

MarQuest meeting at Plymouth Marine Laboratory 9 January
Present: Icarus Allen, Jerry Blackford, Katy Lewis, Corinne Le Quéré, Erik Buitenhuis

Goal of the meeting: identify the degree to which we will undertake a merging between ERSEM and the PlankTOM model (our DGOM), and identify the immediate next step.

o some history

of the ERSEM model development

1990 ERSEM 1 created by merging 2 other models. 15 box model for the North Sea, nutrients to fish

1994 ERSEM 2 1D and 2D physics with ~105 boxes, nutrients to mesozooplankton

2001 coupled to POLCOMS physical model

2001-present: add DOC, Chl:C ratios, carbonate chemistry, bacteria with Droop quota model, plus several branches e.g. DMS, acidification, HABS

current version 41 pelagic + 15 benthic state variables

of the PlankTOM model development

1993 HAMOCC3 GCM with N2D biogeochemistry model (nutrient, POC, CaCO₃)

2003 HAMOCC5 3N2P2Z3D model

2006 PISCES-T 3N2P2Z4D model

2005 PlankTOM5 3N3P2Z4D model

developments since last published version: integration into NEMO GCM, parallelisation, using observation database in microzooplankton, ballast model

current version 27 state variables

time cost of 1 year of simulation: ~56 CPU hours (on 8 CPUs)

o We identified which parts of ERSEM and of the PlankTOM model are currently common:

C, P, Si and O₂ cycles

common PFTs: mixed phytoplankton, diatoms, coccolithophorids, mesozooplankton, microzooplankton (sort of)

semi-labile DOC and 2 particle sizes of POC

variable Chl:C and Si:C ratios

DIC speciation

CO₂ and O₂ fluxes

Technical: both codes are parallelised and run on Linux clusters

o currently different

Only in ERSEM:

N cycle

Additional PFTs: pico-phytoplankton, bacteria, dinoflagellates, heterotrophic nanoflagellates

Additional size of POC, labile and refractory DOC

Benthic model

Quota model with variable C:N:P ratios

preferential remineralisation of N and P

diurnal cycle

effect of pH on biology (preliminary version)

DMS cycle

Only in PlankTOM:

Fe and alkalinity cycles, including explicit CaCO_3
ballast model
diagnostic N_2 fixation

Technical: the codes are structured quite differently

ERSEM:

state variables are 1D, which are equivalenced in the 3D implementation
1 subroutine per PFT
non PFT state variables are changed in the PFT subroutine that affects them
negative concentrations are corrected at the end

PlankTOM

state variables are together in a single 4D array
1 subroutine per process (autotrophy, heterotrophy, etc.)
1 integrative subroutine for all state variables
processes are corrected to prevent negative concentrations
mass balance is maintained by removing particulate material from the bottom
water layer and adding nitrogen fixation at the surface

o strengths and weaknesses

both models underpredict (chlorophyll) variability by about a factor 3.

o immediate next steps

PML will run ERSEM in a configuration that is as similar to PlankTOM5 as is practically feasible, with (1) 5 PFTs and (2) fixed C:N:P ratios and analyse how important these features are for model behaviour, including interannual variability of surface chlorophyll

UEA/BAS will include bacteria and 3 additional PhytoplanktonFTs in PlankTOM, making the bacteria and pico-phytoplankton as similar as possible to ERSEM, and analyse if these improve the model performance, especially with respect to reproducing interannual variability.

Results of these immediate steps will be presented at the **next meeting** in Villefranche-sur-Mer 10-13 April

o The long term goal is to make the structure of the codes more similar. At present the codes are so different that sharing code is not an option, but sharing strengths via the intermediate step of sharing differential equations, and observational databases for constraining parameters and model evaluation can be an intermediate strategy.

Descriptions of the two models are available on the internet:

ERSEM: <http://www.pml.ac.uk/ecomodels/ersem.htm>

PlankTOM: http://lmacweb.env.uea.ac.uk/green_ocean/model/description.shtml