

Responses to the interactive comments
on the model description paper
“ERSEM 15.06: a generic model for
marine biogeochemistry and the
ecosystem dynamics of the lower trophic
level” by M. Butenschön et al.

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1 Answers to Referee P. Wallhead

Dear Dr Phil Wallhead, thank you for the attention given to our manuscript and the extensive and detailed feed-back provided.

In the following we address the individual comments one by one. Where corrections have been applied, these have been included in our current draft manuscript and will be included in the revised manuscript as much as space permits.

1.1 On the general comments

Phil Wallhead:

ERSEM is an important and well-known model in marine biogeochemistry and ecosystem modelling. This manuscript provides a detailed description of the latest version and demonstrates its application in several contexts, including 1D and 3D coupled hydrodynamic models as well as new drivers for 0D simulations ("ERSEM Aquarium") and individual parameterization analysis (Python framework). The new version is a significant update since Blackford et al. (2004) and is presented in unprecedented detail. This, combined with the new drivers for implementation and testing, ensures that the manuscript and its supplement constitute a novel and useful contribution to the marine modelling community. Given the scope and complexity of the model the authors have done an admirable job describing it in such detail within a reasonable number of pages. The manuscript is surprisingly readable: I was able to read it through closely over a few sessions, and can imagine that it could be read fairly quickly by a modeller shopping around for a new model. I can therefore see it functioning both as a reference and as an introduction for potential new users. The example implementations and figures towards the end are particularly useful in this latter regard." Where I think there is the most room for improvement is in the explanation and justification of the model. The model structure and formulation represents a large number of modelling choices: the more these can be explained/justified on rational or empirical grounds, the more useful will be this paper, I believe. Citation is a good way of doing this, but in lieu of that even modelling anecdotes could be helpful. The overall ratio (citations : modelling choices) is acceptable in the present manuscript, but I think it could be higher, and there are a few places where I feel that more explanation is clearly needed. I have indicated some places where more explanation is desirable or needed in my specific comments. Overall, I am pleased to recommend this manuscript for publication subject to minor revisions.

Thank you very much for these comments, we are glad to read that the perceived scope of the manuscript matches our intentions. We agree with you that there is space for more detailed information on the choices

and background of the model formulations and aim to provide these in the revised version of the manuscript.

1.2 On the specific comments

Phil Wallhead:

p7068, Eqn 1. The last term is not explained. If it is already covered by the fluxes across the sea floor (p7069, l3) then the term should be deleted. If it represents some biogeochemical transformations of pelagic state variables which are particular to the bottom layer and not covered by the $\mathcal{F}$ s, this should be explained here.

The last term would represent indeed the fluxes across the sea floor and should indeed not be there. It is a remainder of a previous notation, which was abandoned as these fluxes are in fact boundary conditions of the pelagic system and should not appear in the general equation for the interior. This equation now reads:

$$\frac{\partial c_p}{\partial t} + \vec{u} \cdot \frac{\partial c_p}{\partial \vec{x}} + \overset{c_p}{w}_{\text{sed}} \frac{\partial c_p}{\partial z} = \nu \frac{\partial^2 c_p}{\partial \vec{x}^2} + \left. \frac{\partial c_p}{\partial t} \right|_{\text{bgc}}$$

Phil Wallhead:

Section 2.2 is a nice addition, very useful for work on coupling ERSEM to physical models.

Thank you.

Phil Wallhead:

p7074, Eqn 4. Might be worth explaining the basis for neglecting nutrient excretion by phytoplankton (e.g. Puyo-Pay et al., 1997).

The formulation of nutrient uptake is based on the main function of phytoplankton, photosynthesis (which is seen as an assimilation of carbon and based on the assumption that nutrients and not carbon are the limiting resource, see also the reply to the following comment). Therefore excretion is focused on the release of excess carbon, while we consider the excretion of nutrients largely negligible. However, the model allows for small releases of nutrients to regulate the internal stoichiometry when the actual quota exceeds the storage capacity of the cells and respiration exceeds photosynthesis. In fact the uptake terms (Eq. 5) may turn negative when rest respiration exceeds the assimilated rate or the

internal nutrient content exceeds the storage capacity (p7078 first paragraph). This approach is in line with findings that nutrient excretion plays a minor role in the phytoplankton physiology. (Puyo-Pay et al. 1997).

In order to clarify these concepts we have rephrased the corresponding paragraph in the manuscript and explicitly split the uptake term in Eq. 5 in uptake and release:

Nutrient uptake of nitrogen, phosphorus and iron is regulated by the nutrient demand of the phytoplankton group, limited by the external availability. Excretion is modelled as the disposal of non-utilisable carbon in photosynthesis while the release of nutrients is limited to the regulation of the internal stoichiometric ratio. This approach is consistent with observations that nutrient excretion plays a minor role in the phytoplankton fluxes (Pujo-Pay et al., 1997). Consequently, demand of nutrients may be positive or negative in sign in relation to the levels of the internal nutrient storages and the balance between photosynthesis and carbon losses, so that:

$$\left. \frac{\partial \bar{P}_{N,P,F}^x}{\partial t} \right|_{\text{upt}} = \begin{cases} \min \left(\mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x, \mathcal{F}_{\text{avail}} \bar{P}_{N,P,F}^x \right) & \text{if } \mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x > 0 \\ 0 & \text{if } \mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x < 0 \end{cases}$$

$$\left. \frac{\partial \bar{P}_{N,P,F}^x}{\partial t} \right|_{\text{rel}} = \begin{cases} 0 & \text{if } \mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x > 0 \\ \mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x & \text{if } \mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x < 0 \end{cases}.$$

The nutrient demand (with the exception of silicate) is computed from assimilation demand at maximum quota $\bar{q}_{\text{max},N,P,F:C}^x$ complemented by a regulation term relaxing the internal quota towards the maximum quota and compensating for rest respiration:

$$\mathcal{F}_{\text{demand}} \bar{P}_{N,P,F}^x = \bar{S}_{\text{gpp}} \left(1 - \bar{Q}_{\text{excr}} \right) \left(1 - \bar{q}_{\text{aresp}} \right) \bar{q}_{\text{max},N,P,F:C}^x \bar{P}_{\text{C}}^x + r_{\text{nlux}} \left(\bar{q}_{\text{max},N,P,F:C}^x \bar{P}_{\text{C}}^x - \bar{P}_{N,P,F}^x \right) - \bar{r}_{\text{resp}} \bar{P}_{N,P,F}^x$$

where r_{nlux} is the rate of nutrient luxury uptake towards the maximum quota.

Note, that these terms may turn negative when rest respiration exceeds the effective assimilation rate $\bar{S}_{\text{gpp}} \left(1 - \bar{Q}_{\text{excr}} \right) \left(1 - \bar{q}_{\text{aresp}} \right) \bar{P}_{\text{C}}^x$

or the internal nutrient content exceeds the maximum quota resulting in nutrient release in dissolved inorganic form. The maximum quota for nitrogen and phosphorus may exceed the optimal quota allowing for luxury storage while it is identical to the optimum quota for iron and silicate.

The uptake is capped at the maximum achievable uptake depending on the nutrient affinities $r_{\text{aff}_{\mathbb{P},\mathbb{F},n,a}}^{\chi}$ and the external dissolved nutrient concentrations:

$$\mathcal{F}_{\text{avail}}|_{N_{\mathbb{P},\mathbb{F}}}^{\chi} = r_{\text{aff}_{\mathbb{P},\mathbb{F}}}^{\chi} N'_{\mathbb{P},\mathbb{F}} \bar{P}_{\mathbb{C}}^{\chi},$$

$$\mathcal{F}_{\text{avail}}|_{N_{\mathbb{N}}}^{\chi} = \left(r_{\text{aff}_n}^{\chi} N'_{\mathbb{N}}^{\text{ox}} + r_{\text{aff}_a}^{\chi} N'_{\mathbb{N}}^{\text{amm}} \right) \bar{P}_{\mathbb{C}}^{\chi},$$

where the nitrogen need is satisfied by uptake in oxidised and reduced form in relation to the respective affinities and external availability.

Phil Wallhead:

p7074, Eqn 5. It seems that the ERSEM treatment of nutrient limitation departs from Geider et al., 1997, 1998 and Fasham-type models (Fasham et al., 1990) in another important sense. In ERSEM, nitrogen and phosphorus limitation do not impact the gross primary production (as do silicate and iron limitation) but instead increase the rate of excretion and lysis, and also limit chlorophyll synthesis (Eqns 6, 7, 10). This seems to be a key structural difference and presumably has a physiological/experimental basis — I would like some more explanation/references for this difference in the treatment of limitation by different nutrients. A consequence seems to be that ERSEM phytoplankton in nitrogen-limited regimes, such as the surface waters of the subtropical gyres in summer, will go on happily converting DIC to DOC. Might this help to explain the “paradoxical” summer drawdown of DIC at BATS? Other aspects that may deserve explanation/references: 1) Eqn 5 uses a negative exponential form for the saturation of photosynthesis with irradiance, consistent with target theory / a Poisson process (Sakshaug et al., 1991); 2) Eqn 5 predicts that carbon fixation becomes insensitive to temperature and nutrient limitation at low light (physiological justification?).

The formulation in fact combines the form originally presented with ERSEM II in Baretta-Bekker et al. 1997 for the balance of carbon assimilation, excretion and respiration with the negative exponential light harvesting model based on Jassby and Platt 1976, Platt et al. 1982 and Geider

et al. 1997 and describes the total specific carbon fixation (total GPP, Eq. 5). In this formulation the gross carbon assimilation is assumed to be not depending on nitrogen and phosphorus. Total GPP is assumed to be composed of a fraction which is assimilated (cellular GPP) through photosynthesis and a fraction which is not utilisable, e.g. due to nutrient limitation, and excreted (dissolved extracellular GPP, Eq. 6). A similar approach can be found in Falkowski and Raven (Aquatic Photosynthesis, pg. 315, Eq. 8.16) although that equation includes also respiration which we describe separately in Eq. 12. In ERSEM, nitrogen and phosphorus limitation is assumed to alter the partition of fixed carbon between cellular and extracellular (dissolved) GPP. The idea behind this assumption is that nutrient limitation (nitrogen and phosphorus) affects more the assimilation of newly fixed carbon into cellular biomass (assimilation) than the photosynthesis itself. It should be noted that by reducing the amount of fixed carbon going into cellular biomass nutrient limitation (although not affecting the specific GPP) does affect GPP indirectly. This means that in a fully nutrient limited environment it will lead to a short continuation of conversion of DIC to DOC which will in any case decay gradually with the phytoplankton biomass. This dissolved (extracellular) component of gross primary production is not considered in Geider et al 1997 or 1998.

We have rephrased this answer into a paragraph that we have added in the begining of the section on primary producers:

The formulation of photosynthesis combines the form originally presented in Baretta-Bekker et al. (1997) for the balance of carbon assimilation, excretion and respiration with the negative exponential light harvesting model based on Jassby and Platt (1976), Platt et al. (1982) and Geider et al. (1997) in order to describe the total specific carbon fixation. In this formulation the gross carbon assimilation is assumed to be not depending on nitrogen and phosphorus. Total gross primary production (GPP) is assumed to be composed of a fraction which is assimilated (cellular GPP) through photosynthesis and a fraction which is not utilisable, e.g. due to nutrient limitation, and excreted. A similar approach can be found in Falkowski and Raven (2007). The idea behind this assumption is that nutrient (or specifically nitrogen and phosphorus) limitation affects more the assimilation of newly fixed carbon into cellular biomass (assimilation) than the photosynthesis itself.

As for the temperature nutrient dependence of the phytoplankton carbon assimilation at low light, note that the metabolic temperature

response in form of the Q10 function I_T is not limited to the exponent of the light harvesting, but also included as a proportional factor to the gross carbon assimilation and by that regulates the activity level of phytoplankton at any light level in the same way. Similarly, the internal nutrient limitation will reduce relative carbon assimilation by the same amount at any light level. (In addition nutrient limitation enhances lysis so affects the organism also at rest.)

Phil Wallhead:

p7076, Eqns 9-10. I think it may be better swap the order here. For me, the “acclimated quota” is really defined by Eqn 10, and then parameterized by Eqn 9. Also, I find the term “acclimated quota” confusing — perhaps a better term would be “nutrient-replete ratio of chlorophyll synthesis to carbon uptake”. The word “acclimated” is confusing here because it would seem to imply a ratio under conditions of balanced growth, when C:Chl ratio has adjusted to the ambient light levels. Equation 9 rather seems to parameterize the non-acclimated ratio (cf. Eqn 4 in Geider et al. 1997). Under acclimated conditions, the Chl:C ratio in the denominator might be related to E_{PAR} (cf. Eqn 5 in Geider et al., 1997).

We agree, we have swapped the equations and rephrased accordingly. The corresponding passage now reads:

The synthesis rate of chlorophyll a is given by:

$$\left. \frac{\partial \dot{P}_c}{\partial t} \right|_{gpp} = I_{(NP)}^x \phi^x \dot{S}_{gpp}^x \dot{P}_c^x,$$

where ϕ is the ratio of chlorophyll a synthesis to carbon fixation under nutrient replete conditions. It is given by:

$$\phi = \left(\dot{q}_{\phi \max}^x - q_{\min C:C} \right) \frac{\dot{S}_{gpp}^x}{\alpha_{PI}^x E_{PAR} \dot{q}_{C:C}^x} + q_{\min C:C},$$

where $\dot{q}_{\phi \max}^x$ are the maximum achievable chlorophyll a to carbon quota for each type, $q_{\min C:C}$ is the minimum chlorophyll a to carbon quota.

This formulation differs from the original formulation of Geider et al. (1997) in its asymptotic limit of the carbon to chlorophyll a synthesis at high PAR. In the original formulation the

ratio is unbound, while in this formulation it is bound by the inverse minimum chlorophyll *a* to carbon ratio $q_{\min C:C}$ in order to avoid excessive quotas not observed in nature.

Phil Wallhead:

p7076-7077, Eqns 11-13. It is not obvious to me that the loss rates from excretion, respiration, and lysis should be the same for both carbon and chlorophyll. Can these assumptions be justified? For example Geider et al. (1997) do not immediately assume that the chlorophyll respiration rate equals the carbon respiration rate.

While we have implemented a modulation of the chlorophyll *a* dynamics in photosynthesis regulated by light and nutrient supply, we have simply assumed the loss processes to be proportional to the carbon pool. This is clearly a first order approximation in absence of better knowledge. However, as a side note, also Geider et al. in their 1998 paper in the end assign the specific losses to the same value (eq. 9 of their paper), even if they formally maintain two separate parameters for carbon and chlorophyll *a* losses. In any case, the ratio of chlorophyll *a* to carbon seems to be modelled sensibly considering the results of Pina et al. 2015 (figure 3 panel c) and figure 8 of our paper.

Phil Wallhead:

p7077-7078, Eqns 15-18. Again I think a change in order would make for easier reading, so that the reader is not left wondering why “nutrient demand” should be calculated at all. I would start with Eqn 18 to calculate nutrient uptake, then explain that this is limited by internal cellular “demand” and an upper limit imposed by the capacity to actively take up nutrient at the cell surface (here termed “availability”, but maybe “max uptake” would be better?). Might also help to remind that the affinities have units [carbon⁻¹ time⁻¹] unlike the other “*r*”s. On a scientific note, surely the assumption of a linear dependence of (maximum) uptake rate on external nutrient concentration deserves some comment/references (e.g. Aksnes and Egge, 1991; Franks, 2009)? When a nutrient starved cell is suddenly exposed to a very high external nutrient concentration, it seems likely that the cell-surface uptake capacity would be saturated, which is inconsistent with the linear formulation of Eqns 16, 17. However, internal constraints on nutrient uptake rate (via S_{gpp} and r_{flux}) would then presumably limit the realized nutrient uptake rate to realistic levels, such that a saturation parameter for uptake at the cell surface might be redundant. . .?

Thanks, we have changed the order of equations accordingly (see answer to comment on 7074, Eq. 4 above for the revised formulation if the manuscript) and added a footnote clarifying the units. As for the nutrient uptake capacity, the formulation is indeed formulated as proportional to the affinity, and thus purely linear, rather than limited by a saturation assumption of Michaelis-Menten type (Aksnes-Egge 1991). This is justifiable as our model treats phytoplankton in pools of functional groups, rather than individual species with defined saturation characteristics (Franks 2009). We have rephrased this explanation for the manuscript in the following paragraph:

This purely linear formulation of maximum uptake proportional to the affinity is in contrast to the more widely used saturation assumption of Michaelis-Menten type (Aksnes and Egge, 1991). It is justified here as ERSEM treats phytoplankton in pools of functional groups, rather than individual species with defined saturation characteristics (Franks, 2009).

Phil Wallhead:

p7079, Eqns 21-23. Should explain why silicate gets this special treatment. Something to do with lack of internal storage...?

The variability of the internal silicate quota of diatoms reported in literature is small and there's little or no evidence of luxury uptake capacity for this element (Brzesinszky, 1985; Moore 2013). These factors combined with the large uncertainties in the silicate cycle have led us to this simplified description of the pelagic silicate dynamics. We have added this clarification to the revised manuscript in the form

The variability of the internal silicate quota of diatoms reported in literature is small and there's little evidence of luxury uptake capacity for this element (Brzesinszky, 1985; Moore 2013). The silicate dynamics of diatoms are therefore modelled by a simple relaxation towards the optimal quota given by the equations: ...

Phil Wallhead:

p7080-7081, Eqns 27-31. Again it would be good to briefly explain where this more elaborate multi-source feeding parameterization comes from. As far as I can tell, it is equivalent to a Fasham-type Michaelis-Menten formulation (Fasham et al., 1990, Eqns 8, 9) with the feeding

preference constants multiplied by Michaelis-Menten type “detectability ratios”. But it is not clear to the reader what extra is gained by the f_{min} parameters. Chasing down the reference I find that the ERSEM parameterization is a “Class 2D passive switching model” (Gentleman et al., 2003, Table 3a). But can we say anything about why this particular choice was made for ERSEM, among the many possibilities?

The formulation is since the original ERSEM versions (Broekhuizen et al. 1995; Heath et al. 1997) based indeed on a functional response of type II (Chesson, 1983). The additional parameter f_{min} represents an attempt to include sub-scale processes by adding a detection restriction for an individual prey type on top of the uptake limitation for total prey. In the water volume of a single cell (which within the underlying continuum hypothesis may be considered large with respect to prey individuals and small patches) prey, particularly when it is scarce, may be distributed in separate patches. Consequently, if one prey type is scarce while another one is more abundant, the limitation should consider the distinct prey which is achieved here by the additional Michaelis-Menten terms for individual preys.

We have inserted the following paragraph after the zooplankton uptake equations:

This formulation is similar to the approach used in Fasham et al. (1990), but introduces additional Michaelis-Menten terms for individual prey types. The purpose here is to include sub-scale effects of pooling as preys of different types can be assumed to be distributed in separate patches in the comparatively large cell volume. Consequently, individual prey patches below a certain size are less likely to be grazed upon compared to the larger patches, which is expressed by the h_{min}^{χ} parameter.

Note, that in response to Referee M. Baird we have relabelled the f_{min} parameters by h_{min} .

Phil Wallhead:

p7082, Eqns 32-34. The parameterization of trophic transfer appears to be a large source of sensitivity/uncertainty in biogeochemical models (Anderson et al., 2013). Can anything be said about how ERSEM developers arrived at this particular formulation?

The formulation goes back to the original ERSEM version I (Broekhuizen et al. 1995) which, based on the standard organism layout (Baretta 1995),

uses a fixed assimilation efficiency with a constant fraction lost in faeces. These are accompanied by the activity costs in form of activity respiration, again as a constant fraction of uptake. While there are other approaches to model the trophic transfer, there is no clear indication as to which is the most adequate one (Anderson, 2013).

We rephrased this paragraph in order to include these concepts in the following way:

The ingestion and assimilation of food by the predators is subject to inefficiencies that, given the wide diversity of uptake mechanisms within the zooplankton pools, is for simplicity taken as a fixed proportion of the gross uptake $1 - \bar{q}_{\text{eff}}^{\chi}$. These losses are attributed to the excretion of faeces as a constant fraction ($\bar{q}_{\text{excr}}^{\chi}$) and activity costs in form of enhanced respiration ($1 - \bar{q}_{\text{excr}}^{\chi}$).

The excretion term in Eq. 25 is then given by:

$$\left. \frac{\partial \bar{Z}_{\text{C,N,P}}^{\chi}}{\partial t} \right|_{\text{excr}} = \left(1 - \bar{q}_{\text{eff}}^{\chi} \right) \bar{q}_{\text{excr}}^{\chi} \left. \frac{\partial \bar{Z}_{\text{C,N,P}}^{\chi}}{\partial t} \right|_{\text{upt}} .$$

Respiration losses are composed of the activity costs and a basal respiration term required for maintenance and hence proportional to the current biomass by the constant factor $\bar{r}_{\text{resp}}^{\chi}$ multiplied with the metabolic temperature response (Eq. 231):

$$\left. \frac{\partial \bar{Z}_{\text{C}}^{\chi}}{\partial t} \right|_{\text{resp}} = \left(1 - \bar{q}_{\text{eff}}^{\chi} \right) \left(1 - \bar{q}_{\text{excr}}^{\chi} \right) \left. \frac{\partial \bar{Z}_{\text{C}}^{\chi}}{\partial t} \right|_{\text{upt}} + \bar{r}_{\text{resp}}^{\chi} \bar{I}_{\text{T}}^{\chi} \bar{Z}_{\text{C}}^{\chi} .$$

This simple formulation of assimilation losses is closely related to the phytoplankton losses described in the previous section following the concept of the standard organism (Baretta 1995) pending a better understanding of the underlying physiological mechanisms (Anderson et al. 2013).

Phil Wallhead:

p7086, Eqns 45-46. Why is the maximum uptake flux of R by bacteria capped at a value of rR ? What does this represent ecologically? I would

have expected a maximum flux proportional to bacterial biomass (B), in which case no capping would be needed...

The formulation actually switches from a mode that is proportional to bacteria concentration (when substrate concentrations are sufficiently large with respect to the bacteria concentration) to a mode that is proportional to the substrate biomass (when substrate is scarce compared to bacteria), regulated by the bacteria/substrate ratio. The reasoning behind this approach is that bacteria uptake would be determined by the substrate available up to a certain limit when the individual bacteria uptake is saturated and uptake will become proportional to the bacteria biomass. We have changed the description in the manuscript as follows:

Bacterial uptake of DOM is given by a substrate mass specific turn-over rate r_{lab}^B for labile dissolved organic matter when substrate is scarce and by a maximum bacteria mass specific potential uptake regulated by temperature and limited by nutrient and oxygen conditions when substrate is abundant and the uptake per bacteria is saturated, regulated by the ratio of bacteria over substrate biomass:

$$S_{upt}^B = \min \left(r_{lab}^B, \frac{B}{g_{max}} \frac{B}{I_T} \frac{B}{I_O} \min \left(\frac{B}{I_P}, \frac{B}{I_N} \right) \frac{B_C}{R'_C} \right),$$

$$\left. \frac{\partial B_{C,N,P}}{\partial t} \right|_{upt} = S_{upt}^B R'_{C,N,P},$$

Phil Wallhead:

p7092, l7-15. This is not entirely clear. For example: Does the small POM receive iron input directly from the grazing fluxes of all zooplankton on nano- and picophytoplankton?

That is correct, for the iron component of grazing the size class of particulate matter is given by the prey it derives from, while for silicate it is given by the predator that ingests the material. We have clarified the related description:

In the case of silicate the particulate organic matter types are determined by the predator that ingested the prey and directly releases the silicate contained in the frustule. They are consequently distributed analogous to the zooplankton excretion:

...

For iron, on the contrary, the size of particulate iron is given by the prey size class and taken analogous to phytoplankton lysis reflecting the assimilation of iron into the cytoplasm:

...

Phil Wallhead:

p7098. What about aragonite dynamics?

The parameterisation of calcification adopted is undoubtedly simple with respect to the complexity of the processes, the diversity of calcifiers and of the minerals (aragonite, calcite, high Mg calcite) involved. Given the limited knowledge of the physiological constraint of calcification, and the need to constrain the number of state variables included in the model (see response to Mark Baird as well), we adopted an implicit parameterisation of calcification based on the concept of the rain ratio, i.e. of the $\text{CaCO}_3:\text{POC}$ ratio in the sedimenting flux, where no distinction is made on the type of calcium carbonate.

We have added the following phrase to the manuscript for clarification:

Since the rain ratio has been defined for the sinking fluxes and calcite is the more resistant mineral, we limit the description to calcite in this part of the model, neglecting aragonite.

As a side note, the choice to consider only calcite is common to many biogeochemical models (e.g. PISCES (Gehlen et al., 2007), MEDUSA (Yool et al., 2013), Moore et al., 2002)). In any case, when the carbonate system is solved, saturation state of both forms of CaCO_3 are given.

Phil Wallhead:

p7099, Eqn 92. This makes me uneasy about mass conservation. Sedimentation redistributes the living phytoplankton biomass (Eqn 1). But here the sedimentation flux divergence of living phytoplankton contributes directly to the calcite dynamics without any biogeochemical transformation. Wouldn't this "create" carbon from nothing in the lower levels? Doesn't it duplicate the sedimentation term in Eqn 1 applied to calcite?

In the leading paragraph of the section we have alluded to the reasoning of the calcification module that is not a prognostic model based on the actual processes generating calcite. In this approach the amount of calcification in a given time-step is semi-diagnostically derived from

a postulated rain-ratio that is approximated from environmental conditions (based on the limitation state of nanopytoplankton, temperature and the current calcite saturation level). To achieve this rain-ratio the local change (and not only production) of particulate carbon is accompanied by a corresponding change in dissolved inorganic calcite. The actual processes of calcification are not modelled here. Nevertheless, the carbon mass is conserved by this description as all the calcite added based on the description mentioned is taken out from DIC (see Eq.s 114, 115). We have added the following phrase towards the end of the calcification section:

Note, that while the calcification rates are implicitly derived from the rain-ratio and not directly modelled processes, this formulation is still conservative as all sources and sinks of calcite are balanced by DIC (see Eq.s 114 and 115).

Phil Wallhead:

p7103, Eqn 111. It's not obvious to me why the remineralization flux of dissolved organic iron might be assumed proportional to the grazing flux from medium POM to mesozooplankton. What exactly is the sequence of events that is being parameterized here? Wouldn't it be better related to zooplankton excretion fluxes?

In general, the dissolution of particulate organic iron to dissolved inorganic iron by bacterial remineralisation is described implicitly in Eq. 64, 65 (see also Vichi et al. 2007). The assumption here is that the feeding activity of zooplankton increases the bio-availability of the particles and accelerates the conversion into dissolved inorganic iron. In addition, there was a minor mistake in the formula as the second term shouldn't have had the C , N and P components, so this passage now reads.

$$\left. \frac{\partial N_{\text{Fe}}}{\partial t} \right|_{\text{remin}} = \mathcal{F} \Big|_{\text{med}}^{\text{MESO}} \text{med} R'_{\text{Fe}} + \left. \frac{\partial R_{\text{Fe}}^{\text{X}}}{\partial t} \right|_{\text{decomp}} .$$

It is assumed here that the feeding activity of scavenging zooplankton increases the bio-availability and accelerates the decomposition of particulate iron.

Phil Wallhead:

p7104, l5. Would be nice to have a reference for silicate remineralization being confined to the benthos.

We have added the phrase:

This neglect of silicate conversion into inorganic form in the water column is based on observations that the recycling of this element in particulate form while sinking down the water column is much lower than for the other nutrients, such that most of its remineralisation is confined to the sea-floor (Broecker and Peng, 1982; Dugdale 1995).

Nevertheless, we are aware that this is an oversimplification at least in parts of the open ocean and are currently working on an implementation of remineralisation of silicate in the water column that will be added to the next model release.

Phil Wallhead:

p7105, Eqn 125. How is the calcium ion concentration calculated? From salinity?

In the current form it is assumed constant at the oceanic mean concentration based on the lack of reliable data. The calcium ion concentration is fairly constant in seawater (Kleypas et al., 1999), with a little increase in deep oceans and locally strong decreases towards river water. Consequently a salinity regression as suggested would be desirable, but there is few evidence for a robust formulation of such a relationship and the impact of such a formulation would be minor with the exception of major riverine outflows. We have added the following phrase to the manuscript in order to clarify:

The variability of this ratio is dominated by $c_{[\text{CO}_3^{2-}]}$ as $c_{[\text{Ca}^{2+}]}$ is nearly constant in sea water (Kleypas et al., 1990) and therefore fixed in the model at the oceanic mean value of $0.01028 \text{ mol kg}^{-1}$.

Phil Wallhead:

p7111, l21. If I have understood correctly from reading further, the benthic state variables describe the total content per square metre of all three layers combined (corresponding to the c_b in Eqn 138), so there is strictly no explicit vertical resolution, even between the three layers. When it is necessary to account for layer-specific habitat and predation ranges, the individual layers contents are calculated from the total content and an implicit vertical resolution model (Eqn 151), and a vertical

line is used to denote the restriction. However, only the unrestricted total contents are evolved dynamically. Please add something at this point and/or later to clarify this to the reader.

This is correct. We have amended the core paragraph of the introductory Sec. 4.1 to make this concept clearer in the revised manuscript.

The model includes the functional types of aerobic and anaerobic bacteria as decomposers of organic material, three types of benthic predators (suspension feeders, deposit feeders and meiobenthos), dissolved organic matter and three forms of particulate detritus classified according to their availability and decomposition time scales into degradable, available refractory and buried refractory matter.

Benthic state variables are vertically integrated contents (in mass per area) whose vertical distribution follows the following simplifying assumptions: Three distinct layers are considered in the model, a top, aerobic layer that is oxygenated and delimited by the horizon of dissolved oxygen, an intermediate oxidised layer with no free oxygen, but oxidised nitrogen available (also referred to as denitrification layer) and delimited by the horizon of oxidised nitrogen and a completely anoxic deep sediment layer. Given its very shallow penetration into the sediments, for simplicity, also dissolved organic matter is assumed to be restricted to the aerobic layer. Below these layers, limited by the total depth horizon of the model, no biogeochemical processes take place and only buried refractory matter exists.

The chemical components of the types are identical to the pelagic part consisting of carbon, nitrogen, phosphorus, silicate and iron; the silicate and iron cycles are simplified, bypassing the living functional types, in a similar manner to the pelagic part of the model. The silicate contained in detritus is remineralised implicitly into inorganic form in the sediments, while the iron in detritus is directly recycled and returned to the water column.

The vertical distribution of dissolved inorganic and particulate organic matter is crucial in determining the availability of food and resources to the benthic organisms. It is implicitly resolved assuming near-equilibrium conditions for the inorganic

components determining the diffusion rate with the overlying water body for the inorganic forms and assumes exponentially decaying distributions for particulate organic matter. The vertical dynamics of these distributions are described by dedicated state variables that describe the structure of the sediments. These are given by the oxygen horizon (the lower limit of the oxygenated layer and the upper limit of the denitrification layer), the oxidised nitrogen horizon (the lower limit of the denitrification layer and the upper limit of the strictly anoxic layer) and the mean penetration depths for available refractory carbon, nitrogen and phosphorus and degradable carbon, nitrogen, phosphorus and silicate.

Phil Wallhead:

p7113, Eqn 139. I assume this comes from parameterizing the physical exchange as a linear mixing flux and setting the overall tendency to zero? A little more explanation might help.

p7113, Eqn 140. Please explain where this comes from, and why a different equation is needed when $c_p > c_b$. Moreover, why do we care about c_{bed} ?

The change of concentration between cell centre of the pelagic bottom layer and sediment interface is indeed approximated by a linearisation of the diffusive mixing given the equilibrium flux condition at the sediment interface neglecting all other fluxes. The different formulations for positive and negative fluxes are necessary to guarantee positive concentrations. A standard linearisation would risk to generate negative concentrations at the sea-bed when $c_p < \left| p_{vmix} \frac{\partial c_b}{\partial t} \right|_{bgc}$. Instead we have opted to use the Patanka scheme here (Patanka, 1980, Sec. 7.2-2; Burcharde et al., 2003), which for the case of a net sink in the sediments uses the approximation

$$c_{bed} = c_p + p_{vmix} \frac{\partial c_b}{\partial t} \bigg|_{bgc} \frac{c_{bed}}{c_p} = c_p \frac{c_p}{c_p - p_{vmix} \frac{\partial c_b}{\partial t} \big|_{bgc}}.$$

The concentration at the sea bed c_{bed} is needed as boundary condition for the steady state production-diffusion balance in Eq. 138. We have amended this section as follows:

The sediment surface concentration c_{bed} required as a boundary condition to the production-diffusion balance above is gen-

erally not equal to the concentration at the centre of the lowest pelagic discretisation cell c_p , as diffusion across the sediment surface will be attenuated by the bottom boundary layer. In the simplest case the difference between cell centre and sediment surface concentrations can be estimated assuming a linear diffusive flux as positively proportional to the biogeochemical net change in the sediments. However, a problem arises for this formulation when the sediments act as net sink, as the calculated differences may exceed the cell centre concentration suggesting negative concentrations at the sediment interface. Therefore, for negative net sinks in the sediments the formulation suggested by Patankar (1980); Burchard et al. (2003) is applied, leading to the equation:

$$c_{bed} = \begin{cases} c_p + \rho_{vmix} \frac{\partial c_b}{\partial t} \Big|_{bgc} & \text{if } \frac{\partial c_b}{\partial t} \Big|_{bgc} > 0 \\ c_p \frac{c_p}{c_p - \rho_{vmix} \frac{\partial c_b}{\partial t} \Big|_{bgc}} & \text{if } \frac{\partial c_b}{\partial t} \Big|_{bgc} < 0 \end{cases} ,$$

where ρ_{vmix} is an inverse mixing velocity constant.

Phil Wallhead:

p7114-7115, Eqns 144-147. I would start by assuming Eqn 147 but with a general e-folding depth (say λ). The total c_b is then given by Eqn 144 with D replaced by λ . I think Eqn 145 actually only applies for $d \gg \lambda$ (note the “uv” term = $-\lambda d e^{-d/\lambda}$ when integrating by parts). So then we can say that in the limit $d \gg \lambda$, the mean penetration depth $D \approx$ the e-folding scale λ . Eqn 144 as written then follows.

This makes the derivation indeed a lot clearer, thanks. We have rephrased as:

The penetration of organic matter type ψ into the sediments is assumed as exponential decay of a concentration $c^\psi(\zeta)$ from a sediment surface value c_0^ψ as a function of the e-folding depth λ :

$$c^\psi(\zeta) = c_0^\psi e^{-\frac{\zeta}{\lambda}} .$$

Total content c_b^ψ is then given by the integral

$$c_b^\psi = c_0^\psi \int_0^{d_{tot}} e^{-\frac{\zeta}{\lambda}} d\zeta$$

and the penetration depth $\overset{\psi}{D}$ of matter ψ is defined accordingly as

$$\overset{\psi}{D} = \frac{1}{\overset{\psi}{c_b}} \overset{\psi}{c_0} \int_0^{d_{\text{tot}}} \zeta e^{-\frac{\zeta}{\overset{\psi}{D}}} d\zeta.$$

For $d_{\text{tot}} \rightarrow \infty$ the two integrals of Eq.s 2 and 3 yield

$$\lambda = \overset{\psi}{D} = \frac{\overset{\psi}{c_b}}{\overset{\psi}{c_0}},$$

i.e. the mean penetration depth is given by the e-folding depth of the distribution function:

$$\overset{\psi}{c}(\zeta) = \overset{\psi}{c_0} e^{-\frac{\zeta}{\overset{\psi}{D}}} = \frac{\overset{\psi}{c_b}}{\overset{\psi}{D}} e^{-\frac{\zeta}{\overset{\psi}{D}}}.$$

Phil Wallhead:

p7115, Eqns 148-150. I'm afraid you lost me here. What is the basis for Eqn 148? Eqn 149 appears to relate a function of depth on the LHS to a constant on the RHS. How does this lead to Eqn 150?

We should indeed have been more explicit. Based on the formulas 144-147 the change of penetration depth due to vertically distributed sources and sinks $f(\zeta)$ can then be calculated by the formula:

$$\frac{dD}{dt} = \int_0^\infty (\zeta - D) \frac{f(\zeta)}{c_b} d\zeta$$

(This can be proven by using Eq.s 145 and 146:

$$\begin{aligned} dD &= D(c(\zeta) + f dt) - D(c(\zeta)) = \frac{c_0 \int_0^\infty \zeta (c(\zeta) + f(\zeta) dt) d\zeta}{c_0 \int_0^\infty (c(\zeta) + f(\zeta) dt) d\zeta} - D \\ &= \frac{c_0 \int_0^\infty \zeta c(\zeta) d\zeta + \int_0^\infty \zeta f(\zeta) d\zeta dt}{c_0 \int_0^\infty c(\zeta) d\zeta + c_0 \int_0^\infty f(\zeta) d\zeta dt} - D \\ &= \frac{c_0 \int_0^\infty \zeta c(\zeta) d\zeta + \int_0^\infty \zeta f(\zeta) d\zeta dt - c_0 \int_0^\infty D c(\zeta) d\zeta - \int_0^\infty D f(\zeta) d\zeta dt}{c_0 \int_0^\infty c(\zeta) d\zeta + c_0 \int_0^\infty f(\zeta) d\zeta dt} \\ &= \int_0^\infty (\zeta - D) \frac{f(\zeta)}{c_b} d\zeta dt \end{aligned}$$

)

As the model is not vertically explicit, but based on the model assumptions, processes can be attributed to layers (e.g. activity of aerobic bacteria to the aerobic layer), the changes $\mathcal{F}_i$ caused in a given layer can be attributed to discrete depth levels being the centre of the layer ζ_i , so that

$$\frac{dD}{dt} = \sum_i (\zeta_i - D) \frac{\mathcal{F}_i}{c_b}.$$

This is complemented by movement of sediment material in bioturbation that smoothes the concentration gradient and is therefore implemented as diffusive flux proportional to the difference in concentrations between 0 and a bioturbation length scale δ_{bturb} .

However, there was a typo in Eq. 149 which has obscured this step, the correct form is

$$\left. \frac{\partial D}{\partial t} \right|_{\text{bturb}} = \frac{\nu_{\text{bturb}}}{c_b} (c_0^\psi - c(\delta_{\text{bturb}})^\psi),$$

Eq. 150 is then simply the result of inserting the vertical profile of Eq. 147 into this equation. We have amended the corresponding section of the manuscript as follows:

The change of penetration depth due to vertically distributed sources and sinks $f(\zeta)$ can then be calculated by the formula:

$$\frac{dD}{dt} = \int_0^\infty (\zeta - D) \frac{f(\zeta)}{c_b} d\zeta$$

As the model is not vertically explicit, but, based on the model assumptions, processes can be attributed to layers (e.g. activity of aerobic bacteria to the aerobic layer), the changes $\mathcal{F}_i$ caused in a given layer can be attributed to discrete depth levels being the centre of the layer ζ_i .

The changes of penetration depth due to source and sink terms are complemented by the physical displacement of organic matter by the process of bioturbation, so that the total change is given by the equation:

$$\frac{\partial D}{\partial t} = \sum_i (d_i - D) \frac{f_i}{c_b} + \left. \frac{\partial D}{\partial t} \right|_{\text{bturb}}.$$

Bioturbation smoothes the concentration gradient and is therefore implemented as diffusive flux proportional to the difference in concentrations between 0 and a bioturbation length scale δ_{bturb}

$$\left. \frac{\partial D}{\partial t} \right|_{\text{bturb}} = \frac{\nu_{\text{bturb}}}{c_b} (c_0 - c(\delta_{\text{bturb}})),$$

where ν_{bturb} is the bioturbation diffusivity of particulate matter (Eq. 210). Still assuming that $D \ll d_{\text{tot}}$, this takes the form

$$\left. \frac{\partial D}{\partial t} \right|_{\text{bturb}} = \frac{\nu_{\text{bturb}}}{D} \left(1 - e^{-\frac{\delta_{\text{bturb}}}{D}} \right). \quad (1)$$

Phil Wallhead:

p7117, l13-14. Reference to support exclusive feeding on particulates by anaerobic bacteria?

The exclusive feeding on particulates by anaerobic bacteria is a consequence of the vertical structure of the model design which assumes for simplicity that dissolved matter is confined to the aerobic layer as the reduced solubility in the lower layers doesn't allow organic material in dissolved form. This should have been included in the introduction to the benthic form and is now included in the amended introduction quoted above in the response to the comment on p7111, l21. Consequently the anaerobic bacteria can not obtain dissolved matter.

Phil Wallhead:

p7117, l15-17. Reference to support preferential uptake of organic nitrogen/phosphate?

We have provided a reference:

The uptake of organic nitrogen and phosphorus is enhanced by a nutrient preference factor ρ_{nup}^x supported by observations that the relative nutrient content of benthic DOM decreases under bacteria production (van Duylet al., 1993). It is complemented by the uptake of inorganic forms when organic matter is nutrient-poor with respect to the fixed bacterial stoichiometric ratio.

Phil Wallhead:

p7118, l8. Anaerobic bacteria really only excrete particulate matter? Please provide a reference.

This is again based on the simplifying model assumption that the depth horizon of dissolved matter coincides with the aerobic layer. Consequently all organic matter generated by aerobic bacteria in the sediments is of particulate form.

Phil Wallhead:

p7119, Eqn 163. Doesn't the oxygen dependence only apply to aerobic bacteria?

No, in both layers the mortality is enhanced at low oxygen, but while for the aerobic bacteria the enhancement occurs due to reduced dissolved oxygen leading to a thinner aerobic layer, for the anaerobic bacteria it is enhanced by reduced levels of oxidised nitrogen and a thinning of the reduced layer (see Eq. 244). We have clarified this in the manuscript now:

Bacterial mortality is fully regulated by oxygen (see Eq. 244) and proportional to the bacteria biomass by factor χ_{mort} :

$$\left. \frac{\partial \dot{H}_{\text{C,N,P}}^{\chi}}{\partial t} \right|_{\text{mort}} = \chi_{\text{mort}} \left(1 - I_{\text{O}}^{\chi} \right) \dot{H}'_{\text{C,N,P}}^{\chi} \quad ,$$

where aerobic bacteria use oxygen in dissolved form while anaerobic bacteria satisfy their oxygen requirements from oxidised nitrogen.

Phil Wallhead:

p7120, Eqn 166. Why do we have the food preference constants in the detectability fraction, unlike in the pelagic (e.g. Eqn 27)? Same comment for Eqn 168.

The reasoning here is that while the pelagic predators may be considered more passive feeders benthic feeders are assumed to search for prey more actively. Consequently the detection capability for the benthic fauna is assumed to vary by food-source as preferred food will attract the predator at relatively lower amounts. We have updated the manuscript to include this concept:

The total prey available to each zoobenthos type χ is composed of the individual prey types ψ as

$$\Pr_{\mathbb{C},\mathbb{N},\mathbb{P}}^{\chi} = \sum_{\psi} f_{\text{pr}}|_{\psi}^{\chi} \frac{f_{\text{pr}}|_{\psi}^{\chi} \psi'_{\mathbb{C}}}{f_{\text{pr}}|_{\psi}^{\chi} \psi'_{\mathbb{C}} + h_{\min}^{\chi}} \psi'_{\mathbb{C},\mathbb{N},\mathbb{P}}^{\chi},$$

where $f_{\text{pr}}|_{\psi}^{\chi}$ are the food preferences and $h_{\min}^{\chi}$ is a food half-saturation constant limiting the detection capacity of predator χ of individual prey types similar to the zooplankton predation (Eq. 27). In contrast to the pelagic form the detection capability for the benthic fauna is assumed to vary by food-source assuming that benthic predators search their food more actively. The prey contents in the half-saturation term are consequently multiplied by the food-preferences.

Phil Wallhead:

p7125, Eqn 181-182. I find this whole derivation a bit dubious. Eqn 182 implies that burial only occurs when the mean penetration depth D is changing, but in a system in quasi-equilibrium I would expect a constant burial flux even with a constant D . The argument seems to be based on approximating the burial flux as the product of a 'burial velocity', independent of the concentration, and the concentration at the total depth. But this sounds more like an advective flux, whereas the sediment system is earlier assumed to be diffusion-dominated for inorganic states (Eqn 138). I would have rather expected an argument based on a diffusive flux at the total depth. Assuming the exponential decay profile and a constant organic matter diffusivity ν_{odiff} , this diffusive flux would result in a burial rate independent of the rate of change of D :

$$\left. \frac{\partial Q}{\partial t} \right|_{\text{bur}} = \frac{\nu_{\text{odiff}} Q}{D^2(1 - e^{-d/D})} e^{-d/D}$$

Perhaps there is in fact a good foundation for Eqn 182 but if so it should be better explained here (noting that the Kohlmeier 2004 reference is in German).

The use of the term velocity was misleading here. The reasoning behind this formulation is as follows: bioturbation will inevitably lead to redistribution of matter that will eventually carry matter across the total horizon for biogeochemical processes. As bioturbation is stronger in

the uppermost part of the sediments (as expressed by equation 150), the assumption of a flat diffusivity is unsatisfactory. However, it is possible to derive the burial flux from the time derivative of the integrated sediment content between the surface and the depth horizon, using Eq.s 147 and 152. This derivation is straight-forward, but somewhat lengthy, so we have decided to replace it here by a simple geometric argument assuming that the change of penetration depth maintains its exponential shape stretching the original profile. The flux across any depth interface is then given by the local concentration times the displacement rate of the profile. We stress again that this is a purely geometrical argument here that doesn't correspond to an advective process.

Unfortunately, the explanation was further obscured by the arbitrary use of z and ζ for the depth coordinate (which should have been ζ throughout in this paragraph) and the subscript "diff", which should have been "bturb" as given in Eq. 150.

We have removed these mistakes and replaced the paragraph by the following text in order to clarify the derivation of the burial flux:

The diffusive process of bioturbation leads to the downward displacement of refractory material. The resulting flux of refractory organic matter across the total depth horizon of living organisms in the model d_{tot} may be interpreted as burial flux (activated by the ISWbur switch), as material is removed from the biogeochemical active part of the model.

To derive this flux we use a simple geometric argument here: it is assumed that the diffusive process will preserve the vertically exponential distribution of refractory organic matter (Eq. 147), stretching it. Consequently the flux across any horizontal interface can be expressed as the product of the local concentration $C_{C,N,P}^{\text{refr}}$ and the displacement rate of the exponential profile at the given level. Specifically, we know that the local displacement rate at the level of the penetration depth is precisely the change of penetration depth due to bioturbation

$$\left. \frac{\partial C_{C,N,P}^{\text{refr}}}{\partial t} \right|_{\text{bturb}} .$$

To derive the local displacement rate of the exponential profile at the total depth we can use the displacement time scale at

d_{tot} , that is independent of the local concentration:

$$\frac{1}{\tau_{\text{bur}}(\zeta)} = \frac{1}{c_{\text{C,N,P}}^{\text{refr}}(\zeta)} \frac{\partial c_{\text{C,N,P}}^{\text{refr}}(\zeta)}{\partial t} = \frac{\zeta}{D^{\text{refr}_{\text{C,N,P}}}} \frac{\partial D}{\partial t} \Big|_{\text{bturb}},$$

Scaling the displacement rate with this scale the flux of matter at d_{tot} , and hence the burial flux, can be computed as:

$$\begin{aligned} \frac{\partial Q_{\text{C,N,P}}^{\text{refr}}}{\partial t} \Big|_{\text{bur}} &= c_{\text{C,N,P}}^{\text{refr}}(d_{\text{tot}}) \frac{\tau_{\text{bur}}\left(\frac{D}{D^{\text{refr}_{\text{C,N,P}}}}\right)}{\tau_{\text{bur}}(d_{\text{tot}})} \frac{\partial D}{\partial t} \Big|_{\text{bturb}} = c_{\text{C,N,P}}^{\text{refr}}(d_{\text{tot}}) \frac{d_{\text{tot}}}{D^{\text{refr}_{\text{C,N,P}}}} \frac{\partial D}{\partial t} \Big|_{\text{bturb}} \\ &= \frac{Q_{\text{C,N,P}}^{\text{refr}}}{D^{\text{refr}_{\text{C,N,P}}}} \left(1 - e^{-\frac{d_{\text{tot}}}{D^{\text{refr}_{\text{C,N,P}}}}}\right) e^{-\frac{d_{\text{tot}}}{D^{\text{refr}_{\text{C,N,P}}}}} \frac{d_{\text{tot}}}{D^{\text{refr}_{\text{C,N,P}}}} \frac{\partial D}{\partial t} \Big|_{\text{bturb}} \end{aligned}$$

This result can be formally confirmed by a straight-forward, but fairly lengthy derivation of the time derivative of the integrated content of refractory matter between the sediment surface and d_{tot} using Eq. 147 and Eq. 152.

Note that this process removes biomass from the biogeochemically active part of the model, as there are no processes connected to buried organic matter and the model currently does not consider remobilisation. This means that during long term simulations the loss of nutrients needs to be compensated, e.g. by riverine inputs or atmospheric deposition (carbon is restored by air-sea exchange).

Note, that this formulation is absent in previous references (e.g. Kohlmeier).

Phil Wallhead:

p7135, l6. Only the slowly or never degrading part of the sediment matter is eroded?

The particulate matter in the benthos is actually split in slowly degrading and refractory matter so the “slow” labeled POM is actually the faster degrading one, as the slow was originally intended with respect to the DOM. In resuspension we take only this more available part labeled as slowly degradable into consideration while the fully refractory part is more compact in structure and assumed to have a higher penetration depth. It is therefore not considered in resuspension. In response,

we have in any case decided to relable the slowly degradable matter to degradable matter in order to avoid confusion.

Phil Wallhead:

p7136, l3. Not clear how this slope (units $\text{mass} \cdot \text{length}^{-4}$) is translated into a time scale.

This formulation is indeed not very precise and unclear. We have extended the paragraph which now reads:

For phosphorus, ammonium, silicate and DIC the relaxation fluxes towards equilibrium are computed by assuming a parabolic vertical distribution of excess biomass with 0 surface concentration and 0 bottom flux and assuming contributions to the generation of the excess proportional to the layer depth. The compensation flux across the seabed is then again computed from the production-diffusion balance in Eq. 138.

Phil Wallhead:

p7151, l1-11. It looks like there is also an persistent underestimation of summer nutrient levels, consistent with the weak secondary blooms mentioned in the text. Perhaps the benthic system is not remineralizing fast enough (cf. silicate), or GOTM is not capturing enough summer mixing events... I notice also an apparent decreasing trend in the surface oxidized nitrogen, perhaps also because of too-weak benthic return fluxes. It's also notable that the interannual variability in the model seems consistently weaker than in the data (Figures 2 and 3). Perhaps some aspect of the forcings is responsible?

While there is clearly some weaknesses in the representation of the summer chlorophyll a compared to the observational data, which may well be caused by the slighter underestimation of oxidised nitrogen, speculations as for the cause of these are difficult in the idealised 1D context. The Oyster Ground site is characterised by strong lateral influences including estuarine, coastal and channel waters that include strong direct impacts on the nutrient concentrations in the area. Particularly in the stratified season in summer these lateral effects are dominating the surface water signal while the deeper part of the depression is essentially isolated from the surface layer (see Weston et al. 2008). Similarly, the interannual variability can be expected to be dominated by relative variations in the prevailing currents of the area, that is receiving inflows from the continental coast, the channel, the English coast and the central North

Sea and can not be fully captured in this 1D case study. We have included these considerations in the revised manuscript:

In addition, some deficiencies, in the model simulations are to be expected as the Oyster Ground site is characterised by strong lateral influences including estuarine, coastal and channel waters that include strong direct impacts on the nutrient concentrations in the area that can not be captured in this idealised setting. Particularly in the stratified season in summer these lateral effects are dominating the surface water signal while the deeper part of the depression is essentially isolated from the surface layer (Weston et al., 2008)

1.3 On the technical comments / typos

Phil Wallhead:

"food web" not "food-web"

"North Sea" not "North-Sea"

"case study" not "case-study"

p7065, l1. "Given the importance of these applications, transparent descriptions..."

p7065, l9. "occurred"

p7065, l19. "a scientific tool"

p7065, l22. "Allen et al. (2001) adopted"

p7065, l23. "Holt et al. (2012) and Artioli et al. (2012)"

p7065, l24. "Blackford et al. (2004) applied"

p7065, l25. "Barange et al. (2014) used applications of the model in the major coastal upwelling zones of the planet, and..."

p7066, l1. "(2014) have assessed the skill of the model, demonstrating..."

p7066, l9. "climate change"

p7066, l21. "nitrogen, phosphorus,"

p7066, l24. "The present paper provides a full description of all model components , simple case studies illustrating the model capabilities in an idealised mesocosm type framework and three vertical water-column implementations of opposing character, and a brief illustration of a full-scale three dimensional application."

p7067, l4. "licence" assuming this is UK English.

p7067, l17. "feedback"

These have been corrected, thanks.

Phil Wallhead:

p7070, l7-8. Actually the $\mathcal{F}$ is used in many instances to denote rates with units $[\text{time}^{-1}]$ rather than fluxes with units $[\text{concentration} \cdot \text{time}^{-1}]$ (e.g. Eqns 14, 20, 23, ...). Perhaps those $\mathcal{F}$ s should be changed to $\mathcal{S}$ s?

The different letters as we use them are not so much about their units, but about the underlying processes: while $\mathcal{S}$ is more for rates related to physiological processes of a functional type like specific uptake or lysis, $\mathcal{F}$ is used for uptake fluxes that are directed from one functional type to another.

Phil Wallhead:

p7070, l17. "equations"
p7070, l26. "exception"
p7071, l14. "radiation"
p7071, l16. "coefficients"
p7071, l20. Latex failure.
p7072, l3. "numerical"
p7072, l19. "heterotrophic nanoflagellates"
p7072, l25. "silicic"
p7073, l5. "simplicity; their pathways. . ."
p7073, l7. "dissolved"
p7073, l19. "a net result"

These have been corrected, thanks.

Phil Wallhead:

p7074, l15. Shouldn't this be Geider et al., 1998?

Either of the two works as example here, but we had the Geider et al. 1997 paper in mind, specifically table 2.

Phil Wallhead:

p7075, Eqn6. Q_{exc} should be the fraction excreted, but the RHS appears to be 1 minus this fraction.

In fact, we have corrected this.

Phil Wallhead:

p7075, Eqn7. Doesn't this blow up (or give poor numerics) as either limitation factor approaches zero?

In fact this formula has been transcribed erroneously from the code, the corrected equation now reads:

$$\mathcal{S}_{\text{lys}}^{\chi} = \frac{1}{\min \left(I_{\langle \text{NP} \rangle}^{\chi}, I_{\text{S}}^{\chi} \right) + 0.1} \mathcal{r}_{\text{lys}}^{\chi} .$$

(See also Blackford et al. 2004, Eq. 7.)

Phil Wallhead:

p7076, l5. Break this sentence in two, e.g.: “This formulation differs from the original formulation of Geider et al. (1997) in its asymptotic limit of the carbon to chlorophyll a synthesis at high PAR. In the original formulation...”

p7076, l16. Remove “consequently”.

p7079, Eqn 24. Missing parentheses around pCO₂-379.48.

Corrected.

Phil Wallhead:

p7081, Eqns 28-30. The notation may be a bit confusing here. Eqn 28 uses a “specific uptake capacity” $\mathcal{S}$, but it is not specific to the up-taker concentration (as it was for phytoplankton uptake of nutrients), but rather to the concentration of “total available prey” (this could be made clearer by a second equality in Eqn 30). Seems it would have been better to define $\mathcal{S}_{\text{growth}}$ via Eqn 28 with Pr substituted for $\mathcal{Z}$ (and adjust Eqn 29). Maybe too dangerous to redefine anything now. Perhaps the best solution is to replace “specific” in l1 with “total prey-specific” and in l5 with “prey-specific”.

We should indeed have stated to what state the specific rate refers. We have clarified the use of specific not only here, but throughout the manuscript, in reponse to a similar, more generic comment by referee M. Baird. As for the motivation of the prey uptake formulation we hope our earlier answer on the specific comment related to p7080-81, Eqs. 27-31 has clarified the reasoning behind.

Phil Wallhead:

p7082, l5. “activity-related”

Corrected.

Phil Wallhead:

p7082, Eqn 33. $\left. \frac{\partial \mathcal{Z}}{\partial t} \right|_{\text{growth}}$ is not defined.

This should have been $\left. \frac{\partial Z}{\partial t} \right|_{upt}$ and has been corrected.

Phil Wallhead:

p7084, Eqn 38. It would be better to write this as a sum of concentrations multiplied by layer thickness, divided by the total water column height.

We have voluntarily used the integral in line with all the rest of the mathematical description that is formulated in continuous rather than discrete space. It is not divided by the water column height as the criterium we want to use for hibernation of mesozooplankton (that within limits are able to move vertically) is the vertically integrated prey mass and not an average concentration.

We have in any case corrected the formula, which was missing the final dz .

Phil Wallhead:

p7086, Eqns 45-46. Again I think it would have been better to define the rate S_{upt} as a flux specific to bacterial biomass instead of available DOM.

The formulation of bacteria uptake of substrate is in fact switching between saturated uptake when substrate is abundant (proportional to bacteria biomass) and substrate-limited uptake, which is proportional to the substrate available and consequently substrate specific. See also the answer to the specific comment related to p7086, Eqns 45-46.

Phil Wallhead:

p7087, Eqns 49-50. r_{lab} should be replaced with r_{rel} ?

p7087, l16. "occurs"

Corrected.

Phil Wallhead:

p7091, Eqn 64. Might be clearer to divide by $q_{refN:C}$, so that the ratio $q_{refN:C}/q_{refN:C}$ can be seen as a factor accounting for nutritional status (from the point of view of the decomposing bacteria that are not explicitly resolved).

This would in fact be clearer in the equation, but we have chosen to stick to the $\mathbb{C} : \mathbb{N}$ parameter for easy comparison as this is usually used in literature (e.g. the Redfield ratio is usually expressed as $\mathbb{C} : \mathbb{N}$).

Phil Wallhead:

p7098, Eqns 86 and 87. I think there are three typos: “upt” in overhead of Eqn 86, and “lab” in two overheads in Eqn 87, unless I missed something.

That’s correct, apologies for the careless editing.

Phil Wallhead:

p7098, l16. Replace “where” with something like: “The dynamics of particulate inorganic carbon (or “calcite”) may be decomposed as:”

We have replaced with:

The calcite dynamics are then described by the equation:

Phil Wallhead:

p7100, l1. Insert something like “(plus scavenging of dissolved inorganic iron)”

We have added the phrase:

Dissolved inorganic iron is additionally subject to scavenging.

Phil Wallhead:

p7108, l8. “non-modelled forms of inorganic matter and the background. . .”

Corrected.

Phil Wallhead:

p7110, l10. The R for calcite has changed into an L .

For consistence with the code lable and the state variable table, it is actually the R^{calc} s in the equations above that should have been L^{calc} s. This has been changed consistently throughout the manuscript now.

Phil Wallhead:

p7111, l23-24. “the silicate and iron cycles are simplified, bypassing the living functional types in a similar manner to the pelagic part of the model”

Corrected.

Phil Wallhead:

p7111, l27. Clash of singular “a particularity” with plural “are” - rephrase.

This has been replaced by

In addition, the benthic model includes dedicated state variables that describe the vertical structure of the sediments, given by ...

Phil Wallhead:

p7113, l2. “biogeochemical”

p7114, l9. Should be c_b not c I think.

p7115, Eqn 151. Surplus “/”

p7117, Eqn 158. Shouldn’t the R s be Q s for the benthos?

p7118, Eqn 159. Shouldn’t that be a Q instead of H in the first term on RHS?

p7121, l2. “capable of feeding on itself”

Corrected.

Phil Wallhead:

p7121, Eqns 170-171. The uptake terms should be specific to the ϕ (“upt, ϕ ”), or use the F s.

We have corrected using the F s:

$$\left. \frac{\partial Y_C^\chi}{\partial t} \right|_{\text{excr}} = \sum_{\psi}^{\text{degr med } Q, R} q_{\text{excr}}^\chi \mathcal{F}_{|\psi}^{\chi} \psi_C' + \sum_{\psi}^{\text{degr med } Q, R} q_{\text{pexcr}}^\chi \mathcal{F}_{|\psi}^{\chi} \psi_C'$$

$$\left. \frac{\partial Y_{N,P}^\chi}{\partial t} \right|_{\text{excr}} = q_{\text{dil}}^\chi \left(\sum_{\psi}^{\text{degr med } Q, R} q_{\text{excr}}^\chi \mathcal{F}_{|\psi}^{\chi} \psi_{N,P}' + \sum_{\psi}^{\text{degr med } Q, R} q_{\text{pexcr}}^\chi \mathcal{F}_{|\psi}^{\chi} \psi_{N,P}' \right)$$

Phil Wallhead:

p7125, l1. “Note that this...”

p7125, l3. “does not”

p7131, l2. “atmospheric inputs, otherwise denitrification...”

p7133, Eqn 209. Shouldn’t the “depo” and “sed” be subscripts and the “cp” overhead

Corrected.

Phil Wallhead:

p7133, l10. Is it an R or an L for calcite? Be consistent!

It should in fact be L , we have made this consistent across the manuscript.

Phil Wallhead:

p7135, l2. "In the case"
p7135, l13-14. "towards equilibrium"
p7136, l23. "cycle"
p7137, l16. "identical between"

Corrected.

Phil Wallhead:

p7138, Eqn 229. Should the G be an O ? The " s " is also not defined in the text.

It should indeed, corrected. The oxygen saturation s_0 mentioned here is actually the same as the one in Eq. 240 and is given in the supplements, we have added the reference to the supplements also at this point:

(The regression formula for s_0 is given in the Supplement).

Phil Wallhead:

p7144, l7. Should be $>$ or $<$ 1?

Corrected.

Phil Wallhead:

p7145, Eqn 258. p_{crowd} on the LHS and RHS?

These should have read $\bar{p}_C^x$ throughout the RHS. In addition the result should have been constrained to a lower limit of 0 by a maximum function:

$$\bar{p}_{\text{crowd}}^x = \max \left(0, Y_C^x - \bar{p}_C^x \right) \frac{Y_C^x - \bar{p}_C^x}{Y_C^x - \bar{p}_C^x + h_{\text{sat}}^x}$$

Phil Wallhead:

p7149, l10. Better "strong nutrient limitation"?
p7149, l11. "microbe dominated"
p7149, l14. "an order of magnitude"

Corrected.

Phil Wallhead:

p7155, l22. Shouldn't this read "product of the chlorophyll a content and PAR"?

It should indeed, it's the carbon-specific rate that is proportional to PAR and the chlorophyll a to carbon ratio, so that the actual absolute rate is proportional to irradiation and chlorophyll a. In any case, the corresponding phrase has been removed in response to a comment by Yool et al.

Phil Wallhead:

p7157, l2. "pigment complements"

Corrected.

2 Answers to Referee Mark Baird

Dear Dr Mark Baird, thank you for the attention paid to our manuscript and the extensive feed-back provided. Please find our considerations regarding your comments below.

Marc Baid:

The ERSEM model is one of the most sophisticated biogeochemical models available for shallow water ecosystems. It contains a broad range of elements (C, N, P, Si, Fe), has dynamic quotas for 4 phytoplankton types, 3 zooplankton types, bacteria mediating remineralisation, a carbon / oxygen chemistry suite, as well as a benthos with three zooplankton. There are models with more sophisticated optical sub-models, size-resolution of plankton, benthic plants and sediment chemistry (metals etc.), but in general ERSEM contains one of the broadest set of processes of any available model. The representation of bacteria in the microbial loop is, in particular, world-leading. This manuscript describes in detail the ERSEM model with the ambitious goal to be the definitive complete mathematical description for users of this model at its present, mature state. In general the manuscript achieves this goal, although a significant number of errors appear in the text that need attention, and elements of the structure are worth considering. I am a strong supporter of peer-review publication of this type of work and wish to provide the following comments in order to improve the manuscript. Any bluntness in the comments is due to brevity, as I understand the challenge in achieving an

error-free document with this many details. Thank you for your commitment to the thorough scientific presentation of your biogeochemical model.

Thanks again for your effort and time in reviewing our work, we are glad to receive your constructive feed-back and suggestions.

In the following we address the individual comments one by one. Where corrections have been applied, these have been included in our current draft manuscript and will be included in the revised manuscript as much as space permits.

2.1 On the major comments on clarity

Marc Baid:

1. It is awkward that Eqs. like (3) consider all dP/dt terms to be positive (i.e. $dP/dt|_{pred}$ is positive), such that it must be subtracted from growth in Eq. 3. Of course dP/dt due to predation is negative. This awkwardness is compounded later when the individual terms are calculated. For example Eq. 32 gives excretion being equal to uptake, when in fact the terms are the negative of each other. I would suggest that $dP/dt|_{pred}$ be negative, as well as all other loss terms. This issue comes up many times in the manuscript.

We understand the problem of a loss term being positively correlated to a production term, but we had to make a choice here:

- either we incorporate the sign into the sub-process (as you suggest) to have loss processes anticorrelated to the production term they originate from, stating all processes of the overall balance equations in a simple sum,
- or we distinguish already at the top level between loss and production terms putting the sign in the actual balance equation and assume all sub-processes as positive amounts.

We have voluntarily opted for the latter approach which seemed clearer and more immediate to us to show at a first glimpse what increases and what decreases the respective state. As a side note, this approach is not particular to our work, but has been used in other related works (e.g. Vichi et al. 2007, Fasham 1990, Fennel 1995).

Marc Baid:

2. The symbol 'q' is overused, resulting in confusion. 'q' is used as a quota, a fraction, and a turnover rate. In principle, it would be best to assign a symbol one class of entity to quantify, and then use subscripts and superscripts to be more specific.

We feel that a single letter representing fractions and proportions is restrictive enough to make a logical and conceptual distinction between parameters, but We agree that the letter "q" should not be used as turnover rate, as this is substantially different to the other uses. However, we could not find any such occurrences.

Marc Baid:

3. The quotas are state variables? Wouldn't you need a set of equations to describe their advection and diffusion like Eq. 1 that conserves mass? In Section 3.2 of J. Mar. Sys. 50 (2004) 199– 222 I give a description of how conservation of mass is achieved in the advection of quotas. Is this what you do?

The quotas themselves are not state variables. The actual state variables are the components or constituents of the functional groups, e.g. the diatom carbon concentration and the diatom nitrogen concentration, rather than its carbon to nitrogen quota. Hence the actual differential equations are solved on these (conservative) states, while the quotas are a purely diagnostic consequence. We have clarified this in the statement describing the model state variables under Eq (1):

"...where c_p are the pelagic concentrations (per volume) and c_b the benthic contents (per sediment surface area) of each chemical component of the organic model types or the inorganic model components."

Marc Baid:

4. The use of calligraphic symbols for chemical elements does not abide by conventions in chemistry, although it is still clear.

We assume this refers to the subscripts C, N, P, S, F. We have chosen to distinguish these from the general font used to evidence them with respect to the "descriptive" subscripts. We believe this facilitates the reading of the equation, even if it breaks with the conventions used in purely chemical literature.

Marc Baid:

5. 'Specific' is used regularly though the text, but we are not told whether it is carbons-specific etc. In a model with varying stoichiometries I think this is important. Without this I had trouble with the Eqs. on p7081, as noted below.

Generally, when we say specific, it would be specific with respect to all chemical components of a state. E.g. a specific mortality becomes absolute carbon, nitrogen or phosphorus loss by multiplying it with the current carbon, nitrogen or phosphorus concentration. We agree however that there is considerable ambiguity in our use of specific that led to confusion (see also some of the comments below), particularly in the cases you mention, where rates are specific to prey rather than predator concentrations. We will ensure that all uses of specific rates will be clearly defined in the revised manuscript.

Marc Baid:

6. The terms lysis and mortality are used interchangeably at times. Are they the same thing in the model?

Mostly mortality would consist of lysis, but there are some exceptions. E.g. in the case of zooplankton it would also include predation by non-modelled organisms, which is why we prefer mortality over lysis in these cases.

Marc Baid:

7. Primes are used in the sense of $B' = B + \text{small number}$, to avoid numerical integration issues. I was not confident the prime was used consistently in the text. In any case, this is a numerical integration issue, whereas this manuscript is mostly concerned with the symbolic presentation of processes formulations. I suggest primes are removed from all equations, and an additional section added to describe any numerical approximations that are recommended for the solution of the equations.

We will carefully check again that we have used the primes consistently in the descriptions and the model. Even being a numerical issue, we think that specifying the use of full or "available" biomass in the equations is important as there are cases where the use of either of the two is

ambiguous, such as half-saturation terms (e.g Eq 29 or Eqs 49,50). Therefore, in order to support the reproducibility of the model from the equations given, we have decided to keep the primes in the equations.

Marc Baid:

8. The usefulness of this document would be greatly enhanced by providing a list of parameters for one of the applications given. This is particularly necessary as many of the parameters are not given units in the text. I see this as an advantage, as the model equations are therefore not presented in a specific units system. But at some point units must be given so that the consistency of the model can be assessed.

Indeed, the full parametrisation used in all examples is given in the Supplement, stating the mathematical representation in the equations of the manuscript, the name in the code and the value and units used. Given the volume of these tables and the volume of the manuscript without it and considering the fact that the parametrisation is a customisable element and not strictly part of the model definitions, we felt that the Supplement is the adequate place for this information.

2.2 On the specific major comments

Marc Baid:

1. If Eq. 1 contains a seabed term, then Eq. 2 should have a water column term?

In fact this term should not be there, it is covered by the boundary conditions in form of the fluxes. It remained there by mistake from a previous formulation where we had included these fluxes in the balance equation for the interior, but it shouldn't be there being a boundary condition of the system. Apologies for that. Eq 1 now reads:

$$\frac{\partial c_p}{\partial t} + \vec{u} \cdot \frac{\partial c_p}{\partial \vec{x}} + w_{sed}^{c_p} \frac{\partial c_p}{\partial z} = \nu \frac{\partial^2 c_p}{\partial \vec{x}^2} + \left. \frac{\partial c_p}{\partial t} \right|_{bgc} \quad (2)$$

Marc Baid:

2. Eq. 4 – should this have an excretion term?

Nutrient excretion was covered by the net uptake term (Eq 18,21) which may turn negative, e.g. in conditions of no growth (see pg 7078, lines 2-4. This is not clear from the Eq.4, so we have decided to split the term explicitly into uptake and release. The corresponding passage in the manuscript now reads:

Nutrient uptake of nitrogen, phosphorus and iron is regulated by the nutrient demand of the phytoplankton group, limited by the external availability. Excretion is modelled as the disposal of non-utilisable carbon in photosynthesis while the release of nutrients is limited to the regulation of the internal stoichiometric ratio. This approach is consistent with observations that nutrient excretion plays a minor role in the phytoplankton fluxes (Pujo-Pay et al., 1997) Consequently, demand of nutrients may be positive or negative in sign in relation to the levels of the internal nutrient storages and the balance between photosynthesis and carbon losses, so that:

$$\left. \frac{\partial \tilde{P}_{N,P,F}^{\chi}}{\partial t} \right|_{\text{upt}} = \begin{cases} \min \left(\mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}}, \mathcal{F}_{\text{avail}}|_{\tilde{P}_{N,P,F}^{\chi}} \right) & \text{if } \mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}} > 0 \\ 0 & \text{if } \mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}} < 0 \end{cases}$$

$$\left. \frac{\partial \tilde{P}_{N,P,F}^{\chi}}{\partial t} \right|_{\text{rel}} = \begin{cases} 0 & \text{if } \mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}} > 0 \\ \mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}} & \text{if } \mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}} < 0 \end{cases}.$$

The nutrient demand (with the exception of silicate) is computed from assimilation demand at maximum quota $\tilde{q}_{\text{max},N,P,F:C}^{\chi}$ complemented by a regulation term relaxing the internal quota towards the maximum quota and compensating for rest respiration:

$$\mathcal{F}_{\text{demand}}|_{\tilde{P}_{N,P,F}^{\chi}} = \tilde{S}_{\text{gpp}} \left(1 - \tilde{Q}_{\text{excr}} \right) \left(1 - \tilde{q}_{\text{aresp}} \right) \tilde{q}_{\text{max},N,P,F:C}^{\chi} \tilde{P}_{\text{C}}^{\chi} \\ + r_{\text{nlux}} \left(\tilde{q}_{\text{max},N,P,F:C}^{\chi} \tilde{P}_{\text{C}}^{\chi} - \tilde{P}_{N,P,F}^{\chi} \right) - \tilde{r}_{\text{resp}} \tilde{P}_{N,P,F}^{\chi}$$

where r_{nlux} is the rate of nutrient luxury uptake towards the maximum quota.

Note, that these terms may turn negative when rest respiration exceeds the effective assimilation rate $\dot{S}_{\text{gpp}}^{\chi} \left(1 - \dot{Q}_{\text{excr}}^{\chi}\right) \left(1 - \dot{q}_{\text{aresp}}^{\chi}\right) \dot{P}_{\text{C}}^{\chi}$ or the internal nutrient content exceeds the maximum quota resulting in nutrient release in dissolved inorganic form. The maximum quota for nitrogen and phosphorus may exceed the optimal quota allowing for luxury storage while it is identical to the optimum quota for iron and silicate.

The uptake is capped at the maximum achievable uptake depending on the nutrient affinities $\dot{r}_{\text{aff}_{\text{P},\text{F},\text{n},\text{a}}}^{\chi}$ and the external dissolved nutrient concentrations:

$$\begin{aligned} \mathcal{F}_{\text{avail}} \Big|_{\dot{N}_{\text{P},\text{F}}}^{\dot{P}_{\text{P},\text{F}}} &= \dot{r}_{\text{aff}_{\text{P},\text{F}}}^{\chi} \dot{N}'_{\text{P},\text{F}} \dot{P}_{\text{C}}^{\chi}, \\ \mathcal{F}_{\text{avail}} \Big|_{\dot{N}_{\text{N}}}^{\dot{P}_{\text{N}}} &= \left(\dot{r}_{\text{aff}_{\text{n}}}^{\chi} \dot{N}'_{\text{N}}^{\text{ox}} + \dot{r}_{\text{aff}_{\text{a}}}^{\chi} \dot{N}'_{\text{N}}^{\text{amm}} \right) \dot{P}_{\text{C}}^{\chi}, \end{aligned} \quad (3)$$

where the nitrogen need is satisfied by uptake in oxidised and reduced form in relation to the respective affinities¹ and external availability.

And for silicate:

$$\begin{aligned} \left. \frac{\partial \dot{P}_{\text{S}}^{\text{dia}}}{\partial t} \right|_{\text{upt}} &= \max \left(\dot{q}_{\text{ref}_{\text{S}:\text{C}}}^{\text{dia}} \dot{S}_{\text{growth}}^{\text{dia}}, 0 \right), \\ \left. \frac{\partial \dot{P}_{\text{S}}^{\text{dia}}}{\partial t} \right|_{\text{rel}} &= \max \left(\dot{P}_{\text{S}}^{\text{dia}} - \dot{q}_{\text{ref}_{\text{S}:\text{C}}}^{\text{dia}} \dot{P}_{\text{C}}^{\text{dia}}, 0 \right), \end{aligned} \quad (4)$$

Similarly the uptake and release of nutrients and bacteria was covered by a single term, which has now been split in two explicit terms as well:

¹Note that the dimensions of these are $[\text{volume}^1 * \text{mass}^{-1} * \text{time}^{-1}]$ as opposed to $[\text{time}^{-1}]$ as for most other rates.

$$\frac{\partial B_{\mathbb{P}}}{\partial t} \Big|_{\text{upt}} = \begin{cases} r_{\text{rel}}^B \left(q_{\mathbb{P}:\mathbb{C}}^B - q_{\text{max}\mathbb{P}:\mathbb{C}}^B \right) B_{\mathbb{C}} \frac{N_{\mathbb{P}}'}{N_{\mathbb{P}}' + h_{\mathbb{P}}} & \text{if } q_{\mathbb{P}:\mathbb{C}}^B < q_{\text{max}\mathbb{P}:\mathbb{C}}^B \\ 0 & \text{if } q_{\mathbb{P}:\mathbb{C}}^B \geq q_{\text{max}\mathbb{P}:\mathbb{C}}^B \end{cases}$$

$$\frac{\partial B_{\mathbb{P}}}{\partial t} \Big|_{\text{rel}} = \begin{cases} 0 & \text{if } q_{\mathbb{P}:\mathbb{C}}^B < q_{\text{max}\mathbb{P}:\mathbb{C}}^B \\ r_{\text{rel}}^B \left(q_{\mathbb{P}:\mathbb{C}}^B - q_{\text{max}\mathbb{P}:\mathbb{C}}^B \right) B'_{\mathbb{C}} & \text{if } q_{\mathbb{P}:\mathbb{C}}^B \geq q_{\text{max}\mathbb{P}:\mathbb{C}}^B \end{cases}$$

Marc Baid:

3. Eq. 7 will produce an undefined number when either of the limiting functions is zero.

This is a mistake in the transcription, the formulation in the code in fact augments the denominator by 0.1. The corrected equation reads:

$$\chi_{\mathcal{S}_{\text{lys}}} = \frac{1}{\min \left(l_{\langle \text{NP} \rangle}^{\chi}, l_{\text{S}}^{\chi} \right) + 0.1} \chi_{\text{lys}} .$$

Marc Baid:

4. Eq. 24 – I think there should be a bracket around (p-379.48)

Thanks, this has been corrected in the manuscript.

$$\gamma_{\text{enhC}} = 1.0 + (\text{pCO}_2 - 379.48) \times 0.0005 .$$

Marc Baid:

5. I think Eq. 28 should have Prc on the nominator?

No, not at this stage of prey-specific uptake. The prey biomass comes into play later, when the absolute uptake is computed (Eq. 30). This should be clearer now that we have clarified the meaning of the various occurrences of specific rates (see the response to major comment number 5).

Marc Baid:

6. Eq. 27-30. To illustrate an inconsistency, imagine you have one phytoplankton species $P = 1 \text{ mg C m}^{-3}$, $f_{\min} = 1$. f_{pr} becomes 1, and the grazing rate is proportional to $1 \times 1 / (1+1) = 0.5$. Now split the phytoplankton into two identical populations, indistinguishable to the zooplankton, then f_{pr} becomes 0.5 for both, and the grazing rate is proportional to $0.5 \times 0.5 / (0.5+1) + 0.5 \times 0.5 / (0.5+1) = 0.3333$. I am not sure about the definition of f_{pr} , but the definition of $f_{\min}$ is problematic. This same issue exists for benthic feeders. Here (Eq. 168) a detection capacity is assumed. The only justification I could imagine for a detection capacity is that the concentration is less than one individual. If so, then there would be a calculation that could be made to determine the value. But I don't think this is what you are trying to represent. If it is relative availability, then you could use an affinity for prey in the same manner as you consider NH_4 and NO_3 uptake.

If the two prey types are indistinguishable to the zooplankton, i.e. they are perceived as the same thing by the predator, then the $f_{\min}$, i.e. the detection concentrations for the single perceived prey type, should be split between the two actual prey types equally. Specifically, in your example, if the single prey type has $f_{\min}=1$, then the two prey types perceived as one should have $f_{\min}=0.5$, which then yields 0.5 as prey availability in both cases.

The detection capacity is essentially an attempt to include sub-scale effects, in that different prey types are likely to be distributed in the water column in separate patches. At that point, if one prey type is very rare it is unlikely to be detected with respect to other prey types that are abundant. We have amended the manuscript to explain this concept better:

This formulation is similar to the approach used in Fasham et al. (1990), but introduces additional Michaelis-Menten terms

for individual prey types. The purpose here is to include sub-scale effects of pooling as prey of different types can be assumed to be distributed in separate patches in the comparatively large cell volume. Consequently, individual prey patches below a certain size are less likely to be grazed upon compared to the larger patches, which is expressed by the $h_{\min}^{\chi}$ parameter.

Marc Baid:

7. Eq. 38 might be incomplete. The LHS implies a depth-average concentration, which would require the integral through the water column to be divided by the depth, while the RHS implies the depth integral (although the dummy variable, dz , is not given)

This is a misunderstanding, the “av” subscript here stands for available prey as stated in the phrase on top of the equation. It is given by the vertical integral of prey in each horizontal position. Nevertheless, the integral formula was missing the integrand and has been corrected:

$$\text{Pr}_{\text{av}}^{\text{ow}} = \int_{\text{seafloor}}^0 \text{Pr}_{\text{C}}^{\text{MESO}} dz$$

Marc Baid:

8. Eq. 45,46. I don’t see how these equations work. If Sup is the bacteria-specific uptake rate, then Eq. 46 should be $dB/dt = S B$, where Sup depends on the available organic matter, not the bacterial population? In Eq. 45, should it be R_{lab} ?

There was a minor mistake in the super- and subscripts of these equations: the “lab”s should have been “dis”, so refer to the labile dissolved organic matter. This possibly has caused confusion here and has been corrected. In any case, the uptake rate of equation 45 is specific with respect to the substrate available and not to the bacteria biomass (similar to the predation uptake being specific to prey, see the comment to your point 5). This means that under the condition of the first case of

the minimum function (representing the case that sufficient substrate to saturate uptake by bacteria is available), specific uptake will increase the bigger the bacteria biomass. The second term represents uptake that is limited by scarcity of substrate with respect to the bacteria biomass in a simplified manner as a fixed substrate specific rate, compared to the half-saturation formulation of the predators . The formulation essentially is a switch between uptake proportional to bacteria biomass when enough substrate is available or proportional to substrate if substrate is scarce, regulated by the bacteria over substrate ratio. This explanation was added to the manuscript, which now reads:

Bacterial uptake of DOM is given by a substrate mass specific turn-over rate r_{lab}^B for labile dissolved organic matter when substrate is scarce and by a maximum bacteria mass specific potential uptake regulated by temperature and limited by nutrient and oxygen conditions when substrate is abundant and the uptake per bacteria is saturated , regulated by the ratio of bacteria over substrate biomass:

$$\begin{aligned} \mathcal{S}_{upt}^B &= \min \left(r_{lab}^B, \frac{B}{g_{max}} \frac{B}{I_T} \frac{B}{I_O} \min \left(\frac{B}{I_P}, \frac{B}{I_N} \right) \frac{B_C}{R_{lab}^C} \right), \\ \left. \frac{\partial B_{C,N,P}}{\partial t} \right|_{upt} &= \mathcal{S}_{upt}^B R_{C,N,P}^{lab}, \end{aligned}$$

Marc Baid:

9. I am not sure of the meaning of the bold brackets in Eqs. 57 and 58, but they seem to imply multiplication of local derivatives, which I don't think is the intention.

The squared brackets here and in other places represent terms that hold only for individual functional groups, e.g. the silicate components in the phytoplankton equations that are only present in diatoms. We have added the following phrase to the nomenclature section:

In equations that hold for multiple functional groups or components squared brackets are used for terms that are only valid for a single functional group or component.

However, the terms in Eq 57 sepically shouldn't have had brackets. We have taken them out.

Marc Baid:

10. P7091. Is $r_{\text{decomp}} = r_{\text{remin}}$ by definition in the equations? If so, it would be better to have just one parameter.

" r_{remin} " is not used in the manuscript. If the comment refers to the remineralisation rates from dissolved organic matter to inorganic matter ($r_{\text{remN,P}}$), the decomposition of particulate matter to dissolved matter in the standard bacteria model is in principle independent of the remineralisation of dissolved matter by bacteria, which is why we have preferred to use two parameters.

Note: Point 11 seems to have been removed by the referee?

Marc Baid:

12. P7105 – If alkalinity is correlated to temperature, which is non-conservative, then alkalinity will be non-conservative. Why not initialise the model with alkalinity based on T and S, and then advect total alkalinity (not just the bgc perturbations), with bgc processes as local sink/sources.

Indeed this option is included in the model by switching the regressions off (ISWTALK=5). Then whatever initial condition provided will be advected and diffused conservatively if the transport operator of the physical driver is conservative. This is in fact the option used in the global ERSEM simulation in Kwiatkowski et al. 2014. However, we have chosen to allow a hybrid formulation of alkalinity as not all processes contributing to the carbonate system are included in the model, so conservation is not necessarily a desirable feature in this case. At the same time relatively robust regressions for alkalinity from salinity or alternatively temperature and salinity exist at least for some areas of the world ocean (see e.g. Artioli et al. 2012, Lee et al. 2006), that in combination with the biological changes give a good approximation for the total alkalinity, as demonstrated in the Artioli et al. paper. In these areas this semi-prognostic approach gives a much better representation of the carbonate system compared to the fully prognostic description used in Kwiatkowski that performed comparatively poor. In any case, we have rewritten the final part of the carbonate system section in order to clarify the different options:

Two different modes to compute total alkalinity are provided with the model:

- A diagnostic mode, that computes alkalinity from salinity or salinity and temperature. This mode is non conservative and the field of alkalinity is recomputed at each time step without physical transport. It does not include changes to alkalinity by the biogeochemical processes of the model.
- A prognostic model, that includes biogeochemical changes to alkalinity, is fully conservative and adds a state variable for alkalinity that is subject to physical transport.

As a third semi-diagnostic option, these two modes can be combined as a sum by setting the prognostic alkalinity state to 0, so that the diagnostic mode provides the background field and the prognostic mode gives a trace of the contribution of biogeochemical processes to the total alkalinity.

The recommended option is the semi-diagnostic option for coastal applications and shelf seas, where reliable and robust regressions exist or the fully prognostic mode, where no single reliable regression is available, e.g. in global simulations. (For further detail the reader is referred to Artioli et al., 2012)

The changes of alkalinity due to biological processes are given by sources and sinks of phosphate, oxidised nitrogen and ammonium as well as calcification and dissolution of calcite:

$$\left. \frac{\partial A_{\text{bio}}}{\partial t} \right|_{\text{bgc}} = \left. \frac{\partial N_{\text{N}}^{\text{amm}}}{\partial t} \right|_{\text{bgc}} + 2 \left. \frac{\partial L_{\text{C}}^{\text{calc}}}{\partial t} \right|_{\text{diss}} - \left. \frac{\partial N_{\text{P}}}{\partial t} \right|_{\text{bgc}} - \left. \frac{\partial N_{\text{N}}^{\text{ox}}}{\partial t} \right|_{\text{bgc}} - 2 \left. \frac{\partial L_{\text{C}}^{\text{calc}}}{\partial t} \right|_{\text{calc}} .$$

In three dimensional simulations, these changes are accompanied by the effect of riverine inputs (see Artioli et al., 2012).

Marc Baid:

13. The equation of the vertical attenuation of light (Eq. 128) calculates light at a depth z . But the model considers discrete layers, in which case any single depth (top, centre, or bottom of the layer) does not represent the mean available light in the layer. The correct depth-averaged light within a layer is given by $(E_{\text{top}} - E_{\text{bot}})/(K_d \, dz)$ where K_d

is the vertical attenuation of light coefficient, and dz is the thickness of the layer. A similar problem is described on the ROMS forum: <https://www.myroms.org/forum/viewtopic.php?f=33&t=1314>.

Indeed, this issue relates to the fact that the “average” light in an individual cell should not be the light at the cell centre, but the integral of the exponentially decaying light over the cell thickness, divided by the cell thickness, which is how it is implemented in the aquarium and gotm drivers provided with the model release code and also in the various coupled systems using the POLCOMS and NEMO ocean models cited in the paper. We have amended the corresponding point in the section on dependencies on the physical environment:

- Primary production relies additionally on the photosynthetically active radiation (PAR) as energy input which should be computed from shortwave radiation at the sea surface I_{surf} , taking into account the attenuation coefficients given in Section 3.9. Note, that the model requires the average light in each discrete model cell, which is not given by the light at the cell centre, but by the vertical integral of the light curve divided by the cell depth.

Marc Baid:

14. Eqn 245 has a parameter h with units of $(\text{mass}/\text{length})^3$. If you replace h with h^3 , the units of h will be concentration, and the value will be a meaningful concentration. Same for Eq. 246.

We had considered the option of setting this parameter to the units of simple concentration, but have opted for leaving it cubic at this point for easier comparison with previous parametrisations (Blackford et al., 2004).

Marc Baid:

15. Eqn 247 – is this really a 2. If so explain.

That value has been chosen to limit the impact of pH on nitrification rate at high pH to a factor of 2, to avoid unreasonable extrapolation of Huesmann et al. 2002 Anyway, this limit is purely a safety-valve for pathological cases because such doubling of nitrification rate will occur only when $\text{pH} > 9.637$, i.e. a value that is usually higher than the values simulated by the model in natural environment.

Marc Baid:

16. You could replace equation 254-255 with $x./(abs(x)+hcalc)$ where $x = \omega - 1$, which would be positive for calcification and negative for dissolution.

That would be a possibility, but would still require the “non active” limitations to be set to zero and the dissolution ones to be reset positive in case of a negative result. Overall, this seems less transparent to us, so we prefer the original formulation.

Marc Baid:

17. P7145 – So the calcification is unaffected by temperature above say 10 °C? Rather than use the rain ratio, would it be easier to have an explicit calcifier.

We don't fully understand the first half of the comment: the effect of temperature on calcification is described by a saturating curve (Eq 256), with half saturation constant equal to 2 °C. This implies that at 10 °C calcification is 83% of the maximum value and at 30 °C is about 94%.

Although the implementation of an explicit calcifiers would improve the ability of the model to simulate some aspect of calcification (e.g. the dependency of calcification from the physiological state of the calcifier), including a specific group of calcifier is problematic given the diversity of calcifying organisms in the marine environment and will therefore lead to the exclusion of the contribution of calcifiers that are not included in this new group. Hence, in order to include all possible sources of calcification, and given the limited knowledge on the mechanistic representation of the process involved, we decided to use this implicit parametric formulation, that is similar to the ones used in other biogeochemical models (e.g. PISCES - Gehlen 2007, MEDUSA - Yool 2013).

2.3 On the minor comments

Marc Baid:

1. L10 p7083. I know what you mean, but ‘enhanced inefficiency’ is an oxymoron? Perhaps ‘reduced efficiency’ would be simpler.

Thanks, we have changed this in the manuscript to:

It is capable of scavenging on medium size organic matter whose assimilation is less efficient and therefore subject to enhanced excretion $q_{\text{Rexcr}}^{\text{MESO}}$:

Marc Baid:

2. L9, p7068 replace 'with respect to' with 'compared to'.

Corrected.

Marc Baid:

3. P9 'according to the internal quota and storage capacity' – are these different quantities?

Yes, the internal quota would be the actual internal quota and the storage capacity its maximum threshold (or better the difference of maximum and reference internal quota). This should become clearer in the section on primary producers.

Marc Baid:

4. Eq. 2 direction of z is important in this definition.

The direction of the z coordinate is given in the Nomenclature section just beneath, but to make this clearer at this point of the manuscript, we have inserted the phrase:

$\vec{x}$ represents the vector of spatial coordinates of which z is the vertical coordinate being 0 at sea surface and increasing downwards.

Marc Baid:

5. P7070, l12 'equations'.

We assume this comment is referring to line 17 on the same page and have corrected it.

Marc Baid:

6. P7071, l15 small 'P' production, radiation misspelt.

Corrected.

Marc Baid:

7. P7071, l20 vecu_wind is not defined.

This was a latex typo and has been corrected to $\vec{u}_{wind}$.

Marc Baid:

8. P7072, l3 'numerical' misspelt.

Corrected.

Marc Baid:

9. P7073, l19 'as the net result'

This has been corrected to "as a net result" on suggestion of referee P. Wallhead.

Marc Baid:

10. P7073, l21 'predation by zooplankton'

Corrected.

Marc Baid:

11. P7074 l4 'for diatoms is the'

We have corrected to:

"and where the silicate component (§) is only active for diatoms."

Marc Baid:

12. P7074, l10-l14 quatae? 'in unlimiting conditions at the reference'

13. P7078 l16 replace tendency with rate, and misspelling of luxury.

Corrected.

Marc Baid:

14. P7080 l16 – I thought ‘h’ was going to be for half-saturation constants? Might be worth saying that a low f means better detectability (i.e. f is actually a measure of indetectability!)

Thanks, we have followed the suggestion to label the half-saturation constant with h. Labeled clearly as half-saturation constant now, we believe that the relation of a low half-saturation meaning high detection capacity should be clear.

Marc Baid:

15. P7082 – internal stoichiometric quota.

If this refers to line 10, we couldn’t find any mistake with the original phrase.

Marc Baid:

16. Eq. 57 – the meaning of ‘adj’ is not given.

Apologies, this shouldn’t have read ‘exu’ as in exudation, which is defined below. We have corrected this.

Marc Baid:

17. P7086, l15 – what is the meaning of ‘at rest’

“at rest” here refers to the pure maintenance metabolism of the microbes without any decomposition of substrate. We have added the phrase:

(representing the maintenance cost of the metabolism in absence of uptake activity)

Marc Baid:

18. P7090 l4, ‘excretion by zooplankton’, l6 ‘respectively’

Corrected.

Marc Baid:

19. In some places (Eqs. 144, 145, 152) zeta is used as the dummy variable for distance in the vertical, where z is used elsewhere. Might be clearer to stick with z .

We have chosen to use a separate depth coordinate for the sediments, as for the benthos the level 0 is at the sediment interface, while for the pelagic part it is at the sea surface, so strictly they are separate coordinates.

Marc Baid:

20. P7098. L8 replace 'quota' with 'proportion' or something other than quota.

We have replaced with "ratio".

Marc Baid:

21. P7117 Eq. 158 – the use of the vertical line delimited by depths is unusual.

We agree that the vertical line is a fairly ambiguously used symbol in mathematical notation, but at the same time think that our use here is sufficiently clear ("substrate concentrations available in the respective layer", "where the layer limits d_{low} , d_{up} are 0, $\overset{oxy}{D}$ for aerobic bacteria and $\overset{oxy}{D}$, d_{tot} for anaerobic bacteria") and we don't think our use is particularly uncommon (See e.g. https://en.wikipedia.org/wiki/Vertical_bar: "Sometimes a vertical bar following a function, with sub- and super-script limits 'a' and 'b' is used when evaluating definite integrals to mean 'f(x) from a to b', or 'f(b)-f(a)'.")

Marc Baid:

22. P7138 I5 'through'

Corrected.

Marc Baid:

23. P7141 replace 'M-M constants' with 'half-saturation' constants.

24. P7143 l9 – 'nitrification'

Corrected.

Marc Baid:

25. P7144 l 6 Do you mean > 0 ?

This should indeed read > 1 , it has been corrected.

Marc Baid:

26. P7155 l13-14 – check units of PAR and Ns.

The relevant phrase has been removed as a response to a comment by A. Yool et al. on this section.

3 Answers to Andrew Yool, Tom Anderson and Katya Popova

Dear Dr Andrew Yool, Dear Prof Tom Anderson, Dear Dr Katya Popova,

We'd like to thank you for the thorough and detailed feed-back that you have provided concerning our discussion paper. In the following we will address your individual comments. Where corrections have been applied, these have been included in our current draft manuscript and will be included in the revised manuscript as much as space permits.

Andrew Yool, Tom Anderson and Katya Popova:

In the first instance, we are very pleased to see ERSEM get a thorough and updated description, and the authors are to be commended. As a long-standing and much-used staple of many marine biogeochemistry studies, particularly in the shelf seas region, it is crucial that ERSEM is transparent and accessible to interested researchers. Especially since recent work (e.g. Kwiatkowski et al., 2014) has shown ERSEM now running at the largest possible scales. However, while welcoming this manuscript, there are a number of weaknesses in it that we feel do not allow ERSEM to be shown in its best light. In our opinion, addressing these would make

the resulting manuscript a much more valuable resource, both for existing ERSEM users and as an advert to potential new users of ERSEM. We have divided our comments into general, overarching points and shorter remarks on specific facets of the manuscript.

Thank you again for the attention you have given to our work, we have considered your points carefully and have tried to address them in our answers that you find below.

As a general remark, we believe that some of the criticism raised is based on a misconception of our purpose of this paper having a conceptually different paper in mind that would “show case” the model in its entire broadness with a considerable weight on the variety of full scale applications. This however wouldn’t be possible in reasonable space (as you recognise yourself in point 4), if not at the cost of an incomplete mathematical description which would repeat the short-coming of earlier works on this model. In addition, there is a variety of examples in the scientific literature that illustrate the spectrum of ERSEM applications, so adding these here would only repeat previous efforts, therefore we have limited ourselves in this occasion to refer to these works in the introductory and concluding remarks.

On the contrary our main objectives for this paper were:

- providing a full, transparent mathematical description and a full illustration of the model software.
- provide test cases that demonstrate the main model capabilities, but at the same time allow for a full replication of results within reasonable effort and at a low level of requirements in terms of computational resources.

We realise that this approach may be slightly different to at least some previous papers in GMD on similar types of models, but we believe it is fully supportive of the GMD standards for a model description paper. Specifically it:

- fully supports reproducibility, either of all model equations in a different framework, either of the test cases presented,
- provides examples of model output with comparison to observational data.

We believe that this focus on transparency and reproducibility renders the work interesting and relevant to both, expert modellers familiar to

models of similar type, and modellers of related fields as well as other scientists that are interested in the backgrounds and details of our model.

We have rephrased the beginning of the last paragraph of the introduction in order to reflect these intentions:

Our main objective with this paper is to provide a full description of all model components, accompanied by simple case studies with low resource requirements that illustrate the model capabilities and enable the interested reader to implement our model and reproduce the test cases shown. To this purpose we present the examples of a mesocosm type framework and three vertical water-column implementations of opposing character complemented with basic validation metrics against in-situ observations. A brief illustration of a full scale three dimensional implementation is given to show the model in a large scale application. All material required to replicate the test cases that are given here, such as parameterisation and input files, are provided in the Supplement.

The next section gives...

3.1 On the general points

Andrew Yool, Tom Anderson and Katya Popova:

1. While the model equations are doubtless mathematically correct, they are expressed throughout in an overly nested and quite repetitive style that makes following and interpreting them unnecessarily difficult. We would suggest that the authors examine descriptions of comparable models (e.g. PISCES was very recently published; Aumont et al., 2015) and adopt some of the style conventions there.

The way we have presented the equations follows the strategy to first present the balance equation for each functional class giving an overview of the processes that change it, and then specify the individual processes in more detail. We appreciate that the volume of mathematical descriptions may at first be a bit overwhelming to readers who are not familiar with the model, but at the same time, we think that this is the best way in which a description of a model of this detail can be presented, when completeness of the description is our main goal. This approach allows unfamiliar users to get an idea of what is changing a state by a quick

look at the head of each section, with the possibility to get more into detail, where desired. The same approach has also been followed in other works (e.g. Vichi et al. 2007) of comparable model detail. Specifically, we think that the more “all in one” approach, which works well e.g. for the mentioned PISCES model description, is unsuitable here as the balance equation for the individual states would become excessively long, spreading over several lines, rendering them essentially unreadable. For this reason, we are inclined to stick to our general approach of mathematical representation, also considering, that none of the two referees expressed a similar concern and one of them even finding the current form “surprisingly readable”. Nevertheless, we have reviewed our description and reordered in several places equations where they appeared excessively nested or hard to follow (see e.g. some of the comments raised by Referee P. Wallhead and their response).

Andrew Yool, Tom Anderson and Katya Popova:

2. More broadly, while the model equations are scrupulously documented, their origins are not explained. As such, it is difficult for readers to chase up particular functions to understand the rationale for framing them or their underlying assumptions and limitations. Where possible, we suggest that the authors either make reference to their sources and / or identify where they have used “standard” functions (e.g. type-II or type-III responses).

We agree that the origin of the model formulation is at times weakly motivated and documented and have amended the formulations to improve this point adding the reasoning for a particular formulation, including references where adequate (see some of the responses to the two referees).

Andrew Yool, Tom Anderson and Katya Popova:

3. Oddly, the model description includes a number of additional optional functionalities for particular processes, but it offers no information on how these perform (functionally and computationally), how they impact model performance, or under which circumstances they should be preferred. We would suggest that an obvious inclusion on these occasions would be to perform a simple sensitivity analysis that illuminates on these points. Alternatively, if these options have formed part of a preceding publication, a pointer to this would help.

We agree that the various options of the model formulations are not clear enough. We have decided to add a section on optional model choices to summarise these along with information on their impact, advantages and disadvantages. However, we believe that a sensitivity analysis, even if brief, for each of these options would exceed the volume of the present work (see point 4), whose main purpose is a full description of the model formulations. We will ensure in any case that reference to relevant previous works are in place.

Andrew Yool, Tom Anderson and Katya Popova:

4. The paper is exceptionally long, even by GMD standards, and we appreciate that our suggestions are unlikely to shorten it. One possible avenue might be to separate the manuscript into two shorter manuscripts in which the pelagic and benthic submodels are (semi-)separately described and explored. At present, the manuscript does not do the benthic submodel justice.

This underlines a fundamental problem in accomadating a significant number of your comments. Given the considerable size of the manuscript in the submitted form and the addition of the background information on the various model formulations we can not accomodate a lot of the suggestions you've made without splitting the work into pieces. This would result in a different work, that is against our main purpose with this manuscript which is to provide a description of the model as a whole. On the contrary, we have opted to focus on a full mathematical description in this work accompanied with reproducible examples. Summarising a model of this volume in a single publication will always be a challenge as it is impossible to enter into the details of the individual processes within a reasonable limit of length, but we believe there is merit in presenting the concise description in itself as a reference to interested readers. Furthermore, we have refrained from splitting the benthic from the pelagic model description as the two systems are deeply interconnected therefore both systems should be thought of as a single framework and not as two separate pieces.

With respect to the sediment model, we have amended the section of the benthic model in various parts, which we believe gives now an adequate description of this part of the model.

Overall, we believe that the paper in its current form, including the amendments we suggest for the revised manuscript, is certainly longer than average, but still of acceptable length for GMD.

Andrew Yool, Tom Anderson and Katya Popova:

5. The extensive use of idealised 0D and 1D configurations followed by just two paragraphs on a 3D configuration does something of an injustice to ERSEM's long record in 3D work. While the former configurations have particular uses, as the authors note, they are a poor representation of what ERSEM is capable of. We would suggest that that manuscript would be much improved if the focus was on the 3D model (either in shelf seas or global mode) with passing mention made of these useful, cut-down modes.

Andrew Yool, Tom Anderson and Katya Popova:

6. On a related point, the demonstration of ERSEM's range and utility is very weak. The ways chosen to illustrate this are limited and do not provide any context for the model-observation comparisons (i.e. is ERSEM doing well / badly relative to other models?). This is compounded by some weak figures and analysis, but is principally hampered by the focus on idealised cases rather than ERSEM's work in 3D (which, as already noted, is given seriously short shrift in this draft of the manuscript). Again, we would strongly suggest that the authors examine recent model descriptions in GMD, of which the PISCES model provides (in our opinion) a good example.

Our decision to focus on “simpler” test cases here is following two main motivations in order to support transparency and reproducibility:

- This class of test cases eases the approach to the model to unfamiliar readers as the effect of model mechanisms is more directly tractable and clearer than in a full 3D applications where the interactions with the physical driver are much more complex.
- The 0D and 1D test cases are easier and faster to set-up and have much lower demands on data volumes of in- and output data and much lower requirements in computational power to run the simulations allowing the reader to reproduce our examples on any standard work station or laptop. This enables us to provide the full input data and configuration required to reproduce the test cases, and it enables the interested reader to reproduce all our test cases on a standard work station without the need of access to a high performance computing system.

This approach offers the interested reader the actual possibility of taking the paper, downloading the code and reproducing the examples given at full extent.

In addition, as you rightly state, the model has a long history of simulations in full 3D. But instead of repeating these we have decided to focus on the simpler reproducible applications. The full spectrum of model applications and validation studies it has been subject to is extensively referenced in the introductory and concluding remarks providing providing the background of more detailed work at full scale.

Finally, model intercomparison is surely a useful and interesting exercise (and ERSEM already participated in one of these exercises, see Kwiatkowski et al., 2014), however it is not the aim of this paper that is focussed on describing ERSEM and its ability to reproduce observed patterns in some illustrative test cases (see also point 8).

Andrew Yool, Tom Anderson and Katya Popova:

7. ERSEM's treatment of alkalinity appears to have several confusing elements. Calcifiers are included, but alkalinity is effectively implicit ... while also being open to modification - it's not at all clear how the model can "remember" this modification in the absence of an explicit TA tracer. It is also unclear what this does to carbonate chemistry and air-sea CO₂ exchange. On a related point, if TA is a function of T S, what happens to it at depth where these relationships completely breakdown because of the biological pump? More broadly, either ERSEM or the manuscript (or both?) are not self-consistent when it comes to alkalinity - even simple nutrient-restoring models manage this more straightforwardly.

The description of the alkalinity options in the carbonate system submodule unfortunately hasn't been very clear. We have clarified the options for the alkalinity computation in an amended version of the final part of the carbonate system section:

Two different modes to compute total alkalinity are provided with the model:

- A diagnostic mode, that computes alkalinity from salinity or salinity and temperature. This mode is non conservative and the field of alkalinity is recomputed at each time step without physical transport. It does not include changes to alkalinity by the biogeochemical processes of the model.

- A prognostic model, that includes biogeochemical changes to alkalinity, is fully conservative and adds a state variable for alkalinity that is subject to physical transport.

As a third semi-diagnostic option, these two modes can be combined as a sum by setting the prognostic alkalinity state to 0, so that the diagnostic mode provides the background field and the prognostic mode gives a trace of the contribution of biogeochemical processes to the total alkalinity.

The recommended option is the semi-diagnostic option for coastal applications and shelf seas, where reliable and robust regressions exist or the fully prognostic mode, where no single reliable regression is available, e.g. in global simulations. (For further detail the reader is referred to Artioli et al., 2012)

The changes of alkalinity due to biological processes are given by sources and sinks of phosphate, oxidised nitrogen and ammonium as well as calcification and dissolution of calcite:

$$\left. \frac{\partial A_{\text{bio}}}{\partial t} \right|_{\text{bgc}} = \left. \frac{\partial N_{\text{N}}^{\text{amm}}}{\partial t} \right|_{\text{bgc}} + 2 \left. \frac{\partial L_{\text{C}}^{\text{calc}}}{\partial t} \right|_{\text{diss}} - \left. \frac{\partial N_{\text{P}}}{\partial t} \right|_{\text{bgc}} - \left. \frac{\partial N_{\text{N}}^{\text{ox}}}{\partial t} \right|_{\text{bgc}} - 2 \left. \frac{\partial L_{\text{C}}^{\text{calc}}}{\partial t} \right|_{\text{calc}} .$$

In three dimensional simulations, these changes are accompanied by the effect of riverine inputs (see Artioli et al., 2012).

Andrew Yool, Tom Anderson and Katya Popova:

8. The concluding statement “The ERSEM 15.06 model is the only model currently available that provides the structure for simulating in one coherent system the biogeochemical cycles of carbon, the major macronutrients and iron, the carbonate system and calcification, the microbial food-web and the benthic biogeochemistry” is over-reaching in the extreme. That this description is not backed up in this manuscript by any strong evidence that it does a good job on any of these components makes it difficult to sustain. The manuscript needs to demonstrate ERSEM’s skill (e.g. comparison with a range of other models) to justify as strong a statement as this.

It is not our intention with this phrase to underline that ERSEM would be better with respect to any other models in all these aspects. Given that

we don't provide a model inter-comparison in this paper (which would go beyond the scope of this paper), we have omitted any comment at this point on the actual quality of the model elements mentioned compared to other models. We have simply stated that the model in the current form "*provides the structure*" to include these processes in simulations and that is to our knowledge unique. Given that we also provide a full description of each of these elements, it is transparent to the reader/user how and to what detail these processes are included or not. Based on these considerations, we believe this is a fair statement. In any case, we have slightly changed the phrase to:

The ERSEM 15.06 model is to our knowledge the only model currently available that provides the structure for simulating in one coherent system the biogeochemical cycles of carbon, the major macronutrients and iron (using variable stoichiometric relationships), the carbonate system and calcification, the microbial food web and the benthic biogeochemistry.

3.2 On the specific points

Andrew Yool, Tom Anderson and Katya Popova:

- Why is this version "15.06" of ERSEM?; why not version 15?; like many models, ERSEM is documented sporadically so does it really need a ".06" designation in its version number?; this especially seems odd given that previous manuscripts do not routinely report a specific model revision, and also because this manuscript will presumably be the go-to description for the model for years to come; in the language of modern marketing, Apple promotes iOS 9, not iOS 9.06 ...

The version number refers to the year.month of the release. There are undoubtedly different approaches to versioning computer software, most of them are based on either a running number, like iOS, or on the time of the release, like some windows releases or the ubuntu operating system. We have decided to go for the release number based on the release time in order to avoid the difficulty of attributing an adequate running number given the dispersive development previous to this release. The decision to include year and month leaves us the opportunity to release more than once in a year, which may or may not be necessary, but in this way at least we are not restricted by the version number.

We have added the following phrase to the code availability section:

The versioning convention used with this software refers to the year and month of the release.

Andrew Yool, Tom Anderson and Katya Popova:

- An explanation of the differences between BFM and ERSEM might be helpful; they are introduced as cousins but one is shelf seas while the other is (at least ostensibly) open ocean

Actually also the BFM branch of the ERSEM model has been applied on the shelf and in the global ocean as alluded to in the introduction on pg. 7065, lines 8-13, references to Leeuwen et al. 2012 and van der Molen 2014. As the main concepts of the two models are very similar, but the differences lie in smaller details of the model equations, we believe that a listing of the differences in between the two models would be more confusing to the reader than it would help and would lengthen the manuscript considerably. In addition, we would be obliged to compare an up-to-date description of 2015 with the last publication of the BFM dated 2007, which would probably not give a fair representation of the current state of the BFM. Again, a model comparison is not our purpose here, but on the base of this work any interested reader has full access to the description of our model in order to compare.

Andrew Yool, Tom Anderson and Katya Popova:

- Lots of examples of diverse use are given in the introduction, but it's used in a very narrow way in this manuscript; arguably, the 1D uses are rather passé when we know that it's more routinely used in 3D and even at the global scale (of which, the manuscript is rather coy about its performance)

There is a variety of examples of 0D and 1D uses of the ERSEM model along the 3D works in recent scientific literature and the manuscript gives references to these works. We believe that scrupulous, intensive and well documented model development in idealised 0D and 1D implementations should be at the base of any full scale model implementation, because by simplifying the context they allow to isolate the different model components and to better understand the interaction among these. Up to this day there is a long record of publications using the ERSEM model

in idealised 0D or 1D simulations (including recent ones) and as far as we are concerned, there will be a lot more in the future.

Andrew Yool, Tom Anderson and Katya Popova:

- A “model of intermediate complexity” is an odd way to hear ERSEM described; relative to most other plankton models, it’s more a “kitchen sink” model in which complexity has been successively extended to include functional groups for which there is arguably still only limited knowledge about; perhaps some examples of other models would make this intermediate status clearer?

What we intended here is that the model is certainly on the complex side of biogeochemical models, but compared to some models of the marine food-web, the complexity of the ecosystem representation is rather reduced.

In any case, we have removed the statement concerning the complexity of the model as it is not further explored in this work.

Andrew Yool, Tom Anderson and Katya Popova:

- What does “a particularity of ERSEM” actually mean?; this is not unique to ERSEM by a long chalk

Of all the main models currently in wider use, to our knowledge the majority of models still uses fixed stoichiometric or limited stoichiometric dynamics of individual constituents. So while we don’t insinuate this is an exclusive characteristic of ERSEM, it is still a particular element compared to the bulk of models available. Nevertheless, we have rephrased to:

Importantly, ERSEM uses a fully dynamic stoichiometry in essentially all its types (with the exception of mesozooplankton, benthic bacteria and zoobenthos which use fixed stoichiometric ratios).

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 1 does not do a good job of describing something as complex as ERSEM; it would be far better to separate out the pelagic and benthic components and do a better job separately for each; for instance, the diagram makes it look like all phytoplankton use

all nutrients, that all zooplankton have access to all phytoplankton, and that there's only a single size class of detritus (which the text later makes clear is not the case); also, the diagram has no need of including the carbonate system in this way - one assumes pH and omega; the arrows on the diagram, in particular, for this part are unhelpful since they imply that alkalinity is consumed by not just the phytoplankton (and possibly the "microbes" and zooplankton; which P and Z, incidentally, is left to the imagination of the reader) but also the DIC system, which in turn is consumed by pCO₂

Just as the paper is aiming to give an all-in-one description, the rationale for this figure is to give an overview of the model in its entity, which we believe is a crucial requirement for a manuscript such as this. Consequently much detail is omitted from this diagram, which aims to show the interactions between model components, not just fluxes of biomass or compounds. This is why the links with the carbonate system are appropriate, and we believe pertinent to include. We have however improved the figure in order to make our intentions clearer.

Multiple size classes of particulate organic matter (and labilities of dissolved organic matter) were already implied by the previous diagram, but have been made more explicit. Very similar versions of this figure have been published in many other publications to date as an introductory overview of the model.

We agree that additional diagrams could help to illustrate some of the more detailed aspects of the model in other points of the manuscript (e.g. the connections between prey and predators mentioned in a later comment and diagrams of the two bacteria sub-models) and we will provide these in the revised manuscript.

Andrew Yool, Tom Anderson and Katya Popova:

- Stating "small scale and high resolution applications" would benefit from having scales attributed to them; among other things, the continuity assumption is only ever an approximation

The continuity assumption is in fact always an approximation. The point we are making here is that one needs to keep in mind that this approximation is only justifiable when one is looking at the dynamics from scales coarse enough so that the abrupt discrete changes vanish. A precise limit is hard to define and depends on the precision required, but as

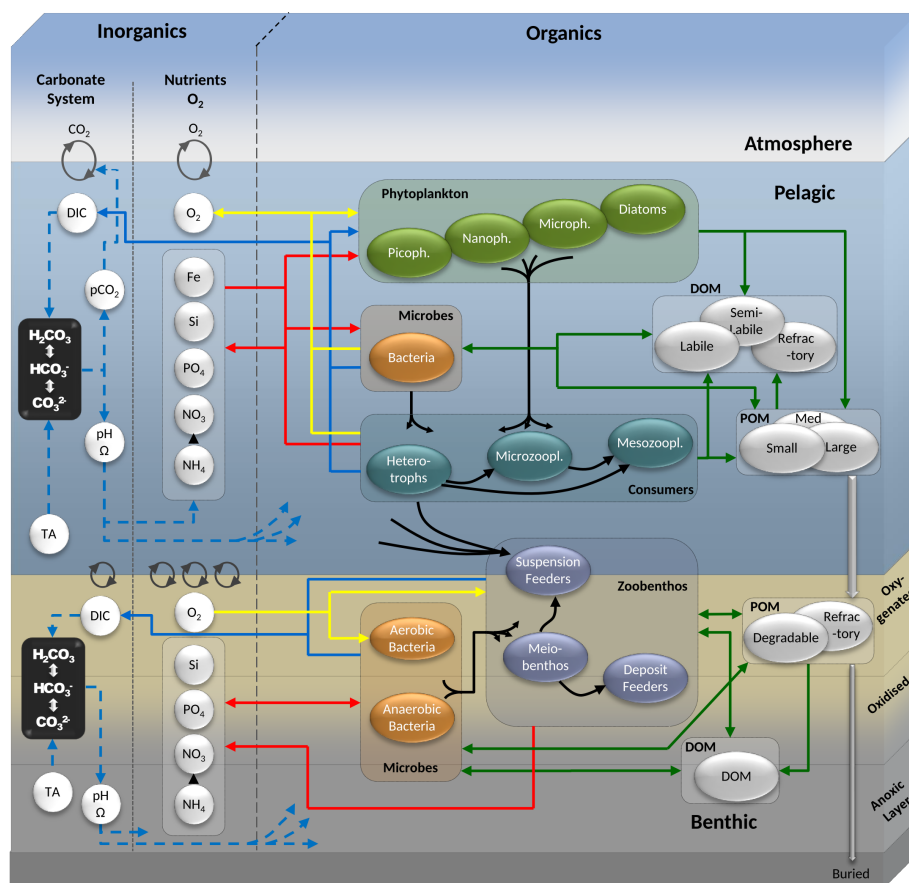


Figure 1: ERSEM schematic showing how model components interact with or influence each other. Blue connectors represent inorganic carbon fluxes, red represents nutrient fluxes, yellow represents oxygen, black represents predator-prey interactions and green represents fluxes of non-living organics. Dashed arrows indicate the influence of carbonate system variables.

a rule of thumb one should use scales that are at least an order of magnitude larger than the body and patch size of the modelled organisms. We have added the following phrase to the manuscript:

As a rule of thumb, in order to guarantee the validity of the equations, the modelled scales should at least be an order of magnitude bigger than the organisms modelled and smaller patches.

Andrew Yool, Tom Anderson and Katya Popova:

- Table 3, which describes the predator-prey relationships in the model, would surely have been better off as a diagram; Figure 1's job should have been this

We agree, we will add these figures to the revised manuscript.

Andrew Yool, Tom Anderson and Katya Popova:

- From the get-go the equations, while doubtless mathematically correct, are fairly impenetrable to read; it would be a lot of work to understand and follow them enough to reproduce them in another model; and why is the format of a vertical line followed by a shorthand description used?; wouldn't underbraces, or just well-chosen names, be better?

The general principle we have followed in presenting the equations, as described in the answer to the similar general comment above (1.), is to give an overview of what processes affect a single organism in form of the general balance equation, followed by the specification of the individual terms. Taking also into consideration the feed-back of the two nominated referees, we don't have the impression that the general layout of the equations is a major problem in principle. However, we admit that on occasions the specification of individual terms was slightly convulsive and has not helped readability. Consequently, we have changed these where they've occurred to us. We believe that these changes have improved the readability of the overall manuscript even further.

As for the notation style of vertical lines specifying types of source-sink terms, the choice between our notations and other forms as underbraces is surely subjective and we have favoured the vertical lines (which has also been used in other works, e.g. Vichi et al., 2007).

Andrew Yool, Tom Anderson and Katya Popova:

- In section 2.3, how sensitive is the model to the size of this number?; while it's small, it's a value that the model could reach relatively easily; also, does this mean that the ocean has an enormous standing stock of biological material when integrated everywhere?

Sensitivity studies we have performed when introducing this threshold have shown that the results in spun-up simulations remain unaltered in between runs using this negativity control and runs that do not use the concentration buffer. The model indeed reaches values of 0.01 mg m⁻³ carbon at times, but these occasions have entirely negligible impact on the model dynamics and overall flux budgets. As for the biomass budgets over entire domains, one should use the available biomasses to compute the overall budgets in order to exclude these background concentrations. We have added a corresponding comment to the revised manuscript:

Note that when calculating the overall budgets of a domain, these background concentrations should be subtracted in order to give adequate results.

Andrew Yool, Tom Anderson and Katya Popova:

- We presume that “hetero nanoflagellates” are “heterotrophic nanoflagellates”?

Thanks, we have corrected this.

Andrew Yool, Tom Anderson and Katya Popova:

- The equations contain a large number of diverse functional forms, but these are neither sourced to particular work, nor are the functional responses of them illustrated diagrammatically - this might help in the more complex cases; for instance, how is the rather complex nitrification equation derived?; is there empirical support for such a multi-factorial form, or is it a composite function based on separate studies for each factor?

We agree and have added a significant amount of background on the origin of the model formulations to the revised manuscript, as stated in response to general comment “2.”. Also we will add some diagrammatical representations of parts of the model (within limits to keep the paper at a sensible length, see also response to the comment on figure 1).

Andrew Yool, Tom Anderson and Katya Popova:

- Is there any exploration in the manuscript of the different bacterial degradation schemes?; if not, why not?; the text makes a point of describing both at length

The DOCDYN sub-model is simply an updated version of the standard ERSEM formulation meant to represent the bacteria-mediated production of recalcitrant DOC. The enhancements offered with this new feature in simulations is already documented in the literature (Polimene et al., 2006, 2007). As such we think that going further in exploring the differences between the two formulations is outside the scope of this paper. The tendency within the group of developers is to use the DOCDYN formulation as default bacteria model. However, for the sake of completeness we have left the possibility to choose the “old” version also considering that, in some cases, it could be convenient to run the model without the semi-refractory DOC (R3 variable in the code) reducing the computational cost. In order to make the differences of the two sub-models more transparent we intend to include diagrams showing the different versions in the revised manuscript.

Andrew Yool, Tom Anderson and Katya Popova:

- Where does this calcification form originate?; it is not sourced; also, extra functionality is described for CaCO₃ dissolution but again appears unexplored; ordinarily one would expect a sensitivity analysis section in the manuscript, not least to help users of ERSEM decide which of the optional functions (here and elsewhere) they should use; of course, it may be obvious from the sources of the functional responses, but - as noted - these are not made clear

We have amended the introduction of the calcification section in order to clarify reasoning and background of this sub-module. It now reads:

The model in its current form does not include calcifiers as a dedicated

functional group given the limited knowledge of the physiological constraint of calcification. Therefore, the process of calcification is not directly modelled, but is treated implicitly by considering part of the nanophytoplankton to act as calcifiers. Calcification processes are inferred from the system dynamics based on the assumption of a given ratio between particulate inorganic carbon over particulate organic carbon in sedimenting material, usually referred to as rain-ratio. Here this ratio is used as a

proxy for the calcite production matching the local increase of POC originating from nanophytoplankton. Since the rain ratio has been defined for the sinking fluxes and calcite is the more resistant mineral, we limit the description to calcite in this part of the model, neglecting aragonite. This approach is similar to the implementations in other biogeochemical models, e.g. PISCES (Gehlen et al, 2007) or MEDUSA (Yool et al., 2013).

Andrew Yool, Tom Anderson and Katya Popova:

- Nice light modelling, but, again, what's the difference in the schemes presented?; is either functionally superior, and does it come at extra cost?

The two models can be tuned to give essentially the same results, but the new formulation includes the major advantage of being formulated on the base of inherent optical properties, which with respect to the apparent optical properties of the earlier formulation are more directly and much more often measured. This gives the possibility to:

- base parameter choices on collected data available,
- validate the optical sub-model against data sets of inherent optical properties,
- constrain the non-modelled optical parts on observed quantities that are closer to the model formulation (e.g. ADYTRACER option),
- assimilate optical data directly rather than the derived product ocean colour.

The computational cost of the two models is comparable.

We have added the following phrase to the manuscript at the end of the section:

The two models can be calibrated to give comparable results, but the latter formulation based on inherent properties has the advantage to be based on quantities that are frequently measured, which helps in constraining the parameterisation, validation and enables the direct assimilation of optical data.

Andrew Yool, Tom Anderson and Katya Popova:

- The second benthic scheme is a bucket; would it be better to present this as tier 1, with the more advanced one as its successor (which is doubtless how the model actually evolved)

We have followed this order as the second scheme is strictly speaking not a full benthic sub-model, but more of an extended boundary condition or benthic closure as no internal process of the sediments is included. Therefore its description in fact resides in section 5 on horizontal interfaces rather than in section 4 on the benthic model. In this context we admit that the introductory section of section 4 is a bit misleading and have rephrased accordingly, see the response to the following comment.

Andrew Yool, Tom Anderson and Katya Popova:

- On benthic schemes, again, is there any sensitivity analysis on the choice?; also, the “complex” scheme is simplified from a model that is 20 years old - why not include the full scheme it’s derived from as an option?; one would expect it to be more computationally tractable now than before

The original full scheme is for most applications of unnecessary detail and numerically significantly more vulnerable than the currently implemented form, which is why it has been abandoned. On the choice of the benthic model, we have rephrased the introductory paragraph of the benthic system as follows:

The benthic model in ERSEM is predicated on muddy sediments of the continental shelf, including zoobenthos, bacteria, different forms of organic matter and implicit vertical distribution of material within the sea-bed. It explicitly describes the main functions of the sediment such as benthic predation, decomposition and recycling of organic matter, bioirrigation and bioturbation. In alternative to using a full benthic model, the benthic-pelagic interface can be described by a simple benthic closure given in Sec. 5.1.5 that adsorbs depositing particulate matter and phytoplankton and returns dissolved inorganic nutrients and carbon to the water column at a given time scale reducing the sediments to a simple buffer layer of organic matter recycling, that however does not involve any explicit benthic processes. It is computationally considerably lighter compared by the full model, but the computational effort in

both cases is neglectible compared to the pelagic component. While the former is more adequate for shelf seas application that are dominated by the sediment type it represents with a close connection to the productive upper ocean, the latter is most suitable in deep domains under oligotrophic conditions, where the sediment processes are of lesser importance.

Andrew Yool, Tom Anderson and Katya Popova:

- In passing, it is difficult to ascertain the total number of tracers (and parameters) in the model; a table could help

The full list of tracers in the model is in fact provided in tables 1 to 6. These tables have been split into various categories in order to fit each table on a single GMD discussion format page, but we aim to merge these into a single table for pelagic and benthic state variables each, which should make the total number of state variables transparent. Tables including all parameters are given in the supplements.

Andrew Yool, Tom Anderson and Katya Popova:

- The information in Section 6 seems oddly placed; should this not have appeared when these terms were first introduced?

The reason they appear in an individual section is that they are overarching formulations used in several parts of the model, e.g. the temperature response factor, or that their detailed description would have interrupted the logical flow of the process description if they would have been left in place, e.g. the internal nutrient limitation factors of phytoplankton. We believe that moving these where they were first introduced would deteriorate the readability of the manuscript.

Andrew Yool, Tom Anderson and Katya Popova:

- Section 6.2's stoichiometric adjustments are presented as if they are a simple fudge rather than being derived from an existing formulation; is this correct?

These terms are indeed stoichiometric correction fluxes in order to close the mass balances, we have clarified this point in the manuscript:

For states ϕ^x with fixed stoichiometric quota $q_{N,P,C}^x$ (mesozooplankton, benthic bacteria and predators) the process rates are complemented by exudation fluxes that regulate imbalances on order to preserve the fixed reference quotas as follows: ...

Andrew Yool, Tom Anderson and Katya Popova:

- ERSEM-Aquarium seems to be a perfect system that could be used to examine the model's sensitivity to the extra functionality that's loaded onto it; but that hasn't been done here

As stated in an earlier point, we are unable to address the suggestions raised that would extend the length of the work considerably, given that we are inclined to stick to our approach of providing a single paper with the full description of the model. To underline our issue here, we are asked to

- consider the excessive length of the paper.
- change the balance of 0D, 1D and 3D applications in favour of 3D applications.
- include more 0D applications with sensitivity studies.

which is simply not possible maintaining the same concept of the paper.

Having to choose, we have decided to show as a 0D simulation an example that illustrates the pathways of the model in contrasting environments to illustrate the overall model dynamics in different conditions rather than an individual sensitivity study.

Andrew Yool, Tom Anderson and Katya Popova:

- The manuscript's imbalance towards idealised frameworks (0D, 1D) is difficult to understand given that ERSEM is largely used in 3D simulations

The motivation for our balance is given by our aim to provide lightweight and easily reproducible examples along with a complete transparent description as described more in detail in the general comments

above, while the full-scale applications are best dealt with within dedicated publications that do justice to the physical processes and their interactions with the biogeochemistry. For this paper that deals specifically with the ingredients of the biogeochemical model we believe that the examples we give provide the better focus. In addition, we are referring to some recent examples that use the ERSEM model in various parts of the manuscript.

Andrew Yool, Tom Anderson and Katya Popova:

- Section 8 is an anomaly; ostensibly about the “Development and Testing Framework”, it wraps up on a discussion of diatoms and chlorophyll which should really appear during the model description

The purpose of this paragraph illustrates on the base of a practical example of how the software infrastructure can be used to test individual components of the model and perform sensitivity analysis. The discussion of the photosynthesis description of the model occurs in this place in order to explain the context of the example plots, but the purpose of the paragraph remains the illustration of the possibilities offered by the software package in isolating the individual process formulation. We have modified passages across the entire section in order to maintain the focus and make its purpose clearer.

In addition to the 0- and 1-D ERSEM implementations a framework is provided with the model that allows developers and users of the code to analyse and plot the result of calls to individual ERSEM procedures from Python. This facility is supported through Fortran-C interoperability, that arrived with the Fortran 2003 standard (ISO/IEC 1539-1:2004(E)), and the Python Ctypes package. ERSEM test harnesses consist of the ERSEM library and a set of C wrappers, which are jointly compiled as a shared library. A Python interface to the shared library permits access to Fortran data structures and procedures from Python. This allows developers and users of the code to quickly interrogate the validity and behaviour of individual procedures, without first reimplementing them in a second language, and without running the full model. Here we illustrate this feature by examining the photosynthesis model implemented in ERSEM.

The photosynthesis model used in ERSEM is based on Geider et al. (1997), and is described in Sect. 3.1. In the model, photosynthetic cells are able to regulate their chlorophyll *a* to carbon ratio in response to changes in irradiance, temperature and silicate (in the case of diatoms) by modifying the proportion of photosynthate that is directed towards chlorophyll biosynthesis ($\bar{p}$; see Eq. 9). Balanced growth is achieved when cells are fully acclimated, in which case:

$$\frac{d}{dt} \left(\frac{\bar{p}_c^x}{\bar{p}_c^x} \right) = 0 \quad (5)$$

Chlorophyll *a* biosynthesis is assumed to be up-regulated in response to a reduction in irradiance and down regulated in response to an increase in irradiance. Through this process, cells are able to balance the rate of energy supply through light absorption, and energy demands for growth. The maximum, light saturated photosynthesis rate $\bar{g}(T)$ is assumed to be independent of changes in irradiance, which is consistent with observations which indicate Rubisco content is relatively invariant with respect to changes in irradiance (Sukenik et al. 1987), and the hypothesis that these cells are adapted to survive and reproduce in dynamic light environments (Talmy et al. 2014).

Using the ERSEM testing framework, it is possible to investigate this process in isolation. Model cells can be artificially acclimated to a given set of environmental conditions by finding a value for $q_{C:C}^x$ which satisfies Eq. (263). Figure 8 shows a plot of $q_{C:C}^x$ vs. I_{PAR} for fully photo-acclimated diatoms in ERSEM. Cells were acclimated to a given irradiance by holding cellular carbon fixed and varying the cellular chlorophyll *a* content within the range $\bar{q}_{min_{C:C}}^x \leq \bar{q} \leq \bar{q}_{\varphi_{max}}^x$ in order to achieve balanced growth. Using the testing framework, the model can be compared with observations in order to sanity check the validity of the implementation, or parameterised against observations using curve fitting procedures. In Figure 8, observations for the diatom *T. Pseudonana* have been overlaid. No attempt was made to fit the curve to this particular set of observations, although the fit appears reasonable. The parameter set is the

same as used in the simulations of Sect. 7 and is given in the Supplement.

Diatoms are a physiologically and morphologically diverse group, which are characterised by their requirement for silicate, which they use to construct their cell wall. It is perhaps unsurprising that model fits to photosynthesis-irradiance curves for different diatom species result in a range of parameter values, including differences in the maximum light saturated carbon specific photosynthesis rate as a function of temperature, and the initial slope of the photosynthesis-irradiance curve (e.g. Geider et al., 1997). Ultimately, many of these differences arise due to differences in organism morphology and physiology, with, for example, different pigment complements or levels of investment in biosynthesis, being reflected in derived parameter values. These within group variations pose a perennial problem to the development of marine ecosystem and biogeochemical models. The diatom group in ERSEM is designed to be representative of diatoms as a whole, and to reflect the important biogeochemical role these organisms perform in nature.

ERSEM includes four phytoplankton functional groups: diatoms, which are characterised by their requirement for silicate, and three further groups which are characterised according to their size. These are the pico-, nano-, and microphytoplankton. The choice to characterise groups according to their size reflects the importance of size as a physiological trait (Litchman et al., 2007, 2010), which influences an organism's competitive ability through its effect on nutrient acquisition, carbon and nutrient storage, the intracellular transport of solutes, photosynthesis rates through pigment packaging effects, and susceptibility to predation (e.g. Chisholm, 1992; Finkel et al. 2010).

Using ERSEM's testing framework it is possible to demonstrate how this classification impacts the competitive ability of the four photosynthetic groups represented in the model. Figure 9 shows photosynthesis-irradiance curves for ERSEM's four phytoplankton groups under the condition of balanced growth. As with the diatoms, the use of a single parameter set for each size-based group ignores within group variations that are observed in nature. It is important to take such abstractions into consideration when interpreting model outputs.

This example illustrates how ERSEM's testing framework can be used to study and check the implementation of different processes within the code. Importantly, this is achieved without having to rewrite sections of the code in a second language with visualisation capabilities, which is an inherently error prone procedure. This capability is designed to complement the 0-D and 1-D drivers that simulate more complex time-varying environments, in which it is often difficult to study processes in isolation.

Andrew Yool, Tom Anderson and Katya Popova:

- Section 8's concluding paragraph on not having to write visualisation for the model in a second language is unnecessary; most users would almost certainly run the model and visualise the output alongside in a separate program anyway

This is a misunderstanding, this statement is not referring to a second programming language in order to perform the visualisation after running the full model. On the contrary the purpose of this part is to demonstrate, that the test harness enables the testing of isolated pieces of the code running only a specific part of it without the need to export it or even rewrite the mathematical formulation in a separate environment. Importantly, this is achieved by directly operating on the same instance of the code that is used for the full simulation, without having to extract and rewrite the part of the code related to the investigated process. It is simply compiled against the test harness library.

This should be clearer now that we have rephrased the section (see previous comment).

Andrew Yool, Tom Anderson and Katya Popova:

- Table 2 - this has got to be among the most arcane naming convention we've seen

We are sorry that you don't appreciate our naming convention. It is an attempt to use a consistent convention throughout, starting from a basis that relates functional types to variables in the model without using numbers for legibility and were possible relating to the code names inherited from the early ERSEM versions.

Andrew Yool, Tom Anderson and Katya Popova:

- Table 3 (and other locations in the text) - “preys” is grammatically incorrect; “prey” is both plural and singular, like “sheep”

Thanks, corrected.

Andrew Yool, Tom Anderson and Katya Popova:

- Table 4 - “particulate” spelt wrong

Corrected.

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 1 - inadequate; would benefit from being split into pelagic and benthic components, and from a focus on the core nutrient cycles rather than including peripheral (in a diagrammatic sense) processes; arrow heads are also missing in places, and sometimes convey implausible pathways (e.g. TA → DIC → pCO₂)

See previous comment on the same topic.

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 2 - the use of line thickness does not make this diagram clear; it’s also missing what would be interesting detail re: differing phytoplankton and zooplankton fluxes between functional types; the diagram also makes it look like different model structures were used rather than just different pathways being favoured; that these different foodwebs are derived from idealised simulations makes the inclusion of this diagram questionable

We are not sure why the use of line thickness would be not clear. The choice to omit details concerning the functional types of phytoplankton and zooplankton was taken to keep this diagram readable and clear. Also, the general behaviour of the modelled phytoplankton community structure is later on illustrated in the summary plot on the 1D simulations (figure 6).

Concerning the model structures, we assume this refers to the benthic components and they are in fact different. As is clearly stated in the text on this test case and referring to this figure, on pg. 7149 lines 1-4 the oligotrophic case uses the simple benthic closure while the eutrophic case uses the full benthic model.

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 3 - are the modelled cycles really out of phase in places?; that's not good; also, these target diagrams would be much more useful if they compared the model to another model (or different versions of the same model; like, for instance, versions using different options); as it stands, all the reader can see is that the model performs differently well for different properties (which, to be fair, is all that showed in our MEDUSA-1 paper, but in MEDUSA-2 we also included model intercomparisons); that the model shows that the relative fit for different properties varies between sites (Figures 3-5) makes it difficult to judge how ERSEM is actually performing.

We are interested here in a full description of the ERSEM model and already push the manuscript to its size limit. The inclusion of a fair comparison to a different model would require an adequate description of this model and planned common joint experiments like the one published in Kwiatkowski et al., 2014, in order to achieve a proper and fair comparison. Comparing different version of the model would be surely interesting, however we believe that this will push the manuscript beyond its limits. That the model behaves quantitatively differently in different environments should not be a big surprise. In our experience, any model will perform differently between fundamentally different sites, the important point here is that it doesn't completely fail in one with respect to the other. As for the chlorophyll-a being out of phase, we have alluded to possible reasons for episodic deficiencies in the text, these occur mainly in periods when data is scarce and is barely sufficient to individuate the seasonal cycle, while for the last, more data rich years, the bloom timing appears to be well captured for a 1D model of a shelf site, where lateral advection is not included. We have added a paragraph explaining the issue and limitations of modelling a shelf site in 1D:

In addition, some deficiencies, in the model simulations are to be expected as the Oyster Ground site is characterised by strong lateral influences including estuarine, coastal and channel waters that include strong direct impacts on the nutrient concentrations in the area that can not be captured in this idealised setting. Particularly in the stratified season in summer these lateral effects are dominating the surface water signal while the deeper part of the depression is essentially isolated from the surface layer (Weston et al., 2008)

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 4 - seems to show the model including a bloom that doesn't occur in the real world at all

We do agree that the simulation of chlorophyll a presents limits (especially at L4). Our intention was to make this clear by the objective comparison with data we presented and by discussing the issue in the text. In particular, as you correctly point-out, some chlorophyll peaks seem to be out of place. However, it should be considered that the L4 station is a highly variable site, strongly affected by riverine inputs (Smyth et al., 2010) which are only partially (through the assimilation of T&S observed profiles) taken into account in our one dimensional framework.

All these issues make the simulation of chlorophyll a at L4 particularly challenging. However, even with all these caveats, the simulated spring bloom (chlorophyll) is still comparable with the climatological values (in terms of both phenology and concentration) for the L4 site. From figure 4 it emerges that the spring bloom is simulated in April which is consistent with Fig 12 of Smyth et al 2010

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 5 - this figure has a number of issues; these include: 1. Including the model spin-up period in the plot when it should be perfectly possible not to do this; 2. Showing the model for a period when there's no data; 3. Not having data on a plot when the data is widely known to exist (this looks suspicious); 4. Showing the same data twice for no good reason

We agree to the first two points. As for the data, we have taken the Turner chlorophyll-a data from the source we are referring to in the manuscript and are not aware of any omission. In any case, in order to address your concern, we have replaced this with the HPLC data available, which doesn't have the gaps and extended the simulation period up to July 2012. In the new Hovmöller plot of chlorophyll-a we have now excluded the scatter plot and show only the interpolated in-situ data. (We had included the scatter plot in order to illustrate to the reader the level of availability of data.) Both, the Hovmöller plot and the statistics now exclude a spin-up period of four years.

Andrew Yool, Tom Anderson and Katya Popova:

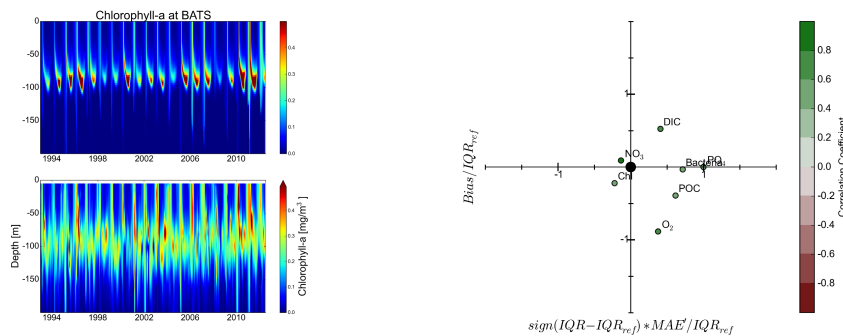


Figure 2: Simulation results vs. in situ data at BATS – left: chlorophyll *a* concentrations (Top – model, bottom – interpolated HPLC data); right: target diagram with bias (abscissa), MAE' (ordinate) and spearman correlation (colour code) for oxidised nitrogen (NO₃), phosphate (PO₄), silicate (Sil), dissolved inorganic carbon (DIC), dissolved oxygen (O₂), chlorophyll *a* (Chl) and particulate organic carbon (POC).

- Figure 6 - any observations here?; for instance, Hirata et al. (2011) and Ward (2015) present absolute and fractional chlorophyll data that would provide a good comparison; as it happens, it looks like ERSEM is going a good job here

We are in fact referring to the Hirata et al. paper in the text discussing the figure and specifically to figure 2a-c therein which shows the close match in community structure (pg. 7154 line 25 to 7155 line 4).

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 7 - while eyeballing model vs. observations is considered bad form these days, would it really hurt here to show the spatial map of observed chlorophyll?; we know it exists because the model has been compared to it

We believe that it is not possible to produce a meaningful comprehensive map comparable to the model based on the data used for the comparison. As stated in the text (7154 lines 22-23) and in the figure caption, we compared the full hindcast with in situ data from the ICES database, i.e. with bottle data. For this reason data are sparse in time and space, therefore a synoptic map cannot be produced without significant interpolation bias. We could produce a comparable map if we used satellite

derived Chlorophyll, however this way we should limit the comparison to a much shorter period. Finally, the aim of section 7.3 and figure 7 is not to provide a comprehensive validation of the 3D implementation of ERSEM in the North Western European Shelf, this has already been done several times (e.g. Lewis et al., 2006, Allen et al., 2007, Allen and Somerfield 2009, Shutler et al., 2011, Artioli et al., 2012, Holt et al., 2012 to name a few) but to illustrate the potential use of ERSEM in a 3D implementation.

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 8 – is this comparing the model to a dataset that was used to parameterise it?; that seems to undercut the rationale for this figure

In the first instance, we are quoting pg. 7156 line 17:

“No attempt was made to fit the curve to this particular set of observations.”

In addition, this figure appears in the section of the testing framework whose purpose is to check the correct implementation of isolated pieces of the model. So we don't think it undercuts the purpose, quite the contrary, it shows that the model behaves as was intended.

Andrew Yool, Tom Anderson and Katya Popova:

- Figure 9 - is there any observational data to add to this plot?; and why is this plot not in colour?; it is difficult to discern the different lines easily

Again, the purpose of this plot is not a model validation, but the possibility to isolate parts of the code and use them on their own for sensitivity studies, in this case an illustration of the effect of different parameter values for the modelled P-I-curve. For this purpose the data is not required. We have included this plot in colour now.

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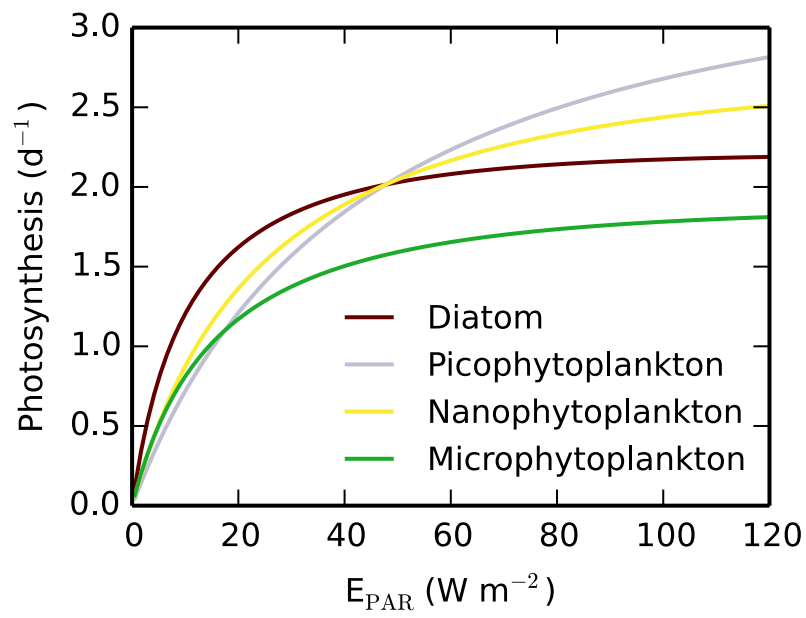


Figure 3: Phytoplankton growth over PAR for the four phytoplankton types.

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