Dear Editor,
Dear Reviewers,

please find our response below:

Editor:

In addition to the comments made by the referees, I note that the acknowledgements section in the last revised manuscript draft contains a "???" mark. Please amend this to the appropriate grant number in the final manuscript.
We added the grant number.

Note, also, that one of the referees has rescinded their anonymity, and can be acknowledged formally by name.
We now explicitly mention Momme Butenschön in the acknowledgements.

Referee 1:

-The authors have added a useful table (210) showing the increase in computing time per tracer versus number of tracers but do not provide any description or comment on the table itself. Maybe a few words after lines 736-738.
Previous passage:
„The MatMult operation takes up 19,8% of computational time for the N model, but 56,7% for the NPZD-DOP model. The implications of these results are discussed in Section 7. Additionally, in Table 210 the absolute timings and the computing time per tracer versus number of tracers are shown."
New Passage:
„The MatMult operation takes up 19,8% of compu- tational time for the N model, but 56, 7% for the NPZD-DOP model. In Table 210 the absolute timings and the computing time per tracer versus number of tracers are shown. The figures confirm the growing dominance of the matrix vector multiplication. The computing time per tracer converges towards 22 s, which is the absolute time spent by the MatMult

operation per tracer in each model. The absolute timings of the biogeochemical model and the interpolation stay (more or less) constant. They are split among all tracers and thus become less significant. The implications of these results are discussed in Section 7.
“

-Line3 931-932: consider being more quantitative here.
Previous passage:
“Using this balancing method a close to optimal speed-up by spatial parallelization was achieved up to the relatively high number of 128 processes. The difference to standard load balancing is immense.„
New passage:
„Using this balancing method a close to optimal speed-up by spatial parallelization was achieved up to the relatively high number of 140 processes. This results in an acceleration factor of four compared to the TMM framework. The factor increases even to five, if 200 processes are used. However, here already 20% of computational resources are wasted.“ (lines 929-935)

<u>Referee 2, Momme Butenschön:</u>

***Lines 73ff**: A fully coupled system includes the computation of the biogeochemical sources and sinks as well, i.e. the actual ecosystem model.*
Yes, of course. Changed to: „For any fully coupled simulation, i.e. simultaneous and interdependent computations of ocean circulation, tracer transport and the biogeochemical sources and sinks in three spatial dimensions, very high computational efforts are needed even at low resolution.“ (lines 55ff)

***Lines 612ff**: That depends on the implementation of the biogeochemical model. Some models have taken into account the preference of order of the transport schemes and operate in the same way as the transport schemes.*
Yes, of course. In general, that is right. But in this case, we think it is clear that we refer to the data alignment used in Metos3D for the application of transport respectively the evaluation of the

biogeochemical (water column) model. We don't see the compelling need to change the statement.

Line 933 *compared*
Corrected. (line 634)