

In regards to the question of the model purpose the answer is rather dull and interesting. It is an EU project funded to bring together modellers so as to produce modelling solutions to indicate the effect of anthropogenic change on MSFD descriptors.

Title : A suggested new title has been proposed in the manuscript: '*Couplerlib: A Metadata driven library for the integration of multiple models of higher and lower trophic level marine systems with inexact functional group matching.*' We will still need to confirm this with the Editors to deal with database problems.

Incidentally

P2 L26-27 Changes – emphasis that this makes the benthic component more top down and expansion of section. In 2<sup>nd</sup> Paragraph of section 2.6 have mentioned that there is active work ongoing in improving LTL models for better benthic community modelling.

P3 L17 I have added a section that adding an integrated section is possible but does not solve the problem of incompatibilities of algorithmic approach and does make it harder to merge code changes.

P5 L9 I have removed '@impressively'. I had previously added the sentence at the end of the paragraph 'However it does achieve a class leading degree of correspondence with observations.' So yes I had qualified my statement as indicated by the reviewer.

P6 L7 'Data consistency' I had already added the phrase '(in terms of names of groups, chemical elements and units)' which is what we are checking when we are trying to be consistent

P7 general. These 4 modes are ways in which the library and associated code has been developed, though the last 2 have not been exemplified in this paper, tags inserted in manuscript.

P7L8 I am slightly surprised this has been flagged – you cannot simply pass an array from FORTRAN to any of the .net languages as used by EwE: It won't even compile! But there are well documented ways of dealing with this. I had stated this in the paragraph in generic terms and have added more technical detail which adds a level of technicality I had not wished to go into.

P7 L22 I did not rely to this one because I am not using a multi-node supercomputer but a shared memory based workstation. I have not tried it and do not know the answer. I used Localhost to emulate networking as a way of running the model across processes. In principle as each node has a separate IP address and this sort of direct use of sockets is permitted then it should work, though I expect it would upset the SYSADMIN for using a low level allocation of resources also the local IP addresses of nodes are unlikely to be available. It is more likely that you would use this methodology to address the head node on a supercomputer running the slow LTL model given that EwE is about 1000 times faster (1 depth layer ton 20-40 and 1 day timestep rather than 10 minutes).

P15 8-12 Some of this is just a statement of what I did: daily timestep, weakly linked benthos. The low frequency response of benthos relative to pelagic has been noted in the text.

P15 L22 This is a good point. We use a system of proportional return (e.g. saying that 0.01 of phytoplankton is consumed in the HTL model in a timestep and then applying this level of consumption across all groups). Noted in text.

P16 L7-13 Comments: EwE does not have separate variables for P and N, but audits on return to conserve P and N Mass. It is a property of the model. A new explanation of the stoichiometric balancing and empirical and modelling levels of nutrient variation are mentioned.

P20 L3 The poor quality of Zoop. Prediction has been discussed 1) In workshops for the Meece and OPEC EU projects, it was discussed at the AMEMR conference and researchers at UBC (the people behind EWE) criticised the mathematical formulation of it. I have references Daewel et al. which argues the main barrier is good estimation of zooplankton mortality

I have to say also with regard your problems with the manuscript I find the GMDD process of typesetting before reviewing has made responding to reviews a particular challenge as I'm dealing with three page and line numbers for everything: My manuscript number, the typeset manuscript page number and revised manuscript. I would strongly recommend that we try and preserve manuscript line numbers for the process somehow!