling models, and there is a trade-off between keeping the model simple and ensuring key drivers are implemented.

High trophic levels as a reservoir of $MMHg^+$

In most marine ecosystems, the annual average biomass of primary producers is relatively low; rather, there is a very high turnover rate of primary producers during the bloom period. While the exact numbers vary depending on the location and seasonality, high trophic levels can make up a major component of the total ecosystem biomass, especially in winter (Bar-On et al., 2018). As high trophic levels have the most $MMHg^+$ per biomass, they can form a major reservoir of $MMHg^+$. Our model, however, shows that this does not have a major effect on the tHg concentration. This indicates that the inclusion of high trophic levels such as fish might be necessary to correctly estimate the $MMHg^+$ budget, but the inclusion of fish is not necessary to correctly model tHg fluxes. One point of uncertainty here is that this conclusion is based on our implementation of the ecosystem.

As discussed in the model limitation segment, several drivers, such as fish migration and the transport of Hg to deep water by sinking carcasses, are not accounted for, and these drivers could still prove to be an essential component of Hg cycling.

Benthic-pelagic coupling

A key component where the ecosystem is essential for a correct understanding of Hg cycling is the Benthic-pelagic coupling. In coastal areas, the consumption of pelagic detritus and Hg bound to it by macrobenthos can be a major flux of organic carbon from the pelagic to the benthic system (Griffiths et al., 2017). The sediment is identified as a key area for Hg methylation; this increased transport of Hg^{2+} from the pelagic to the benthic due to biotic consumption of detritus would constitute a source of $MMHg^{+}$ (Helmrich et al., 2022). Of course, in some areas, sediment is not resuspended, and then increased transport of Hg to the sediment can result in additional burial of Hg. As the macrobenthic influence on the benthic-pelagic coupling are spatially and temporally variable this cannot be accounted for by basic estimation. Rather, the inclusion of a realistic benthic-pelagic coupling is essential for Hg speciation models in coastal areas.

Key species for Hg cycling

In important aspect of estimating the role of the ecosystem in Hg cycling is understanding that not every species affects Hg cycling in a similar way. The clearest of the ecosystem interactions with Hg cycling is the removal of Hg by biota when biomass is high and the release when biomass is low. This is extensively analyzed in this study. However, several species might have an unexpectedly high impact on Hg cycling. The first example of this, which is also evaluated in this paper, is Baltic Sea cyanobacteria, which can facilitate biogenic reduction. But beyond this, it is demonstrated that some species of zooplankton and cephalopods can have *in vivo* Hg speciation (Gente et al., 2023; Gorokhova et al., 2020), and that bioaccumulation is extremely sensitive to *in vivo* Hg speciation (Li et al., 2022). Another example is that sponges are demonstrated to have very high inorganic Hg levels, suggesting an important role in the benthic-pelagic coupling (Orani et al., 2020). Identifying such key species and their effect on the Hg cycle is essential to understand there rol in the Hg cycle and if there implementation in models is needed.

2 Detailed comments

Reviewer Comment

L22: Number of parties now exceeds the number of signatories (over 150), so could update the number https://minamataconvention.org/en/parties

Author Response

The link provided still states that indeed has 152 parties. I suggest to update the statement as below to show both:

Suggested edit

Due to the consumption of polluted marine wildlife, more than 1000 people died, and more were permanently disabled (Harada, 1995). Efforts to control Hg emissions culminated in the Minamata Convention on Mercury, which is a pledge to reduce Hg emissions(Outridge

et al., 2018). It has 152 parties and is currently signed by 128 countries.

Reviewer Comment

L52: "In summary, there are three fractions... in our model." Read as confusing as the model hasn't been introduced yet.

Author Response

I agree that this is incorrect to refer to this in the model before the model is introduced. I also think the rest of the alinea could be clearer. I would suggest rewriting it as:

Suggested edit

Under anoxic conditions, Hg^{2+} binds with S^{2-} to form cinnabar (HgS), which is considered a sink due to its low solubility (Oliveri et al., 2016). In seawater, the abundance of chloride ions causes Hg^{2+} and $MMHg^{+}$ to exist mainly in the form of inorganic chlorine complexes. The neutral forms of these complexes, $HgCl_2$ and MMHgCl, are lipophilic and can diffuse through cell membranes or bind to organic material (Zhong & Wang, 2009). The speciation of Hg with organic carbon in the marine ecosystem, such as detritus and DOM, is a complex interaction that can influence the speciation, solubility, mobility, membrane permeability, and toxicity of Hg (Ravichandran, 2004). In this study, we refer to three distinct fractions of both inorganic Hg and MMHg: 1) dissolved species not bound to organic material, including species such as $HgCl_2$ and MMHgCl, collectively referred to as Hg^{2+} and $MMHg^{+}$, 2) Hg and MMHg bound to dissolved organic matter (DOM), referred to as Hg-DOM and MMHg-DOM, and Hg and MMHg bound to detritus, referred to as Hg-detritus and MMHg-detritus.

Reviewer Comment

L137: As defined in the first sentence, isn't this bioconcentration only?

Author Response

That is indeed badly phrased. I would suggest that I correct it to:

Suggested edit

Bioaccumulation is the increase in Hg^{2+} or $MMHg^{+}$ in the biota relative to the concentration of the surrounding water.

Reviewer Comment

Fig. 1: Typos in title and Scenario C. Could consider overlaying the 1-D vs 3-D component too so that it captures that aspect of the design as well. Could incorporate a map of locations as a side panel for the global audience.

Author Response

I would update the image to the updated images shown in 1

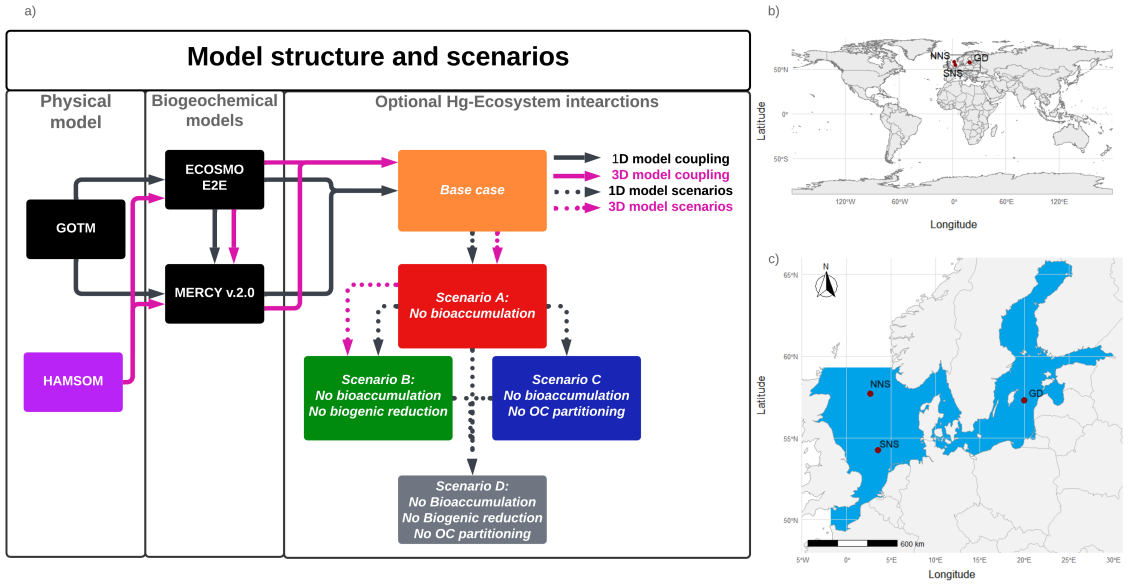

Figure 1: a) Schematic of the model setup. The black lines indicate the 1D setup where GOTM drives the ECOSMO E2E Ecosystem model and MERCY V2.0 Hg speciation model. These are used to simulate a base case and four scenarios with varying Hg–ecosystem interactions. The impact of the ecosystem is evaluated by comparing the base case to a scenario without: bioaccumulation (Scenario A), bioaccumulation and biogenic reduction (Scenario B), bioaccumulation and partitioning to detritus and DOM (Scenario C), and all mentioned ecosystem interactions (Scenario D).The purple lines show the 3D setup, where the HAMSOM model drives ECOSMO E2E and MERCY V2.0 models. The base case, Scenario A, and Scenario B are simulated in the 3D setup. b) Global map with the regional domain highlighted. c) Regional map of the North and Baltic Sea region. The 3D HAMSOM-ECOSMO-Mercy model domain is marked in blue. The three 1D setups, Northern North Sea (NNS), Southern North Sea (SNS), and Gotland Deep (GD), are labeled and marked with red points.

Reviewer Comment

Section 2.4: Include grid resolution for the 3D models (may have missed this)

Author Response

That was indeed not specified in this paper but rather only in the original paper. I would update section 2.4 by adding:

Suggested edit

The 3D HAMSOM-ECOSMO-MERCY domain covers the Baltic Sea and the North Sea with open boundaries at the English Channel and at 63°N, where the North Sea is connected to the Atlantic Ocean, as shown in Fig. 1. The resolution of the model is about 10x10 km2 on a spherical grid with vertical resolution of 20 layers. The upper four layers are 5 m thick, while the deepest layer reaches a thickness of up to 250 m. The maximum water depth is 630 m.

Reviewer Comment

L299: pre-dated?

Author Response

That is indeed wrong and should note have the -. Corrected it to:

Suggested edit

Fish 2 is at the top of the food chain and is therefore not predated upon in the model.

Reviewer Comment

L312-316: A bit more detail on this model tuning/calibration process — what informed the choice of lowered value

Author Response

I would suggest adding the following part at the end of section 2.6, replacing the part from line 316 onward with the expanded explanation below:

Suggested edit

An essential component to estimate bioaccumulation is the uptake efficiency of carbon, known as assimulation efficiency. Biomagnification occurs if the organic material is absorbed less efficiently or respirated more efficiently than a pollutant, as this would result in an increase in this pollutant compared to organic material in the organism compared to its diet. The assimilation of carbon can be seen as two components; the first absorption refers to all carbon that is used by the fish and not directly excreted via feaces, whereas the assimilation refers to the carbon that is build up into the tissue of the fish. This is investigated for fish in Shelley and Johnson (2022). They found that while the fish have an absorption efficiency of 91-92% they only have an assimilation efficiency of 30-49%. Due to uncertainty, we parameterized the higher trohic-level fish with a lower assimilation efficiency than in the previously published ECOSMO E2E version, down to 45% in fish 2. This was done to tune the model to better reproduce higher $MMHg^{+}$ bioaccumulation, which is in line with observations. These interactions remain uncertain in the model, but replicating bioaccumulated concentrations are essential to estimate the bioaccumulation feedback on Hg speciation, which is the core focus of this study.

Reviewer Comment

L468-472: What are the observed values for biomass? Not sure if I missed their reporting somewhere. Could they also be put on Figure 2 for comparison?

Author Response

I would suggest making several changes and changing Fig. 2 by showing chlorophyll-a in the surface water, rather than the fully depth intergrated values. Most measurements measure the concentrations, and hence showing this increases the comparibility to observations. Additionally, I would suggest making the small change to Fig. 2 to make it not based on the last year of the observations but the daily mean of the last 10 years of the simulation to remove the change the plots are influenced by outliers and give a better overview of the behavior of the model. I think the comparison between the model and observations is a bit too nuanced to allow an easy integration of the results into Fig. 2. Because of this, I would suggest adding the Table 1. Then I would add the update Section 3.1 to:

Suggested edit

To evaluate carbon stocks and fluxes of the ECOSMO E2E model we compared the modeled primary and secondary production to the production in the validated 3D ECOSMO E2E version in Daewel et al. (2019). In addition, we compard the model with observations for surface chlorophyll-a and zooplankton concentration, and the total fish and macrobenthos biomass. This comparison evaluated if our simplified 1D models remains consistent with a realistic ecosystem and is shown in Table 1.

The 3D ECOSMO E2E model estimates total primary production between 50 and 90 gC m^{-2} y^{-1} in the open North Sea and between 30-50 gC m^{-2} y^{-1} in the open Baltic Sea. The phytoplankton is initially driven by diatoms, and succeeded by flagellates in the North Sea and a mix of diatoms and flagellates and cyanobacteria in the Baltic Sea. Secondary production is estimated between 20-40 gC m^{-2} y^{-1} in the North Sea and 10-30 gC m^{-2} y^{-1} in the open Baltic Sea (Daewel et al., 2019).

The chlorophyll-a and biomass simulated in our 1D model are presented in Fig. 2. The total yearly primary production in our model is 50, 62, and 61 gC m^{-2} y^{-1}, and the pelagic secondary production is 24, 42, and 29 gC m^{-2} y^{-1}. This means that the primary and secondary production of the 1D model is in line with previously published and validated 3D version of the model.

The plankton concentration during the bloom period is averaged over the bloom period. The phytoplankton spring bloom period is selected as 1^{st} of April - 30^{th} of June and the zooplankton bloom period as 16^{th} of April - 31^{st} of October to select the majority of the bloom. The average chlorophyll-a concentration and zooplankton biomass in the surface (0-10m) is compared to observations.

Chlorophyll-a levels in the Baltic Sea display significant variation. During bloom periods, the Northern Baltic Sea typically has values of 1-2 mg m^3, whereas in the Southern Baltic Sea, values can reach 6 mg m^3, with a basin-wide average of 2.64 mg m^3 (OSPAR, 2017). During the autumn, cyanobacteria can become the dominant species, but there is a large variety in the intensity of the bloom and the relative importance of different species (Hjerne et al., 2019). Our average modeled chlorophyll-a concentrations in the Baltic Sea of 0.92 mg m^3 better resembles the Northern Baltic Sea than the Southern Baltic Sea. While the modeled chlorophyll concentrations in the North Sea are within the range of observations.

Zooplankton concentration range between 50 and 200 mgC m^{-3} in the Northern North Sea and 0-50 mgC m^{-3} in the Southern North Sea (Krause & Martens, 1990). Observations from the coastal Estonia, near the Gotland Deep, report 50 mgC m^3 in measurements furthest from the coast (Ojaveer et al., 1998). The average concentration of zooplankton biomass during the bloom in our model falls within these ranges for all setups.

Total fish biomass in the North Sea is estimated to be between 15 and 23g wet weight m^2 for both the North Sea by Sparholt (1990) and Baltic Seas by Thurow (1997), or between 2.25 and 3.45 gC m^2 assuming the earlier presented conversion rates of wet weight to carbon content of fish. This means that the modeled North Sea fish stocks are in agreement with observatiosn while the modeled fish populuation is in the Baltic Sea is 7% higher than observed. The 7% can indicate the model over estimates fish in the Gotland Deep, but it is low enough that it can originate from uncertainty in the biomass estimate or caused by uncertainty in the conversion from wet weight to carbon.

The peak and mean macrobenthos biomass is 12.3 and 6.84 gC m^{-2} in the Southern North Sea and 3.4 and 0.99 gC m^{-2} in the Northern North Sea, while Macrobenthos biomass estimations range from 1.1 to 35.5 grams of carbon for the open North Sea, with the highest values closer to the coast (Daan & Mulder, 2001; Heip et al., 1992). So the macrobenthos biomass in our model alings with observations. The Gotland Deep has

anoxic deep water, so there is no macrobenthos in the Gotland Deep in our model, which matches observations (Kendzierska & Janas, 2024).

Overal the model produces biomass consistent with observations and the prevously validated 3D version of the model. The only notable deviation is the Chlorophyll-a concentration of the Gotland Deep which closers resembles the Northern than Central Baltic Sea and the fish in the Baltic Sea is above the estimation made by Thurow (1997), this deviation, howeever is only 7% which can also be caused by uncertainty in the original estimation or the conversion of the estimated wet weight to the modeled dry weight.

Table 1: Comparison of modeled and observed values for key ecosystem indicators across three regions.

	Gotland Deep		Northern North Sea		Southern North Sea	
	Modeled	Observed	Modeled	Observed	Modeled	Observed
Surface Chlorophyll ($mg\,m^{-3}$)	0.92 ± 0.11	1–6	1.78 ± 0.12	0.8–2.5	1.68 ± 0.057	0.8–2.5
Surface Zooplankton biomass ($mg\,m^{-3}$)	40.60 ± 4.60	∼50	50.12 ± 3.60	50–200	34.63 ± 5.40	0–50
Fish biomass ($g\,m^{-2}$)	3.70 ± 0.16	2.25–3.45	2.29 ± 0.17	2.25–3.45	2.27 ± 1.16	2.25–3.45
Macrobenthos biomass ($g\,m^{-2}$)	0	0	0.99 ± 0.33	0.6–17.5	6.84 ± 1.16	0.6–17.5

Reviewer Comment

L508: How is “high quality” defined?

Author Response

That is indeed badly phrased. There are many more studies in the Baltic Sea that analyze Hg cycling than in the North Sea. Because of this, I suggest reframing this to:

Suggested edit

The Baltic Sea is studied more extensively for Hg cycling, and articles such as Kuss (2014) provide the opportunity to validate Hg cycling, while studies such as Nfon et al. (2009) allow the validation of low-trophic-level biota, while data on Hg cycling and bioaccumulation in low-trophic-level biota are extremely limited in the North Sea. Because of this, we focus on the evaluation of bioaccumulation of Hg in the Baltic Sea.

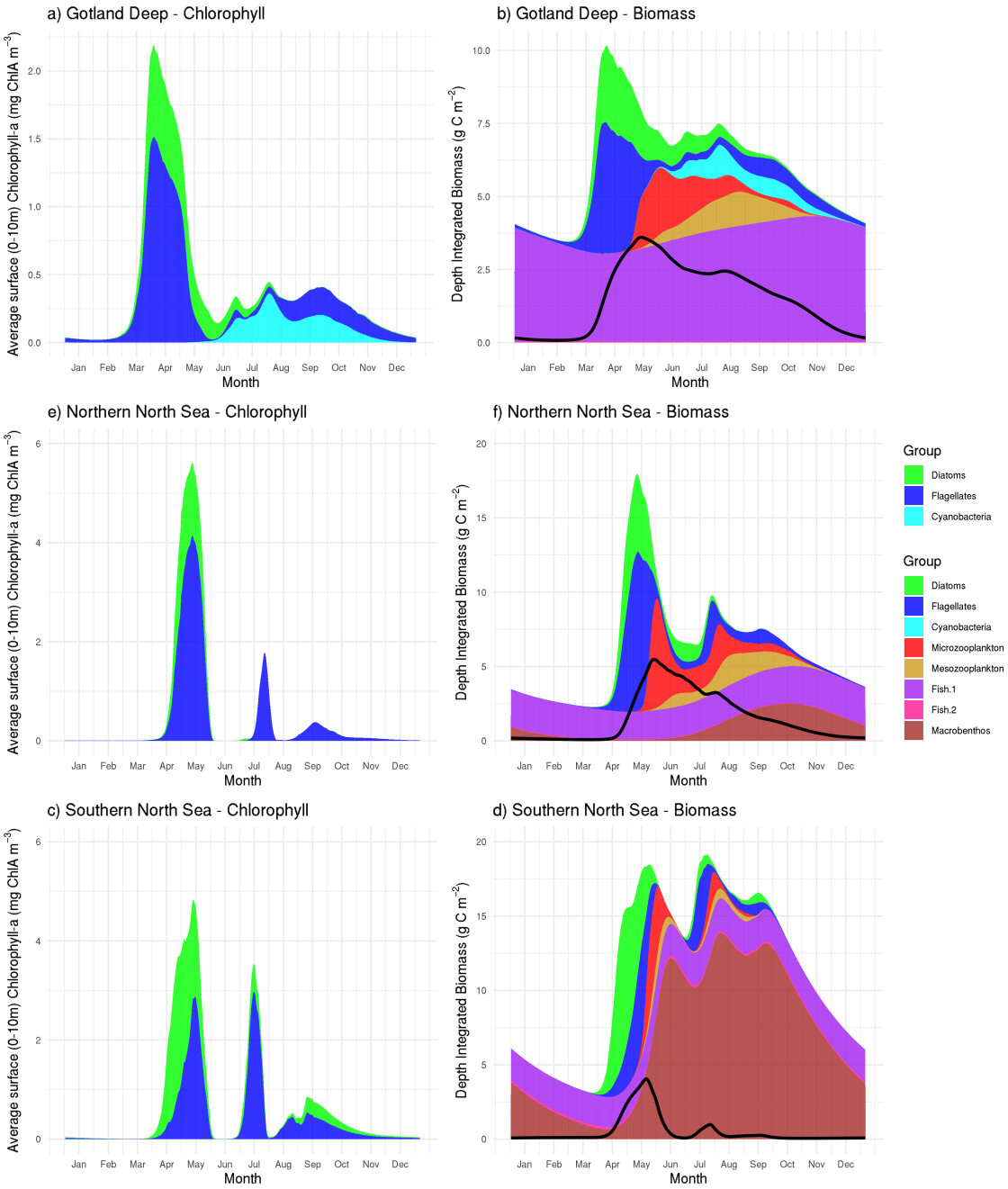

Figure 2: Modeled chlorophyll concentration (left) and organic matter concentration (right). The daily average values over are shown averages over the last 10 years of the simulation (Jan 2001 to Jan 2011). All living organic material is stacked, and detritus and DOM are plotted in the black line on top. Peak spring bloom chlorophyll concentration varies with location. Gotland Deep (a) has 2.2 mg m^{-3} chlorophyll with succession from diatoms to flagellates to cyanobacteria. The Northern North Sea (c) has 5.6 mg m^{-3} chlorophyll and is dominated by flagellates while the Southern North Sea (e) has 4.8 mg m^{-3} chlorophyll and is initially dominated by diatoms and later succeeded by flagellates. All locations have a succession of zooplankton after phytoplankton which microzooplankton and is taken over by mesozooplankton. Fish biomass is stable in the Northern North Sea (fish 1: 1.8-2.6, fish 2: 0.044-0.054 g C m^{-2}), the Southern North Sea (fish 1: 2.0-2.2, fish 2: 0.14-0.16 g C m^{-2}), and the Gotland Deep (fish 1: 3.0-4.3, fish 2: 0.40-0.44 g C m^{-2}). Macrobenthos biomass fluctuates seasonally: Northern North Sea (0.050-2.5 g C m^{-2}), Southern North Sea (0.64-13.8 g C m^{-2}), while macrobenthos is absent in Gotland Deep due to anoxic bottom water.