This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Deliverable No. 2.4

Project acronym:
MareFrame

Project title:
„Co-creating Ecosystem-based Fisheries Management Solutions"

Grant agreement No: **613571**
Project co-funded by the European Commission within the
Seventh Framework Programme

Start date of project: **1st January 2014**
Duration: **48 months**

Due date of deliverable:	31/12/2015
Submission date:	28/12/2016
File Name:	D2.4 MAREFRAME_ For the correct implementation of novel data types
Revision number:	02
Document status:	Final[1]
Dissemination Level:	PU[2]

---

[1] Document will be a draft until it is approved by the coordinator
[2] PU: Public, PP: Restricted to other programme participants (including the Commission Services), RE: Restricted to a group specified by the consortium (including the Commission Services), CO: Confidential, only for members of the consortium (including the Commission Services)

Revision Control

Role	Name	Organisation	Date	File suffix[3]
Author	Montse Pérez	IEO	28/11/2016	MP
Author	Margarita Rincón	CSIC	02/12/2016	MR
Author	Javier Ruiz	CSIC	02/12/2016	JR
Author	Valerio Bartolino	SLU	13/11/2016	VB
Author	Barbara Bauer	SU	14/11/2016	BB
Author	Maciej T. Tomczak	SU	02/12/2016	MTT
Author	John Pope	NRC	14/09/2016	JP
Author	Bjarki Elvarsson	MRI	09/09/2016	BE
Author	Erla Sturludottir	UI	15/12/2016	ES
Author	Alain Baudron	UNIABDN	10/10/2016	AB
Author	Matteo Sinerchia	CSIC	21/11/2016	MS
Author	Francesco Colloca	CNR	21/11/2016	FC
Author	Gheorghe Radu	INCDM	21/11/2016	GR
Author	Ian Tuck	NIWA	01/11/2016	IT
Author	Piotr Margonski	NMFRI	02/12/2016	PM
Author	Jan Horbowy	NMFRI	02/12/2016	JH
Author	Kristinn Ólafsson	Matis	26/12/2016	KO
WP2 leader/Author	Santiago Cervino	IEO	03/12/2016	SC
Coordinator	Anna K. Daníelsdóttir	Matis	28/12/2016	AKD
Administrative Coordinator	Oddur M. Gunnarsson & Kristinn Ólafsson	Matis	27/12/2016	OMG & KÓ
Scientific Coordinator	Gunnar Stefánsson	UI	22/12/2016	GS

---

[3] The initials of the revising individual in capital letters

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Deliverable D2.4

For the correct implementation of novel data types

28/12/2016

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Executive Summary

Work package 2 (WP2) aimed to identify, collect, and evaluate information not usually considered for assessment and management. Deliverable 2.4 (D2.4) contains a list of protocols that describe the final implementation of the novel data into models within each case study (CS). Each of these protocols is written in a similar way as a "Material and Methods" section in a paper. D2.4 is structured as follows for each CS: first a summary of general CS aims, models implemented and novel data explored. This summary ends with an explanation about why this data is considered novel and the definition of the protocols developed in this CS. The number of protocols in each CS ranges between one and three. In some CSs different novel data types were considered but all of them were implemented in the same model. In these cases, only one protocol was written. When more than one model was considered the protocol number equals the number of models. The exception was the Chatham Rise CS, where two different models (EwE and Atlantis) implemented the same novel data types and all were reported in a unique protocol; and SWW-Iberian Peninsula CS were different novel data types were implemented in GADGET although for each data type the GADGET model was different and 3 protocols were presented. The model implementation describes how the data is influencing the model structure, i.e. whether is used to test the validity of assumptions or used to fit parameters; followed by a description of the ecosystem process and how it is related with the novel data. The focus of this section is on the novel data and related processes avoiding extending it to a full model description already presented in other deliverables in WP4 and WP5. A total of 16 different protocols were written. These protocols can be useful to the scientific community to implement similar data in ecosystem models. After the implementation of novel information into assessment models, the utility of this information will be evaluated in a critical report (D2.5). This report will be a synthesis of all the work in WP2 and it will consider the usefulness of each information type in improving the ecosystem models, recommendations to improve future data collection, etc.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Table of Contents

A. Baltic Sea 6

Protocol A.1. Implementation of cod stomach data, fishing effort data and age-length survey data in GADGET. 7

Protocol A.2 Implementation of cod stomach data, zooplankton data and effort data in Ecopath with Ecosim (EwE) model 9

Protocol A.3. Implementation of cod stomach data in the Multispecies stock-production model (MSPM) considering the growth of cod and herring as dependent on environmental variables. 12

B. North Sea 14

Protocol B.1. How to use Isotopes based Trophic Level data in the CSM considering how to capture and use fisherman knowledge in the overview models. 15

C. Northern and Western Waters – Iceland Waters 18

Protocol C.1 - whale genetics (close-kin) to define whale stock structure 18

Protocol C.2. Whale diet implemented in GADGET 22

Protocol C3. Oceanographic data in Atlantis 28

D. Northern Waters – West Scotland 29

Protocol D1. Temperature and NAO index as drivers in the EwE model. 29

E. South-Western Waters – Iberian Peninsula 34

Protocol E.1 - Hake sex ratio-at-length data in GADGET 34

Protocol E.2 - Hake genetic data in GADGET 35

Protocol E.3. Anchovy otholit microchemistry in GADGET 37

F. Mediterranean Waters – Strait of Sicily 41

Protocol F.1. Implementation of isotopes, VMS data and biogeochemical data with Atlantis 42

G. Black Sea 47

Protocol G.1.Turbot diet data implementation on EwE model 47

H. Chatham Rise – New Zealand 56

Protocol H.1. Implementation of isotopes diet data in the balanced foodweb model and Atlantis 57

References 64

List of protocols that describe the final implementation of the novel data into models within each case study:

A. Baltic Sea

The Baltic case study implements ecosystem models able to characterize key species interactions and food-web functioning and fisheries effect within the Baltic Sea. Through increased realism of the models proposed the case study investigates the direct and ecosystem-mediated effects of a trade-off between the different fisheries which operate in the Baltic. This model development will contribute to the implementation of an integrated ecosystem assessment and to the development of a regional ecosystem-based management of the Baltic Sea.

In the Baltic CS three models were used: Gadget (Globally applicable Area Disaggregated General Ecosystem Toolbox), Ecopath with Ecosim (EwE), and Multispecies stock-production model (MSPM). The **Gadget** implementation in the Baltic is a multispecies and multifleet model. Trophic interactions are represented by cod feeding on both herring and sprat. The implement is an age-size based model structured in quarterly time steps from 1974 to 2013. **EwE** model of the open Baltic Proper is a further development of the model described by Niiranen et al. (2013) and Tomczak et al. (2012). In contrast to the above mentioned model, it is parameterised according to post-regime shift conditions. The functional groups included represent the most important groups in the offshore central Baltic Sea, including charismatic species such as grey seals and offshore fish-feeding birds, the four commercially most important fish species, the benthic part of the food web, 4 zooplankton groups and one phytoplankton group. The model includes fishing on all four fish species and environmental effects on their reproduction and on trophic interactions among various groups. The **MSPM** (Horbowy, 2005) is a multispecies simplification of the age-structured multispecies model of Andersen and Ursin (1977). The model was applied to simulate stock dynamics and species interactions of cod, herring, and sprat in the Baltic from 1982 to 2014. It considers the trophic interactions among these species (cod, herring and sprat) and the environmental impact on growth. A complete model description for the 3 models can be found in D5.3.

All models are applied using novel information (data) made available and compiled within MareFrame. The novel information applied in Baltic CS includes: stomach contents data, zooplankton data, age-length data from survey, fishing effort data, and the dependence of cod and herring growth on environmental factors: functional relationship. The stomach contents data is a rich and novel dataset which for the first time could inform on the spatial and temporal dynamics of trophic interactions between cod and its preys in the Baltic. The use of effort data from logbooks represents a novelty within a multispecies model for the Baltic allowing Gadget to estimate the catch or determining fishing mortality rates in EwE. Herring and sprat age-length data, traditionally not used in the assessment of the Baltic Sea fish stocks, are novelty used to inform GADGET in the estimation of growth. The inclusion of cod and herring growth as functionally dependent on area of hypoxic waters (cod) and water salinity (herring) represents novel information in the MSPM

The novel information used is specific for the model applied, however, the stomach contents data are used in all three models, and fishing effort data are used in two models. Novel information includes

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

both new data and new functional relationships applied in the models. The implementation of this data in the 3 different models are presented here as 3 different protocols, one for each model.

Protocol A.1. Implementation of cod stomach data, fishing effort data and age-length survey data in GADGET.

Stomach data

Information on cod diet is available from a number of different sources and time periods. The dataset includes >107,000 cod stomachs collected in a number of different national and international projects which involved several countries around the Baltic. Historical stomach data collected by Latvia spanning from 1977-1993 have been previously compiled and represent the core dataset currently used for multispecies assessment in the Baltic (ICES 2013). In recent years, cod stomach data have been routinely collected during the Baltic International Trawl Survey (BITS) which also provides main information on the abundance and age-length structure of cod in the Baltic. In addition, stomach data collected in 2012-2014 under the new stomach sampling program (EU program Mare/2012/02) was harmonized and included. Prey sizes were mainly recorded by 5 cm groups for the period 1977–1981. Data are compiled by 1 cm length groups for sprat and 2 cm length groups for herring.

Cod stomach data are used in the estimate overall cod consumption based on bio-energetic models and implement trophic interaction between cod, herring and sprat in a Gadget model. Within Gadget stomach data are used to compare the proportion of herring and sprat in the cod diet and the size distribution of these two prey species in the stomachs of cod of different size.

Stomach data stored into mfdb (https://github.com/mareframe/mfdb) are retrieved using the function 'mfdb_stomach_presenceratio' for the time period 1974-2013 and entire eastern Baltic cod distribution at a quarterly aggregation. Prey is aggregated over 1 cm length intervals in the range 4-30 cm for the follow cod length groups: 20-40 cm, 40-60 cm, 60-80 cm, 80-100 cm.

The 'StomachContent' likelihood component is used to compare consumption data sampled from the model with these stomach content data. The likelihood score that is calculated for this component provides some measure of how well the observed stomach content data are represented within the model. A simple ratio function is used in Gadget to compare the ratio of the consumption of herring and sprat in the model for each combination of predator-prey length groups with the same ratio from the data (see Gadget user's guide for more details):

$$l = \sum_{time} \sum_{predators} \sum_{preys} (P_{tpp} - \pi_{tpp})^2$$

where P is the ratio of the stomach content data for that time/predator/prey combination and π is the ration of the modeled consumption for that time/predator/prey combination.

Fishing effort data

One component of the collected data relevant to food web modelling of the Baltic Sea describes fishing effort in units of hours of the vessels in the Community Fishing Fleet Register. At present this data is available for the years 2003-2014, disaggregated at the level of ICES statistical rectangles, and covering

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

the entire Baltic Sea (ICES subdivisions 22-32). Fishing effort data are available for the main fleets catching cod, herring and sprat in the Baltic Sea. In the current implementation quarterly fishing effort is used only to implement the cod fisheries. Fisheries catch of cod is treated differently in the historical and more recent period in the Gadget model. For the period 1974-2003 the harvested catch biomass is assumed without error and removed from the model (i.e., 'totalfleet' type). For the most recent period (2004-2013) catch amount is treated as a likelihood component which means that deviations around the observed catches are allowed and fishing effort information is used (i.e., 'Linearfleet' type). The use of effort data certainly represents a novelty within a multispecies model for the Baltic. In this kind of implementation Gadget estimates the catch amount based on the effort, the available biomass accounting for the selectivity of the fishery and a scaling factor which links to the catchability as follows:

$$C(l) = E\Delta t S(l) N_l W_l$$

where:
<*E*> is the scaling factor for the stock
<Δt> is the quarter
<N> is the number of fish in the length cell
<W> is the mean fish weight in the length cell
<S> is the selectivity of the fishery for the stock (suitability in Gadget terminology)

The catch biomass of cod by quarter and separately for active and passive gears is the likelihood data component used by Gadget and compared with the modelled catches estimated above. A sum of squares function is used to calculate this likelihood component as follows:

$$l = \sum_{time} \sum_{fleets} \left(\log\left(N_{tf} + \epsilon\right) - \log\left(v_{tf} + \epsilon\right) \right)^2$$

where *N* is the catch biomass for that time/fleet combination and *v* is the modelled catch biomass for that time/fleet combination

Age-Length survey data

Gadget can be considered a full age-length model. For this reason, it is suitable to deal with both age and length related dataset. However, several processes are implemented on length in Gadget and they include selectivity and maturation. Moreover, proper estimation of the growth model parameters also requires a certain number of length-related information which is traditionally not used in the assessment of the Baltic Sea fish stocks.

A number of issues, mostly related to the growth of the eastern Baltic cod has prevented in the last few years from having an accepted analytical assessment of this stock (ICES 2014). This has stimulated an intense activity of research on the stock and engagement from the Baltic countries to retrieve commercial length data on this stock and try length-based assessment methods. For this reason, although the use of commercial length data on Baltic cod is not part of the dataset used by other

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

multispecies model for the Baltic, commercial length data on cod are intensively used within the Baltic assessment working group (WGBFAS) and are not considered here strictly as novel information.

Differently from cod, length information from both commercial and scientific surveys on sprat and herring have not been used at all as explicit input for the assessment of these two stocks. An element of novelty in our Gadget model consists in the use of age-length keys from the BIAS survey to inform the estimation of parameters of the von Bertalanffy growth model. Number of sprat and herring by age and length (at 1-cm length interval) is calculated for each year of the BIAS using biological samples collected in the pelagic trawl hauls associated with the acoustic survey. Input data is compiled from mfdb (https://github.com/mareframe/mfdb) so that the contribution of the number of fish for each age-length combination at the ICES rectangle level is weighted by the corresponding acoustic index of abundance. A sum of square likelihood function is used to compare the age-length distribution of the model with the age-length distribution of this dataset as:

$$l = \sum_{time} \sum_{ages} \sum_{lengths} (P_{tal} - \pi_{tal})^2$$

where:
<*P*> is the proportion of the data sample for that time/age/length combination
<*π*> is the proportion of the model sample for that time/age/length combination

Protocol A.2 Implementation of cod stomach data, zooplankton data and effort data in Ecopath with Ecosim (EwE) model

Cod stomach data

The data is the same than those presented for the protocol A.1., although the elaboration for model implementation is quite different. Cod stomach data is used to parameterise diet composition of adult (>=33 cm) and juvenile (<33 cm) cod in the reference year, 2004, in the Ecopath model.

Stomach data stored in the MareFrame database (https://github.com/mareframe/mfdb) was extracted using the query functions mfdb_stomach_preymeanweight and mfdb_stomach_preymeanlength. We used the following procedure to calculate diet composition of cod stanzas from the data: We took the mean weight of each species of prey in all stomach samples from >=33 cm and <33 cm fish for adult and juvenile cod, resp., in SD 25-26, years 2003-2005. Mean weights of individual prey species were added up to correspond to functional groups in Ecopath. Weights from species that are not included in the Ecopath model (e.g. eelpout, sand goby, three-spined stickleback) were added to the 'import' diet part. Weights were then turned into diet fractions (DC_{ij} expressing fraction of a prey group *i* in the diet of predator *j* in wet weight). Juvenile and adult herring and sprat in diet were separated based on their observed length distribution in the cod stomachs, whereby adult herring was defined as >=13 cm, and adult sprat >=11 cm.

In Ecopath DC_{ij} values together with the biomass (B_j) and consumption per biomass ($\left(\frac{Q}{B}\right)_j$) values of predator j (here adult or juvenile cod), are used to calculate Q_{ij}, the absolute amount of prey i consumed by predator j in the Ecopath model:

$$Q_{ij} = B_j \cdot \left(\frac{Q}{B}\right)_j \cdot DC_{ij}$$

According to the mass balance requirement of Ecopath, total biomass removals from each group (including its total consumption by all of its predators) cannot exceed the group's production:

$$P_i = Y_i + E + BA + \sum_{j=1}^{n} Q_{ij}^{*} + P_i \cdot (1 - EE_i)$$

where P_i is produced biomass, and Y_i is the yield (catch in biomass), E_i is net emigration (emigration – imigration, in units of biomass) and BA_i is biomass accumulation of group *i*. $EE_i \in [0,1]$ is group *i*'s ecotrophic efficiency and 1-EE_i is the fraction of its production assumed to be dying from causes other than predation ("other mortality"), which constitutes a biomass flow to the detritus.

Besides being a component of the Ecopath model, Q_{ij} is used to calculate several parameters of the dynamic Ecosim model. One of these is the effective search rate $a_{ij0} = Q_{ij}^{*}/B_i^{*}B_j^{*}$, calculated from Ecopath values (indicated by * superscript) in the first time step, and subsequently recalculated in every time step as $a_{ijt} = a_{ij0} \cdot T_j \cdot S_{ijt}$, where T_j is the relative feeding time of predator *j* and S_{ijt} represents the effects of environmental forcing variables, such as hypoxia, on the predator-prey interaction. The other is vulnerability exchange rate $v_{ij} = k_{ij} \cdot \frac{Q_{ij}^{*}}{B_i^{*}}$, where k_{ij} is the user-defined vulnerability multiplier $k_{ij} \in [1, \infty]$. These are used to calculate vulnerable prey biomass at time *t* (V_{it}) as

$$V_{it} = \frac{v_{ij} \cdot B_{it} \cdot T_i}{2v_i + a_{ijt} \cdot B_{jt}}$$

which is used to calculate time variable Q_{ijt} in Ecosim as

$$Q_{ijt} = a_{ijt} \cdot B_{jt} \cdot V_{it}.$$

Zooplankton data

Mesozooplankton is a key element in marine food web. In the southern Baltic Sea conditions, it is extremely vulnerable to environmental forcing. Observed changes in temperature and salinity have an impact on zooplankton community structure. Recently recovered data are the Polish contribution to the HELCOM COMBINE Program. The longest data series (since 1979) were collected at deepwater stations whereas those taken at more coastal ones started within the last twenty years. In most of the cases, samples were taken 5 times per year using the WP-2 net. Profound changes in zooplankton community were recorded at the deep water stations of the southern Baltic Sea. This is mostly caused by a decrease in abundance of Pseudocalanus copepods. Pseudocalanus is correlated with salinity and,

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

thus, positively responding to each of the inflows from the North Sea. Presented data was applied for the EwE modelling of the Baltic Proper. This data provides additional and more reliable info on food web structure and seasonal dynamics at the regional scale.

The zooplankton monitoring data is used as a reference time series (2004-2014) for fitting vulnerability multipliers (k_{ij}) which are used to calculate vulnerability exchange rates in the Ecosim model. The data format needed for this is a yearly time series of biomass densities of the functional groups: *Acartia sp.*, *Temora sp.*, *Pseudocalanus sp.* and other zooplankton species. During the fitting procedure, the relative change of biomass densities of the above mentioned groups in the reference time series is compared to those predicted by the model by calculating a goodness-of-fit measure SS. More specifically, SS is the weighted sum of squared deviations of log rescaled observed biomasses to log predicted biomasses by EwE. Observed biomasses (y) are rescaled according to the equation $y=q*B$, where q is the maximum likelihood estimate of the relative abundance scaling factor and B is absolute abundance. During the fitting process, first those k_{ij} values are identified that affect SS the most by varying them iteratively and rerunning the model each time. Second, a nonlinear SS minimization procedure based on a Marquardt nonlinear search algorithm with trust region modification of the Marquardt steps chooses such values for the vulnerability multipliers identified in the first step that minimize SS. As this procedure only takes relative changes into account, the absolute values in the time series are less important. Thus, we calculated the time series as the yearly average of monthly average values from months 8 and 9 only as data from these months are available every year 2004-2014.

Fishing effort data

Data on fishing efforts is used together with landings and discards data collected within the DCF (reported by STECF), and landings data from ICES reports to determine fishing mortality rates in EwE. More specifically, relative amounts of landings and discards in weight disaggregated by fish age and fleet segment, total amount of landings per species (from ICES reports) and time series of efforts were used to calculate a fishing mortality time series (2004-2014) for demersal fish species in Ecosim. Relative amounts of landings and discards at age were taken from ICES data. We define adult cod and flounder as Age 3+. The effort time series is constructed as the relative change (compared to 2004) in kW days at sea for each fleet segment. We only use data from gear types contributing most to catches in the fleet segment: otter trawls for active gears, gillnets (and longlines, pots depending on vessel size in the fleet segment) for passive gears and pelagic trawls for pelagic fishery. We excluded data from Finland and Estonia because they started reporting in 2013 and 2005 only, resp., and inclusion of their data would have introduced an artificial jump in the effort time series. We always used STECF data collected in SD 25-28.

In EwE, fishing mortality of a certain stanza i in a given time step t, F_{it} is calculated from the sum of the relative efforts of each fleet j fishing them, E_{tj}, multiplied by the partial fishing mortality F_{ij0} caused on stanza i by fleet j, m being the total number of fleets:

$$\boldsymbol{F_{it}} = \sum_{\boldsymbol{j=1}}^{\boldsymbol{m}} (\boldsymbol{E_{tj}} \cdot \boldsymbol{F_{ij0}})$$

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Protocol A.3. Implementation of cod stomach data in the Multispecies stock-production model (MSPM) considering the growth of cod and herring as dependent on environmental variables.

Cod stomach data

In previous applications of the MSPM the data on cod stomach contents used to fit the model were constrained to years 1982-1990. Recently historical data from different sources have been provided and compiled with newly collected data, so the stomach data available for the model fitting cover period 1982-2014 with gaps in years 1992, 1994, 1997-1998, and 2001-2003. This data represents novel information in the model.

The data is the same than those presented for the protocol A.1 and A.2 although the elaboration for model implementation is quite different. Data were available at length basis and separated into adult and young components of both predator (cod) and prey (herring and sprat) as required in MSPM. The separation length for adult and young components of the cod, herring and sprat was set at 33 cm, 17 cm, and 11 cm, respectively. The adult fish component for cod should represent approximately fish at age 3 and older, while for herring and sprat fish at age 2 and older. The allocations of length (and ages) into components is presented in the text table below.

species	Young component	Adult component
cod	<33 cm (age 1-2)	>=33 cm (age 3+)
herring	<17 cm (age 0-1)	>=17 cm (age 2+)
sprat	<11 cm (age 0-1)	>=11 cm (age 2+)

The separation of the data into young and adult components differs somewhat from the separation used for Ecopath with Ecosim (EwE) model as the time range and the area of model applications differ. The stomach contents data are used to fit the MSPM by adding the following term to the minimized sum of squared residuals

$$StomachContentsTerm = \lambda \sum_{t,s} (\ln SC_{t,s}^{obs} - \ln SC_{t,s})^2$$

where SC is relative stomach contents, index obs refers to observed data, s is species component, t is year, and λ is statistical weight of stomach contents term in the total sum of squared residuals.

Growth of cod and herring as dependent on environmental factors

The growth of cod, herring, and sprat undergoes large changes in the Baltic. Withinthe recent 3 decades the difference between maximal and minimal growth was 40% for cod, 60% for herring, and 50% for sprat. In the former model applications only growth rate of sprat was modelled as dependent on environmental factors (density dependence); for herring and cod time trends in growth were considered.

Now growth rates of cod and herring have been related to environmental variables, growth of cod was made dependent on areas of hypoxic waters, while growth of herring was presented as dependent on water salinity in Bornholm Basin. Both hypoxic areas and water salinity explain quite large amount of variance in cod and herring growth (58% and 65%, respectively, see Fig. A.1-2 below).

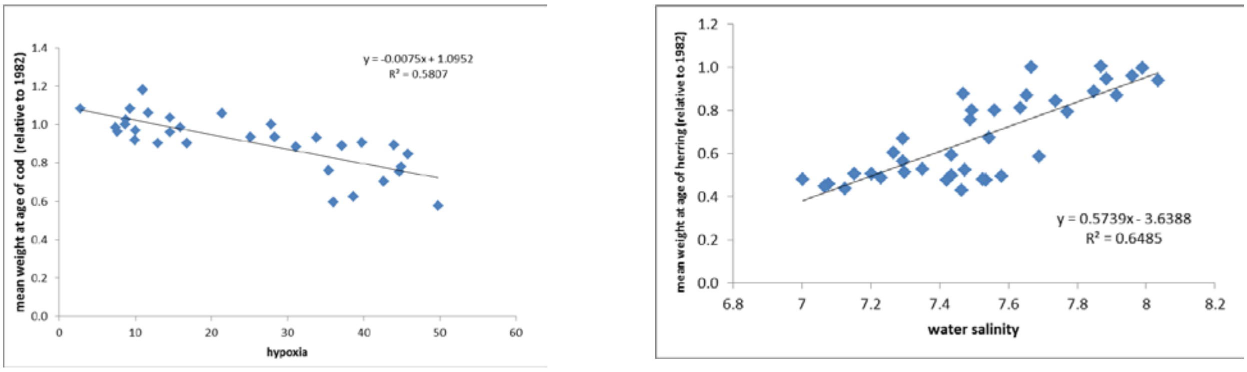


Figure A1-2: Dependence of cod and herring growth on area of hypoxic waters (cod) and water salinity (herring)

The inclusion of cod and herring growth as functionally dependent on area of hypoxic waters (cod) and water salinity (herring) represents novel information in the MSPM. Technically it is implemented by modelling the anabolism coefficients (from differential form of the von Bertalanffy growth equation) of these two species as dependent on above environmental variables.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

B. North Sea

The North Sea case study aims to provide user friendly models for stakeholders that integrate all current knowledge of the likely consequences of changes in management: to fish stocks, to industry catches, to their social and economic outcomes, and to wider EAFM concerns. The modelling philosophy for the North Sea has thus been to provide fast running transportable approximate overview models (The so called green, and possibly the amber and red models) that cover as many aspects of EBFM trade-offs as possible. Such models draw on more detailed models of how the North Sea ecosystem works, particularly its commercial fish stock components, together with information on the social and economic situation of the fisheries.

The Charmingly Simple Model (CSM) was initially developed to explain the changes in the North Sea wide size spectra slope, which is considered a quite stable indicator about ecosystem status. This steady state method predicted that in the long term the log linear size spectrum slope is linearly related to fishing mortality. The North Sea CSM is based upon 13 idealised species of fish whose maximum size (Linf) range from 10 to 130 cm. Other parameters are based upon life-history invariants (e.g. growth, maturity and non-predation natural mortality rates) or common size based processes (e.g. predation, stock recruitment). Model details can be consulted in Deliverable 4.1. Under the MAREFRAME project this model has already be developed to provide a time varying version. This was based upon the moment based approach of Pope, (2003), which describes population numbers and size compositions by their uncentrered moments. (i.e. as the sum over all sizes of Numers at length *Length^i where i=0:4.

How might new data be incorporated into this process? In the case of the North Sea the new data considered are trophic level measurements based upon isotope studies. This is a very specific novel technological data set that might be used to inform the underlying biological models. The other new data to be considered for the North Sea is fishermen information. The latter is far more wide ranging and will help inform the overview models. Its incorporation into models will depend to some extent on the questions fishers, or more likely their representatives, wish to ask. However, since a key question is how fishermen will respond to changes in management, their knowledge of both fisheries and their knowledge of their own likely behaviours are vital to take into account. This is likely to be particularly important in questions of compliance functions where Stakeholder information is likely to be the only feasible data source.

How to incorporate fisher's information into our overview models? The nature of the questions that may be posed to the overview models are open-ended and consequently to some extent so must be our use of fishermen's knowledge. The important point will be the need to be flexible in adding information on elements such as price or costs or behaviours that ongoing stakeholder interactions suggest are important. However, a specific question could be the extent that any new regulations will be complied with. It would be useful to capture this if at all possible. This protocol describes how these two novel data sources (isotopes and fisherman knowledge) might be used in the North Sea models.

Protocol B.1. How to use Isotopes based Trophic Level data in the CSM considering how to capture and use fisherman knowledge in the overview models.

Isotopes data

Trophic Level estimated with isotopes data from 2060 specimens collected between 2002 and 2006 in the North Sea were kindly made available by Simon Jennings of CEFAS (Jennings et al., 2007). These were from the following species *Amblyraja radiata, Clupea harengus, Eutrigla gurnardus, Gadus morhua, Hippoglossoides platessoides, Limanda limanda, Lophius piscatorius, Melanogrammus aeglefinus, Merlangius merlangus, Microstomus kitt, Pleuronectes platessa, Pollachius virens, Scomber scombrus, Trachurus trachurus* and *Trisopterus esmarkii*. These species cover most of the abundant commercial species included in the ICES North Sea multispecies model (ICES 2013), sprat, sandeel and sole being the only un-sampled species. The intention is to try to include these new data in the charmingly simple model (CSM) to test and extend if needed its assumption and hence, if necessary, those of the more detailed models that it emulates. Some fisheries data not previously included in the CSM will also be needed. Data on catch at age and weight at age are available from ICES sources. To link results to the assumptions of the initial CSM the reported weights were first transformed into species equivalent lengths (SEL's) as SEL= (Wt/condition factor)^(1/3). Catch at age data may then be converted to equivalent SEL catch by moment.

A preliminary statistical analysis of the trophic level data indicates size is the chief determinant of a species trophic level. Most individual species of pescivores and benthivores broadly responded by increasing trophic level with length while apparently showing some detailed variations in their response. Not surprisingly the planktivores did not show this response. Notably the trophic level of herring decreases significantly with length and Horse mackerel and Norway pout show negative though non-significant trends with length, this perhaps suggesting that any predation by these species, on the young of other fish species, may be mostly confined to their early stages. Given the systematic changes in trophic level with length it is considered that a modified version of the Charmingly Simple Model (CSM) (Pope et al 2006) may be the most suitable and simplest way of assimilating the available trophic level data set (N.B. these are estimated from isotopes data) into a modelling framework that could then be used for the wider purposes of the project.

Questions to address will be to what extent are more realistic food size and food type preferences required to fit the trophic level data and do any necessary changes markedly affect the model's responses to changes in fishing mortality rate.

***Fishers Information*.**

Fishermen's information is naturally wide-ranging. The strategy to date to gather this information has been to listen carefully to stakeholder's comments on the effects in particular of the landings obligation at two sessions of the NS-ACs demersal working group and in the light of the insights obtained there to provide scope for stakeholders to input their own assumptions into a key part of the integrative models that interprets how closely the fishing patterns of the past will operate in the future. The approach of allowing the prototype integrative model to include stakeholder's views on "species F linkage" has been advanced at a web meeting held with key demersal stake-holders (following very useful suggestions from a web meeting with key members of the Pel-RAC). This is now incorporated into the model in the form of two sliders where the industry can input their own ideas as to the correct form of the relationship. Overtime this will allow their knowledge to be

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

crystalised (Ramirez-Monsalve et al., 2016). This approach to collecting information has the merit of direct involvement and discussion of industry representatives on key issues.

In the same way it is intended extend the approach to other key parameters by leaving certain parameters adjustable by sliders so that industry representatives can include their own estimates. Discussion of the appropriate values should then yield at least some plausible values. This will likely be particularly useful in the weighting the factors relating to compliance. We know something of the links of compliance to economic, social and other factors (Hatcher and Gordon, 2005) but not the case specific parameters that apply them to specific fleets and fisheries. The slider approach to capturing industry knowledge should help clarify these issues. These ideas have been present at the ICES ASC and at a lunchtime seminar at DG MARE as well as to subgroups of the PelAC and NSAC.

Model implementation

The CSM is fully described in Pope et al. (2006) and MareFrame Deliverable 4.1. However, to accept the Trophic Level Data this version of the CSM will need to be modified further so that actual species is fitted rather than the idealised species adopted in the original formulation. It will also need to be extended so that planktonic and benthic food sources are described. These necessary modifications needed to adapt the CSM described in are as follows:

1. *Rescale model to a logarithmic size scale to allow zooplankton and fish eggs to be included.*

The transient moment based version of the CSM operates by updating the column vector of the 0 : 4th moments of the size distribution at time t ($\Psi(t)$) by the equation

$$\Psi(t+1) = G^*(\Psi(t)\ \exp\ (\text{-total mortality rate})^*G + R^*\rho \qquad \text{eq. B.1}$$

Where G is a matrix describing half period growth. R is a scaler of recruitment and ρ a column vector of the moments of average length at recruitment.

In practice except in very simple cases $\Psi(t)\exp(\text{-total mortality rate})$ cannot be adequately described in moment terms and has to be converted to a pseudo length distribution to calculate the impact of mortality on different sizes. This is achieved by converting $\Psi(t)$ to a plausible size distribution ($\theta(t)$) using a pseudoinverse matrix. This is constructed as follows. A square m*m matrix P is constructed from stacking two component matrices M and Λ. Where m is the number of lengths in the size distribution.

M is a 5*m moment generating matrix such that

$$\Psi(t) = M^*\theta(t)$$

Λ is a m-5*m constraint matrix such that

$$O = \Lambda^*\ \theta(t)$$

Where O is a m-5 column vector of zeros. Elements of Λ are bidiagonal or tridiagonal terms that constrain all elements of the psudo size distribution to follow a exponential decline with periodic steps.

We may then right Inverse(P) = $(\text{Stack of } M \text{ and } \Lambda)^{-1}$

The first 5 columns of Inverse (P) are then used as the pseudo inverse PI such that

$\theta(t) = PI * \Psi(t)$

Equation B.1 may then be rewritten as

$\Psi(t+1) = G*(M*SS*PI*G*\Psi(t) + R*\rho$ eq. B.2

Where SS is an m*m diagonal matrix containing the survival proportion from the mortality at each size group. These equations remain essentially unchanged if the elements of $\theta(t)$ are measured on a linear scale or a log scale although these are some minor adjustments to their inner details between the two cases.

2. Compute a trophic level at size spectrum in addition to current numbers at size spectrum (ideally both expressed as moments rather than numbers) (in progress).

It will be necessary either as a distribution by length or in moment terms to construct a tropic level vector T for each predator species such that in length terms T(t, l) is the trophic level of a species at time t and length l.

$T(t+1,l+i) = (T(t,l)*B(t,l) + \text{Trophic Level of food intake}(l)*\text{Wt of food ingested})/(B(t,l+i)$ eq. B.3

Where i is the growth increment at length l and B(t,l) is the biomass of the predator at time t length l. The trophic level of food will need to be computed from the predation on each food item.

3. Two aditionnal modifications, still in planning stage are: (a) allow species in the model extra traits in addition to Linf such as K and food size and type preference. The K, M1 and L_∞ and food size preferences characteristic of each stock will be based upon literature values and (b) develop Zooplankton and Benthic sub spectra for numbers and Trophic Level. To all feeding on “other food“ items simple fixed zooplankton and benthic size spectra with given trophic levels by size will be included to complement the fish spectra. They will be based upon literature values.

*4. Optimising the model to use the Trophic level data based on isotopes***.** With these modifications the model will then be in a shape where its relevant parameters can be adjusted to fit to the trophic level data of each species. The parameters needing optimising will be those of the feeding relationships and potentially those of the bulk trophic level spectra of the “other food species“ of plankton and benthos. Adjustments to these parameters will give a basis for including feeding by species not sampled or not fully sampled in the ICES years of the stomach that consequently are not included as predators in current multispecies models of the North Sea. It may also provide checks on the results of those species that are currently included.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

C. Northern and Western Waters – Iceland Waters

In the Icelandic case study, a complex model incorporating the major gadoid stocks and fleets participating in the fishery was constructed. The interactions among these stocks in terms of predator-prey relationships and mixed fisheries issues is being investigated in the model. Stocks of lesser commercial importance such marine mammals are also incorporated in the model. The impact of changing stock dynamics on the whole system in terms of ecosystem approach to fisheries (EAF) is a key importance in the case study.

The case-study in Icelandic waters will see the development of ecosystem models using three different modelling frameworks, Gadget (Begley and Howell, 2004) with case-study details in Deliverable 4.1, Ecopath with Ecosim (EwE, described in Christiansen et. al., 2004) and ATLANTIS model (Fulton et al., 2004), based on the Icelandic continental shelve area (see deliverable 4.6 for details). Novel data implementation is applied to Gadget. A number of novel data sources and/or novel applications have been considered. A particular emphasis has been made on two different types of novel data i) genetic information on close kin and feeding ecology of minke whales. Genetic information are new technological data for WP2 purposes. Minke whale diet observed recently differed markedly from the previous limited data in Icelandic waters. These changes make this novel data of main interest to be used by the multispecies Gadget model with the aim of understand and quantify the total effect of minke whale in the stocks and in the Iceland fisheries

The genetic information on close kin is model agnostic as it guides the model development, although was implemented in a gadget-like model implemented in R (Rgadget), the feeding ecology of minke whales are implemented in Gadget and the oceanographic data is implemented in ATLANTIS. Three different protocols are defined for this case study each one for each data type an model.

Protocol C.1 - whale genetics (close-kin) to define whale stock structure

This protocol was elaborated based on an already published paper (Elvarsson, 2015) developed in Mareframe taking most of the information from the Material and Methods section.

Data

Certain facets of the population dynamics of a species are hard to quantify, including stock structure. In particular, geographical boundaries of stocks or populations are often hard to estimate, and data often hard to obtain due to issues such as cost per sample. Recent developments that allow for the detection of close-kin has the possibility of giving further insights into stock structure. To investigate the potential utility of augmenting a traditional tag-recapture experiment with information on close-kin the North Atlantic fin whale (*Balaenoptera physalus*) population was used as a case-study.

For management areas in and next to the Irminger Sea, that are East-Greenland (EG), West-Iceland (WI), and East-Iceland (EI), two different stock structure hypotheses have been suggested that could explain the fin whale distribution: 1) a mixing hypothesis, where it is assumed that the fin whales originate in three separate breeding stocks with no dispersion (no sharing of genetic material or no gene flow) between the breeding grounds and 2) the dispersion hypothesis assumes that there is some degree of dispersion on the breeding grounds. However, for the information to be useful when determining stock boundaries sampling from other areas is required. This will require additional sampling outside of the Icelandic EEZ and the question is how many samples are needed. A simulation study of a (genetic) mark-recapture experiment, that has been augmented using information on genetically determined close relatives was set to determine the required amount of genetic samples to eventually determine the minke whale stock structure.

Model implementation

To compare the two stock structure hypotheses of dispersion vs. mixing, a genetic tagging experiment (biopsy collection) in the EG subarea has been suggested. During which time, for a 10-year period, a quota of 150 fin whales annually would be set in the WI subarea. Augmenting the genetic tagging experiment with information on close relative would potentially show greater contrast between the two hypotheses than a conventional tag-recapture experiment.

Simulation model

The stock dynamics in this study were implemented in a computer program, `Rgadget` (https://github.com/Hafro/rgadget), set up in such a way as to closely mimic the dynamics of the Baleen II model as described in Punt (1999). In the analysis which follows comparison will be made on the basis of two possible stock structures, mixing or dispersal type, as shown in Elvarsson (2015), Fig. A1. When mixing dynamics are assumed, separate breeding stocks overlap (to some fixed degree) on the feeding grounds, while dispersion denotes the permanent migration between breeding stocks. The general dynamics of the population is described in Elvarsson (2015). To define the migration process, let α denote the mixing proportion, i.e. the proportion of a stock which migrates to a specific different feeding ground, and let β denote the proportion of animals which “move” to a different stock. The stock distribution on feeding grounds is defined by a mixing matrix $\mathfrak{V} = V_{jk}$, where V_{jk} denotes the proportion of stock j that migrates to area k annually. Under the mixing hypothesis it is assumed that the sub–stocks, even though separate on the breeding grounds, overlap on the feeding grounds. The feeding grounds have been split up into three distinct subareas. The subareas represent the main feeding ground for each of the sub–stocks. While a simulation baseline $1 - 2\alpha$ of the stocks’ individuals migrate to their own feeding ground, regardless of where they were last year, α migrate to each of the areas adjacent to their native feeding ground. The dispersion hypothesis assumes that individuals stray between sub–stocks while the sub–stocks migrate to a fixed feeding area. In general, the stock overlap (mixing) is according to:

$$\mathfrak{V} = \left(\begin{array}{c|ccc} & \mathbf{C1} & \mathbf{C2} & \mathbf{C3} \\ \hline \mathbf{EG} & 1-\alpha & \alpha & 0 \\ \mathbf{WI} & \alpha & 1-2\alpha & \alpha \\ \mathbf{EI} & 0 & \alpha & 1-\alpha \end{array}\right)$$

where the columns represent the breeding stocks (C1, C2, C3) and the rows feeding areas (EG, WI, EI).

Under the dispersion hypothesis the annual straying between three sub–stocks is only defined between adjacent stocks (i and j).

$$D_{i\to j} = d_{i\leftrightarrow j}\frac{K_i + K_j}{2K_i}$$

where

$$d_{ij} = \begin{cases} \beta & \text{if i=1 and j = 2} \\ \beta & \text{if i=2 and j = 3} \\ 0 & \text{if } |i-j| > 1 \\ d_{ji} & \text{j<i} \end{cases}$$

Under the mixing hypothesis $\alpha = 0.05$ and $\beta = 0$, while under the dispersion $\alpha = 0$ and $\beta = 0.05$.

Tagging can, as noted above, be used to estimate stock migrations. Although it is assumed here that all tagging will be made using skin biopsies to obtain genetic material the biopsies can also be used in a conventional mark–recapture analysis. The dynamics of the tagged sub–population in the simulations is the same as for the untagged population. For the sake of simplicity only a single tagging experiment, conducted in a single area, is considered in this analysis. The initial ($t = 0$) number of tagged animals is distributed across stocks j, ages a and genders g, according to the equation:

$$\mathfrak{T}_{gj0a} = \frac{N_{gj0a} * \phi_0}{\sum_{gja} N_{gj0a}},$$

where ϕ_0 is the total number of tagged animals. The expected number of animals recaptured is a function of the dynamics applied to the population, both tagged and untagged. The recaptures, $\hat{U}_t$, were considered to be distributed according to

$$f(\hat{U}_t) = \prod_t \frac{\Gamma(\frac{U_t}{\lambda}+\hat{U}_t)}{\Gamma(\hat{U}_t+1)\Gamma(\frac{U_t}{\lambda})} (\frac{1}{1+\lambda})^{\frac{U_t}{\lambda}} (\frac{\lambda}{1+\lambda})^{\hat{U}_t}, \qquad \text{eq C.1}$$

i.e. a negative binomial distribution with a dispersion[4] parameter U_t defined to be the predicted number of animals recaptured by commercial whaling fleets and λ controls the detection probability. Here a negative binomial distribution for the tag-recaptures is used, instead of a more commonly used Poisson model, which is intended to allow for greater variation in recaptures.

Comparing hypotheses

In the setting described above two different stock structure hypotheses are to be contrasted. To compare these stock structure hypotheses three potential methods of comparison are studied here.

- Time–trend analysis using regression.
- Total number of recaptured animals by area.
- Number of recaptured animals by area in relation to number of intra–related individuals within the catch.

To compare the two hypotheses using direct (genetic) tagging a Poisson regression model for a time trend in the recapture rates can be fitted. The regression model is offset by natural mortality as the tagged population in the model is expected to trend downwards due to it. The dispersion hypothesis is expected to have an increased recapture rate while the rate should be constant under the mixing hypothesis. The model for trend can be compared, using a likelihood ratio test, with a model with no time trend. The rejection interval was set such that the type I error, i.e. the rejection probability when mixing is the true stock structure, was 5%.

---

[4] Not to be confused with stock dispersion

In genetic tagging augmented with information regarding genetically determined close relatives (parent-offspring or half-siblings), a skin sample from a single whale can, in the case of NA–fin whales, effectively tag 2.5 – 3.5 other whales, as shown in Gunnlaugsson (2011). Using information on close relative's time trends in occurrence at feeding grounds are expected to be harder to detect. Intuitively this can be explained by noting that with a dispersing stock relatives are already present at all three feeding grounds at the time of tagging. The total number of caught animals that are related to tagged individuals, i.e. the number of **effectively tagged** individuals is:

$$T_{..k} = \sum_t \sum_{j\in\mathfrak{J}} T_{jkt} \qquad \text{eq C.2.}$$

where T_{jkt} is the number of animals related to the tagged animals from stock j, caught in area k at time t and $\mathfrak{J}$ denotes the set of breeding stocks. $T_{..k}$should, given a similar degree of dispersion and mixing, be somewhat higher for dispersing stocks than mixing, based on a similar argument as before.

Untagged whales caught are also a source of information regarding the stock structure. Consider the total number of animals caught in area k from stock j, denoted by c_{jk}. This number is not observable but if one assumes only one genetic relation can be detected per individual within a stock, then the total number of possible detections is $\frac{c_{jk}(c_{jk}-1)}{2}$. One measure of the magnitude of genetic relatedness detected between all whales caught of stock j, denoted R_k, in area k is therefore:

$$R_{jk} = \frac{c_{jk}(c_{jk}-1)}{2n_j} \qquad \text{eq C.3}$$

Note that R_{jk} tends be smaller as n_j grows larger. Furthermore, the total number of relations detected in the total catch for the time period, which can be observed directly from the catches:

$$R_{.k} = \left(\sum_{j\in\mathfrak{J}} R_{jk}\right) \qquad \text{eq C. 4}$$

becomes smaller with fixed total abundance as the number of breeding stock decreases.

Using the information on related individuals one can augment equation C.1 by calculating the following ratio for each area:

$$\rho_k = \frac{T_{..t}}{R_{.k}}$$

The above quantity should become larger for dispersing stocks as there is genetic interchange, even if the total number of effectively tagged individuals is similar.

For each of the stock structure hypothesis the number of simulated datasets per hypothesis was 1000 for each number of tags. The number of tags in this experiment varied between 100 to 1500. The tag–recaptures were simulated using equation C.2. Under the mixing hypothesis the stock proportions within the catch (c_j from equation C.3) were simulated using a multinomial distribution parametrised

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

by the expected value of number of individuals caught from each stock. Assuming the dispersion hypothesis of $R_{.k}$, as defined by equation C.4, is constant. Here $R_{.k}$ is assumed to be a Poisson process with mean $\frac{c(c-1)}{2n}$ where c is the total catch and n is the total abundance of all stocks.

The distribution of the three test statistics was analysed and for the null hypothesis, which is in this case the mixing hypothesis, the rejection interval was chosen in such a way that it would have a rejection probability of 0.05. Using simulated data based on the alternative hypothesis, which is the dispersion hypothesis, the power of the test was calculated as a function of the number of tags.

Protocol C.2. Whale diet implemented in GADGET

Data

The common minke whale (*Balaenoptera acutorostrata*) is the most abundant whale species in Icelandic continental shelf waters. Previous studies have indicated that cetaceans, and in particular minke whales, play an important role in the marine ecosystem by consuming several times the total Icelandic fishery landings. There the annual consumption by minke whales alone was estimated as around 2 million tonnes in the 1990's. There was, however, considerable uncertainty associated with this estimate. One of the greatest sources of uncertainty regarding the effects on the cod stock was associated with the very limited knowledge of the diet composition of minke whales in Icelandic waters. It was therefore of prime importance for further development of multispecies modelling in Icelandic waters to obtain data on the diet of minke whales and investigate multi-species interactions in more detail, in particular those between minke whales and the cod stock.

The main objective of the research programme on common minke whales, conducted in the years 2003 – 2007, was to address these questions as a pilot study using various methods (Vikingsson et al., 2014). A total of 190 minke whales (96 males and 94 females) sampled during April and September 2003- 2007 were examined with respect to stomach contents. In total, 14 prey types were found in the stomachs, including 10 species of fish and 2 species of euphausids. Sandeel was the most frequently encountered prey, followed by gadoids, capelin and herring. The diet differed markedly from the previously available, limited data from Icelandic waters with less krill and capelin and more gadoids and herring in the more recent period. These changes make this novel data of main interest to be used by the multispecies Gadget model with the aim of understand and quantify the total effect of minke whale in the stocks and in the Iceland fisheries. This whale diet data are saved in the MareFrame data base system dbmf.

Model implementation

for the time period 2003-2007 and entire eastern Baltic cod distribution at a quarterly aggregation. Data format for whale data implementation in GADGET is as follow. Whale total landings are assumed to be known and their abundance data for model implementation (see eq. C.5) is listed in a column format in a separate file with the following fields: *year, step, area, fleetname,* and *amount*. On the other side, whale stomach contents are used as a likelihood component to compare observed and modeled proportions of species consumed by whales (see eq. C.6). Stomach data stored into the Mareframe Data Base - mfdb (https://github.com/mareframe/mfdb) are retrieved using the function 'mfdb_stomach_presenceratio'. The text file format of this likelihood component has the following fields: *year, step, area, predator, prey* and *ratio*.

The following describes stock dynamics of the common minke whale and cod as implemented within the Gadget framework, where species specific formulations are highlighted where appropriate. The model for cod is described in detail in Taylor et. al (2007) and subsequently Elvarsson et. al 2014. In the model the simulated quantity is the number of individuals in a cell, $N_{gralsyt}$ where g denotes the species, r denotes the area in which the individuals within the cell live, a is the age, l the cells length group, s is the maturity status, where $s = 0$ denotes immature animals while $s = 1$ mature, at year y, ranging from 1960 to 2011 and t is the quarter within the year. Age ranges between a_{0g} and $a_{\infty g}$ years while the length ranges from l_{0g} to $l_{\infty g}$ cm, with δl_g cm length increments. The population is governed by the following equations:

$$
\begin{aligned}
N_{alsy,t+1} &= \sum_{l'} G_l^{l'}\left[(N_{al'syt} - C_{fal'st})e^{-M_a \Delta t} + I_{al'syt}\right] && \text{if } t < 4\\
N_{a+1,ls,y+1,1} &= \sum_{l'} G_l^{l'}\left[(N_{al'sy,4} - C_{fal's,4})e^{-M_a \Delta t} + I_{al'sy,4}\right] && \text{if } t = 4 \text{ and } a < a_\infty\\
N_{a,ls,y+1,1} &= \sum_{l'} G_l^{l'}(N_{al'sy,4} - C_{fal'sy,4} + N_{a-1,l'sy,4} - C_{f,a-1,l'sy,4})e^{-M_a \Delta t} && \text{if } t = 4 \text{ and } a = a_\infty
\end{aligned}
$$

where $G_l^{l'}$ is the proportion in length group l, of species g, that grows $l' - l$ length groups in a time period of length Δt, C_{falsyt} denotes the catches by fleet $f \in \{S_c, C_c, S_m, C_m\}$, $S_{\cdot}$ and $C_{\cdot}$ denote the survey and commercial fleets respectively, M_{ga} the natural mortality at age a of species g and $I_{gralsyt}$ denotes the movement from the immmature to the mature stock components. [5]

Growth in length is modelled as a two–stage process, an average length update in Δt and a growth dispersion around the mean update. The average length update per time step is set according to a simplified form of the Von Bertanlanffy equation:

$$\Delta l_g = (l_{g,\infty} - l)(1 - e^{-k_g \Delta t})$$

where $l_{g,\infty}$ is the terminal length and k_g is the annual growth rate of species g. In the second step the growth is dispersed according to a beta–binomial distribution parametrised by the following equation:

$$G_{gl}^{l'} = \frac{\Gamma(n_g + 1)}{\Gamma((l' - l) + 1)} \frac{\Gamma((l' - l) + \alpha_g)\Gamma(n_g - (l' - l) + \beta_g)}{\Gamma(n_g - (l' - l) + 1)\Gamma(n_g + \alpha_g + \beta_g)} \frac{\Gamma(\alpha_g + \beta_g)}{\Gamma(\alpha_g)\Gamma(\beta_g)}$$

where α_g is subject to

$$\alpha_g = \frac{\beta_g \Delta l_g}{n_g - \Delta l_g}$$

where n_g denotes the maximum length group growth of the species within a timestep and $(l' - l)$ the number of lengthgroups grown.

---

[5] A short note on notation, here l is used interchangeably as either the lengthgroup or the midpoint of the length interval for that particular lengthgroup, depending on the context.

The minke whales stock components, i.e. immature and mature, are assumed to have started at their mutual carrying capacity in 1960 when the model simulation starts. Birth rate of minke whales follows a variant of the Pella–Tomlinson spawning model:

$$b_t = BN_{ft}[1 + A(1 - (\frac{N_{ft}}{K_f})^z)]$$

where B_j is the birthrate per mature female in the pristine population, N_{ft} number of mature females (assumed to be 50% of the mature population), A and z are determined by MSY level and rate, and $K_f$the carrying capacity of mature females.

Two types of recruitment approaches are used for cod, depending on the time period. For the data rich time period, that is 1984 and onwards, the total number of recruits is estimated per year. Recruitment enters to the population according to:

$$N_{1l0yt'} = R_y p_l$$

wheret' denotes the recruitment time-step and R_y is the yearly recruitment. $p_l$is the proportion in lengthgroup l that is recruited which is determined by a normal density with mean according to the growth model and variance σ_y^2. For the period before 1984 the number of recruits per year is considered to be constant for all years, i.e. $R_y = R\forall y < 1984$.

Maturity is modelled and represented by the two stock components of each species. The movement between the two components is formulated as

$$I_{alsyt} = \begin{cases} \sum_{l'} N_{al'0y,t-1} \times m_{l'}^{l} & if\ \ s = 1\ and\ t > 1 \\ \sum_{l'} N_{al'0y-1,4} \times m_{l'}^{l} & if\ \ s = 1\ and\ t = 1 \\ -\sum_{l'} N_{al'0y,t-1} \times m_{l'}^{l} & if\ \ s = 0\ and\ t > 1 \\ -\sum_{l'} N_{al'0y-1,4} \times m_{l'}^{l} & if\ \ s = 0\ and\ t = 1 \end{cases}$$

where $s = 0$, as noted above, denotes the immmature stock component and m_x is the proportion mature defined as:

$$m_x = \frac{1}{1 + e^{-\lambda_g(x - x_{50})}}$$

where$x$ is either length or age for cod and minke respectively and x_{50} representes the mid-point of the maturity ogive.

Under the assumption that minke whales have a preference for pelagic fish stocks such as sandeel and capelin the fluctuation in minke whale abundance is in the model explained by linking the abundance to indices of sandeel biomass by a migration matrix:

$$I_{alsyt} = \begin{cases} N_{al0yt} \times m_x & \text{if s = 1} \\ -N_{al0yt} \times m_x & \text{if s = 0} \end{cases}$$

where I_s is the sandeel abundance index and m and m_x are the relative proportion of minke whales that migrate to the Icelandic continental shelf during the summer. Autumn migration is estimated similarly but in the opposite direction.

Catches are simulated based on reported total landings and a length based suitability function for each fleet, both commercial fleets and surveys. Total landings are assumed to be known and the total biomass (or in the case of minke whales, abundance) is simply offset by the landed catch. The catches for length group, fleet f at year y and time step t are calculated by:

$$C_{flsyt} = E_{ft} \frac{S_f(l) N_{lsyt} W_{ls}}{\sum_{s'} \sum_{l'} S_f(l') N_{l's'yt} W_{l's'}} \qquad \text{eq. C. 5}$$

where E_{ft} is the landed biomass (or numbers with $W = 1$) at time t and $S_f(l)$ is the suitability of lengthgroup l by fleet f defined as:

$$S(l) = \begin{cases} \frac{\delta}{1-e^{-(\alpha+\beta l)}} & \text{For whaling and fishing operations} \\ p_0 + p_1 e^{-\frac{(\log(l/L)-p_2)^2}{p3}} & \text{For whaling operations in the early years} \end{cases}$$

where the whaling fleet went through a gradual shift from a dome-shaped selectivity to a logistic curve between the years 1970 to 1980.

Consumption by minke whales of cod is modelled in a similar fashion as fleets, i.e. through a length based suitability function. However, the amount is determined based on the energy requirement of the predator, which is in this case minke whales. In the simple predator-prey relation between the species the prey availability to a predator becomes:

$$\frac{F_{Ll}}{\sum_{l'} F_{Ll'} + \mathfrak{s}OA}$$

where $F_{Ll} = S_{Pp}(L,l) N_{pl} W_{pl}$ is the prey biomass of length l that the predator could consume,

$$S_{Pp}(L,l) = \frac{1}{1 - e^{-(\mathfrak{a}+\mathfrak{b}l)}}$$

the suitability of a prey p for predator P, W_{pl} is the average weight for prey of length l, O is the density, per unit area, of other unspecified food sources and A is the size of the area. Here OA is defined such that enough food is available to minke whales other than cod.

The feeding level of the predator is:

$$\Psi_L = M_L \frac{\sum_{l'} F_{Ll'} + \mathfrak{s}OA}{\sum_{l'} F_{Ll'} + \mathfrak{s}OA + HA}$$

where M_L is the maximum consumption of a predator of length L for a particular time step length Δt. It is determined by:

$$M_L = m_0 L^{m_4} \Delta t$$

where m_0 and m_4 are user defined constants[6]. H is the density (biomass per area unit) of available food at which the predator can consume half maximum consumption. Note that H should reflect the ability of the predator to pursue its prey, which should factor in variables such as temperature and the cost of search. H determines how quickly the predators consumption reaches M_L. $H = 0$ would indicate that the predator would easily consume M_L of the available biomass. A larger value for H would indicate that prey is harder to find and therefore prey needs to be more abundant for the predator to reach M_L.

Given the feeding level and the prey availability the desired consumption of minke whales predators of length L is

$$C_{L,l} = N_L M_L \frac{F_{L,l}}{\sum_{l'} \mathrm{F}_{\mathrm{L,l}'} + OA + HA}$$

The parameter settings for the consumption are based on Lindstrom et. al (2009) and references therein.

Following Stefansson et. al (1997) natural mortality of cod is here factored into two parts, one induced by the consumption of minke whales and the second due to other sources.

$$M_a = M_{0a} + M_{ma}$$

where M_{0a} is the baseline mortality due to other sources and M_{ma} is the mortality induced by minke whales at age a. In the case where consumption is not modeled $M_a = M_{0a}$. When consumption is modelled M_{ma} is assumed *a priori* to be 0.08 and the modeled total natural mortality is adjusted accordingly. This results in a M_{0a} of 0.12 for most age classes which is in line with a recent estimate of the natural mortality reported by Gudmundsson (2013).

Observation model

In Gadget data are assimilated using a weighted log–likelihood function. Here five types of data enter the likelihood, absolute abundance and relative biomass indices, length distributions from survey and commercial fleets combined into a single likelihood, age – length distribution from the survey, maturity at length for all ages, and stomach contents from minke whales.

Survey indices

Abundance estimates for minke whales enter the likelihood using the following equation:

$$l_{gf}^{SI} = \sum_y \sum_t (N_{gfy} - \hat{N}_{gyt})^2$$

where $\overline{N}_y$ is the observed abundance estimate and

$$\widehat{N_{yt}} = \sum_l \sum_a \sum_s N_{alsyt}$$

The survey indices for cod are defined as the total number of fish caught in a survey within a certain length interval. The intervals used here are 16 – 25 cm, 26 – 38 cm and larger than 38 cm. These intervals are chosen such that they roughly represent age 1, age 2 and age 3^{+}.

For each length range g the survey index is compared to the modelled abundance at year y and time-step t using:

$$l^{SI}_{gf} = \sum_y \sum_t (\log I_{gfy} - (\log q_f + \log \widehat{N}_{gyt}))^2$$

where

$$\widehat{N_{gyt}} = \sum_{l \in g} \sum_a \sum_s N_{alsyt}$$

For implementation details see the annex to Elvarsson et al. (2014).

Maturity at length
Length at maturity comparison uses either the number of mature males observed in the scientific survey of minke whales or the number of immature and mature at age 3 from the Icelandic groundfish survey. The observed proportions are compared to the modelled proportion using sum of squares:

$$l^{M} = \sum_y \sum_t \sum_l (\mathrm{p}_{lyt} - \hat{\mathrm{p}}_{lyt})^2$$

whereπ_{lyt} and $\hat{\pi}_{lyt}$ are the observed and modelled proportions mature respectively in length group l, year y and timestep t.

Fleet data
Length distributions are compared using either 2 cm or 50 cm lengthgroups for cod and minke whales respectively for both commercial and survey fleets using

$$l^{LD}_{f} = \sum_y \sum_t \sum_l (\pi_{flyt} - \hat{\pi}_{flyt})^2$$

where$f$ denotes the fleet where data was sampled from. Similarly, age – length data are compared using 4 cm (or 50 cm) length groups:

$$l^{AL}_{f} = \sum_y \sum_t \sum_a \sum_l \sum_s (\pi_{falyt} - \hat{\pi}_{falsyt})^2$$

Stomach data
Stomach contents of minke whales are compared to modelled consumption in a similar manner as fleet data or by:

$$l^{ST}_{f} = \sum_y \sum_t \sum_a \sum_l \sum_s (\pi_{falyt} - \hat{\pi}_{falyt})^2 \qquad \text{eq. C.6}$$

where π_{lyt} and $\hat{\pi}_{lyt}$ are the observed and modelled proportions of stomachs with prey respectively in length group l, year y and timestep t.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Protocol C3. Oceanographic data in Atlantis

Data

Water flux, salinity, and temperature data were obtained from the Cartesian coordinates Ocean model with three-Dimensional adaptive mesh refinement and primitive Equations (CODE) (Logemann et al., 2013). Daily data were obtained from CODE for each spatial layer within each spatial box in the Atlantis model from 1948 to 2012. This oceanographic data is considered novel in two ways: first, the oceanographic model we are using, CODE (http://www.marsyn.is/), has never gone back as far as 1948 and oceanographic data has never been used in ecosystem models for Icelandic waters.

Model implementation

The water fluxes, temperature and salinity are read into the model as daily time-series for each box and layer. The water fluxes control the advection of nutrients and plankton in the model. The nutrients along with the temperature and salinity affect the primary production in the model which is the basis for the growth of other functional groups. A model with these data should be more realistic as reduced growth during cold periods should come from the underling oceanographic model. The oceanographic data can have an effect on the spatial distribution of the functional groups. If groups are allowed to have density dependent movement they will move to boxes within the model that will give the most possible growth, i.e. boxes with the most available prey but both the growth and distribution of the plankton is affected by the oceanography data. The oceanographic data is therefore fundamental for a spatial model like Atlantis.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

D. Northern Waters – West Scotland

The West of Scotland Ecosystem comprises the shelf area west of Scotland and supports several valuable fisheries. The EAF issues addressed in this case study are: what are the management measures required to recover the stocks of cod and whiting, what is the impact of seal predation, how to achieve maximum revenue, with achieving Good Environmental Status being an overarching goal in all management strategies tested.

The Ecopath with Ecosim (EwE) model developed to address these issues is largely based on previous studies (Bailey et al., 2011 and Alexander et al., 2014). It covers the period from 1985 to 2014 including 41 functional groups (marine mammals, seabird, fish, invertebrates, cephalopods, zooplankton, benthos, primary producers and detritus) and five fleets. The model was developed in order to simulate and compare alternative management strategies designed to achieve multiple goals: (1) recovering the depleted stocks of cod and whiting, (2) achieve sustainable exploitation of profitable fisheries and (3) achieve a healthy ecosystem.

For the West of Scotland case study both temperature and NAO index time series are available. Incorporating such data as a driver into a complex food web model including 41 groups is considered as innovative in this area. These environmental drivers can act as forcing function on primary producers in the model in order to assess whether the driver impacts the food web and also to predict changes in ecosystem.

In the West of Scotland area both temperature and NAO index time series, are recognised as being major drivers of marine ecosystems. This CS develops one protocol about the consideration of these data in EwE model.

Protocol D1. Temperature and NAO index as drivers in the EwE model.

Data

Ocean surface temperatures (SST), for the period 1960–2009, were obtained using Hadley Centre HadISST v1.1 and Climate Research Unit CRU TS3.1 data sets. Spatial data extracted within the study area ICES VIa rectangle, and the annual averages were calculated. These results were also validated using the Millport temperature time series previously used to describe the WCS Ecosystem (Bailey et al., 2011). Assuming that surface and bottom temperature showed the same annual trend (Berx and Hughes, 2009), SST trend was then scaled down to obtain depth integrated temperature (DIT), calculating the differences between high resolution surface and bottom temperatures averaged in the study area within 1971-2000 time series data (Berx and Hughes, 2009). DIT time series was used as a temporal time-series in Ecosim.

North Atlantic Oscillation (NAO) index data was obtained from the Climate Prediction Centre at NOAA (http://www.cpc.ncep.noaa.gov/products/precip/CWlink/pna/nao.shtml). The values were then averaged per year in order to get a time series of annual values.

The preliminary data analysis performed (see Del 2.2) shows that the temperature increased by around 0.8 degrees between the mid-1990s and the mid-2000s. In comparison the NAO index shows a very slight decline over the time period considered (1985 to 2013). Explanatory analyses show no obvious correlations between the environmental drivers and primary production although phytoplankton appears to show a very slight increase concomitant with the temperature increase

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

from mid-1990s to mid-2000s, while small zooplankton appears to loosely follow the NAO index up to the early 2000s. The analyses can help to assess the environmental impact on the West of Scotland ecosystem and the knock-on effects on fish production and the fisheries. If identified, such effects will have to be taken into account when designing alternative management strategies to address the management issues.

Model implementation

EwE allows for environmental drivers to be included as a forcing function on primary producers in the model in order to assess whether the driver impact the food web and predict changes in ecosystem to the driver.

Time series of data are imported into Ecosim (the dynamic component of the model) via a unique .csv file. This file contains, in columns, time series of biomass and catch data for each group in the model depending on availability. Each row then corresponds to a year of the time series. In addition, time series of forcing data e.g. temperature can be added to this file. Each data type i.e. catch, biomass, forcing data is identified by a code at the top of the column in order for the model to process the data accordingly. Forcing data can be imported on a yearly or monthly basis. Forcing data can also be standardised as the trend rather than the absolute values are used to force the model.

Forcing functions represent physical or other environmental parameters that may influence trophic interactions. These forcing functions can be used to directly influence primary production or to influence consumer groups in the model (higher trophic levels). Here we focus on the impact on primary production. Forcing data e.g. temperature can be directly input in the model if the effect is known, from previous published work for instance, and needs to be accounted for. The most common way however, as done by Alexander et al. (2015), is to fit the model with a primary production (PP) anomaly and then investigate whether this PP anomaly is statistically related to an environmental driver i.e. the forcing function. This driver can then be added to the model as a time series of forcing data which will influence the PP. This process was applied to the MareFrame west Scotland case study as detailed below.

In EwE, for each value in the prey/predator diet matrix corresponds a vulnerability value which is used in Ecosim i.e. the dynamic component. The vulnerability parameter is of crucial importance for Ecosim since it describes interactions between preys and their predators (i.e. how preys respond to a change in predator's biomass) and therefore has a direct impact on the ability of the model to capture and predict foodweb processes (Walters & Christensen, 2007). For each prey/predator interaction, a vulnerability at default value ($v_{ij} = 2$) means that the interaction is neither top-down nor bottom-up controlled (Walters et al., 1997; Christensen & Walters, 2004). A low vulnerability ($v_{ij} < 2$) means that an increase in predator (*j*) biomass causes little increase in the corresponding predation mortality of prey (*i*) (i.e. bottom-up control). A high vulnerability ($v_{ij} >> 2$) means that if predator (*j*) biomass increase *x*-fold, the corresponding predation mortality of prey (*i*) will increase nearly *x*-fold (Walters & Christensen, 2007). The parameterisation then consists in adjusting these vulnerabilities until the best 'fit' of the model outputs to historical time series is achieved. Goodness-of-fit is assessed by the sum of squared differences between the predicted and observed values on log scale (Christensen *et al.*, 2001). The fitting procedure described in Alexander *et al.* (2015) was applied and the following candidate models were tested (see Alexander *et al.*, 2015 for more details):

(i) Baseline: no fishing or environmental forcing and vulnerabilities set at 2

(ii) Baseline + trophic effects: same as (i) except vulnerabilities are adjusted to fit the data

(iii) Baseline + environmental forcing: same as (i) except the 'fit to time series' identifies a time series of values (forcing function) that improves the fit by impacting the predicted biomasses through primary production (subsequent analyses can be performed to link the forcing function to existing environmental drivers)

(iv) Baseline + trophic effects + environmental forcing: combination of (ii) and (iii)

(v) Fishing: fishing mortalities are included to drive the model, no environmental forcing and vulnerabilities set at 2

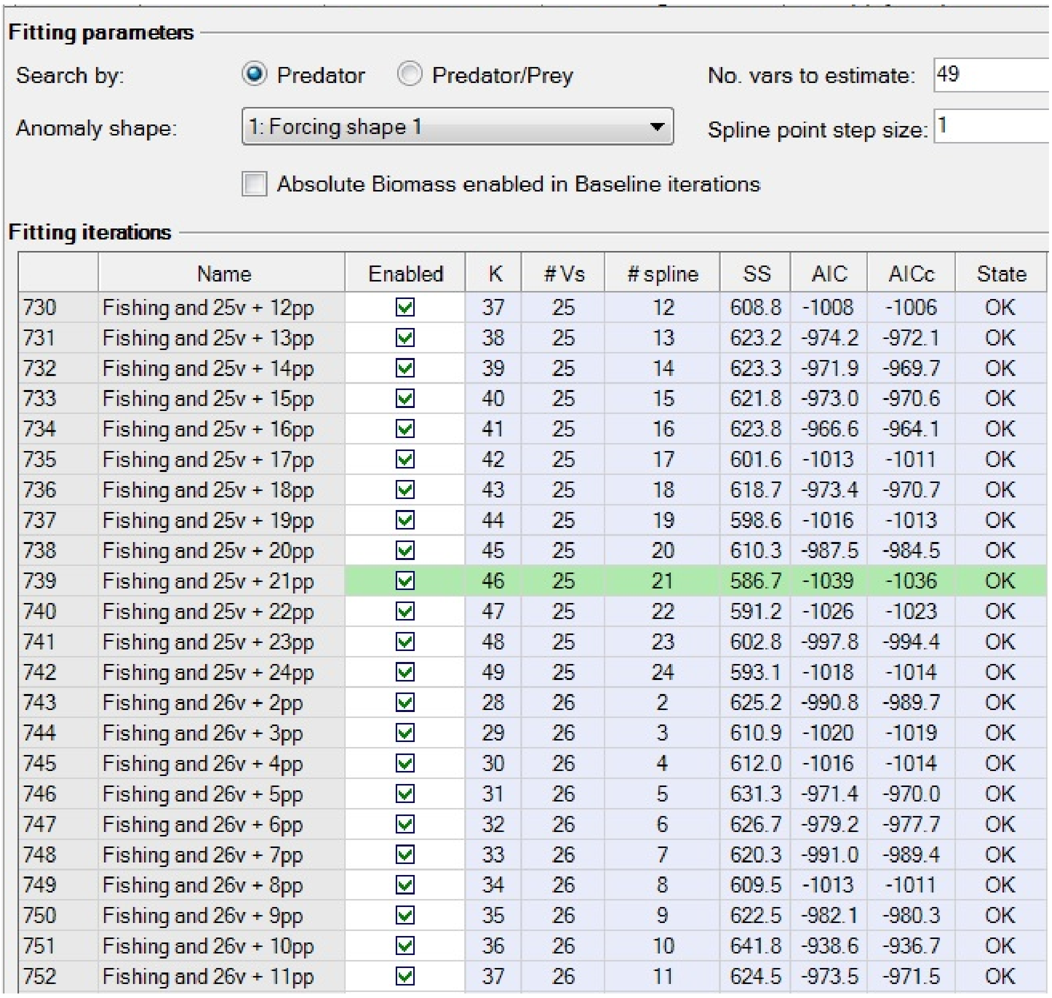
(vi) Fishing + trophic effects: fishing mortalities are included to drive the model and vulnerabilities are adjusted to fit the data

(vii) Fishing + environmental forcing: combination of (iii) and (v)

(viii) Fishing + trophic effects + environmental forcing: combination of (vi) and (vii)

The best candidate was selected with Akaike's Information Criterion (AIC) which identifies the best trade-off between goodness-of-fit and number of parameters (Mackinson *et al.*, 2009). Instead of manually selecting the number of vulnerabilities to adjust prior to running the 'fit to time series' module (Tomczak*et al.*, 2012; Alexander *et al.*, 2015), an automated stepwise fitting procedure (Scott *et al.*, in press) was used. This 'stepwise fitting' module has been included in the latest release of the EwE software (version 6.5) and allows for testing every possible combination of parameters by automatically running the 'fit to time series' with successive increments of the number of vulnerabilities and/or spline points of the forcing function for each candidate model (ii) to (viii).

Upon running the fitting procedure, the best model identified by the lowest AIC had been fitted by adjusting 25 vulnerabilities and with an environmental forcing function with 21 spline points (Fig D1). The fact that the forcing function has 21 spline points when the hindcasting is done over a 29 years' period is a clear indication of over parameterisation (Tomczak et al., 2012). As a result, it was chosen to not fit the model with a forcing function, as done by Tomczak et al. (2012), in order to avoid over parameterisation. The best model identified was fitted by adjusting 29 vulnerabilities (Fig. D2). Since no forcing function was included in the final model, no oceanographic data (temperature and NAO) was included in the subsequent analysis.



Fitting parameters

Search by: ● Predator ○ Predator/Prey

No. vars to estimate: 49

Anomaly shape: 1: Forcing shape 1

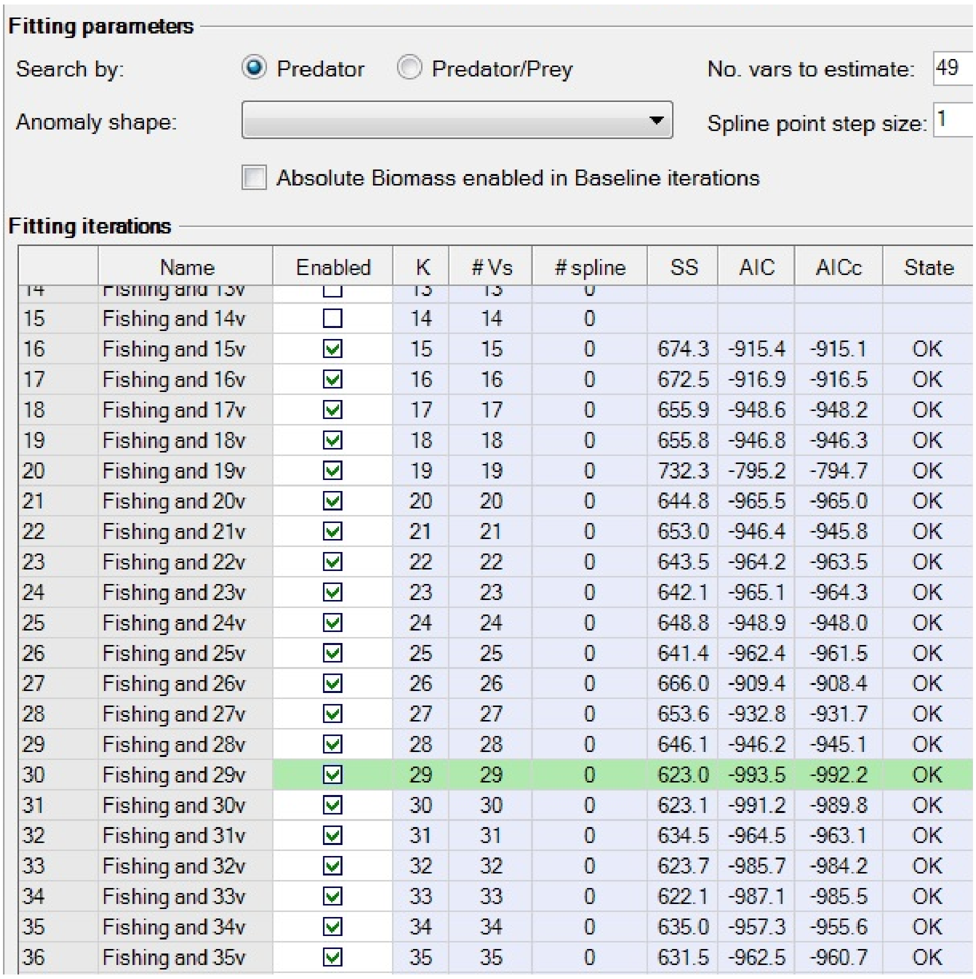
Spline point step size: 1

☐ Absolute Biomass enabled in Baseline iterations

Fitting iterations

	Name	Enabled	K	# Vs	# spline	SS	AIC	AICc	State
730	Fishing and 25v + 12pp	☑	37	25	12	608.8	-1008	-1006	OK
731	Fishing and 25v + 13pp	☑	38	25	13	623.2	-974.2	-972.1	OK
732	Fishing and 25v + 14pp	☑	39	25	14	623.3	-971.9	-969.7	OK
733	Fishing and 25v + 15pp	☑	40	25	15	621.8	-973.0	-970.6	OK
734	Fishing and 25v + 16pp	☑	41	25	16	623.8	-966.6	-964.1	OK
735	Fishing and 25v + 17pp	☑	42	25	17	601.6	-1013	-1011	OK
736	Fishing and 25v + 18pp	☑	43	25	18	618.7	-973.4	-970.7	OK
737	Fishing and 25v + 19pp	☑	44	25	19	598.6	-1016	-1013	OK
738	Fishing and 25v + 20pp	☑	45	25	20	610.3	-987.5	-984.5	OK
739	Fishing and 25v + 21pp	☑	46	25	21	586.7	-1039	-1036	OK
740	Fishing and 25v + 22pp	☑	47	25	22	591.2	-1026	-1023	OK
741	Fishing and 25v + 23pp	☑	48	25	23	602.8	-997.8	-994.4	OK
742	Fishing and 25v + 24pp	☑	49	25	24	593.1	-1018	-1014	OK
743	Fishing and 26v + 2pp	☑	28	26	2	625.2	-990.8	-989.7	OK
744	Fishing and 26v + 3pp	☑	29	26	3	610.9	-1020	-1019	OK
745	Fishing and 26v + 4pp	☑	30	26	4	612.0	-1016	-1014	OK
746	Fishing and 26v + 5pp	☑	31	26	5	631.3	-971.4	-970.0	OK
747	Fishing and 26v + 6pp	☑	32	26	6	626.7	-979.2	-977.7	OK
748	Fishing and 26v + 7pp	☑	33	26	7	620.3	-991.0	-989.4	OK
749	Fishing and 26v + 8pp	☑	34	26	8	609.5	-1013	-1011	OK
750	Fishing and 26v + 9pp	☑	35	26	9	622.5	-982.1	-980.3	OK
751	Fishing and 26v + 10pp	☑	36	26	10	641.8	-938.6	-936.7	OK
752	Fishing and 26v + 11pp	☑	37	26	11	624.5	-973.5	-971.5	OK

Figure D1: Results from the fitting procedure for the model with PP anomaly. The best model is identified by the lowest AIC (highlighted in green)



Fitting parameters

Search by: ● Predator ○ Predator/Prey

No. vars to estimate: 49

Anomaly shape:

Spline point step size: 1

☐ Absolute Biomass enabled in Baseline iterations

Fitting iterations

	Name	Enabled	K	# Vs	# spline	SS	AIC	AICc	State
14	Fishing and 13v	☐	13	13	0				
15	Fishing and 14v	☐	14	14	0				
16	Fishing and 15v	☑	15	15	0	674.3	-915.4	-915.1	OK
17	Fishing and 16v	☑	16	16	0	672.5	-916.9	-916.5	OK
18	Fishing and 17v	☑	17	17	0	655.9	-948.6	-948.2	OK
19	Fishing and 18v	☑	18	18	0	655.8	-946.8	-946.3	OK
20	Fishing and 19v	☑	19	19	0	732.3	-795.2	-794.7	OK
21	Fishing and 20v	☑	20	20	0	644.8	-965.5	-965.0	OK
22	Fishing and 21v	☑	21	21	0	653.0	-946.4	-945.8	OK
23	Fishing and 22v	☑	22	22	0	643.5	-964.2	-963.5	OK
24	Fishing and 23v	☑	23	23	0	642.1	-965.1	-964.3	OK
25	Fishing and 24v	☑	24	24	0	648.8	-948.9	-948.0	OK
26	Fishing and 25v	☑	25	25	0	641.4	-962.4	-961.5	OK
27	Fishing and 26v	☑	26	26	0	666.0	-909.4	-908.4	OK
28	Fishing and 27v	☑	27	27	0	653.6	-932.8	-931.7	OK
29	Fishing and 28v	☑	28	28	0	646.1	-946.2	-945.1	OK
30	Fishing and 29v	☑	29	29	0	623.0	-993.5	-992.2	OK
31	Fishing and 30v	☑	30	30	0	623.1	-991.2	-989.8	OK
32	Fishing and 31v	☑	31	31	0	634.5	-964.5	-963.1	OK
33	Fishing and 32v	☑	32	32	0	623.7	-985.7	-984.2	OK
34	Fishing and 33v	☑	33	33	0	622.1	-987.1	-985.5	OK
35	Fishing and 34v	☑	34	34	0	635.0	-957.3	-955.6	OK
36	Fishing and 35v	☑	35	35	0	631.5	-962.5	-960.7	OK

Figure D2: Results from the fitting procedure for the model without PP anomaly. The best model is identified by the lowest AIC (highlighted in green)

E. South-Western Waters – Iberian Peninsula

The SWW case study is comprised of two different subcases where models are firstly developed independently. Models in both subcases are developed with GADGET. In the Atlantic area of the Iberian Peninsula a model for cetacean fishery interactions is being implemented, two dolphins are the top predators and hake is the main prey although other pelagic are also considered as other food in the model. The main aim of this model is to evaluate the trade-offs of current management strategies when a predator-prey system with conflicting objectives is considered. In the Gulf of Cadiz area, the main goal of the model is to understand the interactions between anchovy and the physical environment affecting recruitment and early life stages, with the aim of recommend optimal management strategies.

Novel information identified by SWW-IP includes hake genetic data from literature reviews; hake sex ratio-at-length data and anchovy otolith microchemistry data in Gulf of Cadiz. Hake genetics and anchovy microchemistry are novel since they are new technological information that have never been considered in the models in the area. Sex ratio is novel in the way that can be used as a new likelihood component helping to define growth in sex separated models.

The Iberian Peninsula multiespecies model ranges from 1982 to 2014 (quarterly) in ICES division VIIIc and IXa. It is an age-length forward projection model using hake landings and discards. For the purpose of the evaluation of this novel information (genetics and sex ratio) a hake single species model is being used instead of the complex multispecies model. However, for the genetic data implementation requires a development of a GADGET model for Northern hake and a spatial link between the Southern and the Northern hake model.

The anchovy model in Gulf of Cadiz ranges from 1988 to 2014. It is a quarterly model using information on length and age distributions of landings and acoustics. Two approaches have been developed to include the main environmental variables affecting anchovy survival, the first one, expanding the Beverton-Holt stock-recruitment relationship and the second one, using the correlation between estimated recruitment and environmental covariates for forward projections. Environmental data such as Easterlies strength, Guadalquivir River discharges and microchemistry of otolith are a very important component of this ecosystem model. The 3 novel data types (hake sex ratio, hake genetics and anchovy microchemistry) will be evaluated in 3 separated models in this CS. 3 different protocols are developed for novel data in this Case of study.

Protocol E.1 - Hake sex ratio-at-length data in GADGET

Data

Data consist of 58145 samples from Iberian Peninsula hake sex-at-length data from 1982 to 2014 ranging from 19 to 84 cm. Growth is affected by sexual development that is frequently reached at a different size in males and females. Differences in growth by sex after maturity produce different patterns in sex proportions-at-length in the population. If these patterns are the consequence of changes in growth, it should be expected that sex ratio-at-length data can help to estimate the growth parameters. The implementation of this data in the model should allow us to know whether this data can help to develop a more accurate model and whether the growth at sex can also be estimated.

This project has received funding from
the European Union's Seventh Framework
Programme for research, technological
development and demonstration under
grant agreement no. 613571

Model implementation

GADGET can deal with this data with the aim of answer these questions developing a likelihood that compares the observed sex ratio-at-length with the modelled one. The required format for the observed sex ratio data is a text file with the following columns: *year; step; area; stock; age; length; number*. *Year* ranges from 1982 to 2014; since the data comes for a sampling for maturity at the beginning of the year *step* is set to 1; *area* is the same for all data; *stock* set the 4 different biological groups in the model (male and female, mature and immature); *age* is not known for hake and all ages are grouped togheter; *length* represents the length groups range (each 2 cm) and *number* is the observed amount (sex ratio) in each length class.

The GADGET likelihood component for this action is the *StockDistribution* that is used to compare distribution data sampled from the model with distribution data sampled from landings or surveys for different stocks within the Gadget model. This is typically used to compare Gadget stocks that are based on the same species, but have differing biological properties (e.g. immature and mature or males and females fish). The likelihood score that is calculated gives some measure as to how well the data from the model fits to the observed data. The sum of squares likelihood function to be minimized is the following:

$$l = \sum_{time} \sum_{length} \sum_{sex} \left(Po_{t,l,s} - Pm_{t,l,s} \right)^2 \qquad \text{eq. E.1}$$

Where *Po* is the proportion observed and *Pm* the proportion modelled at each year (*time*), length group (*length*) and each of the 4 sex group for immature and mature stock *(sex*).

GADGET structure requires 4 different "stocks". GADGET names "stock" as a group of modelled fish with the same life history and fishing selectivity properties. To model different growth in males and females we need separate "stocks", and to model different length-at-maturity in males and females we need also different "stocks". This results in 4 required "stocks"wich are: male immature, male mature, female immature and female mature which have different biological features, although in this case they have the same length dependent exploitation pattern. Male and female immature stocks share the same growth parameters although they mature at different lengths. Male matures at lower length (~28 cm) than female (~45 cm). Immature stocks are moved to mature stocks at the aforementioned length of maturity. Mature stocks have different growth parameters. Growth is modelled following the Von Berttalanfy model. Preliminary analysis suggests that keeping male Linf = 80 cm and female Linf = 112 cm are good estimates for Southern hake (Cerviño, 2014). This would allow estimating the growth rate parameter for male and female through the likelihood that compares the observed and modelled sex ratio-at-length.

To validate this approach, we will compare the model diagnostics with the model where sex is not considered. Likelihoods, residuals and estimated parameters will provide the basis to evaluate the validity of this new approach.

Protocol E.2 - Hake genetic data in GADGET

Data

Hake genetic available data was gathered from published studies about genetic connectivity among hake in different places, using different markers (microsatellites, allozimes or SNPs) both in the

Atlantic and the Mediterranean. Independently of marker used, the papers present the connectivity between areas using F_{st} (genetic differentiation) and N_{me} (effective number of migrants), although one paper (Pita et al., 2016) reported migration rates (m) between specific places in both Northern and Southern stocks in a temporal framework of ten years of sampling. Genetics studies showed that there is a restricted gene flow between Southern hake and Mediterranean hake; however, there is a high connectivity between Southern and Northern stocks in the Atlantic. This can be in conflict with current management structure with two independent Atlantic stocks. The migration hypothesis proposed by Pita et al. (2011) suggest that no barriers to migration seem to exist between the main Atlantic hake stocks, and there is a migrant flow from Porcupine Bank and Great Sole to the Bay of Biscay, the Cantabrian Sea and the Iberian Atlantic waters. Effective number of migrants range among Genetic studies can provide working hypothesis for migration rates between Northern and Southern stock with the aim of test the potential impact of migration on Southern hake assessment and management.

Model implementation

Figure E1 summarizes the elements to consider when modelling the impact of migration on Southern hake assessment and management. These elements are the two stocks modelled with GADGET as a single model with two areas and the coupling hypothesis which represented different plausible scenarios based on the genetic analysis of published works.

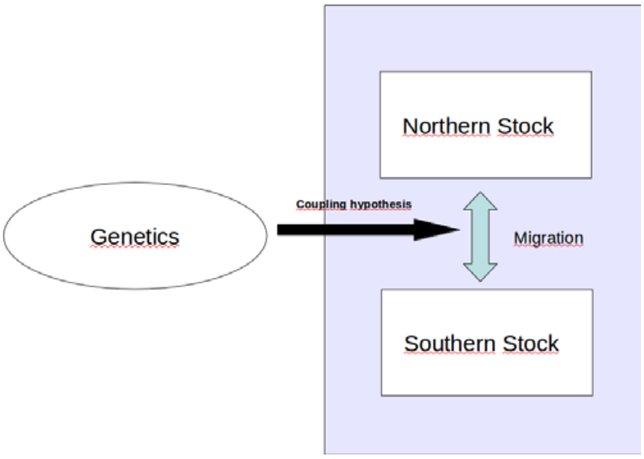


Figure E1: Scheme of the modelled process (migration between Northern and Southern hake stocks) based on genetic information

Genetic results (F_{st} and N_{me}) are estimated based on a different paradigm than population dynamic models; this is the evolutionary paradigm, where the cohesive forces are genetic vs. the ecological paradigm where the cohesive forces are demographic (Waples et al., 2008). These different approaches are the main difficulty to define parameters useful for management, that in this case are migration rates, i.e. the fraction of individuals in one population that was born in another. Furthermore, the genetic results are shots based on equilibrium assumptions that do not allow to identify the migration stage (larva, juveniles or adults) or the migration frequency (yearly or extraordinary). With these difficulties in mind, the approach proposed is using the genetic results to define plausible scenarios considering alternative options that allow checking the conditions that can make the current management of Southern hake inefficient.

The two areas GADGET model links the two hake stocks for North and South. Both stocks share the same time structure (quarterly from 1982 to 2014) and length structure (from 1 to 130 cm) as defined by ICES. GADGET specifies the migration of the stock by defining the ratio of the stock that will migrate between the two areas (Northern and Southern stocks). To use this format for the migration data, the main stock file needs to specify the name of a data file containing information about when the migration will take place, and the name of a data file containing information about the migration ratios. The migration time step file contains a list of the time steps that the migration will take place on, along with the name of the migration matrix that is to be used on each time step. The migration ratio file contains the ratios to be used by Gadget to construct the migration matrices to move the stock between the two areas.

To compare the performance of the different connectivity hypothesis we used in all the cases a short term advice based on MSY. Little is known about the level of migration required to produce demographic coupling. Hastings (1993) suggest m=0.1. Migration rates above this 10% could make ineffective the advice based on single stock assessment. Pita et al (2014) estimate migrations from Northern to Southern stocks ranging from 0.003 and 0.14. However, these figures depend on the proximity of the sampling location in both stock areas. In absence of a well-defined sampling design, the genetic results observed can be useful as a reference for demographic migrations. These results suggest that the migration rates can be in the limit of the demographic coupling proposed by Hastings (1993) so a simulation approach based on different migration scenarios for migration from and to Southern hale stock are proposed:

Scenario base: Southern stock independent (zero migration rate)

Scenario 1: age 0 migration (rate: 0.05, 0.1 and 0.15). North to South.

Scenario 2: adult migration (rate: 0.05, 0.1 and 0.15). North to South.

The impact of different scenarios will be contrasted against the base case evaluating the impact on scientific advice for management purposes (short term).

Protocol E.3. Anchovy otholit microchemistry in GADGET

Data

Collection of specimens and otolith pre-processing

Age-0 anchovy (N = 100) were obtained from a commercial purse seine operating in the Gulf of Cádiz on 29 September 2011. Fish total length (TL, mm), standard length (SL, mm), and weight (W, g) were measured in fresh individuals, which were then frozen and sent to the laboratory for analysis. Their sagittal otoliths were removed using clean methods as in Morales-Nin et al. (2014) and stored in acid-cleaned, plastic vials until further handling. The right otoliths were individually glued onto glass microscopic slides with a thermoplastic resin for age determination; the left otoliths were similarly mounted with distal side up and used for Laser Ablation Inductively Coupled Plasma Mass Spectrometry (LA-ICPMS) analysis.

Age estimation

Otoliths were processed for age and growth determination following the otolith core to post-rostrum axis and using standard polishing methods. All readings were conducted on composite images from light microscopy (x1000 magnification for the central part, x100 magnification for the rest) by two experienced readers using the Age & Shape 2.1.1 (Infaimon©, 2007) software, and only agreed readings were accepted. The Double Band reading criterion described by Cermeño et al. (2008) was applied, and one day was attributed to each increment and double band (Cermeño et al., 2003; Aldanondo et al., 2008). The spawning date was calculated as the date of hatching (estimated from the number of increments and the date of capture) minus 2.5 days, corresponding to the mean embryonic period at the water temperature registered in the area (Bernal et al., 2012). It was possible to determine the daily growth increments for 56 individuals.

Otolith chemical analyses

The aged otoliths were prepared for LA-ICPMS analyses following Morales-Nin et al. (2014). Otolith chemical quantifications for Mg24, Ca43, Ca44, Sr88 and Ba138 were determined using a Nd:YAG UP-213 laser ablation system (NewWave Research) coupled to an ElementXR plasma mass spectrometer (Thermo-Finnigan). Two different analytical methods were used. First of all, primordium to posterior axis transects (hereafter transects) were performed on a sub-sample (13 otoliths) to inspect fine-scale variations in microchemical signal associated with otolith growth. Then, individual spot samples were taken in triplicate, and orthogonal to the reading axis (henceforth triplets), from 43 otoliths on the core and edge (posterior) areas, as proxies to the natal and sampling period signatures, respectively. Three additional spot samples were collected at approximately 300 µm from the primordium (posterior direction) to sample an otolith area suspected to correspond with periods when the juvenile anchovy is expected to ocuppy areas close to guadalquivir estuary (juveniles approximately two months old, [Drake et al., 2002]). Laser spots were 25 µm in diameter centre-to-centre separated by 45 µm in the transects and by 75 µm in the triplets. Laser conditions were set to a frequency of 10 Hz and 60% energy. The typical Certified Reference Materials (CRMs) were used (Yoshinaga et al., 2000; Sturgeon et al., 2005), and sampled using the same instrument conditions at the beginning and end of each working session and after every 20 LA-spots. LA-ICPMS output data were processed using Glitter software (GEMOC, Macquarie University) to obtain element concentrations (µgMe/gotolith) based on natural isotope ratios and using Ca43 as an internal standard. The analyzed CRMs were used to calibrate element concentrations. The election of one specific CRM was determined following Geffen et al. (2013). To reduce bias, the detection of outliers on the CRMs and the election of the concrete CRM was conducted through an ad-hoc script from R software (http://www.r-project.org/) (last accessed February 5, 2014).

Only elements were not under the detection limit (DL) for at least 80% of the spots were used, and only the standards showing no significant differences between sessions (ANOVA). In the case of Ba138, for the few values that were below the DL we used DL as the value. Both for transects and the triplets, the elemental ratios (molar ratios) used for comparisons were Sr/Ca, Mg/Ca and Ba/Ca. After the LA-ICPMS analyses, calibrated digital images from the slides were used to measure the otolith diameter (anterio-posterior axis) and the spot distances to the otolith primordium using ImageJ free software (Schneider et al., 2012).

The information provided by the otolith microchemistry is connected to the use of different habitats over the ontogeny of anchovy. In the Gulf of Cádiz this includes the critical occupation of the estuary of Guadalquivir and its area of influence during the juvenile stage. The data obtained, as shown in the table E1 below, manifest a significant increment of Ba in the portion of the otolith corresponding to the juvenile period. This increment of Ba is usually associated to waters of low salinity and high productivity characteristics of estuarine environments ant the waters they influence.

Table E1: Otolith microchemistry data on anchovies in the Gulf of Cádiz

Ratio	Otolith area	Mean spot age, days ± SD	N	Mean elemental ratio ± SD	TEST	Post-hoc
	Core	25 ± 10.9	32	1.70 ± 0.287		a
Sr/Ca	Middle	49 ± 9.8	32	1.66 ± 0.405	F=54.4**	a
	Edge	130 ± 20.7	31	1.07 ± 0.199		b
	Core	25 ± 10.6	27	0.38 (0.29-0.68)*		a
Ba/Ca	Middle	48 ± 9.1	27	0.69 (0.39-2.46)*	Chi^2= 61.02**	b
	Edge	129 ± 19.3	27	11.76 (8.63-16.93)*		c
	Core	25 ± 10.9	32	131.26 ± 47.561		a
Mg/Ca	Middle	49 ± 9.8	32	147.97± 54.267	F=45.53**	a
	Edge	130 ± 19.3	32	73.19 ± 11.790		b

Model implementation

The model implemented is critically dependent on an assumption whose validity was tested with these new data. Thus, the formulation of the model assumed that all the population of anchovy in the Gulf of Cádiz occupies the estuary of Guadalquivir and its area of influence during the juvenile period to find more productive environments in an ontogenic period when high concentration of food is necessary as well as to avoid predation while occupying more turbid waters. This assumption was based on previous observations of high abundances of juveniles in the estuary during the summer period. However, this assumption needed an independent test to confirm that the conceptual assumptions (better environment for feeding and avoiding predation) and the observations (high juvenile abundances) affected the majority of the population.

The microchemistry data shows that most of the adult population in the Gulf of Cádiz have a *Ba* distinctive signal in their otoliths in coincidence with their juvenile period. This suggests that most of this population is influenced by the Guadalquivir River and its discharges. The consequences for the model are significant since summer discharges abruptly decreases during drought years. The lack of fertilization during these years brings dramatic consequences for the recruitment of anchovy in the region. The michrochemistry were key in the model formulation. Should the microchemistry data suggest that a significant portion of the population was not influenced by Guadalquivir waters during the juvenile period, a re-formulation of the model would be necessary (with that portion of the population not being affected in the model by freshwater discharges).

To include the effect of environmental variables in the model two approaches have been developed. In the first one, a Beverton-Holt like stock-recruitment relationship is included in GADGET using the following stock-recruitment equation:

$$R = \frac{\mu S e^{\rho W} \delta D}{\lambda + S} + \varepsilon \qquad \text{eq.E.2}$$

Where μ and λ are the parameters from original Beverton Holt relationship, $\rho W, \delta D$, account for the effect of the wind and discharges on survival, respectively, and ε is an error term. Particularly δ is the proportion of individuals affected by the discharges of the River. Otolith microchemistry allows to reduce the number of parameters in the previous equation because there is enough evidence to assumeδ=1. A nonlinear regression assuming landings older than 1 year during the first semester as a proxy of SSB and landings younger than 1 year during the second semester as recruits, was used to estimate the initial values (Parameter File) of the parameters μ, λ and ρ. The equation can be included in GADGET using a TimeVariablefile linked to the spawnfile (see GADGET userguide: Begley, 2012).

For the second approach, it is necessary to calculate the relationship between estimated recruitment by GADGET and, W and δD, to include it in the gadget.forward function from *Rgadget* R package. which is again simplified due to otolith microchemistry information provided.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

F. Mediterranean Waters – Strait of Sicily

The Strait of Sicily (SoS) case study (CS) focuses on the development of a reliable approach to the implementation of the ecosystem approach to fisheries management (EAFM) in a key fishing area in the Mediterranean Sea. The objectives of the CS have been progressively refined through the application of a co-creation approach with relevant stakeholders (i.e. fishers and fishers representatives, managers of local and national administrations, conservation NGOs, FAO and GFCM functionares) and taking into account the objectives of the GFCM international management plan for bottom trawl fisheries exploiting hake (HKE: *Merluccius merluccius*) and the deep water rose shrimp (DPS: *Parapenaeus longirostris*) in GSAs 12-16 (i.e. Strait of Sicily, GFCM, 2016)[7].

The overall goal of the CS has been adapted to provide a tool for the application of EAFM in the SoS which can support the achievement of long term sustainability finding a balance between ecological and human well-being through good governance. More specifically four main objectives have been identified during case study meetings with stakeholders, namely: i) rebuilding overexploited stocks; ii) long-term continuity of the fishing activities; iii) same rules for all the actors involved in fisheries exploitation; iv) good environment status.

An operating environment supporting continuity of the fisheries is fundamental and it contains economic, social, and resource considerations. Management strategies will respect Fmsy targets and, at the same time, take into account the impact of the applied management measures on other ecosystem components and possibly the effect of the ongoing climate change. To this aim, ATLANTIS and GADGET have been implemented to investigate the direct and indirect effects of multi-fleet and multispecies fisheries on the ecosystem and food web functioning of the Strait of Sicily. Trophic flows between components of the ecosystem, in particular HKE, horse mackerel (HOM: Trachurus trachurus) and DPS, are investigated to improve the understanding of the dynamics of these stocks under different scenarios. The impact of alternative technical measures (e.g. area closure, mesh sizes, gear restrictions), on the ecosystem and fisheries is investigated in connection with WP6 also taking in consideration the climate forcing effects.

ATLANTIS (Fulton et al., 2004) is chosen for model data implementation in WP2. It is an ecosystem box-model aimed to assess the effects on management measures on commercial stocks and the different components of the SOS ecosystem as well as on key ecosystem processes. It is composed by a set of sub-models for hydrography, community, fishing and management. The case study area corresponds to the North sector of the Strait of Sicily and includes the FAO-GFCM geographical sub-areas (GSAs) 15 (Malta Island) and 16 (South of Sicily). The ATLANTIS model domain was divided into 37 polygons vertically divided in up to five water layers. ATLANTIS was made up of functional groups (aggregate groups of species with similar size, diet, predators, habitat preferences, migratory patterns and life history strategy). The biological community was constructed using time series (1995-2012) of density and biomass data observed during the MEDITS survey. A total of 354 species sampled were aggregated into 55 functional groups with some of the most commercially important species. An extended description of the ATLANTIS model in this CS can be seen in Deliverable 4.1.

---

[7] GFCM, 2016.REC.CM-GFCM/40/2016/4 establishing a multiannual management plan for the fisheries exploiting European hake and deep-water rose shrimp in the Strait of Sicily (GSA 12 to 16)

The main sources of novel information identified for this CSto be implemented in Atlantis are: stable isotopes, which can help to define Atlantis functional groups with similar trophic level; fleet data from vessel monitoring system (VMS), which is rarely used to feed assessment models although can inform the CS model about fishing mortality distribution or effort re-allocation under restricted area scenarios; and finally, biogeochemical data which are used as a link between temperature based climate change scenarios and the ecosystem impact. The following protocol describes how this data and these ideas are implemented in the Atlantis model in the area.

Protocol F.1. Implementation of isotopes, VMS data and biogeochemical data with Atlantis

Data

The dataset is made up by 87 measures of Carbon (δ13C) and Nitrogen (δ13N) stable isotopes for 42 of the most important species in the trawlable are (33 shelf species + 9 slope species) from three different Sicilian coastal areas (Gulf of Castellammare, Termini Imerese and Santa Agata (NW Sicily) in spring 2005 (Table F1).

Table F1: Stable isotope data for the SoS case study

Data	Area	SPECIES	N. samples	Size (mm)	SD	Weigth (g)	SD	δ ^{15}N	SD	δ ^{13}C	SD	δ ^{13}C correct for lipids	SD	Trophic guild	ATLANTIS functional group
Spring 2005	Castellammare	Alloteuthis media	3	46.7	5.8	4.7	1.53	11.14	0.04	-18.52	0.08	-16.76	0.02	C Feeding on pelagic resources	Pelagic cephalopods shelf
Spring 2006	Castellammare	Arnoglossus laterna	3	100.0	13.2	8.3	2.52	9.80	0.39	-18.06	0.80	-16.85	0.84	B Epibenthic/suprabenthic feeder	Demersal fish shelf crustacean feeders
Spring 2007	Castellammare	Callionymus maculatus	3	73.3	15.3	2.7	1.15	9.12	0.23	-18.86	0.32	-17.32	0.30	B Epibenthic/suprabenthic feeder	Demersal fish slope
Spring 2008	Castellammare	Capros aper	3	68.3	10.4	8.0	4.00	9.33	0.32	-18.95	0.32	-17.80	0.27	B Epibenthic/suprabenthic feeder	Demersal fish slope
Spring 2009	Castellammare	Cepola rubescens	3	335.0	42.7	22.7	4.93	8.77	0.18	-19.72	0.16	-18.53	0.19	A Plankton feeder	Demersal fish shelf crustacean feeders
Spring 2010	Castellammare	Dicentrarchus labrax	3	600.0	155.9	3092.7	1812.30	10.74	0.81	-17.79	0.17	-16.59	0.13	Nectobenthic Piscivorous	Demersal fish shelf rocky habitats
Spring 2011	Castellammare	Diplodus annularis	3	125.0	8.7	34.3	4.51	9.91	2.00	-14.87	2.52	-13.61	2.52	D Benthic feeders	Demersal fish shelf rocky habitats
Spring 2012	Castellammare	Eledone cirrhosa	3	353.3	238.0	1049.9	1769.11	9.81	0.99	-17.46	2.44	-16.07	3.48	D Benthic feeders	Benthic cephalopod slope
Spring 2013	Castellammare	Engraulis encrasicolus	3	150.0	10.0	14.0	12.49	7.79	0.24	-19.09	0.07	-17.69	0.17	A Plankton feeder	E. encrasicolus (single group)
Spring 2014	Castellammare	Epinephelus aeneus	5	851.0	32.9	9384.8	2288.22	12.64	0.27	-17.36	0.50	-15.96	0.47	Benthic Piscivorous	Demersal fish shelf rocky habitats
Spring 2015	Castellammare	Gadiculus argenteus	3	93.3	2.9	7.0	1.00	9.65	0.15	-18.79	0.10	-17.59	0.06	C Feeding on pelagic resources	Demersal fish slope
Spring 2016	Castellammare	Gobiidae	3	65.0	8.7	2.0	1.00	10.12	0.20	-18.12	0.64	-16.85	0.64	D Benthic feeders	Demersal fish shelf crustacean feeders
Spring 2017	Castellammare	Illex coindetii	3	135.0	5.0	105.3	34.78	9.54	0.37	-18.78	0.25	-17.34	0.26	C Feeding on pelagic resources	Pelagic cephalopods slope
Spring 2018	Castellammare	Lepidotrigla cavillone	3	105.0	5.0	13.3	2.08	9.72	0.33	-17.66	0.20	-16.47	0.32	B Epibenthic/suprabenthic feeder	Demersal fish shelf crustacean feeders
Spring 2019	Castellammare	Loligo vulgaris	3	101.7	35.1	40.2	56.67	9.80	0.29	-18.19	0.56	-16.89	0.44	C Feeding on pelagic resources	Pelagic cephalopods shelf
Spring 2020	Castellammare	Lophius budegassa	11	447.3	81.2	1515.4	752.40	11.51	0.67	-18.32	0.67	-17.09	0.63	Demersal piscivorous	Demersal fish slope piscivorous
Spring 2021	Castellammare	Merluccius merluccius	8	713.8	90.8	3256.1	1437.68	11.64	0.93	-18.29	0.44	-16.86	0.41	Demersal piscivorous	M. merluccius (single group)
Spring 2022	Castellammare	Mullus barbatus	3	136.7	24.7	31.7	20.21	11.39	0.34	-18.06	0.47	-16.89	0.53	D Benthic feeders	M. barbatus (single group)
Spring 2023	Castellammare	Octopus vulgaris	3	121.7	17.6	647.0	331.45	10.16	0.51	-17.39	0.45	-16.01	0.49	D Benthic feeders	Benthic cephalopod shelf
Spring 2024	Castellammare	Pagellus acarne	3	168.3	20.8	65.0	24.98	10.67	0.43	-17.42	0.29	-15.94	0.26	B Epibenthic/suprabenthic feeder	Demersal fish shelf crustacean feeders
Spring 2025	Castellammare	Pagellus erythrinus	8	318.8	27.0	401.1	101.80	12.29	0.40	-16.69	0.55	-15.57	0.49	Crustacean feeder	Demersal fish shelf crustacean feeders
Spring 2026	Castellammare	Parapenaeus longirostris	3	19.0	2.6	4.8	1.86	8.84	0.08	-18.17	0.05	-17.02	0.07	B Epibenthic/suprabenthic feeder	P. longirostris (single group)
Spring 2027	Castellammare	Sardina pilchardus	3	158.3	11.5	33.7	7.77	7.36	0.65	-19.81	0.78	-17.97	0.47	A Plankton feeder	S. pilchardus (single group)
Spring 2028	Castellammare	Seriola dumerili	8	488.8	38.2	1374.8	109.10	10.07	0.30	-17.71	0.16	-16.48	0.16	Pelagic Piscivorous	Demersal fish shelf piscivorous
Spring 2029	Castellammare	Serranus cabrilla	8	216.9	8.4	121.5	19.34	10.04	0.53	-18.25	0.55	-16.82	0.52	B Epibenthic/suprabenthic feeder	Demersal fish shelf mixed food
Spring 2030	Castellammare	Sparus aurata	4	276.3	41.5	335.3	160.37	11.88	0.80	-15.97	1.95	-14.62	1.40	D Benthic feeders	Demersal fish shelf rocky habitats
Spring 2031	Castellammare	Serranus hepatus	3	85.0	5.0	11.7	3.06	10.23	0.33	-18.29	0.24	-17.09	0.24	B Epibenthic/suprabenthic feeder	Demersal fish shelf crustacean feeders
Spring 2032	Castellammare	Spicara flexuosa	3	108.3	7.6	14.0	2.00	8.48	0.20	-18.79	0.46	-17.67	0.34	A Plankton feeder	Epipelagic fish
Spring 2033	Castellammare	Spicara spp	3	58.3	1.7	2.4	0.12	7.95	0.18	-18.64	0.13	-17.27	0.16	A Plankton feeder	Epipelagic fish
Spring 2034	Castellammare	Torpedo torpedo	7	377.1	74.5	1040.0	480.66	12.13	0.65	-16.34	0.23	-15.02	0.21	Benthic Piscivorous	Demersal rays shelf
Spring 2035	Castellammare	Trachurus trachurus	3	191.7	25.7	65.0	26.46	10.44	0.49	-18.69	0.23	-17.45	0.35	C Feeding on pelagic resources	Other small pelagics
Spring 2036	Castellammare	Trisopterus minutus	3	145.0	13.2	31.7	5.69	10.45	0.32	-17.97	0.20	-16.90	0.19	B Epibenthic/suprabenthic feeder	Demersal fish shelf crustacean feeders
Spring 2037	Castellammare	Uranoscopus scaber	6	238.3	16.6	298.5	58.07	11.04	0.29	-17.52	0.19	-16.31	0.14	Benthic Piscivorous	Demersal fish shelf piscivorous
Spring 2038	Castellammare	Centrophorus granulosus	6	831.7	13.3	3101.3	535.41	11.70	0.57	-17.37	0.32	-16.03	0.28	Mix fish-cephalopods	Demersal sharks slope
Spring 2039	Castellammare	Dalatias licha	3	995.0	109.7	5802.3	2325.62	11.38	0.59	-17.82	0.23	-16.17	0.22	Mix fish-cephalopods	Demersal sharks slope
Spring 2040	Castellammare	Etmopterus spinax	7	356.3	41.8	214.1	73.97	11.02	0.37	-17.50	0.21	-16.07	0.20	Mix fish-cephalopods	Demersal sharks slope
Spring 2041	Castellammare	Galeus melastomus	8	428.8	77.6	281.8	172.78	10.55	0.58	-17.53	0.34	-16.19	0.33	Mix fish-cephalopods	Demersal sharks slope
Spring 2042	Castellammare	Heptranchias perlo	3	1495.0	456.5	26996.4	29657.98	11.93	0.61	-17.50	0.32	-16.05	0.26	Mix fish-cephalopods	Demersal sharks shelf
Spring 2043	Castellammare	Hexanchus griseus	3	1703.3	95.0	42500.0	38890.87	11.13	0.61	-17.48	0.47	-16.14	0.40	Mix fish-cephalopods	Demersal sharks slope
Spring 2044	Castellammare	Raja radula	3	345.0	18.0	296.5	92.63	10.43	0.53	-16.47	0.03	-14.94	0.04	Mix fish-cephalopods	Demersal rays shelf
Spring 2045	Castellammare	Scyliorhinus canicula	8	418.1	39.9	245.9	71.34	10.54	0.35	-17.54	0.16	-16.20	0.13	Mix fish-cephalopods	Demersal sharks slope
Spring 2046	Castellammare	Torpedo marmorata	3	335.8	89.1	877.6	640.62	11.51	0.88	-17.01	0.79	-15.59	0.67	Benthic Piscivorous	Demersal rays shelf

VMS were introduced in 2002 by the European Union for the remote control of fishing vessels and collected within the Data Collection Framework since 2006. In Strait of Sicily (GSA 16) VMS data are available for about 300 vessels operating in the area, providing geo-referenced information for effort covering the years 2006–2015 as produced for the calculation of spatial ecosystem indicators included in the Italian National plan for fisheries data collection (Russo et al., 2013, 2014).

Biogeochemical data available for the SoS include the time series for the major macronutrients of the system (phosphate, nitrate, silicate), phytoplankton, zooplankton and bacteria biomass, dissolved and particulate organic matter, dissolved inorganic carbon (DIC) and dissolved oxygen. A request to the coordinator of the project VECTOR was done in order to use the climate change simulations recently produced by the project for the Mediterranean Sea. The scenarios for the Mediterranean predict by mid-century an increase of the average sea surface temperature (+ 0.6°C), as well as of net primary production and community production (Fig. F1). These data will be used to force the model during future projection scenarios.

Model implementation

Isotope data.

Isotopes information was used to aggregate species with similar trophic preferences in functional groups (*functionalgroups.csv* file in Atlantis). Diet connection matrix in the biol.prm file is structured as a predator and prey (for vertebrates, both divided into juvenile and adults) indicating the maximum availability of prey to a predator. This was then adjusted using stomach content data collected in the Strait of Sicily and refined with the inclusion of different functional groups and by gathering novel information from isotope analysis on the trophic linkages between groups. In addition, ontogenetic changes in isotopic composition of target commercial species (e.g. hake, red mullet) were used to better separate specimens in size classes to be incorporated into Atlantis food web structure.

Information on species trophic level from stable isotopes data was combined with stomach contents data to better classify species into the ATLANTIS functional groups. These groups pool together species with similar trophic behaviour, trophic level, habitat preferences (e.g. coastal rocky bottoms, coastal sandy bottoms, etc.) and behaviour (e.g. pelagics demersal) and are represented in the *functionalgroups.csv* file.

The trophic level is estimated through the equation:

$$\mathrm{TP}_{\delta 15\mathrm{N}} = (\delta^{15}\mathrm{N}_j - \delta^{15}\mathrm{N}_{\mathrm{Base}})/\Delta^{15}\mathrm{N} + \lambda$$

where $\delta^{15}N_j$is the isotopic composition in nitrogen of the studied species, $\delta^{15}N_{Base}$ is the isotopic composition of the baseline, $\Delta^{15}N$ is the isotopic fractionation expected for $\delta^{15}N$, finally λ is the trophic level of the baseline.

Stable isotope data have therefore used to refine and complement the dataset on the diet composition and trophic levels of the species included in the ATLANTIS diet matrix in *biol.prm* file. For example, some species, such as the fish *Uranoscopus scaber* and *Lophius boudegassa,* were assigned to the "*Demersal fish piscivorous*" trophic guild based on their trophic level estimation from isotope data. In this regard, stable isotopes data were used as background information to build the conceptual structure of the ATLANTIS model rather than for model calibration purposes.

Vessel Monitoring System

Vessel Monitoring System (VMS) data are elaborated as an index of fishing pressure (total number of fishing hours carried out over 3kmx3km spatial grid) to derive an accurate information on the spatial distribution of the effort in the ATLANTIS model domain and subsequently allocated to boxes using the fishing forcing time series that can be adjusted in the *harvest.prm* and *MPA.ts* files

These data have been used to inform the model about fishing mortality spatial distribution and reallocation to adjacent boxes under Fishing Restricted Area scenario. In the SoS area (GSA 16) there is no spatial information associated with official catch data that can be used to split the catches proportionally in the in the ATLANTIS boxes. Electronic loogbooks are not yet used within the DCF to produce catchstatistics, because considered poorly consistent. Catch data collection is based on the sampling of vessels landings in the main ports of the area combined with direct samplings on board of commercial vessels, following a well-defined stratified sampling design. We used VMS data to spatially distribute the reported catch of target commercial stocks and by-catch species in the ATLANTIS boxes. This exercise was done assuming the reported catch proportional to the effort displayed. The total annual effort (n trawling hours km^{-2}) was split in the ATLANTIS boxes assuming a constant spatial catchability so that:

$$C_t = \sum_{i=1}^{k} \frac{e_i}{E} C_t$$

where $C_t$is the total annual observed trawl catch of a given stock or functional group, E is the total annual trawl effort (total number of trawled hours from VMS), e_i is the VMS effort observed in the Atlantis box *i.*

Fig. F1 shows VMS data for 2015 the distribution of the observed total effort in the Atlantis model domain (boxes). VMS data are incorporated in scenario simulations of spatial closures as described in Deliverable 5.3. This scenario is aimed at assessing the effects of the implementation of three Fisheries Restricted Areas (FRAs), designed to protect hake and deep-water rose shrimp juveniles (Fig. F1). Simulation will include the actual fleet distribution and the re-allocation of the fishing mortality in the adjacent Atlantis boxes. The proportion of fishing effort displayed in the three FRAs was 4.3% (7.830 hours) of the total effort for the area (182.917 hours) in 2015. The change in F in the FRA and adjacent boxes was proportional to the percentage effort in the box.

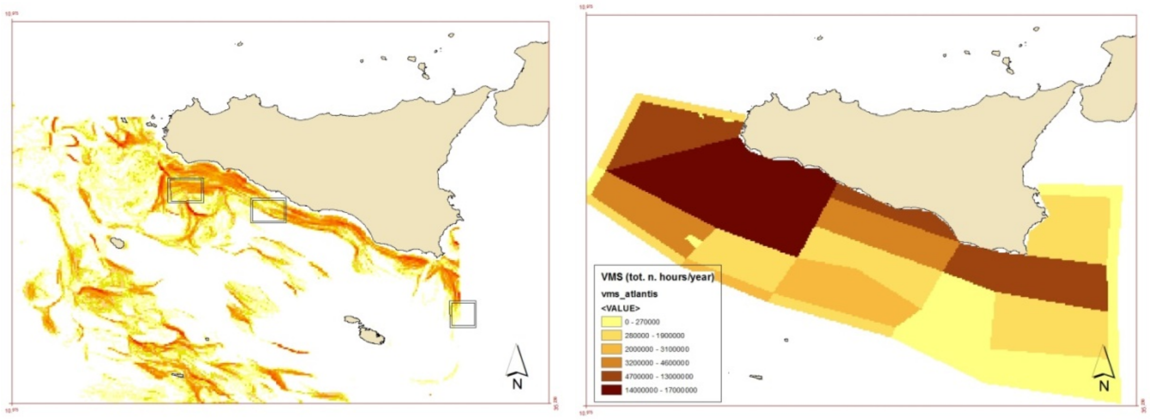


Figure F1: Map showing the distribution of fishing pressure in the SoS area and in the established FRAs, calculated as total number of trawl hours in 2015 (left panel), and in the ATLANTIS boxes (right panel)

Different possible scenarios for the fleet re-distribution, following area closures, will be simulated starting from the current displacement of the vessels based on the analysis of VMS data, in particular related to the inclusion of 3 FRAs in the Strait.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Oceanographic and biogeochemical forcing data

Oceanographic and biogeochemical data forcing to the model is provided by the output of the POLCOMS-ERSEM model (Allen et al. 2001). In particular, for the first set of climate change scenarios, the only change will occur to the *temp.nc* file, which includes water temperature per time step, per box, per layer. The second set of climate change scenarios will also consider the influence of changes in river run-off in coastal areas, modifying the *pointsource.ts* files.

The SoS case study is going to include such simulations into the ATLANTIS model to forecast the long term impact of change in community productivity on key functional groups (i.e. commercial stocks) and fisheries. Biogeochemical data can be used to predict how much the ecosystem productivity and fisheries catches will be impacted by climate change. Two different approaches were undertaken to evaluate the impact of climate change in the SoS ecosystem.

The first approach will be to set-up some simple climate change scenarios to test the ecosystem reaction to a progressive increase in water temperature. Three different scenarios were considered corresponding to increments in the average local sea water temperatures (SWT) over the next 50 years of 1, 2 and 3°C with respect to the present day values.

The spatial and temporal variability of the SWT was reproduced by post-processing of the already existing set of oceanographic data obtained from scenarios IPCC RA and A2 (IPCC, 2007). In particular, we estimated, for each box and levels of the model domain, the differences between the temperature values obtained by A2 and RA scenarios on daily basis. This procedure allowed us to estimate a delta matrix system (DM hereafter) describing both the temporal and spatial variability of the variation of T between the two scenarios. The obtained differences were then averaged obtaining the average difference in water temperature between the RA and A2 scenario at basin scale and for the whole decade. This value was then compared with the predefined set of new sea water temperature differences, 1, 2 and 3°C respectively, obtaining 3 different multiplication factors. Finally, each multiplication factor was applied to the matrix system DM in order to obtain a new set of water temperature delta values to be added to the RA water temperature dataset. The described procedure allowed to obtain 3 different dataset of temperature forcing, one for each new scenario.

The second approach will simulate future scenarios based on the SRES approach taken by the IPCC since 2000, incorporating socio-political drivers as well as projected climate change (IPCC, 2007). Two distinct socio-political scenarios, broadly consistent with the IPCC A2 (National Enterprise) and B1 (Global Community) storylines, formulated as part of the FP7 project VECTORS, will be tested. The effect of these changes is an increase of air temperatures at sea-level in the region of 1°C with respect to present day for the A2 scenario, and about 0.7°C for B1 leading to an average increase of around 0.6°C for both scenarios (Fig. F2). Wind speeds will not change significantly in the Mediterranean. For the future scenarios, values for nutrient levels will be adjusted in ATLANTIS according to the respective future scenario based on the assessments given in the European Lifestyles and Marine Ecosystems report (www.elme-eu.org, Langmead et al. 2007), where a large change in nutrients was taken to be 60%, a standard change 30%. The A2 scenario will therefore include a 60% increase in nutrient output by rivers. These changes will be included in the *pointsource.ts*file for all affected coastal boxes.

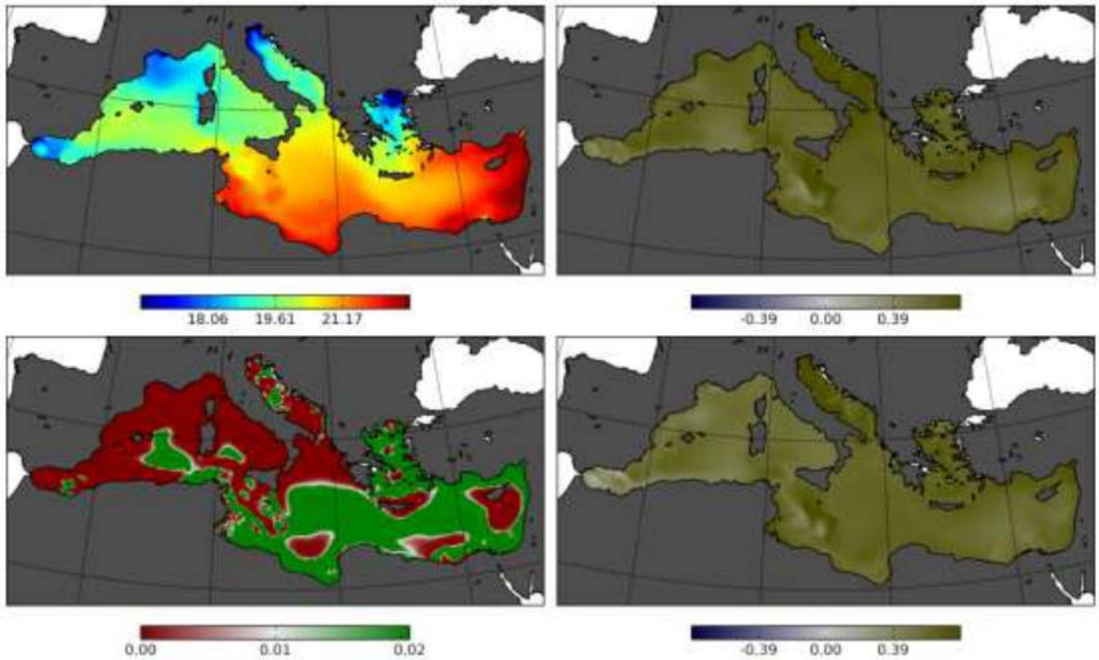


Figure F2: Sea surface temperature change (°C) - Top Left: present day mean, Top Right: A2change with respect to present day conditions, Bottom Right: B1 change with respect to present day conditions, Bottom Left: p-value of significance for difference between A2 and B1

These scenarios will be compared with the Business As Usual (BAU) scenario to assess the effect of climate change to the ecosystem structure and functioning in the short (2020) and medium term (2030). In particular indicators relating to descriptors 1, 3 and 4 will be analyzed: Biomass:

- Catch
- Fishing mortality
- Catch to biomass ratio
- Fishing revenues: using mean price/tonnes

G. Black Sea

Black Sea ecosystem is seriously affected by dynamic changes directly related to fishing, climate change and pollution. Fishery is the most affected sector by the changes of the Black Sea ecosystem. In the same time, fishing activities contribute themselves to the worsening of the ecological situation and for the depletion of the fish stocks. The objective of the Black Sea case study is the restoration of turbot fisheries to more productive levels, considering both the effect of fisheries and the ecosystem change that has occurred in the last 30 years.

The ecosystem models employed in this case study are GADGET and Ecopath with Ecosim (EwE), with the aim of increasing the knowledge about the Black Sea ecosystem functioning and thereby serve to advise on the rebuilding of the turbot stock. These models will allow providing input to the development of a management plan.

The **GADGET model** developed included 7 different populations or functional groups (turbot, anchovy, sprat, gobies, whiting, molluscs, cetaceans), with 3 fleets acting in 3 different areas (Romanian area, West Black Sea area and all Black Sea). Both the impact of the interactions between species and the impact of fisheries harvesting the species have been included in the model. A detailed description can be found in D4.1.

EwE is designed for construction, parameterization and analysis of mass-balance trophic models. The EwE model developed in this CS considers 10 species or pool of species (turbot, anchovy, sprat, whiting, gobies, mussel, cetaceans, zoobenthos, zooplankton, and phytoplankton). Trophic relationships are modelled with a diet matrix representing the proportion of a prey in the diet of the predator. Other data used in the EwE model are: biomass (t/km2), commercial landings (t/km^2/year), IUU catches (t/km2/year), P/B= Z (total mortality), Q/B (consumption rate).

Turbot diet novel data obtained from a stomach content analysis has been implemented in a multispecies model in the area for the first time. A protocol for this implementation is presented here.

Protocol G.1.Turbot diet data implementation on EwE model.

Data

The turbot individuals analysed were collected in May 2013, during the breeding period (when feeding becomes less intensive); depth range = 10 - 70m. A total of 61 turbots were collected in the North and South areas of Romania. Fishes were measured and weighed before and after removing their digestive tracts and gonads. Gut contents were preserved in formalin for diet composition analyses. The study of the food array was performed by analysing the gastro-intestinal content and determining as accurately as possible the type of food contained in the stomach, followed by determining the species or groups of species. Two methods were used, namely the qualitative and quantitative methods. The qualitative analysis consisted in the full identification of the food components found in the fish's stomach. The quantitative method consisted in numerical analysis (frequency of occurrence, dominance) and gravimetrical analysis (feeding coefficient, Index o fRelative Importance - IRI).

The **frequencies of occurrence (FO%)**, as numerical percentages of prey items, were calculated to characterize the stomach contents (Hyslop, 1980, Hansson, 1998). The frequency of occurrence calculates the percentage of the total number of stomachs in which the specific prey species occurs:

$$FO\% = FO_i / FO_t x\ 100$$

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

where FO_i is the number of stomachs in which the species" I" occurs, and FO_t is the total number of full stomachs.

The **dominance** was calculated as the proportion of stomachs dominated by a certain prey type and expressed as a percentage of the total number of stomachs.

The **feeding coefficient** results from multiplying the weight of the stomach content by 10,000 and dividing the result to the full body weight of the fish (Porumb, 1961).

The**Index ofRelative Importance (IRI)** is an integration of measurements of number, volume and frequency of occurrence to assist in evaluating the relationship of the various food items found in the stomach.It is calculated by summing the numerical and volumetric percentage values andmultiplying with frequency of occurrence percentage value (Pinkas et al., 1971, Ahlbeck et al., 2012):

$$IRI_i=(\%N_i + \%V_i)*\%FO_i$$

where, N_i, V_i and FO_i represent percentages of number, volume and frequency of occurrence of prey **i**, respectively. To estimate the importance of diet comparisons among species, IRI was standardized to% IRI (Cortés, 1997).

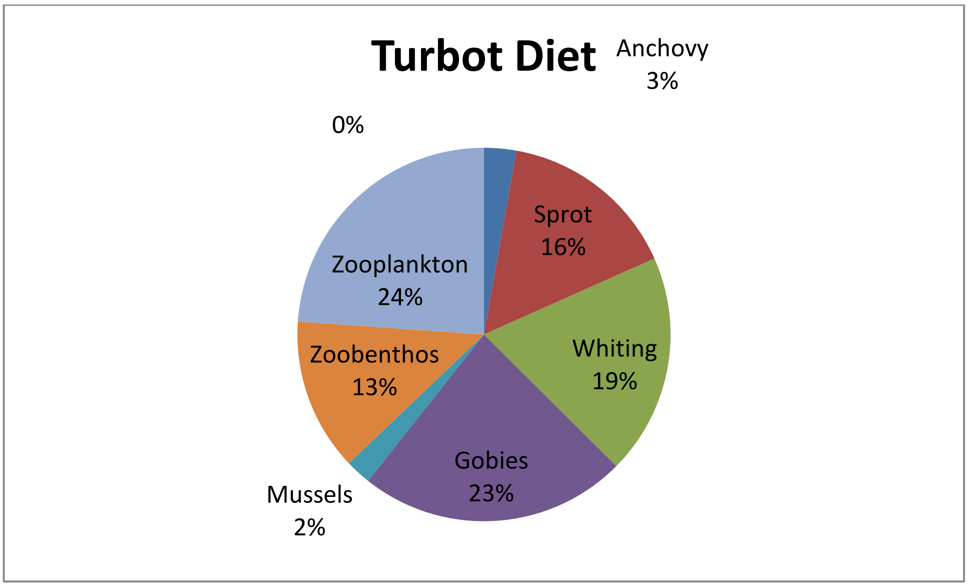


Figure G1: Turbot's Diet

Turbot is supposed to feed mainly on gobies, horse mackerel, crustaceans and molluscs (Bănaru et al., 2009). However, the analysis performed shows that gobies was the main prey (Fig. G1). These modifications in diet can reflect changes in the availability of prey which influenced fish diet composition and were probably related to the loss of biodiversity in the Black Sea benthic communities, which became dominated by some opportunistic species (Bănaru et al., 2009). The favourite prey for turbot at age 1 and age 2 is zooplankton, for turbot at age 3 it is zoobenthos, for turbot at age 4 to 7 it is gobies, for turbot at age 8 and age 9 it is sprat, whiting and gobies (Table G.1). So, generally, the favourite prey are gobies.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Table G.1: Diet for turbot by age groups

	Anchovy	**Sprot**	**Whiting**	**Gobies**	**Mussels**	**Zoobenthos**	**Zooplankton**
Turbot – Age1	0	0	0	0	0	0	1
Turbot – Age2	0	0	0	0	0	0.25	0.75
Turbot – Age3	0	0	0	0	0	0.6	0.4
Turbot – Age4	0.05	0.2	0.16	0.35	0.05	0.19	0
Turbot – Age5	0	0.15	0.39	0.29	0.05	0.12	0
Turbot – Age6	0	0.1	0.37	0.45	0.05	0.03	0
Turbot – Age7	0.1	0.3	0.2	0.35	0.05	0	0
Turbot – Age8	0.1	0.3	0.3	0.3	0	0	0
Turbot – Age9	0	0.35	0.3	0.35	0	0	0
Total	0.25	1.4	1.72	2.09	0.2	1.19	2.15

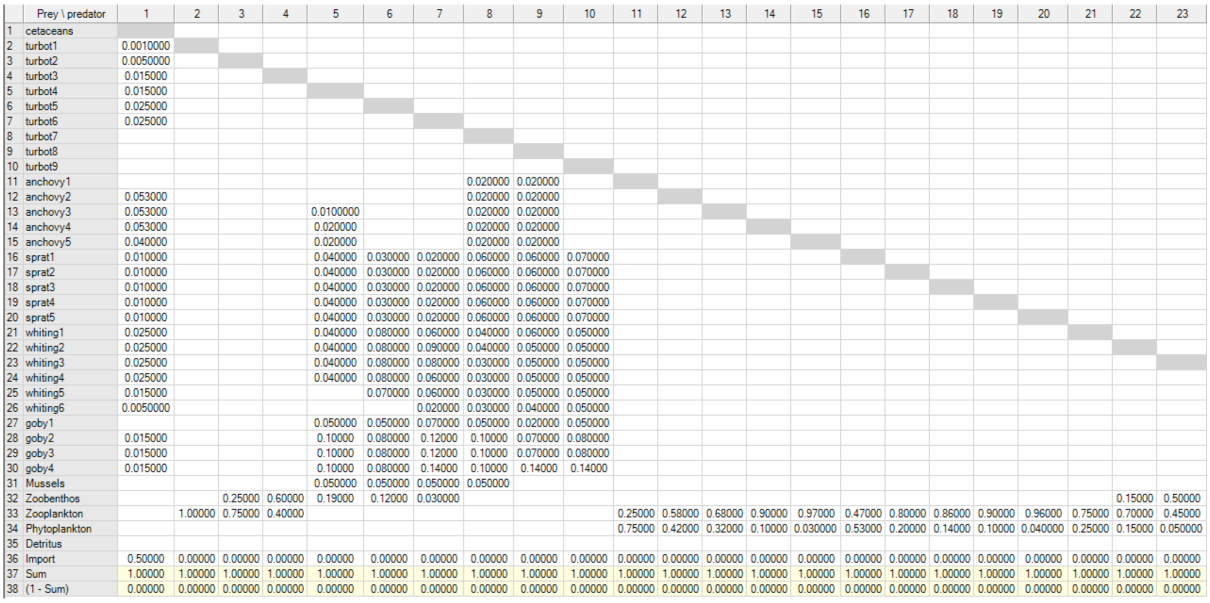
Model implementation

Stomach content data are used to define the turbot food web structure in the EwE model in the Black Sea. Ecopath parameterizes models based on two process, one to describe the production and one to describe the energy balance of each group. Ecopath bases the parameterization on an assumption of mass balance over a year creating a static mass-balanced picture of the resources in an ecosystem and their trophic interactions. Once Ecopath has been built, it can be used directly for dynamic modelling using Ecosim.

Ecopath parameterization.

Modelled species (or pools) are further split into ontogenetic groups as follow: 9 turbot age groups, 5 anchovy age groups, 5 sprat age groups, 6 whiting age groups, 4 gobies age groups, mussel, cetaceans, zoobenthos, zooplankton, and phytoplankton. Trophic relationships are modelled with a diet matrix, i.e. the proportion of a prey in the diet of the predator (Fig G2).

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571



	Prey \ predator	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1	cetaceans																							
2	turbot1	0.0010000																						
3	turbot2	0.0050000																						
4	turbot3	0.015000																						
5	turbot4	0.015000																						
6	turbot5	0.025000																						
7	turbot6	0.025000																						
8	turbot7																							
9	turbot8																							
10	turbot9																							
11	anchovy1								0.020000	0.020000														
12	anchovy2	0.053000							0.020000	0.020000														
13	anchovy3	0.053000				0.0100000			0.020000	0.020000														
14	anchovy4	0.053000				0.020000			0.020000	0.020000														
15	anchovy5	0.040000				0.020000			0.020000	0.020000														
16	sprat1	0.010000				0.040000	0.030000	0.020000	0.060000	0.060000	0.070000													
17	sprat2	0.010000				0.040000	0.030000	0.020000	0.060000	0.060000	0.070000													
18	sprat3	0.010000				0.040000	0.030000	0.020000	0.060000	0.060000	0.070000													
19	sprat4	0.010000				0.040000	0.030000	0.020000	0.060000	0.060000	0.070000													
20	sprat5	0.010000				0.040000	0.030000	0.020000	0.060000	0.060000	0.070000													
21	whiting1	0.025000				0.040000	0.080000	0.060000	0.040000	0.060000	0.050000													
22	whiting2	0.025000				0.040000	0.080000	0.090000	0.040000	0.050000	0.050000													
23	whiting3	0.025000				0.040000	0.080000	0.080000	0.030000	0.050000	0.050000													
24	whiting4	0.025000				0.040000	0.080000	0.060000	0.030000	0.050000	0.050000													
25	whiting5	0.015000					0.070000	0.060000	0.030000	0.050000	0.050000													
26	whiting6	0.0050000						0.020000	0.030000	0.040000	0.050000													
27	goby1					0.050000	0.050000	0.070000	0.050000	0.020000	0.050000													
28	goby2	0.015000				0.10000	0.080000	0.12000	0.10000	0.070000	0.080000													
29	goby3	0.015000				0.10000	0.080000	0.12000	0.10000	0.070000	0.080000													
30	goby4	0.015000				0.10000	0.080000	0.14000	0.10000	0.14000	0.14000													
31	Mussels					0.050000	0.050000	0.050000	0.050000															
32	Zoobenthos			0.25000	0.60000	0.19000	0.12000	0.030000															0.15000	0.50000
33	Zooplankton		1.00000	0.75000	0.40000							0.25000	0.58000	0.68000	0.90000	0.97000	0.47000	0.80000	0.86000	0.90000	0.96000	0.75000	0.70000	0.45000
34	Phytoplankton											0.75000	0.42000	0.32000	0.10000	0.030000	0.53000	0.20000	0.14000	0.10000	0.040000	0.25000	0.15000	0.050000
35	Detritus																							
36	Import	0.50000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
37	Sum	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000
38	(1 - Sum)	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000

Figure G2: Screenshot of diet composition (DC) matrix from Ecopath showing the predator -prey interactions for Black Sea model

According to the mass balance requirement of Ecopath, total biomass removals from each group (including its total consumption by all of its predators) cannot exceed the group's production:

$$P_i = Y_i + E + BA + \sum_{j=1}^{n} Q_{ij}^{*} + P_i \cdot (1 - EE_i)$$

where P_i is produced biomass, and Y_i is the yield (catch in biomass), E_i is net emigration (emigration – immigration, in units of biomass) and BA_i is biomass accumulation of group *i*. $EE_i \in [0,1]$ is group *i*'s ecotrophic efficiency and 1-EE_i is the fraction of its production assumed to be dying from causes other than predation ("other mortality"), which constitutes a biomass flow to the detritus.

Ecopath uses the diet matrix (DC_{ij}) values together with the biomass (B_j) and consumption per biomass $\left(\frac{Q}{B}\right)_j$ values of predator *j*, to calculate consumption (Q_{ij}), the absolute amount of prey *i* consumed by predator *j* with the following equation:

$$Q_{ij} = B_j \cdot \left(\frac{Q}{B}\right)_j \cdot DC_{ij}$$

Ecopath master equation can be parameterized as: Q/B = P/B + UN/Q + R/B, where B is biomass; Q is consumption, P is production, UN is non-assimilated food and R is respiration. The condition for mass-balanced model: Q/B > P/B. The consumption / biomass ratio (Q/B) is defined by the parameters presented in Fig. G.3.

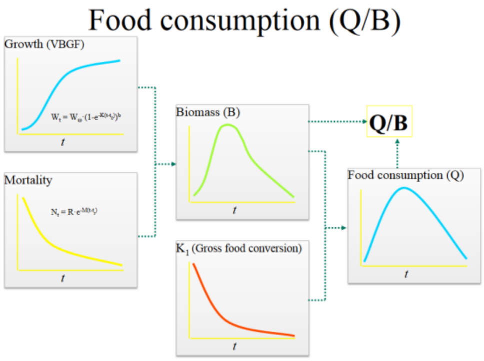


Figure G3: Factors affecting food consumption to estimate Q/B ratio

Consumption is the intake of food by a group over the time period considered. It is entered in Ecopach as the ratio of consumption over biomass (Q/B). Absolute consumption has units t/km² /year, while the corresponding Q/B would be /year. Consumption over biomass is entered in Ecopath on the Basic Input form. There are various approaches for obtaining estimates of the consumption/ biomass ratio (Q/B). In order to calculate the Q/B figure for turbot, the following empirical formula was used:

$$\mathrm{Ln}(Q/B) = -0.1775 - 0.2018 * \ln(W_\infty) + 0.6121 * \ln(T) + 0.5156 * \ln(A_r)$$

where W_∞ is the von Bertalanfy weight infinity; T is the temperature; and A_r is the aspect ratio.

For Ecopath, we need only one Q/B value for every species, so we calculated only for the leading group (turbot at age 9, anchovy at age 5, sprat at age 5, whiting at age 9, gobies at age 4):

Table G2: Data input for Q/B calculation

	W_∞	**T**	**A_r**	**Q/B**
Turbot_9	6500	11.75	1.771	0.863
Anchovy_5	8.35	11.75	1.188	2.694
Sprat_5	10.04	11.75	1.581	3.008
Whiting_9	41	11.75	1.91	2.496
Gobies_4	52	11.75	0.892	1.606

The turbot diet data implemented in the balanced model allows to estimate the following indicators:

First, the Ecotrophic Efficiency (EE), that represents the fraction of the production that is either passed up the food web or exported was analysed. The values should be between 0 and 1(inclusively). A value of 0 indicates that any other group does not consume the group in the system. In our model, for cetaceans, turbot at age 8 and turbot at age 9, we have 0 values; for turbot at age 4, turbot at age 5 and phytoplankton, we have values close to 1.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

For each group, the flow to the detritus consists of what is egested (the non-assimilated food) and those elements of the group, which die of old age, diseases, etc., (i.e., of sources of 'other mortality, expressed by 1 - EE). The flow to the detritus should be positive for all groups.

The net food conversion efficiency is calculated as the production divided by the assimilated part of the food:

Net efficiency = P/B / (Q/B· (1 - GS))

where P/B is the production / biomass ratio, Q/B is the consumption / biomass ratio, and GS is the proportion of the food that is not assimilated.

The omnivore index (OI) is calculated as the variance of the trophic level of a consumer's prey groups:

$$OI_i = \sum_{j=1}^{n} (TL_J - (TL_i - 1))^2 * DC_{ij}$$

where, TL_j is the trophic level of prey j, TL_i is the trophic level of the predator i, and, DC_{ij} is the proportion prey j constitutes to the diet of predator i. When the OI is almost 0 (e.g.: turbot at age2, gobies at age 2), the consumer in question is specialized, i.e., it feeds on a single trophic level. A large value indicates that the consumer feeds on many trophic levels (e.g.: cetaceans).

Trophic levels, as initially conceived (Lindeman, 1942) characterized the position of organisms within the food webs: 1 for primary producers and detritus, 2 for first-order consumers, 3 for their predators, etc. This conceptual approach leads, among other things, representation of ecosystem as trophic pyramids (Elton, 1927), where the biomass of each of the various components of ecosystems had to be shoehorned into one of a few integer trophic levels. This approach has been (rightly) questioned, because most consumers feed on different prey, each with its own trophic level. The result, as noted by Odum and Heald (1975) is that these consumers have fractional trophic levels, which can be calculated from:

$$\tau_j = 1 + \sum\nolimits_j (D_{ij} * \tau_j)$$

where D_{ij} is the proportion of the prey j in the diet of consumer i, and τ_j is the mean trophic level of its prey.

Respiration includes all non-usable 'model currency' that leaves the box representing a group.

The respiration of any living group (i) can be expressed as,

$Resp_i = (1 - GS_i) * Q_i – (1 – TM_i) * P_i$

where $Resp_i$ is respiration of group i, GS_i is the fraction of its consumption that is not assimilated, Q_i is the consumption of i, and TM_i is the proportion of the production that can be attributed to primary production.

Assimilation = the part of the food intake that is assimilated is computed for each consumer group from:

$$B_i * \left(\frac{Q}{B_i}\right) * (1 - GS_i)$$

where B_i is the biomass of group i; Q/B_i is the consumption / biomass ratio of group i; and GS_i is the part of the consumption that is not assimilated.

The (dimensionless) ratio o respiration to assimilation cannot exceed 1, because respiration cannot exceed assimilation. For top predators, whose production is relatively low, the respiration/assimilation ratio can be expected to be close to 1, while it will tend to be lower, but still positive, for organisms at lower trophic levels.

The (dimensionless) ratio production/respiration express the fate of the assimilated food. Computationally, this ratio can take any positive value, though thermodynamic constraints limit the realized range of this ratio to values lower than 1.

The respiration / biomass(R/B) ratio can be seen as an expression of the activity of the group. The higher the activity-level is for a given group, the higher the ratio. The R/B ratio is strongly impacted by the assumed fraction of the food that is not assimilated. If the ratio is too high, this may be due to GS being too low.

Mortality coefficients. Under the assumption that Z_i , the mortality of group i, is constant for the organisms included in i, it turns out that, for a large number of growth functions (including the von Bertalanffy Growth Function, or VBGF):

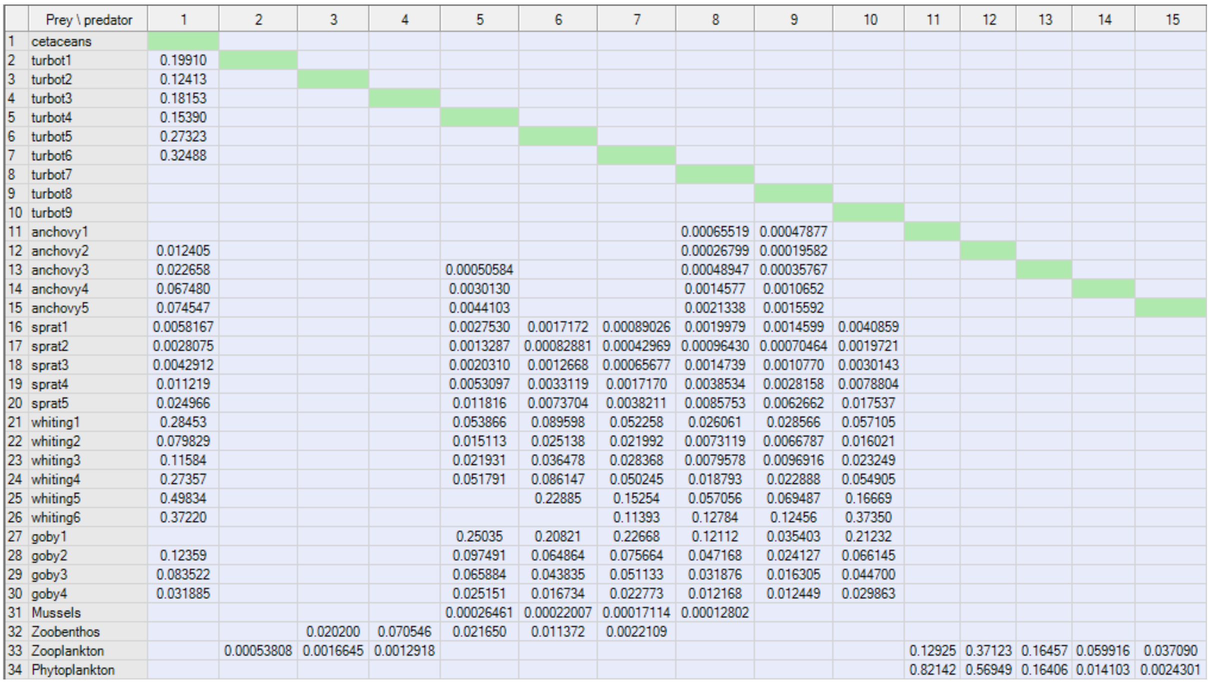
Z_i = (production/biomass)$_i$ = P/B$_i$

or instantaneous mortality equals total production over mean biomass.

The mortality coefficient can be split into its components:

Z_i = P/B$_i$ = fishing mortality + predation mortality + BA + net migration + other mortality

The predation mortality of a group (i) is the sum of the consumption of (i) by the other groups, divided by the biomass of group (i). Predation mortality is calculated in the program, i.e., it is not an input parameter. The coloured diagonal highlights 'cannibalism' (Fig.G4) which should be kept at a low level. As you can see in Fig.G4, we don't have cannibalism.



	Prey \ predator	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	cetaceans															
2	turbot1	0.19910														
3	turbot2	0.12413														
4	turbot3	0.18153														
5	turbot4	0.15390														
6	turbot5	0.27323														
7	turbot6	0.32488														
8	turbot7															
9	turbot8															
10	turbot9															
11	anchovy1								0.00065519	0.00047877						
12	anchovy2	0.012405							0.00026799	0.00019582						
13	anchovy3	0.022658				0.00050584			0.00048947	0.00035767						
14	anchovy4	0.067480				0.0030130			0.0014577	0.0010652						
15	anchovy5	0.074547				0.0044103			0.0021338	0.0015592						
16	sprat1	0.0058167				0.0027530	0.0017172	0.00089026	0.0019979	0.0014599	0.0040859					
17	sprat2	0.0028075				0.0013287	0.00082881	0.00042969	0.00096430	0.00070464	0.0019721					
18	sprat3	0.0042912				0.0020310	0.0012668	0.00065677	0.0014739	0.0010770	0.0030143					
19	sprat4	0.011219				0.0053097	0.0033119	0.0017170	0.0038534	0.0028158	0.0078804					
20	sprat5	0.024966				0.011816	0.0073704	0.0038211	0.0085753	0.0062662	0.017537					
21	whiting1	0.28453				0.053866	0.089598	0.052258	0.026061	0.028566	0.057105					
22	whiting2	0.079829				0.015113	0.025138	0.021992	0.0073119	0.0066787	0.016021					
23	whiting3	0.11584				0.021931	0.036478	0.028368	0.0079578	0.0096916	0.023249					
24	whiting4	0.27357				0.051791	0.086147	0.050245	0.018793	0.022888	0.054905					
25	whiting5	0.49834					0.22885	0.15254	0.057056	0.069487	0.16669					
26	whiting6	0.37220						0.11393	0.12784	0.12456	0.37350					
27	goby1					0.25035	0.20821	0.22668	0.12112	0.035403	0.21232					
28	goby2	0.12359				0.097491	0.064864	0.075664	0.047168	0.024127	0.066145					
29	goby3	0.083522				0.065884	0.043835	0.051133	0.031876	0.016305	0.044700					
30	goby4	0.031885				0.025151	0.016734	0.022773	0.012168	0.012449	0.029863					
31	Mussels					0.00026461	0.00022007	0.00017114	0.00012802							
32	Zoobenthos			0.020200	0.070546	0.021650	0.011372	0.0022109								
33	Zooplankton		0.00053808	0.0016645	0.0012918							0.12925	0.37123	0.16457	0.059916	0.037090
34	Phytoplankton											0.82142	0.56949	0.16406	0.014103	0.0024301

Figure G4: Screenshot of diet Predation mortality rates

Ecosim.Using vulnerabilities to select the time series model.

Once Ecopath model has been parametrized, a biomass dynamic model can be built with Ecosim based on the Ecopath results. For a time dynamic simulation with Ecosim, we used time series data from 2007 to 2013; and the total duration of simulation extended until 2020 is 14 years(2007 - 2020).The Time series data grid used were: biomass, catches, IUU (Illegal, Unreported and Unregulated fishing-only for turbot), fishing effortfor different fleets (GNS, OTM, FPN, FPO, LLS, LHP, SB, TBB). The time series fitting used fishing effort data as driving factors for the Ecosim model runs.

The consumption estimated in the Ecopath model, Q_{ij} is used to calculate other parameters of the dynamic Ecosim model such as vulnerability exchange rate $v_{ij} = k_{ij} \cdot \frac{Q^*_{ij}}{B^*_i}$, where k_{ij} is the user-defined vulnerability multiplier $k_{ij} \in [1, \infty]$. These are used to calculate vulnerable prey biomass at time t (V_{it}) as:

$$V_{it} = \frac{v_{ij} \cdot B_{it} \cdot T_i}{2v_i + a_{ijt} \cdot B_{jt}}$$

, which is used to calculate time variable Q_{ijt} in Ecosim as

$$Q_{ijt} = a_{ijt} \cdot B_{jt} \cdot V_{it}.$$

After time series data have been loaded and applied (Time series→Time series grid), a statistical measure of goodness of fit to these data is generated each time Ecosim is run. This goodness of fit measure is a weighted sum of squared deviations (SS) of log biomasses from log predicted biomasses, scaled in the case of relative abundance data by the maximum likelihood estimate of the relative abundance scaling factor q in the equation y = q*B(y = relative abundance, B = absolute abundance).

One key feature of Ecosim is its ability to allow exploring the implications on system dynamics of different views of how the biomass of different groups in ecosystem is controlled. The two extreme views are ‘predator’ control’ (also called top-down control) and ‘prey (or bottom-up) control’. We model this using ‘vulnerabilities,’ which represent the factor that a large increase in predator biomass will cause in predation mortality for a given prey. Low vulnerability (close to 1) means that an increase in predator biomass will not cause any noticeable increase in the predation mortality the predator may cause on the given prey. A high vulnerability, e.g., of 100, indicates that if the predator biomass is for instance doubled, it will cause close to a doubling in the predation mortality it causes for a given prey. The vulnerability parameters are among the most important parameters that users change to improve the agreement of the model's predictions with historical data.

We determined the sensitivity of SS to the critical Ecosim vulnerability parameters, by changing the vulnerability multiplier k_{ij} slightly (e.g. 1%) then rerunning the model to see how much SS is changed (i.e., how sensitive the time series predictions ‘supported’ by data are to the vulnerabilities). This is doing by following steps: Tools → Fit to time series →Sensitivity of SS to V → by Predator → Search. Then we go to 'Iteration' tab and click on Search button. After 12 iterations, SS was 858.4521 for our model. When all tests are completed or the testing is stopped by clicking the red box above the vulnerability grid, relative sensitivities are shown on a colour code scale on the vulnerability grid. A grid cell shown in red (for prey type in row i, predator type in column j of the grid) is one for which SS was most sensitive (among those tested) to changing that vulnerability, while a grid cell shown in blue is one for which SS was not sensitive to changing that vulnerability.

Scenarios for future projections

We developed three scenarios to estimate the impact of measures regulating the IUU fishing in order to obtain data needed for a Bayesian Belief Network. Dataset used from West Black Sea, i.e. from Romania, Bulgaria, Ukraine.

To develop scenarios, we considered three levels of measures for IUU:

- Business As Usual = 100 % IUU
- Soft Measures = 50% IUU
- Hard Measures = NO IUU

And three kind of Harvest Control Rule: Fishing Mortality(F), Total Allowable Catch(TAC), Maximum Sustainable Yield(MSY). The desire output: SSB, catches, landing.

For variable F: Run Ecosim→ecosim group plots → check turbot at age 2,3,4,5,6,7, where F exist→ save data to csv → average of F/year

For variable TAC: we consider TAC = an imposed catch. Next, we make a new CSV file with TAC instead of catches → load CSV → Run Ecosim→Ecosim group plots

For MSY: $MSY = 0.37 * M * B_{med}$

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

H. Chatham Rise – New Zealand

The Chatham Rise is a broad ridge lying to the east of central New Zealand and extending for c. 1400 km. Subtropical convergence gives the region high biodiversity, and makes it the most productive in New Zealand waters. The ecosystem supports substantial commercial fisheries production, and also a high diversity of seabird, cetacean, and large pelagic fish species, many of which are protected under New Zealand law but threatened by human activities. The main aims of the Chatham Rise case study are to develop approaches by which stakeholders and managers can balance the trade-offs between potentially conflicting views about future management of the region, and tools to understand the implications of different environmental or management scenarios.

Two different ecosystem models are being developed in this case of study. These models are an Ecopath-like balanced foodweb model and Atlantis. A balanced model of the food web of the Chatham Rise was developed by bringing together information on all biota in the ecosystem. Key information includes main species, their biomass, energetics (feeding and growth rates; assimilation efficiencies) and diets. The model has 37 groups: seabirds, toothed whales & dolphins, baleen whales, seals; 9 demersal fish groups; 4 mesopelagic groups; 10 groups of benthic invertebrates; 3 groups of small zooplankton; phytoplankton, bacteria and detritus. An extended description of this model can be found in the D4.1. The Atlantis model provides a spatially explicit biophysical model of the Chatham Rise region to depths of 1300 m, bounded to the west by the 400 m depth contour within the Mernoo Gap. Both models are applied to the same area (Fig. H1), but the balanced foodweb model has no spatial structure. The spatial and depth structure of the Atlantis model (Fig. H1) have been developed on the basis of a wide range of studies investigating fish community composition in the region (Bull et al. 2001, Livingston et al. 2002, Leathwick et al. 2006, Tuck et al. 2009). Water movement within the model region is driven by a revised Regional Ocean Modelling System model for the area (developed from Hadfield et al. 2007). The model uses 53 functional groups to model the biological processes, with 15 vertebrates and one invertebrate group representing single species, and other groups representing two or more species. The main component species of the groups are presented in Table H1. Primary producers and most invertebrate groups are modelled as biomass pools (mg N^{-3}). Within the Chatham Rise implementation, arrow squid and the general cephalopods are modelled as vertebrates, but with two age classes (juveniles and adults). The vertebrate groups are divided into age classes (10 age classes, with varying number of years per class, depending on the longevity of the primary species in the group), with each age class tracked by abundance (numbers) and weight-at-age (mg N). Weights are separated into structural and reserve nitrogen, with structural nitrogen (Ns) representing bones and other hard parts and reserve nitrogen (Nr) representing flesh, fat, reproductive components, and other soft tissue. The division of vertebrate groups into age classes allows for ontogenetic variations in the parameterisation. Zooplankton are divided into four species groups, based largely on distinct species, size and diet. Further details are provided in D4.6.

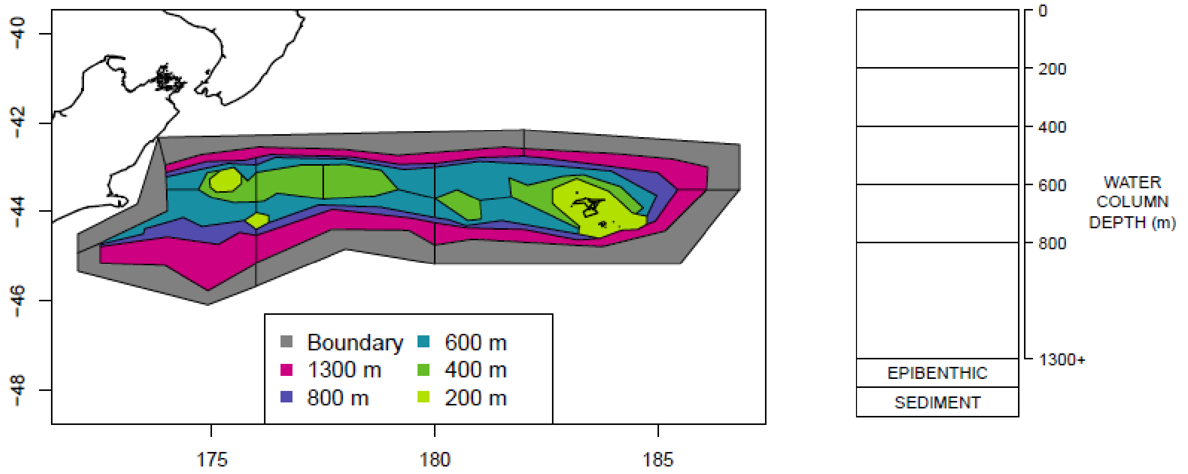


Figure H1: Bioregionalisation and depth structure implemented within the Chatham Rise Atlantis model

Within the MareFrame project, a range of new diet data, including isotopes, have been collected and analysed to improve our understanding of food web dynamics in the region, and calibrate the ecosystem models being developed. Diet data analysed included published papers and the recent collected data on diet from stomach contents. The analysis of diet from stomach contents have been now completed for previously unstudied groups such as rattails and mesopelagic species which are being used for first time in the ecosystem models in the area. Isotopes together with diet data for rattails and mesopelagic fish are being used in the calibration of both the balanced foodweb and Atlantis models. One protocol for this novel data implementation is presented here.

Protocol H.1. Implementation of isotopes diet data in the balanced foodweb model and Atlantis

Data

The protocol describes the implementation of 3 novel data types: rattail and mesopelagic fish diet, mesopelagic species composition and biomass, and trophic level estimates from stable isotopes.

The diet of 8 key rattail species was determined based on 5 years of feeding data from 4500 rattails stomachs. The niche separation (the way different species use resources (e.g., habitat and prey) differentially to help them coexist) between species, and the diet in key deepwater rattail (grenadier) species living between 1000 and 1300 m which are a common bycatch of the orange roughy and oreo fisheries have been analysed, with data being collated for incorporation into food webs within the ecosystem models to determine the role rattails have in the ecosystem. The new diet data are summarised in Table H2.

Table H2. New stomach contents composition for key rattail species. %F, frequency percent of occurrence; %IRI, percentage Index of Relative Importance

	Coelorinchusaspercephalus		*Coelorinchusbollonsi*		*Coelorinchusoliverianus*		*Lepidorhynchusdenticulatus*		*Idiolophorhynchusandriashevi.*		*Coryphaenoidesmcmillani*		*Coryphaenoides murrayi*		*Coryphaenoidesstriaturus*	
	%F	%IRI	%F	%IRI	%F	%IRI	%F	%IRI	%F	%IRI	%F	%IRI	%F	%IRI	%F	%IRI
Polychaeta	28.9	3.9	78.6	72.9	12.9	0.3	3.8	0.1			8.3	0.2	7.7	0.1	25	7.4
Copepoda	10	0.2	8.5	0.2	99.4	90.1	57.4	37.1	100	100	100	88.4	84.6	78.3	91.7	39
Isopoda	15.4	1.7	10.5	0.4	3.7	0.2	1.2	0.1					3.8	0	37.5	4.4
Chaetognatha							1.5	0.1			12.5	0.2			8.3	0.4
Euphausiacea	6	1.3	2	0.1	1.8	0.1	9.4	0.7			12.5	0.3				
Natantdecapoda	37.8	7.1	10.5	0.3	24.5	5.2	36.8	38					3.8	0.6	8.3	0.4
Astacidea	1.5	0.1	0.7	0.1												
Anomura	64.2	57.2	7.5	0.5	0.6	0.1	2.4	0.1					7.7	0.7		
Brachyura	18.9	5.1	29.2	10.4	4.3	0.1										
Corophiidea	4.5	0.1													4.2	0
Gammaridea	61.2	17.4	48.5	13.3	41.1	2.3	33.5	2.8			20.8	1.5	42.3	6	91.7	41.9
Hyperiidea	2	0.1	2	0.1	20.3	0.6	32.9	7			12.5	0.2			4.2	0
Other Arthropoda	12.4	0.4	8.8	0.3	27	1	9.1	0.3			12.5	7.5	26.9	9		5.6
Osteichthyes	8	0.5	2	0.1	4.9	0.2	25.9	11.5			8.3	1.9	7.7	5	8.3	0.1
Cephalopoda			0.7	0.1	2.5	0.1	29.1	2.4					3.8	0		
Other Mollusca	5.5	0.1	5.8	0.1	0.6	0.1	2.9	0.1							4.2	0
Salpida	2.5	0.1	3.1	0.1	2.5	0.1					4.2	0	3.8	0.4		
Foraminfera					0.6	0.1									12.5	0.2
Echinodermata	31.3	4.6	24.8	1.5												
Cnidaria			0.7	0.1												
Porifera			0.3	0.1												
Priapulida			0.3	0.1												
Ascidiacea			0.7	0.1												

A range of studies are underway to examine the role that mesopelagic species play in the trophic linkage between the benthos and epibenthos and higher trophic levels. Mesopelagic diet studies have focussed on 20 main species, with analysis complete for 15 of these, but more samples required for the others. An approach to estimate the abundance of mesopelagic species with hydroacoustics has been developed (Oeffner et al. unpublished). Acoustic backscatter has been partitioned into its individual species contingents using multi-frequency acoustics, mark morphology, and environmental data, with a decision tree correctly identifying 89.9% of species from a training set. The approach has been applied to acoustic data from random trawl surveys to provide information on the spatial distribution and biomass of mesopelagic species (Fig. H2).

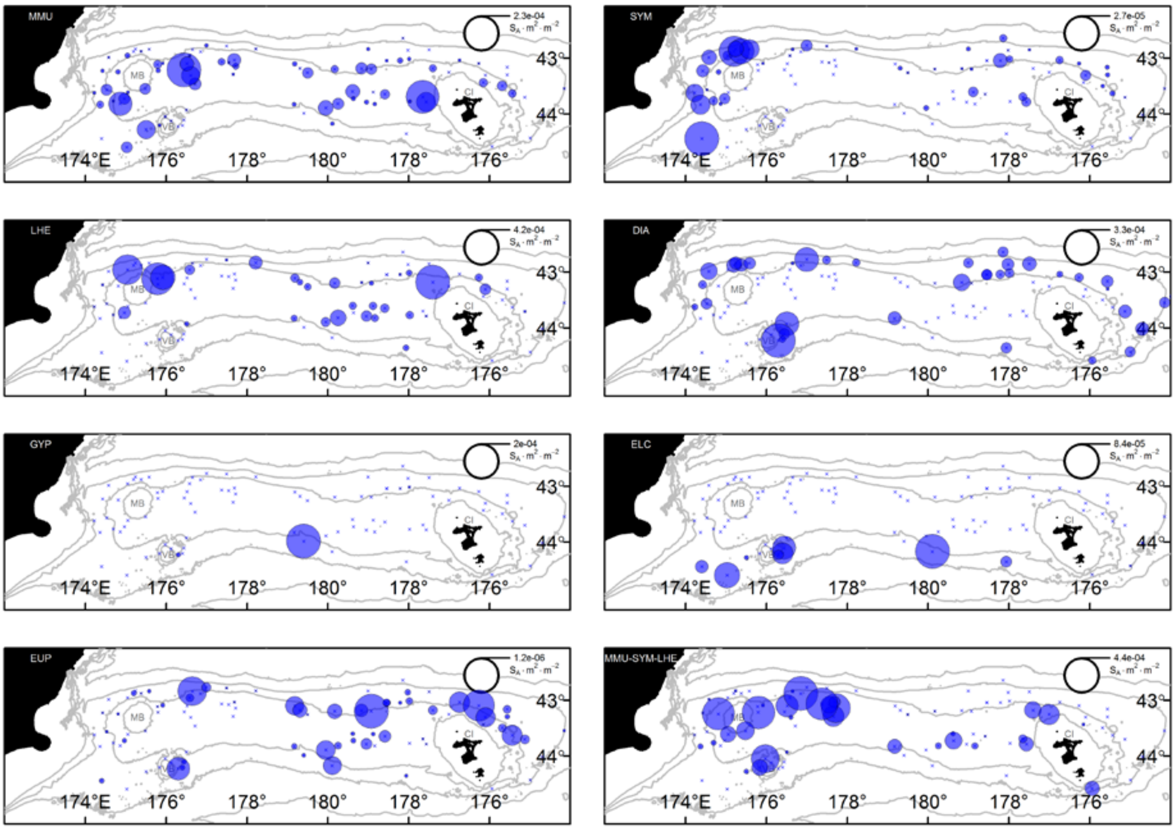


Figure H2: Spatial distribution (blue circles) of acoustic backscatter from 38 kHz data per species/classification category, as classified with the decision tree model (**Error! Reference source not found.**), of the application dataset (trawl files from the 2013 survey) on the Chatham Rise. Blue crosses show location of all trawls. First seven panels represent decision tree model outputs for *Maurolicus australis* (MMU), *Symbolophorus boops* (SYM), *Lampanyctode shectoris* (LHE), *Diaphus dan*ae (DIA), *Gymnoscopelus piabilis* (GYP), *Electronacarls bergi* (ELC) and krill (EUP). The last panel represents the species-mix classification category MMU-SYM-LHE – data that the decision tree model did not categorize into single species. Legend in top right corner shows maximum circle size which is proportional to maximum area acoustic backscatter coefficient (S_A in m^2 m^{-2}). Note that the size of each circle varies between each panel. Grey lines show bathymetry contours of 200 m, 500 m, 1000 m and 2000 m; locations of Mernoo Bank (MB), Veryan Bank (VB) and Chatham Islands (CI) are highlighted. Source: Oeffner et al. (unpublished)

Stable isotope analysis has been completed for the 30 most abundant species in surveys. Measurements of stable isotopes of nitrogen δ15N in fish muscle from the Chatham Rise ranges from 10.4 to 15.4 allowing to estimate the trophic level of each specie ranging from 3.09 (Spiny dogfish) to 4.66 (ling or bigeye rattail). This trophic level information can help to validate the ecosystem model helping to understand how well the model estimates the feeding patterns.

Model implementation

In quantifying the trophic structure of the ecosystem, the fundamental information includes the species present, abundances in terms of weight, the energetics of species (i.e., production, consumption, growth efficiency, respiration), and trophic interconnections between species through information on diets of predators. For rattails and the mesopelagic groups, new data includes their abundances in terms of biomass and trophic interconnections. The stomach content data of rattails and mesopelagic species informs both models (balanced foodweb and Atlantis) about food web structure, particularly about the role of these group species in the ecosystem. The biomass (and spatial distribution, for the Atlantis model) of the mesopelagic species will also help inform the trophic linkages through the system. Once the models are balanced the estimated trophic levels can be validated with the isotopes information providing an observed trophic level.

Implementation in Ecopath-like balanced food web model

Data format for model implementation

Diet data is provided to the model in the form of a Diet matrix, showing the percentages of each prey by weight (species or group) in the diet of each predator. Biomass within the model is presented in units of organic carbon density (gC m^{-2}). New biomass estimates for mesopelagic species provided from the acoustic data are used to inform the initial model estimates of average annual biomass.

Operative process description

The trophic model developed here quantifies the transfer of organic material through a food web based on the widely used mass-balance identities of the Ecopath trophic model (Christensen and Pauly 2002, Christensen and Walters 2004). Production is defined according to Equation H.1. For non-detrital groups, production represents the intrinsic rate of growth of all individuals in the population. For detrital groups, production is the total net flow of organic matter into the group, including fecal material (unassimilated consumption) from consumers, dead organisms, non-consumed predation ("messy eating"), planktonic exudates, and transfers between groups. These latter transfers include, for example, the sinking of detrital/ungrazed material to the benthos. Carbon flow through each trophic group per year is balanced according to Equation H.2 (for detrital and non-detrital groups) under the assumption that all parts of the ecosystem will be in balance in an average year. These balance equations provide a number of equality constraints to the system. Another set of equality constraints are provided by the fact that diet fractions of each predator sum to unity. The new diet data for rattails and mesopelagic species is used directly within equation H.2, defining the percentages of each prey in the diet of each predator.

$$P_i = B_i \left(\frac{P}{B} \right)_i$$ Non-detrital groups [Eq H.1a]

$$P_j = \sum_{i=1}^{n} P_i \left[T_{ij}^{1-E} + U_{ij}\left(\frac{Q}{P}\right)_i + T_{ij}^{s} \right]$$

Detrital groups [Eq H.1b]

$$P_i\left[1-\sum_{j=1}^{n}(T_{ij}^{1-E}+T_{ij}^{g}+T_{ij}^{s})-X_i-A_i\right]-\sum_{j=1}^{n}P_j\left(\frac{Q}{P}\right)_j D_{ij}-F_i=0$$

[Eq H.2]

In these equations for trophic group *i*:

B_i	annual average biomass (gC m^{-2})
P_i	annual production (gC m^{-2} y^{-1}). Autotrophic production rate is net of respiration but assumed to include production of phytoplankton exudants and other detrital material.
Q_i	annual consumption (gC m^{-2} y^{-1}). Note that autotrophs and detritus have Q_i=0.
$(P/B)_i$	production/biomass ratio (y^{-1})
$(Q/P)_i$	reciprocal of the growth efficiency (dimensionless)
D_{ij}	average fraction of prey *i* in the diet of predator *j* by weight (dimensionless)
X_i	fraction of production exported over year due to advection and migration (dimensionless)
A_i	fraction of production accumulated over a year (dimensionless)
F_i	fishing removals (gC m^{-2} y^{-1}).
T_{ij}^{1-E}	detrital transfer: fraction of production transferred from group *i* to detrital group *j* as non-living material, i.e. excluding direct predation but including phytoplankton exudants, parts of organisms (e.g. due to "messy eating"), whole dead organisms and carcasses (dimensionless)
T_{ij}^{g}	growth transfer: fraction of production transferred from group *i* to group *j* due to growth, i.e. as an organism gets older and/or larger it changes from one group to another (dimensionless)
T_{ij}^{s}	seasonal transfer: fraction of production transferred from group *i* to group *j* by non-trophic, seasonal processes, e.g. due to vertical flux of material (dimensionless)
U_{ij}	fraction of food that has been consumed by component *i* but which is not assimilated, instead being passed to detrital group *j*, (dimensionless)
n	total number of groups in the model
R_i	loss of organic carbon from the system due to respiration (gC m^{-2} y^{-1}). Respiration can be calculated as $R_i=Q_i\cdot(1-U_i)-P_i$

Note that Equations H.1 and H.2 differ from the standard Ecopath equations (Christensen & Walters 2004; Christensen &Pauly 2002). Details for these differences were described in Deliverable 4.1.

Model validation

Stable isotope analysis has been completed for the 30 most abundant species in surveys to estimate trophic levels, and uncertainty around these estimates. This data will be used to validate the trophic level values estimated within the balanced food web model. We calculated trophic levels (Lindeman 1942, Christensen and Pauly 2002) in the balanced model using matrix inversion based on two rules. First, primary producers, detritus and bacteria were defined as having a trophic level of 1. Second, a consumer's trophic level was defined as the sum of the trophic levels of their prey items, weighted by diet fraction, plus one. Previous model implementations appear to overestimate trophic level of predatory fish compared to values cited in the literature (see Deliverable 4.1.), although the appropriateness of some of the literature values is unclear. As a means of validation of the model, and testing the sensitivity of the model to specific data sets (i.e., the new rattail and mesopelagic diet data) the trophic levels estimated within the model will be compared directly with those estimated from stable isotope analysis. For the species for which stable isotope trophic level estimates are available, the ability of the food web model to estimate trophic level within appropriate bounds of uncertainty of the stable isotope estimate, or the magnitude and direction in any bias in the estimate, will be taken as a measure of model performance.

Implementation in Atlantis model

Data format for model implementation

Diet data is used within Atlantis to initially help inform the pPREY matrix (the proportion of biomass of a prey species available to a predator), confirming which species should or shouldn't be available, and then used (along with the trophic level data) in the model validation, to confirm that the predator diet realised within the model is realistic. In a similar way, the biomass estimates for mesopelagic species provided from the acoustic data are used to initially inform starting values for spatial distribution and biomass, and then validate model runs.

Operative process description

Consumers in Atlantis are modelled as biomass pools, age-structured biomass pools or age-structured groups. The age-structured groups are typically used for vertebrates, while non-vertebrates are largely modelled as biomass pools. A detailed description of how predation is modelled within Atlantis is provided by Audzijonyte et al. (2016). Predatory interactions are modelled in a similar way for both biomass pools and age-structured groups (although age-structured groups have additional options). Feeding interactions are modelled through biomass, which in age-structured groups are then converted to numbers to track individual mortality. In Atlantis predatory interactions are determined by:

1) Physical overlap – prey and predator must be in the same cell at the same time (determined by vertical and horizontal distribution parameters), and if prey is in the sediment the predator must be able to reach it.

2) Diet connection matrix (pPREY matrix or detailed ontogenetic diet preferences) that indicate maximum availability of prey to a predator. The actual realised consumption will depend on refuge factors, but if the value in the pPREY matrix is set to 0, no predation will occur.

3) Gape limitation for age-structured prey – prey that is too small or too big for the predator (either age-structured or biomass pool) will not be consumed.

4) Habitat refuge.

5) Environmental factors (temperature, salinity, pH) that can modify predator's feeding rates, prey's availability and nutritional content.

Using the standard Holling type II predator response relationship, grazing term (*Gr*), the amount of biomass of a specific prey (*prey*) consumed by a consumer *CX* is calculated as:

$$Gr_{prey} = \frac{B.C.B^{*}_{prey}}{1+C.HT.\sum_{i} B_{prey,i}} \qquad \text{[Eq H.3]}$$

where

$$B^{*}_{prey} = p_{prey,CX}.\delta_{overlap}.\delta_{habitat}.\delta_{size}.B_{prey} \qquad \text{[Eq H.4]}$$

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

is the available biomass of *prey* in an area, taking into account refuge (δ) options.

B is the feeding biomass of predator CX in a cell (mgN m^{-3}).
B_{prey} is the biomass of prey in that cell (mgN m^{-3}).
$p_{prey,CX}$ is the maximum availability of the *prey* to the predator CX defined in the pPREY matrix
C is the clearance rate of predator CX
HT is handling time

In biomass or age-structured biomass pool consumers (CP) the only variable tracked is N. Flux through a consumer biomass pool is determined by growth (G_{CP}), natural mortality (M_{CP}), predation for i predators ($Gr_{CP,i}$), fishing mortality (F_{CP}), and optional encystment in (Ec_{in}) and out (Ec_{out}) of the system.

$$\frac{d(CP)}{dt} = G_{CP} - M_{CP} - \sum_{i=predators} Gr_{CP,i} - F_{CP} - Ec_{out} + Ec_{in} \qquad \text{[Eq H.5]}$$

In age-structured consumers (CX) the nitrogen pool is partitioned into the reserve (RN) and structural nitrogen (SN) of an average individual of each age, and the numbers of individuals per age group are tracked.

$$\frac{d(Nm_{CX})}{dt} = Nm_{CX-1,ageup} - Nm_{CX,ageup} - M_{CX} - \sum_{i}^{predators} Gr_{CX,i} - F_{CX} - T_{CXout} + T_{CXin} \qquad \text{[Eq H.6]}$$

$Nm_{CX-1,ageup}$ is recruitment or ageing into the age group
$Nm_{CX,ageup}$ is the ageing up into the next age
T_{CXout} and T_{CXin} are migration out of and into the model domain

Model validation

It is important that our simulation model is validated before it is used to inform management decisions. Having run the model to replicate real world conditions (having extracted known fishery removals), model realised biomass trajectories and predator diets can be extracted from model outputs for comparison with real world observations. The mesopelagic biomass (and additional species breakdown) provides a valuable validation dataset beyond the traditional trawl survey abundance index data, and is likely to be very useful, given the important trophic role linking the benthic and pelagic systems these species have. Also, the trophic level data from the stable isotope study forms a valuable validation opportunity, which will be used in a similar way to Olsen et al. (2016). From the model realised feeding patterns, the trophic level of each component of the modelled food web can be estimated using the approach described above for the balanced food web model (primary producers, detritus and bacteria defined as having a trophic level of 1, a consumer's trophic level defined as the sum of the trophic levels of their prey items, weighted by diet fraction, plus one), and compared with externally estimated values.

References

A. Baltic Sea

Andersen, K. P.; Ursin, E., 1977.A multispecies extension to the Beverton and Holt theory of fishing with accounts of phosphorus circulation and primary production. Meddr.Danm. Fisk- Havunders: N. S. 7, 319–435.

Horbowy, J., 2005. The dynamics of Baltic fish stocks based on a multispecies stock production model. J. Appl. Ichthyol. 21: 198–204.

ICES. 2013. Report of the Baltic Fisheries Assessment Working Group (WGBFAS). 10-17 April 2013, ICES Headquarters, Copenhagen. ICES CM 2013/ACOM:10. 747 pp.

M.T. Tomczak, S. Niiranen, O. Hjerne, T. Blenckner 2012. Ecosystem flow dynamics in the Baltic Proper using a multi-trophic dataset as a basis for food–web modelling. Ecol. Model., 230 (2012), pp. 123–147

B. North Sea

Hatcher, A and Gordon, D. 2005.Further Investigations into the Factors Affecting Compliance with U.K. Fishing Quotas. Land Economics • February 2005 • 81 (1): 71–86.ISSN 0023-7639; E-ISSN 1543-8325.

Jennings, S., De Oliveira, J. A., Warr, A., Karema J. 2007. Measurement of body size and abundance in tests of macroecological and food web theory. Journal of Animal Ecology 76, 72–82.

Pope, J.G., Rice, J.C., Daan, N., Jennings, S., Gislason, H. 2006. Modelling an exploited marine fish community with 15 parameters - results from a simple size-based model. ICES Journal of Marine Science 63, 1029–1044.

Pope, John VI. 2003 Golden Ages Or Magic Moments? Natural Resource Modeling. Volume 16, Number 4, Winter 2003.

Ramírez-Monsalve, P., Raakjær, J., Nielsen, K. N., Santiago, J. L., Ballesteros, M., Laksá, U., & Degnbol, P. (2016). Ecosystem Approach to Fisheries Management (EAFM) in the EU–Current science–policy–society interfaces and emerging requirements. Marine Policy, 66, 83-92.

C. NWW - Iceland Waters

Elvarsson, B. P. 2015. Evaluating stock structure hypotheses using genetically determined close relatives: a simulation study on North Atlantic fin whales. ICES Journal of Marine Science, 72 (2): 661-669. doi: 10.1093/icesjms/fsu140.

Elvarsson, B., Taylor, L., Trenkel, V. M., Kupca, V., Stefánsson, G. 2014. A bootstrap method for estimating bias and variance in statistical multispecies. African Journal of Marine Science. 36(1):99–110.

Fulton, E.A., M. Fuller, A.D.M. Smith, and A.E. Punt. 2004. Ecological Indicators of the Ecosystem Effects of Fishing: Final Report. Australian Fisheries Management Authority Report, R99/1546.

Gunnlaugsson, T. 2011. Relatedness between samples quantified and an optimal criterion for match detection approximated. Journal of Cetacean Research and Management, 12: 12.

Lindstrøm, U., Smout, S., Howell, D., and Bogstad, B. 2009. Modelling multi-species interactions in the Barents Sea ecosystem with special emphasis on minke whales and their interactions with cod, herring and capelin. Deep Sea Research Part II: Topical Studies in Oceanography, 56(21-22):2068–2079.

Logemann, K., Ólafsson, J., Snorrason, Á., Valdimarsson, H., & Marteinsdóttir, G. (2013). The circulation of Icelandic waters–a modelling study. Ocean Sci, 9(5), 931-955.

Punt, A. 1999. A full description of the standard baleen II model and some variants thereof. Journal of Cetacean Research and Management, 1: 267–276.

Taylor, L., Begley, J., Kupca, V. and Stefansson, G. 2007. A simple implementation of the statistical modelling framework Gadget for cod in Icelandic waters. African Journal of Marine Science 29(2): 223–245, 2007.

Stefánsson, G., Sigurjónsson, J., and Víkingsson, G. 1997. On dynamic interactions between some fish resources and cetaceans off Iceland based on a simulation model. J. Northwest Atl. Fish. Sci., 22:357–370.

Vikingsson, G.A., B. T. Elvarsson, D. Olafsdottir, J. H. Sigurjonsson, V. Chosson and A. Galan. 2014. Recent changes in the diet composition of common minke whales (*Balaenoptera acutorostrata*) in Icelandic waters. A consequence of climate change? Vol. 10, No. 2, 138-152, http://dx.doi.org/10.1080/17451000.2013.793812.

D. NWW - West of Scotland

Alexander, K. A, Heymans, J. J., Magill, S., Tomczak, M. T., Holmes, S. J. and Wilding, T. A. 2014. Investigating the recent decline in gadoid stocks in the west of Scotland shelf ecosystem using a food web model. ICES Journal of Marine Science; doi:10.1093/icesjms/fsu149

Bailey, N., Bailey, D., Bellini, L., Fernandes, P., Fox, C., Heymans, S., Holmes, S., et al. 2011. The West of Scotland Marine Ecosystem: a Review of Scientific Knowledge.

Berx, B. and Hughes, SL. 2009. Climatology of surface and near bed temperature and salinity on the north west European continental shelf for 1971-2000. Continental Shelf Research 29(19): 2286-2292.

Christensen,V., and Walters, C. J. 2004. Ecopath with Ecosim: methods,capabilities and limitations. Ecological Modelling, 172: 109–139.

Christensen,V.,Walters, C. J., and Pauly,D. 2001. Ecopath with Ecosim:a User's Guide.

Mackinson S, Daskalov G, Heymans JJ, Neira S, Arancibia H, Zetina-Rej´on M, Jiang H, Cheng HQ, Coll M, Arreguin-Sanchez F, Keeble K,Shannon L. 2009. Which forcing factors fit? Using ecosystem models toinvestigate the relative influence of fishing and changes in primary productivity on the dynamics of marine ecosystems. Ecol Model ;220(21):2972–87.

Scott, E., Serpetti, N., Steenbeck, J., Heymans, J. J. A Stepwise Fitting Procedure for automated fitting of Ecopath with Ecosim models. Software X, In Press

Tomczak, M. T., Niiranan, S., Hjerne, O., Blenckner, T. 2012. Ecosystem flow dynamics in the Baltic Proper – Using a multi-trophic dataset as a basis for foo-web modelling. Ecological Modelling 230 (2012) 123-147

Walters, C., Christensen, V. 2007. Adding realism to foraging arena predictions of trophic flow rates in Ecosim ecosystem models: Shared foraging arenas and bout feeding. Ecological Modelling Vol. 209. 342–350

Walters, C., Christensen, V., and Pauly, D. 1997. Structuring dynamic models of exploited ecosystems from trophic mass-balance assessments. Reviews in Fish Biology and Fisheries, 7: 139–172.

E. SWW - Iberian Peninsula

Aldanondo, N., Cotano, U., Etxebeste, E., Irigoien, X., Alvarez, P. et al., 2008. Validation of daily increments deposition in the otoliths of European anchovy larvae (Engraulis encrasicolus L.) reared under different temperature conditions. Fisheries Research, 93 (3), 257-264.

Bernal, M., Jiménez, M. P., Duarte, J., 2012. Anchovy egg development in the Gulf of Cádiz and its comparison with development rates in the Bay of Biscay. Fisheries Research, 117-118, 112-120.

Cermeño, P., Uriarte, A., de Murguia, A.M., Morales-Nin, B., 2003. Validation of daily increment formation in otoliths of juvenile and adult European anchovy. Journal of Fish Biology, 62 (3), 679-691.

Cermeño, P., Uriarte, A., Morales-Nin, B., Cotano, U., Álvarez, P., 2008. Setting up interpretation criteria for ageing juvenile european anchovy otoliths. Scientia Marina, 72 (4), 733-742.

Cerviño, S. 2014. Estimating growth from sex ratio-at-length data in species with sexual size dimorphism. Fisheries Research. 160:112-119. doi:10.1016/j.fishres.2013.11.010

Catalán, I. A., Pérez-Mayol, S., Álvarez, I., Ruiz, J., Palmer, M., Baldó, F., Peliz,A., Morales-Nin, B. 2015. Daily otolith growth and ontogenetic geochemical signatures of age-0 anchovy (*Engraulisencrasicolus*) in the Gulf of Cádiz (SW Spain). Mediterranean Marine Science, 15(4), 781–789.

Hastings, A. 1993. Complex interactions between dispersal and dynamics: lessons from coupled logistic equations. Ecology 74, 1362–1372.

Morales-Nin, B., Pérez-Mayol, S., Palmer, M., Geffen, A.J., 2014. Coping with connectivity between populations of *Merluccius merluccius*: An elusive topic. Journal of Marine Systems, 138, 211-219.

Pita , A., Pérez, M., Cerviño, S. and Presa, P. 2011. What can gene flow and recruitment dynamics tell us about connectivity between European hake stocks in the Eastern North Atlantic? Cont. Shelf Res. 31, 376-387.

Pita, A., Pérez, M., Balado, M., Presa, P. 2014. Out of the Celtic cradle: the genetic signature of European hake connectivity in South-western Europe J. Sea Res. 93, 90-100.

Pita, A. A. Leal, A. Santafé-Muñoz and P. Presa. 2016. Genetic inference of demographic connectivity in the Atlantic European hake metapopulation (*Merluccius merluccius*) over spatio-temporal framework. Fisheries Research. 179: 291-301.

Waples, R.S., A. Punt and J.M. Cope. 2008. Integrating genetic data into management of marine resources: how can we do it better? Fish and Fisheries, 9, 423–449

Yoshinaga, J., Nakama, A., Morita, M., Edmonds, J.S., 2000. Fish otolith reference material for quality assurance of chemical analyses. Marine Chemistry, 69 (1-2), 91-97.

F. Mediterranean Waters - Strait of Scilly

Allen, J. I., Blackford, J. C., Holt, J., Proctor, R., Ashworth, M. and Siddorn, J. 2001. A highly spatiallyresolved ecosystem model for the North West European Continental Shelf Sarsia: 86,423-440.Fulton, E.A., FullerM., SmithA.D.M., and Punt. A.E. 2004. Ecological Indicators of the Ecosystem Effects of Fishing: Final Report. Australian Fisheries Management Authority Report, R99/1546.

IPCC, Solomon, S.; Qin, D., M. M.; Chen, Z.; Marquis, M.; Averyt, K.; Tignor, M. & Miller, H. 2007.(Eds.) Summary for Policymakers Climate Change 2007: The Physical Science Basis. Contribution of Working Group I to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change, Cambridge University Press, Cambridge, United Kingdom and NewYork, NY, USA., 1-18.

Langmead O., McQuatters-Gollop A., Mee L.D. (eds), 2007. European lifestyles and marine ecosystems: exploring challenges for managing Europe's seas. University of Plymouth Marine Institute, Plymouth

Russo T., Parisi A., Cataudella S. 2013. Spatial indicators of fishing pressure: Preliminary analyses and possible developments. Ecol Ind 26: 141–153.

Russo T., Parisi A., Garofalo G., Gristina M., Cataudella S., Fiorentino F., 2014. SMART: A Spatially Explicit Bio-Economic Model for Assessing and Managing Demersal Fisheries, with an Application to Italian Trawlers in the Strait of Sicily. PLoS ONE 9(1): e86222. doi:10.1371/journal.pone.0086222.

G. Black Sea

Ahlbeck I, Hansson S, Hjerne O. 2012. Evaluating fish diet analysis methods by individual-based modelling. Can. J. Fish. Aquat. Sci. 69(7): 1184-1201.

Bănaru, D., M. Harmelin-Viviena. 2009. Feeding behaviour of Black Sea bottom fishes: Did it change over time?, Acta Oecologica: 35, 6: 769-777.

Cortes, E., 1997. A critical review of methods of studying fish feeding based on analysis of stomach contents: application to elasmobranch fishes. Can J. Fish Aquat. Sci 54 (3): 726- 738;

Elton, C. 1927. Animal Ecology. N. Y.MacMillan Co., 260 p.

Hansson, S. 1998. Methods of studying fish feeding: a comment. Can. J. Fish. Aquat. Sci. 55(12): 2706–2707. doi:10.1139/f98-158. Heincke, F. 1908. Berichtüber die Untersuchungen der Biologischen

Hyslop E. J., 1980, Stomach contents analyses – a review of methods and their application, J. Fish Biol. (1980) 17:41 1-429.

Lindeman, R. 1942. The Trophic-Dynamic Aspect of Ecology. Ecology, 23(4), 399-417. doi:10.2307/1930126.

Odum, W. E., &Heald, E. J. 1975. The detritus-based food web of an. Estuarine Research: Chemistry, biology, and the estuarine system, 265.

Porumb I. I., 1961.Contribuţii la cunoşterea biologi eiguvizilor (Gobius batrachocephalus, Gobius cephalargesşi Gobius melanostomus) din dreptu llitoralului Romanesc al Mării Neagre (date preliminare), Hidrobiologia, 3, 271-282.

Pinkas L., Oliphant M.S., Iverson I.L.K., 1971. Food habits of albacore, bluefin tuna and bonito in Californian waters. CalifDep Fish Game Fish Bull 152:l-105.

Villy Christensen, Carl J. Walters, Daniel Pauly and Robyn Forrest. 2008. Ecopath with Ecosim version 6, User Guide.

http://www.boblme.org/documentRepository/Ecopath%20parameters.pdf

H. Chatham Rise - New Zealand

Audzijonyte, A., R. Gorton, I. Kaplan, I. van Putten, S. Richards, and E. A. Fulton. 2016. Atlantis User's Guide. CSIRO.

Bull, B., M. E. Livingston, R. Hurst, and N. Bagley. 2001. Upper-slope fish communities on the Chatham Rise, New Zealand, 1992-1999. New Zealand Journal of Marine and Freshwater Research 35:795–815.

Christensen, V., and D. Pauly. 2002. The ECOPATH II - a software for balancing steady-state ecosystem models and calculating network characteristics. . Ecological Modelling 61:169-185.

Christensen, V., and C. J. Walters. 2004. Ecopath with Ecosim: methods, capabilities and limitations. Ecological Modelling 172:109-139.

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Hadfield, M., G. Rickard, and M. J. Uddstrom. 2007. A hydrodynamic model of Chatham Rise, New Zealand. New Zealand Journal of Marine and Freshwater Research 41:239-264.

Leathwick, J. R., J. Eldith, M. P. Francis, T. Hastie, and P. Taylor. 2006. Variation in demersal fish species richness in the oceans surrounding New Zealand: an analysis using boosted regression trees. Marine Ecology Progress Series 321:267–281.

Lindeman, R. L. 1942. The trophic-dynamic aspect of ecology. Ecology:399-418.

Livingston, M. E., B. Bull, D. W. Stevens, and N. Bagley. 2002. A review of hoki and middle depth trawl surveys of the Chatham Rise, January 1992–2001. NIWA Technical Report 113:145p.

Oeffner, J., S. Gauthier, M. Pinkerton, and R. O'Driscoll. unpublished. A decision-tree model for species identification of acoustic marks: moving beyond acoustic indices to estimate mesopelagic biomass.

Olsen, E., G. Fay, S. Gaichas, R. Gamble, S. Lucey, and J. S. Link. 2016. Ecosystem Model Skill Assessment. Yes We Can! PLoS ONE 11.

Tuck, I. D., R. Cole, and J. Devine. 2009. Ecosystem indicators for New Zealand fisheries. New Zealand Aquatic Environment and Biodiversity Report No. 42:180p.