



Seventh FRAMEWORK PROGRAMME THEME 6 Environment

Collaborative Project (Large-scale Integrating Project)

Project no. 212085

Project acronym: **MEECE**

Project title: Marine Ecosystem Evolution in a Changing Environment

D4.2 Scientific Papers

Due date of deliverable: 28/02/2013

Actual submission date: 28/02/2013

Lead partner responsible for deliverable: All

Project co-funded by the European Commission within the Seventh Framework Programme, Theme 6 Environment		
Dissemination Level		
PU	Public	x
PP	Restricted to other programme participants (including the Commission)	
RE	Restricted to a group specified by the consortium (including the Commission)	
CO	Confidential, only for members of the consortium (including the Commission)	

Start date of project: 01.09.09 Duration: 54 months (including extension)

Project Coordinator: Icarus Allen, Plymouth Marine Laboratory

D4.2 Scientific Papers from WP2: Ecosystem Response to Direct Anthropogenic Drivers

*Contributors: The MEECE Community
List compiled April 2013*

Executive Summary

The overall objective of WP4 was to address, through a coupled physical-biogeochemical-higher trophic level modelling approach, the potential response of the marine ecosystem to direct anthropogenic stress in future climate change scenarios. It aimed to integrate and contribute to the analysis of the marine ecosystem evolution in a changing environment by using the modelling tools delivered by WP2 and used in parallel in WP3, and by focusing on drivers expressing directly the anthropogenic pressure on the marine ecosystem. The overall objective was to explore the response of marine ecosystems to combinations of direct anthropogenic drivers on a regional scale and to analyse the impact on ecosystems end to end of changes in pollution, fishing effort, fluvial nutrient and CDOM inputs, focusing on physics, biogeochemistry and ecosystem productivity and higher trophic levels. The final objective was to publish the advances in technical and scientific knowledge generated in the peer reviewed literature.

To date MEECE WP4 has published 13 papers in a variety of journals. The published papers represent aspects of the diverse range of activities. Particular focal points of published activity thus far have focused on end to end models and foodweb dynamics. It should be noted that while WP4 is now complete, the work of writing up the results and completing the publishing process is on-going and it is anticipated that further publications will be produced.

1. Allen JI, (2010). Marine ecosystem response to multiple climatic and anthropogenic drivers: A modelling approach. Comparative Biogeochemistry and Physiology A-Molecular & Integrative Physiology 157, 1, S1-S1.

Marine ecosystems are sensitive to the impacts of both climatic change and the direct effects of human activity. Predictive models that consider the full range of drivers (e.g. Climate and Ocean Acidification, Pollution, Fishing, Invasive Species) are required to elucidate the responses of the marine ecosystem in a holistic manner, rather than driver by driver as has been done in the past. One of the challenges is to integrate the response of ecosystems to multiple drivers across a range of trophic levels by developing coupled models to assess key vulnerabilities and risks of global change for the marine ecosystem. A focus for this work is MSFD which distinguishes 11 qualitative descriptors that together determine the characteristics of Good Environmental Status (GES). Underpinning this activity is the requirement for a range of scenarios which take account of the impacts of multiple climatic and anthropogenic drivers on marine ecosystems. Recently the FP7 MEECE has simulated present and future primary production states in several regions and this is being expanded to include simulations with coupled plankton fish models along with the effects of pollution and ocean acidification. Implementation of such models requires addressing challenges such as the choice of model structure, scaling processes from physiology to functional types to fish, the ecosystem model sensitivity to changes in the physical environment, new methods for the

evaluation and comparison of ecosystem and biogeochemistry models and the quantification of simulation uncertainty. These points are illustrated with examples.

2. Andonegi E, Fernandes JA, Quincoces I, Irigoien X, Uriarte A, Pérez A, Howell D, and Stefánsson G, (2011). The potential use of a Gadget model to predict stock responses to climate change in combination with Bayesian networks: the case of Bay of Biscay anchovy. *ICES Journal of Marine Science*, 68: 1257–1269.

The European anchovy (*Engraulis encrasicolus*) is a short-lived pelagic species distributed in Atlantic European waters, with the Bay of Biscay being one of the main centres of abundance. Because it is a short-lived species, the state of the stock is determined largely by incoming recruitment. Recruitment is highly variable and depends on a variety of factors, such as the size of the spawning stock and environmental conditions in the area. The use of a coupled model that could serve to predict the evolution of the anchovy stock in the short, medium, and long term under several fishing-pressure scenarios and given climate scenarios is demonstrated. This coupled model consists of a Gadget (Globally Applicable Disaggregated General Ecosystem Toolbox) model that was used to analyse the status of the Bay of Biscay anchovy population and to simulate future scenarios based on the estimated recruitment levels, combined with a probabilistic Bayesian network model for recruitment estimation based on machine-learning methods and using climatic indices as potential forecasting factors. The results indicate that certain combinations of medium to high fishing pressure and adverse environmental conditions could force the stock outside its biological reference boundaries.

3. Christensen A, Butenschon M, Gurkan Z, Allen JI (2013). Towards an integrated forecasting system for fisheries on habitat-bound stocks. *Ocean Sci.*, 9, 261–279, 2013

Abstract: First results of a coupled modelling and forecasting system for fisheries on habitat-bound stocks are being presented. The system consists currently of three mathematically, fundamentally different model subsystems coupled offline: POLCOMS providing the physical environment implemented in the domain of the north-west European shelf, the SPAM model which describes sandeel stocks in the North Sea, and the third component, the SLAM model, which connects POLCOMS and SPAM by computing the physical–biological interaction. Our major experience by the coupling model subsystems is that well-defined and generic model interfaces are very important for a successful and extendable coupled model framework. The integrated approach, simulating ecosystem dynamics from physics to fish, allows for analysis of the pathways in the ecosystem to investigate the propagation of changes in the ocean climate and to quantify the impacts on the higher trophic level, in this case the sandeel population, demonstrated here on the basis of hindcast data. The coupled forecasting system is tested for some typical scientific questions appearing in spatial fish stock management and marine spatial planning, including determination of local and basin-scale maximum sustainable yield, stock connectivity and source/sink structure. Our presented simulations indicate that sandeel stocks are currently exploited close to the maximum sustainable yield, even though periodic overfishing seems to have occurred, but large uncertainty is associated with determining stock maximum sustainable yield due to stock inherent dynamics and climatic variability. Our statistical ensemble simulations indicates that the predictive horizon set by climate interannual variability is 2–6 yr, after which only an asymptotic probability distribution of stock properties, like biomass, are predictable.

4. Myksvoll M, Sundby S, Ådlandsvik B, Vikebø F. (2011). Retention of coastal cod eggs in a fjord caused by interactions between egg buoyancy and circulation pattern. *Marine and Coastal Fisheries* [Volume 3, Issue 1](#), 279-294.

Norwegian coastal cod form a stationary population of Atlantic cod *Gadus morhua* consisting of several genetically separated subpopulations. A small-scale differentiation in marine populations with pelagic eggs and larvae is made possible by local retention of early life stages in coastal environments. A numerical model was used to simulate the circulation in a fjord system in northern Norway over 2 years with different river runoff patterns. The dispersal of cod eggs was calculated with a particle-tracking model that used three-dimensional currents. The observed thickness of the low-salinity surface layer was well reproduced by the model, but the surface salinity was generally lower in the model than in the observations. The

cod eggs attained a subsurface vertical distribution, avoiding the surface and causing retention. Interannual variations in river runoff can cause small changes in the vertical distribution of cod eggs and larger changes in the vertical current structure. Retention in the fjord system was strong in both years, but some eggs were subjected to offshore transport over a limited time period. The timing of offshore transport depended on the precipitation and temperatures in adjacent drainage areas. A possible match between maximized spawning and offshore transport may have a negative effect on local recruitment.

5. Salihoglu B, Fach BA, Oguz T. (2011). Control mechanisms on the ctenophore *Mnemiopsis leidyi* population dynamics: A modelling study. *Journal of Marine Systems*, Volume 87, Issue 1, Pages 55-65

A comprehensive understanding of the mechanisms that control the ctenophore *Mnemiopsis* blooms in the Black Sea is gained with a zero-dimensional population based model. The stage resolving model considers detailed mass and population growth dynamics of four stages of model-ctenophore. These stages include the different growth characteristics of egg, juvenile, transitional and adult stages. The dietary patterns of the different stages follow the observations given in the literature. The model is able to represent consistent development patterns, while reflecting the physiological complexity of a population of *Mnemiopsis* species. The model is used to analyze the influence of temperature and food variability on *Mnemiopsis* reproduction and outburst. Model results imply a strong temperature control on all stages of *Mnemiopsis* and that high growth rates at high temperatures can only be reached if food sources are not limited (i.e. 25 mg C m⁻³ and 90 mg C m⁻³ mesozooplankton and microplankton, respectively). A decrease of 5 °C can result in considerable decrease in biomass of all stages, whereas at a temperature of 25 °C a 40% decrease in food concentrations could result in termination of transfer between stages. Model results demonstrate the strong role of mesozooplankton in controlling the adult ctenophore biomass capable of reproduction and that different nutritional requirements of each stage can be critical for population growth. The high overall population growth rates may occur only when growth conditions are favorable for both larval and lobate stages. Current model allows the flexibility to assess the effect of changing temperature and food conditions on different ctenophore stages. Without including this structure in end-to-end models it is not possible to analyze the influence of ctenophores on different trophic levels of the ecosystem.

6. Salihoglu B, Neuer S, Painting S, Murtugudde R, Hofmann EE, Steele JH, Hood RR, Legendre L, Lomas MW, Wiggert JD, Ito S, Lachkar Z, Hunt G, Drinkwater KF, Sabine CL, (2012). Bridging marine ecosystem and biogeochemistry research: lessons and recommendations from comparative studies. *Journal of Marine Systems* doi: [10.1016/j.jmarsys.2012.07.005](https://doi.org/10.1016/j.jmarsys.2012.07.005)

Abstract: There is growing interest in linking marine biogeochemistry with marine ecosystems research in response to the increasing need to understand and predict the effect of global change on the marine ecosystem. Such a holistic approach combines oceanographic and biogeochemical processes and information on organisms, ranging from microbes to higher-trophic-levels. Comparative studies offer a means to improve understanding of critical mechanisms that influence marine systems by showing differences in ecosystem response to changing ocean conditions. Comparing similar biomes that differ in a particular set of physical or biological characteristics can provide insight into the susceptibility of the key features of a system to perturbation. Also, comparative studies based on long-term observations at fixed time-series stations enable the evaluation of long-term changes in the physical and biological environment, such as those driven by climate patterns. Moreover, the comparative approach provides a feasible alternative to costly and complex research programs designed to provide detailed end-to-end evaluations of marine systems. Planned and unplanned perturbations allow the investigation of the sensitivity of ecosystems and their biogeochemical processes to change at different time and space scales. In well-studied regions where sufficient data are available, models can provide comprehensive syntheses, mechanistic insights and even predictions. We present examples of successful comparative studies that incorporate both biogeochemical and ecosystems aspects. A framework for a basic approach for comparative studies is proposed that considers the interactions between

biogeochemical cycles and ecosystems. This approach is based on constructing a minimalistic observational framework grounded within a conceptual model.

7. Shin YJ, Travers M, Maury O, (2010). Coupling low and high trophic levels models: Towards a pathways-orientated approach for end-to-end models. *Progress In Oceanography* 84 (1-2): 105-112 Sp. Iss.

Abstract: Existing models of marine ecosystems address specific issues related to the bottom-up forcing of production or to the top-down effects of fishing on a limited range of the trophic spectrum. Very few existing models explicitly incorporate the dynamics from one end of the ecosystem to the other and thus allowing the exploration of interplay between exploitation and climate effects. The shift to an ecosystem approach to fisheries and concerns about the ecological effects of climate change require the assemblage of knowledge assembled from the respective marine disciplines with the view to build end-to-end models of marine ecosystems.

Here, with a focus on plankton and fish models, we present some issues and recommendations for the integration of models between trophic levels (vertical integration) and within functional groups (horizontal integration within trophic levels). At present, vertical coupling of plankton and fish models is mainly realized through predation processes, generally represented as a functional response. In the absence of empirical evidence and quantification, the choice of the functional response term is often made by default, and is reduced to a parameterization problem. A strategy is proposed to overcome this arbitrary choice.

In addition to the vertical coupling of trophic models, the structure of end-to-end models incorporates biodiversity via horizontal integration of trophic levels. For guiding the selection of key components to be included in end-to-end models, the idea that marine food webs are structured as alternative trophic pathways is highlighted and related to observed dynamics. We suggest that an important early step in model development is the identification of major trophic pathways and bottlenecks in an ecosystem using a historical perspective.

8. Tomczak MT, Niiranen S, Hjerne O, Blenckner T, (2012). Ecosystem flow dynamics in the Baltic Proper—Using a multi-trophic dataset as a basis for food–web modelling. *Ecological Modelling* 230: 123-147

Abstract: The Baltic Proper is a semi-enclosed, highly productive basin of the Baltic Sea with a low biodiversity, where only a few key species drive the system's dynamics. Recently, an ecosystem regime shift was described having pronounced changes at all trophic levels, driven by changes in fishery and climate and leading to a food–web reorganisation. An Ecopath with Ecosim Baltic Proper food–web model (BaltProWeb) was developed to simulate and better understand trophic interactions and their flows. The model contains 22 functional groups that represent the main food–web components. BaltProWeb was calibrated to long-term monitoring data (1974–2006), covering multiple trophic levels and is forced by fisheries and environmental drivers. Our model enables the quantification of the flows through the food–web from primary producers to top predators including fisheries over time. The model is able to explain 51% of the variation in biomass of multiple trophic levels and to simulate the regime shift from a cod dominated to a sprat dominated system. Results show a change from benthic to more pelagic trophic flows. Before the reorganisation macrozoobenthos was identified as an important functional group transferring energy directly from lower trophic levels to top predators. After the regime shift, the pelagic trophic flows dominated. Uncertainties and limitations of the modelling approach and results in relation to ecosystem-based management are discussed.

9. Travers M, Watermeyer K, Shannon LJ, Shin YJ, (2010). Changes in food web structure under scenarios of overfishing in the southern Benguela: comparison of the Ecosim and OSMOSE modelling approaches. *Journal of Marine Systems*, 79: 101-111.

Ecosystem models provide a platform allowing exploration into the possible responses of marine food webs to fishing pressure and various potential management decisions. In this study we investigate the particular effects of overfishing on the structure and function of the southern Benguela food web, using two models with different underlying assumptions: the spatialized, size-based individual-based model, OSMOSE, and the trophic mass-balance model, Ecopath with Ecosim (EwE). Starting from the same reference state of the southern Benguela upwelling ecosystem during the 1990s, we compare the response of the food web to scenarios of overfishing using these two modelling approaches. A scenario of increased fishing mortality is applied to two distinct functional groups: i) two species of Cape hake, representing important target predatory fish, and ii) the forage species anchovy, sardine and redeye. In these simulations, fishing mortality on the selected functional groups is doubled for 10 years, followed by 10 years at the initial fishing mortality. We compare the food web states before the increase of fishing mortality, after 10 years of overfishing and after a further 10 years during which fishing was returned to initial levels. In order to compare the simulated food web structures with the reference state, and between the two modelling approaches, we use a set of trophic indicators: the mean trophic level of the community and in catches, the trophic pyramid (biomass per discrete trophic level), and the predatory/forage fish biomass ratio. OSMOSE and EwE present globally similar results for the trophic functioning of the ecosystem under fishing pressure: the biomass of targeted species decreases whereas that of their potential competitors increases. The reaction of distant species is more diverse, depending on the feeding links between the compartments. The mean trophic level of the community does not vary enough to be used for assessing ecosystem impacts of fishing, and the mean trophic level in the catch displays a surprising increase due to the short period of overfishing. The trophic pyramids behave in an unexpected way compared to trophic control theory, because at least two food chains with different dynamics are intertwined within the food web. We emphasize the importance of biomass information at the species level for interpreting dynamics in aggregated indicators, and we highlight the importance of competitive groups when looking at ecosystem functioning under fishing disturbance. Finally, we discuss the results within the scope of differences between models, in terms of the way they are formulated, spatial dimensions, predation formulations and the representation of fish life cycles.

10. Utne KR, Hjøllø SS, Huse, G, Skogen, MD, (2012). Estimating the consumption of *Calanus finmarchicus* by planktivorous fish in the Norwegian Sea using a fully coupled 3D model system. *Marine Biology Research*, 8(5-6):527-547. DOI: 10.1080/17451000.2011.642804

Energy flow and trophic regulation are often well understood in closed freshwater ecosystems. Such regulation is harder to understand in large marine ecosystems, as they extend over vast areas and are influenced by adjacent marine areas. Fully coupled biophysical models have increased in popularity during recent years, but these models are still in their infancy. Here we present a coupled model system of the Norwegian Sea, including an ocean model, a phytoplankton model and individual-based models of the copepod *Calanus finmarchicus* and planktivorous fish. The fish migration model is driven by survey observations, but the *C. finmarchicus* densities also affect the fish migrations. This leads to a realistic predation pressure on zooplankton by fish in time and space. The predation pressure of fish on zooplankton is calculated by modelling individual fish growth using bioenergetics models. We estimated that the major pelagic fish stocks in the Norwegian Sea, herring, mackerel and blue whiting, consumed a total of 82 million tonnes of zooplankton, including 35 million tonnes *C. finmarchicus*, in 1997. Furthermore, the interspecific competition has the greatest effect on blue whiting consumption, while herring consumption is unaffected by the other fish species in this one-year simulation. We also analysed the spatial distribution of *C. finmarchicus* in June and August and found the highest densities in the northern Norwegian Sea and around Iceland. The results give us a better understanding of the effect from fish predation on the Norwegian Sea ecosystem, and how it affects the *C. finmarchicus* stock.

11. Utne KR, Huse G, (2012). Estimating the horizontal and temporal overlap of pelagic fish distribution in the Norwegian Sea using individual-based modelling. *Mar. Biol. Res.* 8, 548-567

The most abundant pelagic fish species in the Norwegian Sea, Norwegian spring-spawning herring, Northeast Atlantic mackerel and Northeast Atlantic blue whiting have inter-annual variation in their summer feeding migrations. Knowledge about the spatial distribution and overlap is essential for understanding the species' interactions and their impact on the ecosystem. Here we attempt to recreate the annual feeding migrations with individual-based modelling and use the results to estimate the daily horizontal overlap between the three species. Species-specific swimming velocities and direction, and the degree of random walk for each year 1995–2003 are found by using a genetic algorithm through calibration with survey observations. From the results it can be concluded that herring and mackerel have a very low horizontal overlap during the feeding season, while herring and blue whiting have a high horizontal overlap. Blue whiting and mackerel have some horizontal overlap in late summer, but a very limited vertical overlap. There is generally a high variability in the horizontal overlap between the species both seasonally and inter-annually. The species utilize many of the same feeding areas in the Norwegian Sea, but often at different times. The modelling approach developed can be useful for implementation of dynamic fish distribution in end to end ecosystem models.

**12. Utne KR, Hjøllø SS, Huse G and Skogen M., 2012. Annual consumption of *Calanus finmarchicus* by planktivorous fish in the Norwegian Sea estimated from a coupled 3D model system. *Marine Biology Research*, 8: 548_567.
<http://dx.doi.org/10.1080/17451000.2011.642804>**

Abstract: Energy flow and trophic regulation are often well understood in closed freshwater ecosystems. Such regulation is harder to understand in large marine ecosystems, as they extend over vast areas and are influenced by adjacent marine areas. Fully coupled biophysical models have increased in popularity during recent years, but these models are still in their infancy. Here we present a coupled model system of the Norwegian Sea, including an ocean model, a phytoplankton model and individual-based models of the copepod *Calanus finmarchicus* and planktivorous fish. The fish migration model is driven by survey observations, but the *C. finmarchicus* densities also affect the fish migrations. This leads to a realistic predation pressure on zooplankton by fish in time and space. The predation pressure of fish on zooplankton is calculated by modelling individual fish growth using bioenergetics models. We estimated that the major pelagic fish stocks in the Norwegian Sea, herring, mackerel and blue whiting, consumed a total of 82 million tonnes of zooplankton, including 35 million tonnes *C. finmarchicus*, in 1997. Furthermore, the interspecific competition has the greatest effect on blue whiting consumption, while herring consumption is unaffected by the other fish species in this one-year simulation. We also analysed the spatial distribution of *C. finmarchicus* in June and August and found the highest densities in the northern Norwegian Sea and around Iceland. The results give us a better understanding of the effect from fish predation on the Norwegian Sea ecosystem, and how it affects the *C. finmarchicus* stock.

13. Utne KR, Huse G 2012. Estimating the horizontal and temporal overlap of pelagic fish distribution in the Norwegian Sea using individual-based modelling *Marine Biology Research*, 2012; 8: 527_547

Abstract: The most abundant pelagic fish species in the Norwegian Sea, Norwegian spring-spawning herring, Northeast Atlantic mackerel and Northeast Atlantic blue whiting have inter-annual variation in their summer feeding migrations. Knowledge about the spatial distribution and overlap is essential for understanding the species' interactions and their impact on the ecosystem. Here we attempt to recreate the annual feeding migrations with individual-based modelling and use the results to estimate the daily horizontal overlap between the three species. Species-specific swimming velocities and direction, and the degree of random walk for each year 1995_2003 are found by using a genetic algorithm through calibration with survey observations. From the results it can be concluded that herring and mackerel have a very low horizontal overlap during the feeding season, while herring and blue whiting have a high horizontal overlap. Blue whiting and mackerel have some horizontal overlap in late

summer, but a very limited vertical overlap. There is generally a high variability in the horizontal overlap between the species both seasonally and inter-annually. The species utilize many of the same feeding areas in the Norwegian Sea, but often at different times. The modelling approach developed can be useful for implementation of dynamic fish distribution in end to end ecosystem models.