

Strolling through end-to-end bioenergetic ecosystems: On-line comparison of NEMURO.FISH and APECOSM equations

by Ivo Grigorov

With the reaffirmed role of anthropogenic contribution to global climate change (4th IPCC Assessment Report, 2007), the development of predictive capability of marine ecosystem models end-to-end has found even greater context. In order to capture the essence of the combined impacts of climate forcing and overfishing on the dynamics of marine ecosystems, two recent bioenergetic models have attempted to bridge the two ends of the trophic chain.

NEMURO.FISH (NEMURO For Including Saury and Herring; Megrey *et al.*, *Ecological Modelling*, 2007, 202: 144–165) and APECOSM (Apex Predators ECOSystem Model; Maury *et al.*, *Progress in Oceanography* 2007, doi:10.1016/j.pocean.2007.05.002) are both upper trophic-level bioenergetic models expressing energy flow through individuals in terms of gain as consumption and losses due to respiration, excretion, and reproductive output. The two approaches are, however, quite different.

The former follows the rhomboid approach proposed by de Young *et al.* (*Science*, 2004, 304: 1463–1466), whereby a maximum functional complexity is used at a targeted trophic level (in this case Pacific herring), with increasing degree of simplification at the trophic levels below (food) and above (predators) acting as closure terms. The exception with NEMURO.FISH is the dynamic coupling to the nitrogen-based biogeochemical model (NEMURO) that supplies the prey for the model-targeted species. While the dynamic coupling NEMURO–NEMURO.FISH provides a more realistic closure term for Pacific herring and a high level of functional complexity at three separate trophic levels, the coupling of multiple trophic-level-centered

models can become increasingly complex if the ecosystem is to be represented in an end-to-end manner.

An alternative approach is proposed for the APECOSM model. As with NEMURO.FISH, the energy fluxes through individuals are expressed as a function of their physiological processes, but APECOSM treats all processes in the trophic chain as size-dependent, thus avoiding the limitation of the rhomboid approach and being capable of representing all trophic levels based on size allometry. As with NEMURO.FISH, APECOSM will be coupled on-line to the PISCES (Pelagic Interaction Scheme for Carbon and Ecosystem Studies) biogeochemical model to be linked to the primary producers.

The model equations behind the formulation of these two bioenergetic upper trophic-level models are now available on-line (<http://www.eur-oceans.eu/models>) through the Model Shopping Tool (MoST) database, a product of the EUROpean Network of Excellence for OCEan Ecosystem ANalysis (EUR-OCEANS, <http://www.eur-oceans.eu>). The aim of MoST is to provide a quick method of model equation inter-comparison for recent and mature pelagic ecosystem models. The database allows process scientists and non-ecosystem modelers an easy access to the inner detail of pelagic ecosystem models. NEMURO.FISH and APECOSM can be compared rapidly through this on-line tool, at the equation level, and based on individual processes (where available, the individual parameter values and sources are included). MoST also provides the model equations for the biogeochemistry models, NEMURO and PISCES, coupled to NEMURO.FISH and APECOSM.

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