ICES International Council for the Exploration of the Sea
CIEM Conseil International pour l'Exploration de la Mer

Theme Session L –Spatially explicit models for plankton and fish: processes, model integration, and forecasts

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Summary

Coupled models of the ocean circulation and plankton continue to improve their representation of the spatial and temporal variability of the marine environment. These models provide a solid basis for describing the current state of the ocean and projecting future states. To project changes in fish distribution and productivity under global change, models of different fish life cycle stages are also being developed. Models of lower and upper trophic levels can now be integrated. This theme session targeted presentations that attempted to meet current challenges faced in constructing spatially-explicit plankton, fish and coupled plankton-fish models.

The session was separated into four sub-sessions: 1) zooplankton models, 2) larval fish individual-based models, 3) full life cycle models, and 4) end-to-end models. Within these sub-sessions there were 5, 4, 4 and 6, oral presentations, respectively. One talk was withdrawn and this time slot was devoted to briefly presenting the 15 posters that were on display from session L. In the following, we briefly summarize the oral presentations made in each sub-session as well as the highlights and the general discussion points of this session.

Zooplankton sub-session

All presented zooplankton models were based on the individual-based modeling concept. Life cycle and life history of zooplankton species were implemented at different levels of complexity. All of these models were coupled to 3D hydrodynamic models providing explicit spatial impact on the zooplankton dynamics. One presentation (L:17) highlighted the importance of including detailed aspects of specific life history characteristics in terms of the ability to depict observed patterns of spatial habitat residence and changes in long-term time series data. That study utilized a four-stage model that was parameterized for three species (*Pseudocalanus spp., Centropages typicus, and Calanus finmarchicus*). In a second pair of presentations, a spatially-explicit population model for *C. finmarchicus* was described for the Atlantic Basin including aspects related to overwintering and comparison with observations within the region in the Norwegian Sea (L:09, see Figure 1). An associated talk (L:16) utilized these estimates of zooplankton as prey in bioenergetics models for herring, blue whiting, and mackerel, three key pelagic fish species in that region. A fourth paper (L:19) examined how changes in physical processes (strength of tidal components) could impact zooplankton estimates from a nutrient, phytoplankton, zooplankton and detritus (NPZD) model.

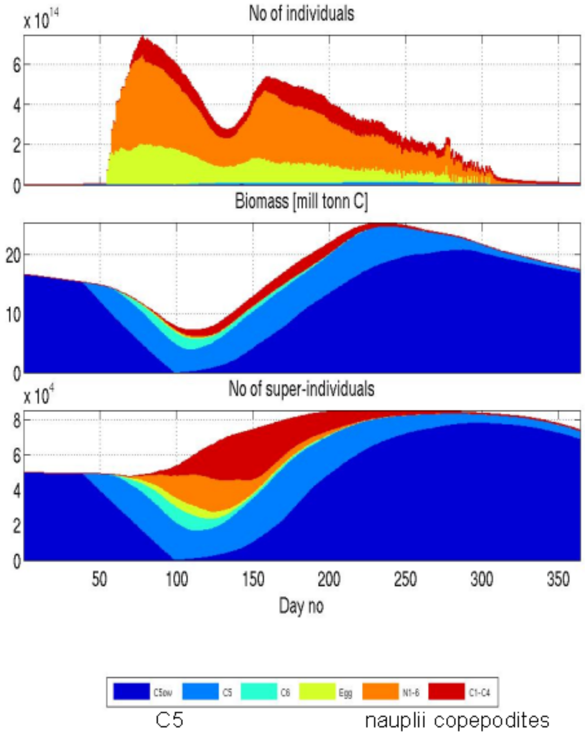

Figure 1 Output data from an IBM developed for *Calanus finmarchicus* population dynamics in the Norwegian Seas and greater Atlantic basin area (L:09).

Most simulations in the zooplankton sub-session were restricted to time periods of a few years. Longer simulation periods will be necessary to examine climatic- driven changes in populations and their tropho-dynamic impacts (e.g., in coupled zooplankton-fish models). The lack of validation data is a challenge in terms of developing and making robust hindcasts and projections using zooplankton / lower trophic level ecosystem models. One presentation on the "FEAST" Bering Sea project (L:21) provided an excellent example of how to cope with this shortcoming by com-piling a common data base of the available data.

Larval fish IBM sub-session

The development and use of coupled biophysical individual-based models for the larvae of various marine fish species were discussed in four talks covering applications for haddock on Georges Bank (L:18), Chilean jack mackerel in the south Pacific (L:20) and Atlantic cod, sprat and herring in the North Sea (L:12). These three presentations highlight the potential species-specific differences that exist in important aspects of foraging (prey selectivity, behaviour) and growth (metabolic and feeding rates) that interact with physical processes to impact survival, drift routes (patterns of advection) of larval cohorts. In terms of coupling to lower trophic levels using bulk zooplankton carbon estimates from an NPZD model highlighted the sensitivity of larval IBM estimates of survival and growth to changes in the slope of the plankton size spectrum. A second presentation (L:18) also employed coupled model approach (*Pseudocalanus* stage-based model) to examine the fate of haddock larvae in contrasting years of low and high recruitment. The model served as a "virtual laboratory" allowing various mechanisms to be tested (e.g., partitioning larval mortality into advective losses, those that died from starvation and those that died due to predation) (Figure 2). To assess model performance, another study employed empirical orthogonal function (EOF) and frequency domain (multitaper method, MTM) analyses to compare modeled and in situ data in terms temporal, spatial and frequency patterns.

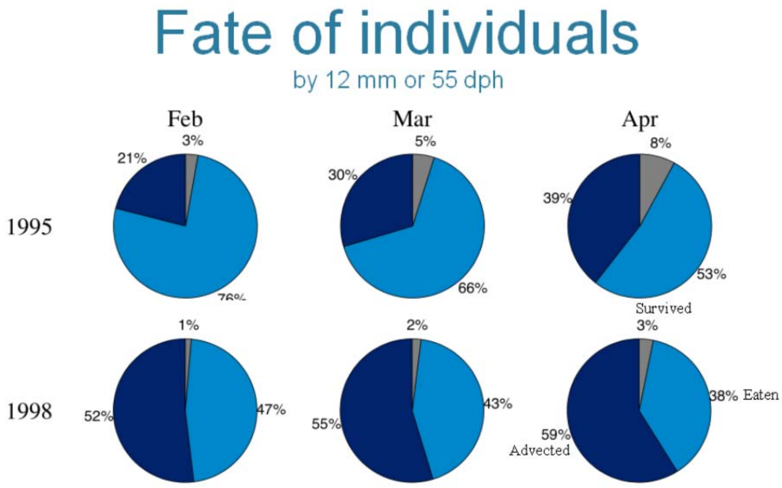

Figure 2) Fate of individual haddock larvae hatched on Georges Bank in each of two years from presentation L:18. In this case, advective mortality (loss off the bank) was estimated to be the most important mortality source of larvae in 1998 whereas predation contributed more to losses in 1995.

A fifth talk (L:15) provided an overview of an online Lagrangian tool that simulates ichthyoplankton drift dynamics within various regions of the world's oceans. A simple user interface allows the tool to be utilized for teaching / classroom situations (e.g., to demonstrate how changes in various features affect the potential drift trajectories of marine fish early life stages).

Full life-cycle models sub-session

Representing the whole life cycle of key fish species within models poses a number of challenges and clear progress was presented within presentations in this sub-session. One presentation linked the outputs from an IBM (mixing rates among sub-populations) directly into a statistical catch-at-age model. This was one of the few examples of how IBM results could be directly integrated into stock an assessment framework. A second presentation (L:13) discussed how the "Eulerian SEA-PODYM "Spatial Ecosystem And Population Dynamics Model" was being developed to test the factors shaping the spatial distribution of Peruvian anchovy spawning. That work in the Humboldt system illustrated some of the challenges facing full-life cycle models that include adult feeding, behavior and spawning

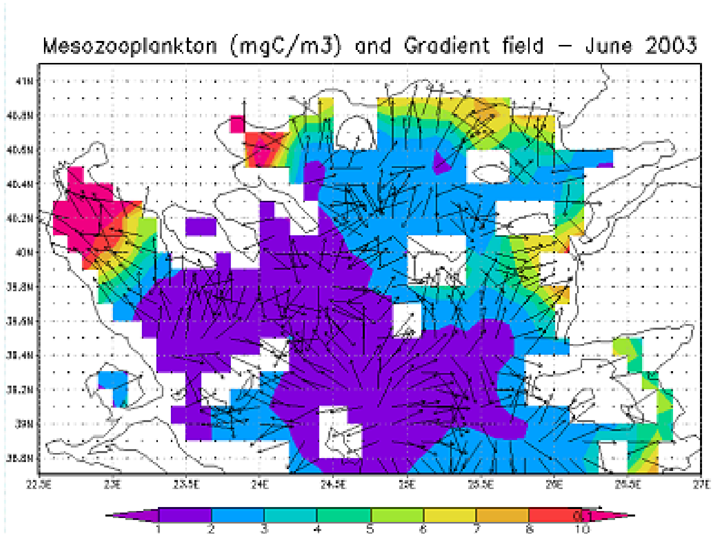

Figure 3 Movement vectors for European anchovy plotted with mesozooplankton biomass in the Northern Aegean (L:14). Behavior rules included movement towards higher mesozooplankton biomass and movement towards shallower waters during the night. Vertical movements were also simulated.

and coupling to lower trophic levels. In that case, the ROMS-PICES model was too coarse to provide robust depiction of mesoscale features. In a third presentation (L:14), the life cycle dynamics of another anchovy species (European anchovy) was examined using a 3-D IBM in the northern Aegean Sea. That and other presentations highlighted the importance of adult movement schemes in terms of model spatial predictions (Figure 3). Finally, in the fourth presentation (L:06), a dynamic energy budget approach was used to simulate ontogenetic changes in the feeding and growth of European plaice juveniles and adults. That tool was utilized with productivity estimates from ERSEM to reveal how climate variability and change may have affected the spatial extent of suitable habitats in the North Sea with results agreeing with trends of greater offshore movements in the most recent decade. In this case, an indirect link was used to estimate benthic prey available for plaice based upon model-derived estimates of pelagic productivity and a type-II functional response.

End-to-end sub-session

End-to-end (E2E) models often provide the potential to simulate how environmental and anthropogenic factors interact to affect marine fisheries resources. Two presentations (L:04, L:10) provided examples of complex models that include spatially-explicit full life cycle population dynamics / demographics, full life cycles of target species and the dynamics of (or mortality from) fishing fleets. In the first example (L:10), scenarios of different wind strength (climate forcing) and fishing pressure were utilized to examine the trophodynamic consequences (changes in top predators, mid-predators, and the productivity of zooplankton and phytoplankton) to reveal whether climate and fishing acted in an additive, synergistic or antagonistic manner on each of those trophic levels. A total of 10 fish species were included in the modeled foodweb (Figure 5). In the second presentation (L:04), a preliminary version of an E2E model of anchovies and sardines in the California Current system with the vision including long-term (1958-2006) simulations on the development of those species within that system (including fishing fleets with profit-based decision rules). A third presentation (L:08) examined historical and projected climate-driven changes in lower trophic levels of the Baltic Sea ecosystem using A1B and B1 emission scenarios for the period 1960 to 2100 while a fourth presentation (L:03) focused on changes in the higher trophic levels of that ecosystem. The challenge of realistic movement patterns of predators was highlighted by examining spatial predator fields with and without specific behavioral rules.

An alternative approach to E2E modeling of Georges Bank, the North Sea and Northern California Current ecosystems was presented within L:05. This approach lacks spatial resolution and merges various species into functional groups to examine energy cycling in a tractable manner (16 state variables) while still attempting to reproduce all relevant processes affecting trophodynamic structure and function. This presentation provided an interesting contrast to the parameter-rich "virtual word" approach of other E2E models. The final presentation (L:02) provided a mechanistic glimpse of how models with different structures and/or elements are being coupled to one another using a tool called "Couplerlib". An example was provided for coupling of a biogeochemical model (GOTM-BFM) and a higher trophic level (ECOSIM) model allowing the models to exchange information on a daily time step.

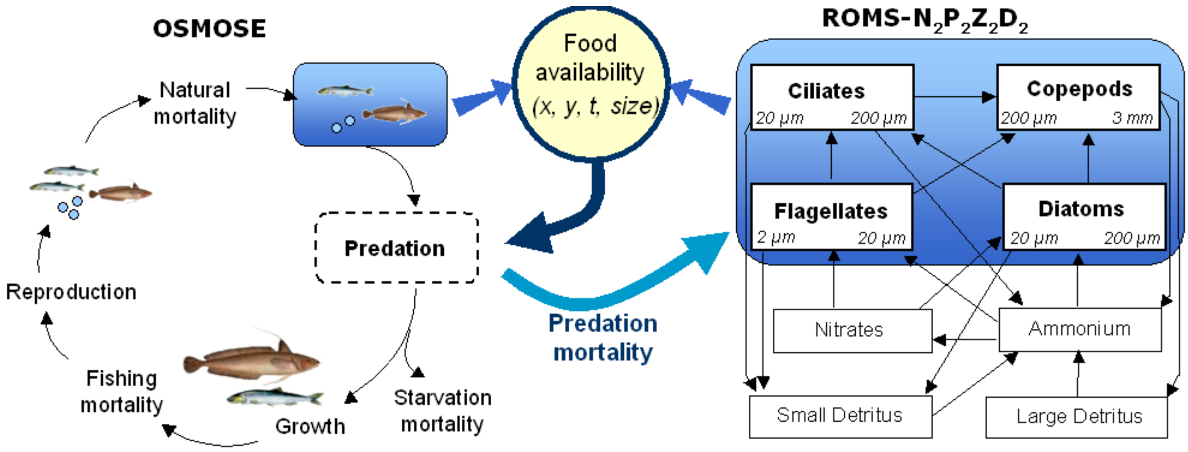

Figure 4 Foodweb and biogeochemical components within a coupled E2E model designed to simulate the Bengula Current ecosystem (L:10). A total of 10 species are represented in the OS-MOSE model that account for 76% of the total fish biomass and 94% of the commercial catch.

Highlights (including discussion)

Coupling higher trophic levels such as fish populations to lower trophic levels such as a zooplankton compartment in an NPZD model is now routinely performed in a 3D setting with IBM approaches, and is a rapid developing field of research that follows the increase in computer capacities (L:04).

Full life cycle fish models (egg, larvae, juveniles, spawning adults) are becoming more common in part due to the recognition that climate-driven changes in key species may occur through mechanism acting on all life stages (from eggs to adult spawners). Fish egg and larval stages are relatively easy to model as movement of these life stages are the direct result of passive drifting and advection. Finding methods to describe juvenile and adult movement present new challenges and is a growing field of research. Different aspects were presented: movement oriented by food gradients (L:03), movement based on fish condition (L:16, L:14) or migrations constrained based on fishery knowledge (L:04). Fish movement implies representing different processes at different scales (i.e., searching for food as well as seasonal / ontogenetic migrations) and stochastic approaches are possible (L:34).

In nearly all examples where fish populations were coupled to lower trophic levels, fish bioenergetics models were implemented to represent ingestion and resulting fish condition to simulate its effects on swimming, growth and reproduction. Coupling of lower and upper trophic level models poses the problem of adequately representing prey resources, whether predators feed on pelagic zooplankton (L:12) or benthic prey (L:06). Size classes but also prey functional groups often need to be resolved. Therefore coupling models involves a better representation of the food for upper trophic levels in lower trophic models. Moreover, behavioural responses to prey resources is also an important aspect to be included in model formulations as this will markedly impact on the spatio-temporal patterns of predation.

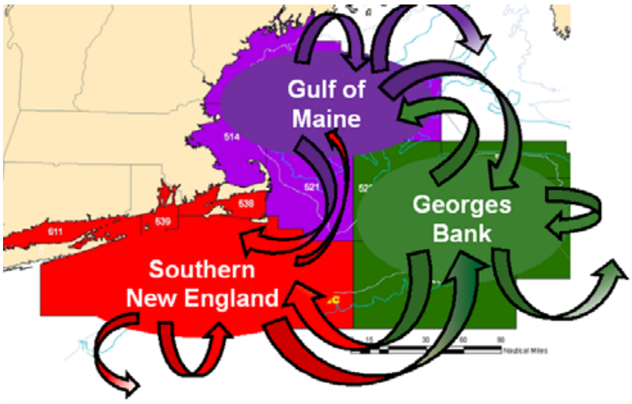

Figure 5 Example of model domain and the types of connectivity estimates obtained from a larval IBM. Connectivity values were then utilized as larval proportions entering specific sub-units for meta-population modelling.

While complex E2E models can be developed to explore the role of different processes, the complexity of coupled models can be much reduced depending upon the application. Tradeoffs obviously exist between model complexity and the level of biological realism. On the one hand, the ability to represent the appropriate amount of biological realism (e.g., species-specific physiology and life history attributes) may be critical to provide insight regarding the mechanism behind historical and ongoing changes in marine ecosystems / key players. On the other hand, corroborating the outputs of complex models and the increased computer time associated with simulations are two potential drawbacks. Despite these two emerging schools of thought (complexity versus parsimony), coupled models have a great potential for helping resolve spatial management issues. In particular, L:01 suggested (Figure 5) how results of larval IBM simulation runs could be integrated into the parameterisation of a multi-site population model developed for designing spatial management plans.