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Towards an ecosystem approach to fisheries for
Nephrops norvegicus and *Merluccius merluccius*
inhabiting the Central Adriatic Sea

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Abstract

This study presents the development of a Model of Intermediate Complexity for Ecosystem assessments (MICE; Plagányi et al., 2014) towards evaluating different scenarios for the management of the European hake and Norway lobster bottom trawl fishery in the central Adriatic Sea. These two species represent the target species, as well as the predators, of this study; they are two of the most important species fished by the bottom trawl fishery, accounting for both the highest landings and commercial value among demersal species in the area.

The study area represents a zone of particular relevance for both economic and biological reasons. Economically, because the majority of catches of the northern and central Adriatic Sea come from this area and they account for an high commercial value; and biologically because it represents a nursery ground for hake and hosts a distinctive population of Norway lobster. Moreover, thanks to the peculiar circulation of the Adriatic Sea, upwelling phenomena occur in this area allowing the formation of a rich planktonic community that supports a richness in pelagic and demersal resources (Adriamed, 2006). This richness in species, as well as the significant importance of the area for the target species of this study and its considerable exploitation by fishing fleets of at least two countries (Italy and Croatia), make it an interesting case study for the development of an ecosystem approach to fisheries (EAF).

Different models are available to reach EAF purposes, here the choice was made to develop a MICE approach, since it is well adapted to test specific management questions, as required by this study, and accounts for an intermediate complexity. The MICE was developed in a step-wise manner. Firstly, the conceptual model was defined: this represents the interaction between the trawl fishery, the two target species (Norway lobster and European hake) and their prey (grouped in four meaningful groups). Discards were also considered, representing a source of food for Norway lobster and being important in terms of management options. Secondly, management scenarios to be tested were determined: (i) base case (BC): an investigation into the effects of continuing the current situation, (ii) decrease in recruitment (DR): the effects of a 50% reduction in predator recruitment, (iii) increase in net selectivity for smaller individuals (S1), (iv) protection of larger individuals (S2) and (v) the imposition of a discard ban *sensu* Reg. EC No.1380/2013.

The management scenarios were tested by linking predators and their prey, and projecting their dynamics ten years into the future (2013 – m 2022).

Predator dynamics were reproduced by developing single species stock assessment models to evaluate the status of these resources and produce the input values to be included within the MICE. Three different models were compared for hake: a Length Cohort Analysis (LCA) with VIT (Lleonart and Salat, 1992; 1997), a statistical catch at length model, “Mark3”, and an integrated assessment (IA), Stock Synthesis 3 (SS3; Methot and Wetzel, 2013). Two models were tested for the Norway lobster: LCA with VIT (Lleonart and Salat, 1992; 1997) and an IA using CASAL (C++ algorithmic stock assessment laboratory; Bull et al., 2012). The results from the VIT assessments were those chosen as inputs to the MICE model as they represented the least complex models, thus satisfying the underlying MICE philosophy, which embraces simplicity, and allowing the implementation of the MICE model to be more expedite. However, since both species lack assessments that address all important intrinsic complexities (e.g. those related to their biology) , the investigation of a number of more complex stock assessment methods (Mark 3, SS3, CASAL) represents an important part of this study, and their outputs will be included in future developments of this study.

The description of prey dynamics required the collection of a large amount of data. Firstly, prey were pooled into four prey groups according to similarities in their life history characteristics and the role they play in the ecosystem. Then, for each group information about their biomass within the study area was collected, and a number of life history parameters necessary to describe the rate of increase of each prey group were defined. The prey preference probability of each predator for each prey group was also estimated and used to model the prey-predator functional response, assumed to be a Holling Type II. The rate at which a predator obtains its prey, together with all other information collected, allowed us to model the dynamics of each prey group.

Finally, predator and prey dynamics were linked within the MICE model and projected into the future under the different management scenarios. The best management scenario resulted to be the protection of adults, which produced the most beneficial results for both predator species (in terms of spawning stock abundance and adult size) and prey groups. Under this scenario, prey groups showed a visible decrease compared to the base case scenario but this was not important enough to discard the option. The other management options showed modest (if any, in the case of the discard ban) tangible beneficial effects on predator or prey groups. Moreover, results also

highlighted the importance of predation as the main factor regulating the biomass of the prey groups. This is not surprising as they mainly comprise species not targeted by the fishery.

This MICE application has demonstrated a capacity of a multispecies model for producing valuable management options to avoid ecosystem degradation sustaining the well-being of marine ecosystems and the fisheries they support; i.e. the crucial objective of an ecosystem approach to fisheries (Garcia et al., 2003; Pikitch et al., 2004). Moreover, the role of multispecies models of intermediate complexity in complementing single-species models in terms of simulating alternative management strategies and evaluating associated trade-offs (i.e. in a tactical, rule-based, management context), especially when taking trophic interactions into account, is highlighted.

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CHAPTER 1 – Introduction

1.1 General features of the Adriatic Sea

The Adriatic Sea is an elongated and semi closed basin in central Mediterranean Sea between Italy and the Balkan peninsula (Fig. 1.1). From an FAO point of view, the northern and central Adriatic sea together comprise Geographical Sub-Area (GSA) 17, whereas the southern Adriatic comprises GSA 18. GSAs were established by the FAO General Fisheries Commission for the Mediterranean (GFCM) to facilitate the management of the fisheries resources.

The Adriatic sea extends for *ca.* 800 km in a NW to SW direction and is 100 to 200 km wide (Fonda Umani et al., 1990), occupying 138 595 km² and representing 4.6% of the total Mediterranean surface (Buljan and Zore-Armanda, 1971). The northern Adriatic shallow with an average depth of about 35 m, whereas the central part accounts has an average depth of 140 m, reaching *ca.* 270 m in its deepest part, which is represented by the Pomo/Jabuka pits (Fig. 1.2). The southern basin is characterized by a wide depression reaching more than 1200 m deep (Artegiani et al., 1997a) and ending in the Otranto Channel, the connection with the rest of the Mediterranean Sea.

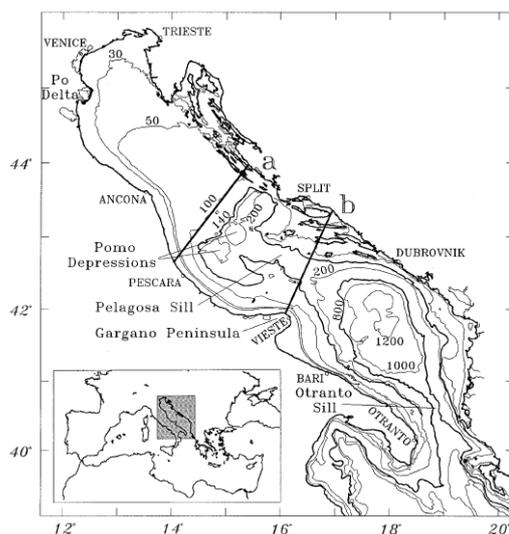


Fig. 1.1 The Adriatic Sea. Lines a and b define the northern, central and southern Adriatic Sea (source: Artegiani et al., 1997a)

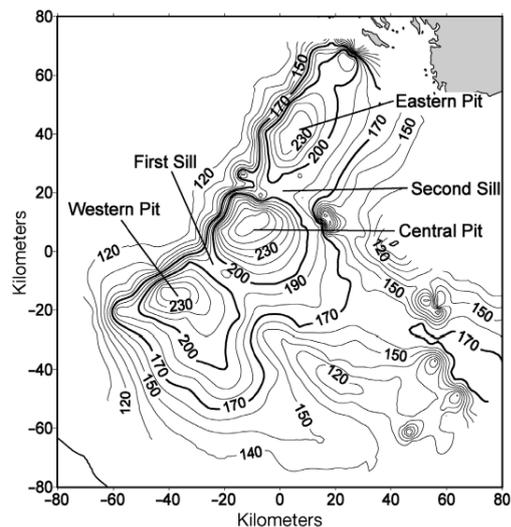


Fig. 1.2 High resolution bathymetric map of the Pomo/Jabuka Pits (source: Marini et al., 2006)

The Adriatic Sea is characterized by a distinct circulation pattern (Fig. 1.3): new water masses (Levantine Intermediate Water, LIW) coming from the Mediterranean enter

from the Otranto Channel and proceed northerly along the eastern coast. When the LIW reaches the northern Adriatic, the NE cold wind (“Bora”), together with the Po river runoff cause a decrease in salinity and density, transforming it into the Northern Adriatic Deep Water (NAdDW). The NAdDW flows back down towards the southern Adriatic, travelling mainly along the Italian coast (Franco 1982; Artegiani and Salusti, 1987; Gacic et al. 2001). On its way, the NAdDW mixes with warmer and saltier water masses increasing its temperature and salinity. A characteristic water mass, the Middle Adriatic Deep Water (MAdDW), sits year-round on the bottom of the Pomo/Jabuka pits. When the NAdDW flows southwards, it may stop in this area and since it is denser than the resident water mass it will sink to the bottom, displacing old MAdDW and increasing the density and oxygen concentration of the bottom layer. This water renewal occurs in late-winter/early-spring every two or three years (Artegiani et al., 2001; Vilibić, 2003). Displacement of old MAdDW is dependent upon the strength of the Bora winds and the extent of the Po river runoff (Marini et al., 2015).

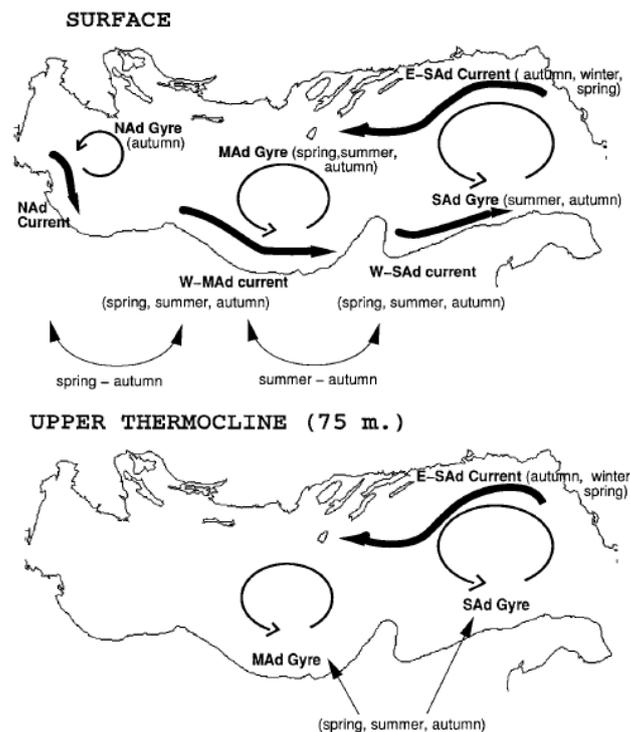


Fig. 1.3 Baroclinic circulation in the Adriatic Sea (source: Artegiani et al., 1997b).

Upwelling phenomena take place in the Pomo/Jabuka pits, allowing the formation of a rich planktonic community that supports a richness in pelagic and demersal fishes (Adriamed, 2006). Here, the bottom sediment is composed of fine mud, appropriate for *Neprhops* burrows, whereas the surrounding seabed is much shallower, typically less

than 100 m, and formed by coarser sandy sediments less suitable for this species. The Pomo/Jabuka pits thus host a distinct population of Norway lobster (*Nephrops norvegicus*), characterised by a high density of small-sized individuals; they also represent a nursery area for European hake (*Merluccius merluccius*) (Županović and Jardas, 1986; Froglija and Gramitto, 1981). These features make this area an important fishing ground both for Italian and Croatian bottom trawling fleets.

1.1.1 Study area

The study area is located in the central Adriatic sea, it includes the Pomo/Jabuka pits and takes in account the fishing activity of the principal harbours exploiting this zone at depths greater than 100 m (Ancona, San Benedetto, Martinsicuro, Giulianova, Pescara and Termoli for the Italian side and Split and Šibenik for the Croatian side) (Fig. 1.4). This area is important both economically and biologically.

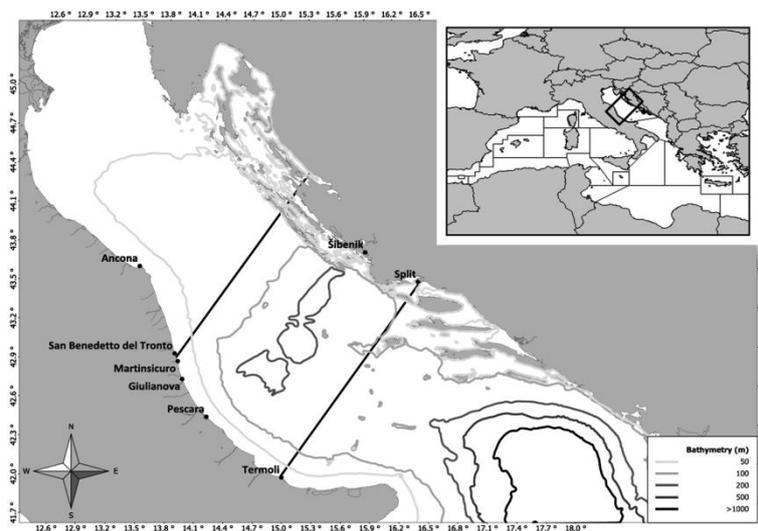


Fig. 1.4 Map of the northern and central Adriatic Sea. Black lines define the study area; within this area, the 200 m isobath defines the edge of the Pomo/Jabuka pits.

1.2 Fishery in the study area

1.2.1 Italian fishery

Fishing represents an important economic sector for Italy, especially for the northern and central Adriatic Sea where the highest effort (in terms of fishing days), income (in millions of €) and catches (tonnes) are recorded (Fig.1.5).

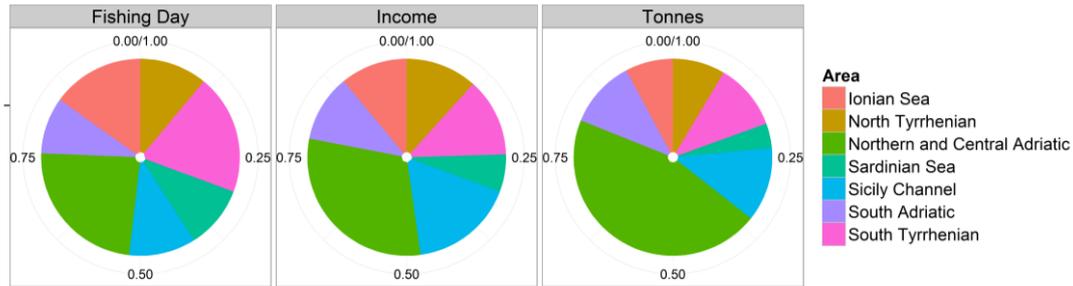


Fig. 1.5 Italian productivity per fishing area – data source IREPA, 2012 (<http://www.irepa.org/it/dati-sistan/dati-nazionali/2012.html>)

In 2012, 45% of total Italian catches came from the northern and central Adriatic Sea: the Marche region above all, followed by Emilia-Romagna, Veneto, Abruzzo, Friuli-Venezia-Giulia and Molise. Catches were taken mainly by pelagic pair trawls targeting small pelagic species (e.g. anchovy and sardine), followed by boat dredges targeting clams, then bottom trawls exploit principally demersal species (hake, red mullet, sole), and finally set gillnets and purse seines (IREPA, 2012) (Fig. 1.6). The activity of the Italian fleet is principally carried out within the territorial and extraterritorial waters.

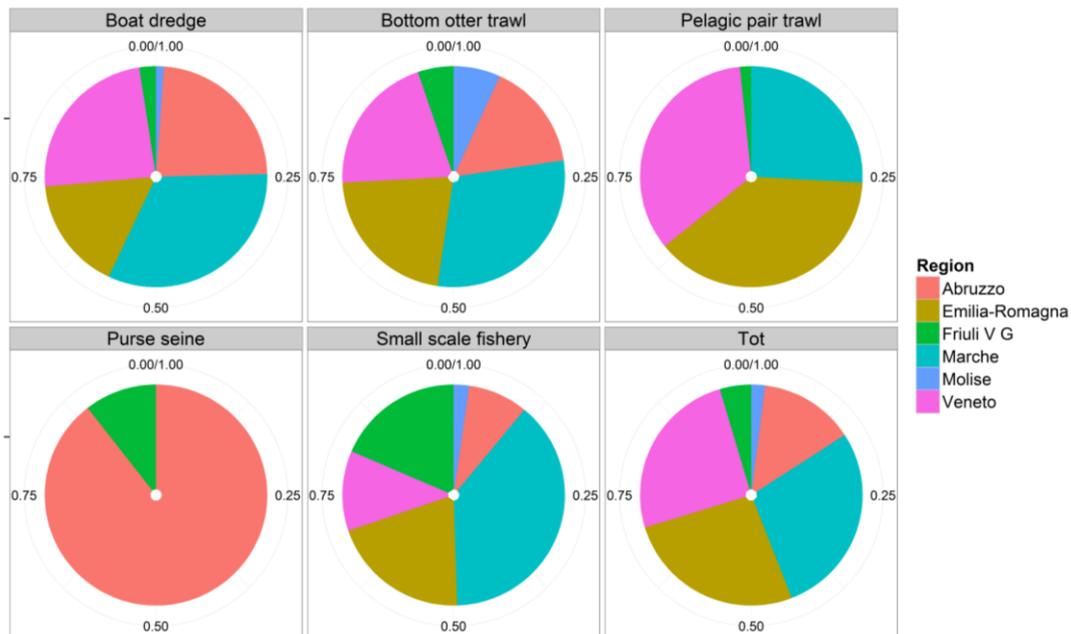


Fig. 1.6 Catches by metier and region for north and central Adriatic Sea in 2012 - data source IREPA, 2012 (<http://www.irepa.org/it/dati-sistan/dati-nazionali/2012.html>)

Within the study area of this research and the regions exploiting it (Marche, Abruzzo and Molise), this study focuses its attention on the activity of bottom trawlers and two target species: European hake (*Merluccius merluccius*) and Norway lobster (*Nephrops norvegicus*). To identify the amount of catch and effort coming from the study area, data

for to the whole northern and central Adriatic Sea were scaled considering the information collected by the Vessel monitoring system (VMS – see Paragraph 2.2).

1.2.2 Croatian fishery

Croatian waters extend for 12 NM starting from the coastline all the way down the country; for statistical purposes they are separated into zones and the one included within the study area is zone C (Fig. 1.7). Zones H, I, J and K are in international waters on the Croatian side of the midline. Croatian fishing activity is mainly carried out within its territorial water.



Fig. 1.7 Croatian territorial waters. Source: Croatian Institute of Oceanography and Fisheries in Split.

Zone C seems to be the most exploited area, accounting for the highest number of fishing days, number and length of hauls and hours of trawling (Vrgoč et al., 2005). The importance of zone C, for the two target species in particular (hake and Norway lobster), is also highlighted by the MEDITS survey (Bertrand et al., 2002, see paragraph 2.3) (Fig. 1.8; data provided by Croatian Institute of Oceanography and Fisheries in Split). More specifically, hake is well represented in all areas and mostly in areas E and F, G and C. Biomass indices in Zone C have a fluctuating trend with peaks in 2004, 2008 and 2012. Norway lobster, on the other hand, are only found in a few zones, principally C, E and F, D and occasionally in zone B. Zone C accounted for the highest biomass in 2000, 2006, 2007 and 2013.

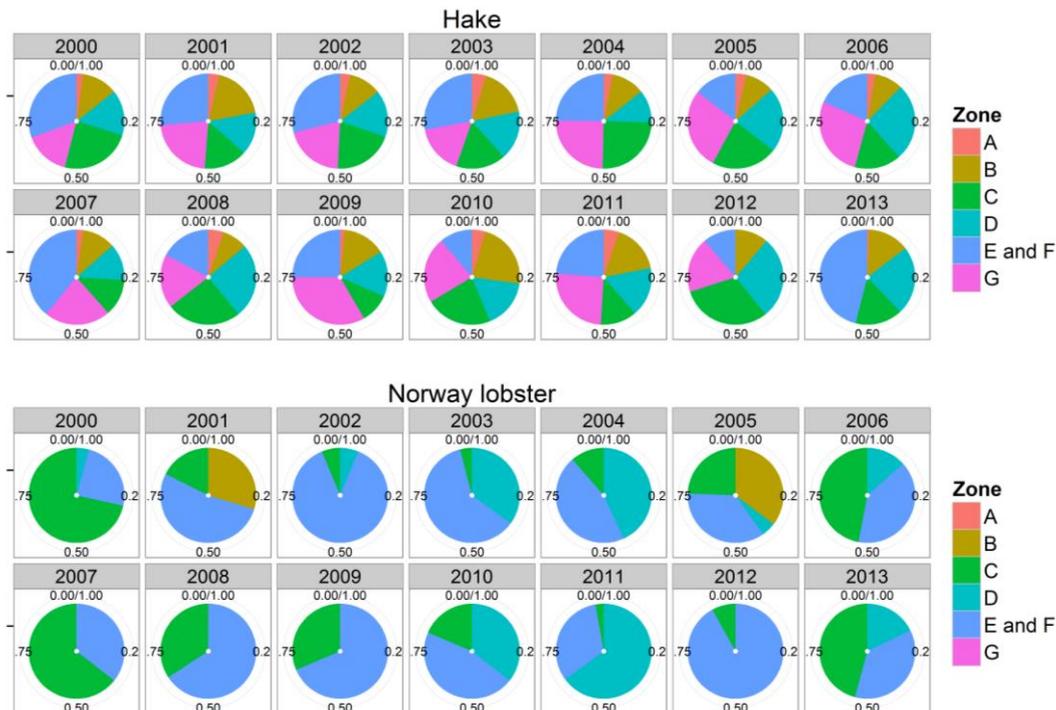


Fig. 1.8 Biomass index (kg/km²) from MEDITS survey for years from 2000 to 2013 for hake (top) and Norway lobster (bottom). Source: Croatian Institute of Oceanography and Fisheries in Split.

The annual Economic Report on the EU Fishing Fleet (STECF 14-16, 2014) provides information on the status of Croatian fisheries, reporting an increase in the number of vessels (by 3% from 2012) and fishing effort (increase in GT and kW by 2% and 6% from 2012) in 2013. Unfortunately VMS data are not accessible for this country and the information on fishing effort is not adequate to extract data for the study area only. Thus to represent the proportion of fish caught by the Croatian fleet in the study area, landings were decreased to 40% of their original value for hake, to 85% for *Nephrops* and to 30% for the other species considered in this study (N. Vrgoč, pers. comm.).

1.3 Stock assessment

1.3.1 Aim and history of the stock assessment

“Stock assessment is the part of Fisheries Science that studies the status of a fish stock as well as the possible outcomes of different management alternatives. It tells us if the abundance of a stock is below or above a given target point and by doing so lets us know whether the stock is overexploited or not; it also tells us if a catch level will maintain or change the abundance of the stock.” (Musick and Bonfil, 2005).

This science has a long history: already at the beginning of the twentieth century a correlation between the size of fish stocks and fishing activity was recognized (Quinn, 2003). In particular, Baranov identified catches as the decisive factor controlling the state of fish resources and developed the fundamental and well-known “Baranov catch equation” (Baranov, 1918). During these same years, precisely in 1902, the International Council for the Exploration of the Sea (ICES) was founded; this promoted the collection of fisheries data and scientific studies on growth, recruitment and ageing of fishes (Quinn, 2003).

Fisheries science was established properly only in the mid-twentieth century, when various mathematical models were developed. In particular, the work of Ray Beverton and Sydney Holt (1947-1953) has to be noted: they developed the proper theory of fishing taking in account all the factors influencing fish dynamics (i.e. growth, mortality, recruitment). Later, thanks to Ricker’s studies (Ricker, 1945), the importance of statistics in fisheries modelling was recognized, contrary to the work of Beverton and Holt that was more mathematical. In the years following the focus was on the development of deterministic models, such as Virtual Population Analysis (VPA, Gulland, 1965), cohort analysis (Pope, 1972), surplus production models (Pella and Tomlinson, 1969; Schnute, 1977; Hilborn, 1979), that all made use of fixed parameters to make estimates. Whereas, the first statistical catch at age approach was conducted by Doubleday in 1976. Statistical models were initially abandoned to then become fundamental in most recent years. Meantime multispecies models were diffused thanks to the increasing attention for the ecosystem. However, the development of these models was limited by the absence of data about species and trophic level interactions and it was recouped and improved only recently (Quinn, 2003).

The late 20th century, from 1980, was characterized by an explosion of quantitative fisheries papers, thus Quinn (2003) defined this period as the *Golden Age*. Different nonlinear, statistical and stochastic age-based models taking into account different sources of data were developed (e.g. ASPIC by Prager, 1994). The inclusion of more information, e.g. selectivity, catchability, recruitment, lead to the production of less biased results. The development of length-based approaches, that are models where the length of an individual is considered a proxy for its age, also started, but they bumped into several difficulties for the principal reason of not having proper growth pattern estimations. Consequently, the application of these methods was considered doubtful and their diffusion was limited (Hilborn and Walters, 1992). During this period the

importance of including Bayesian approaches in stock assessment methods was also recognized (Hilborn, 1992), owing to their ability at explaining uncertainty and evaluating the validity of data included in the stock assessment (Quinn, 2003). At the same time, a methodology called retrospective analysis was also developed: this allows the identification of problems within a stock assessment model by comparing results obtained after removing one year at time (Deriso, Quinn and Neal, 1985; Parma, 1993; NRC, 1988).

The numerous and important improvements that occurred in these years contributed to the development of the complex stock assessment models developed in the most recent years. More specifically, features of the more recent stock assessment methodologies include the possibility of (i) quantifying measurement and process errors, (ii) applying Bayesian methodologies, and (iii) taking into account complex dynamics of the species examined, e.g. spatial movements, different growth patterns. Moreover, the need for estimating the effects of environmental changes on the species assessed has been addressed and socioeconomic variables have been taken in account (Quinn, 2003). The need of understanding interactions between species was resumed, leading to the development of multispecies approaches, e.g. MSVPA (Sparre, 1991; Magnusson, 1995), MULTSPEC (Bogstad, Hauge and Ulltang, 1997), that finally led to the development of the ecosystem approach to fisheries (Plagányi, 2007; see below).

1.3.2 Classification of single species stock assessment models

The long history of stock assessment produced different methodologies, some dismissed, others still in use and others under development. Basically stock assessment models can be divided into 1) deterministic models, in which parameters remain constant over the considered time series, and 2) stochastic models, in which at least one parameter varies randomly over the time scale of the model's application. Nowadays stochastic models are the most widespread, since it was recognized that the inclusion of uncertainty and variation can produce finer results and consequently better recommendations (Hoggarth et al., 2006).

Choosing the most appropriate model is of essence and depends above all on the species considered and the data available. Particularly, stock assessment methods need: i) information coming from the commercial fishing activity, defined as fishery-dependent data, ii) data providing information on the population at sea, i.e. scientific surveys, defined fishery-independent data and iii) life history information (e.g. growth

parameters, natural mortality estimates, percentage of mature individuals at a given age or length). The more information available, the more precise and reliable the estimates generated by the model of choice.

Currently different stock assessment methodologies are available; they can be grouped into three main approaches: i) biomass dynamic models, i.e. surplus production models or global models, ii) delay-difference models, and iii) analytical models based on the investigation of catch-at-age data (Hoggarth et al., 2006).

Biomass dynamic or surplus production models (e.g. Schaefer, 1954; Pella and Tomlinson, 1969) represent the simplest stock assessment method: all they need is a time-series of catches and effort data to rebuild biomass population over the considered years. Their principal aim is to determine the maximum sustainable yield (MSY), represented by the best level of effort, that is the maximum yield that the stock can sustain without affecting its long term productivity (Sparre and Venema, 1998).

Extensions of surplus production models are presented by delay-difference models (Deriso, 1980): these also include biological information, like natural mortality, growth and recruitment. The fact that these methods assume that the population is closed to immigration and recruitment, make them less used (Punt et al., 2013).

Analytical models are generally more diffused than the methods described previously; one of the most widespread methodologies belongs to this category: the Virtual Population Analysis (VPA). VPA approaches (e.g. XSA (Shepherd, 1999), ADAPT (Parrack, 1986; Gavaris, 1988), VPA2BOX (Porch, 2003)) basically use catch-at-age data to derive estimates of stock abundance and fishing mortality by age and year (Gulland, 1965). The word 'virtual' highlights the fact that the resulting population is estimated by the model using real total catch data and estimates of natural and terminal fishing mortality. This method is based on the idea of using the part of the stock that can be fished (the catch) to estimate the population at the sea that allows to obtain such catch (Sparre and Venema, 1998). The stock is rebuilt through a back-calculation from the oldest age and the most recent year assuming no errors in catches. The principal limitations are the need to know precise catch at age data and the absence of uncertainty estimation.

Recently, VPA approaches have been surpassed by Statistical Catch-At-Age (SCAA) models, e.g. ASAP (Legault and Restrepo, 1999), SAM (Gudmundsson, 1994; Berg et al., 2014), a stochastic version of age-structured dynamic models. These models do not present particular limitations, since they are developed using a very flexible framework.

Latest development is represented by Integrated Analysis (IA) models, that are built to include several sources of data into a unique analyses (Maunder and Punt, 2013) (e.g. Stock Synthesis (Method and Wetzel, 2013), CASAL (Bull et al., 2012), Multifan-CL (Fournier et al. 1998)). These methods tend to use input data with reduced pre-processing, for example by inputting catch-at-length and information on growth it is possible to estimate catch-at-age within their framework. They can work both by fixing parameters but can also use stochastic processes and are also able to work with limited and fragmented data sets (although results will be of poor quality). These methods include the possibility of making forecasts and estimating management reference points. Limitations to these approaches could be the complexity of results, the necessity to have high trained computational skills and the need to include information about a number of biological processes which is not always available (ICES, 2012).

1.3.3 Age based vs. length based stock assessment methods

Stock assessment models are aimed at estimating and keeping track of the number of individuals entering each single year, and defined “cohort”. Two categories of methods are available to reach this purpose: length-based and age-based stock assessment models. The approach that best describes the growth of each cohort is heavily influenced by the data available.

Length data are generally easier to collect and to process because they do not require others steps before being used. However, age-based models are the most common in particular for fish species; these rely on otolith readings to determine age. This is true for many species, but for many others the determination of age is complex (e.g. hake) or impossible (e.g. some crustaceans). In these cases length-based methods become essential. Attempts to determine age in crustacean species are being carried out (e.g. Leland et al. (2011), Kilada et al. (2012), Sheridan et al. (2015)), but none of them are yet used in a stock assessment.

Age-based models are preferable whenever possible, because they better describe the concept of cohorts and their progression through time, performing better than length-based models (Hoggarth et al., 2006). To facilitate the use of age-based stock assessment models, a procedure defined age-slicing was developed; this assigns an age-classes to length-classes based on the von Bertalanffy growth parameters and then these data are used as inputs for age-based models. This procedure is useful whenever age determination is not possible. Different age-slicing methodologies are available: from

the simpler, e.g. ELEFAN (Pauly and David, 1981), to the more complex, e.g. MULTIFAN-CL (Fournier et al., 1998), and they are normally used for the stock assessment of some migratory (e.g. swordfish (*Xiphias gladius*), yellow fin tuna (*Thunnus albacares*), Atlantic Bluefin tuna (*Thunnus thynnus*); ICCAT, 2010, 2011, 2012a,b, 2014) and demersal species (e.g. witch flounder (*Glyptocephalus cunoglossus*); ICES, 2012), including hake (*Merluccius merluccius*; Aldebert and Recasens, 1996; GFCM, 2014). However, some concerns are expressed about the use of age-slicing methodologies, because they tend to underestimate recruitment variability and estimate individuals older than they actually are producing incorrect stock evaluations (Goodyear, 1987; Mohn, 1994; Restrepo, 1995; Kell and Kell, 2011, Ailloud et al., 2014). For these reasons, in most recent years efforts have been undertaken to develop length-based models less dependent by age composition.

Initially, stock assessment models able to include both length and age composition were developed. These methods are able to perform an age-slicing within them and give results structured both by ages and sizes. Stock Synthesis (SS; Method and Wetzel, 2013) represents an example of these methods; it incorporates MULTIFAN-CL which allows to input data by size and then estimate stock by age and length. The disadvantage of this kind of method is the fact that some processes, for example selectivity, are modelled by age so they do not change over the time causing a possible misspecification of the stock structure (Punt et al., 2013).

To avoid this problem methods based on size-structure alone have been developed. They track growth from one size class to the next using a transition matrix to describe the probability of animals in a given length to growth into the following length (Hillary, 2011; Punt et al., 2013). This approach is quite common and used for fish (e.g. Hillary et al., 2010), crustaceans (e.g. Punt et al., 1997) and molluscs (e.g. Breen, 2003). The transition matrix can be pre-specified or estimated within the model; if possible the second option is preferable because in this way the transition matrix will be more consistent with the information included in the assessment, and also the uncertainty can be considered (Punt et al., 2013). Length-based models have to be handled with attention because growth estimation by transition matrices makes it harder to identify cohorts, especially if there are big changes in size at age from year to year: this problem can be reduced using tag recapture data, being able to explicitly capture the growth of a given species, without assuming it from a von Bertalanffy growth equation (Punt et al., 2013).

However, when only von Bertalanffy parameters are available, as well as catch-at-length data only for few years, it is possible to apply a Length Cohort Analysis (LCA; Leonart and Salat, 1997), a simplified VPA that assumes that the stock is in a state of equilibrium, that is that biomass gains are compensated by the losses. This methodology, that permits to work directly by length and to take into account different fishing gears, was used a lot in Mediterranean during the 1990's, mainly owing to the lack of long time series of data (Oliver, 2002). Nowadays, with the availability of longer time series of catch data, this methodology is no longer recommended because the steady-state assumption is not realistic and causes some imprecisions, e.g. it can underestimate stock biomass, as well as overestimate fishing mortality. However, when applying this method to short time-series with no strong variations among estimated parameters, quantitative estimations can be considered valid (Rätz et al., 2010).

For the species object of this study (hake and Norway lobster) length-based stock assessment models have been explored and developed. This choice was guided by the fact that reliable age determination is not available for either. Details about single-species stock assessment are given in Chapter 3 for hake and in Chapter 4 for Norway lobster.

1.4 Towards an ecosystem approach to fishery

The Nineteenth Session of the FAO Committee on Fisheries (COFI) of 1991, underlined the need for new approaches to fisheries management that involved not only the conservation of the species subjected to fishing activity but also the related socioeconomic aspects and the protection of the ecosystem in general (FAO, 2003). These objectives were gathered underneath the term ecosystem approach to fisheries (EAF) and ecosystem-based fisheries management (EBFM), and have become common concepts in the 21st century (Garcia et al., 2003; Pikitch et al., 2004). The main aims of these approaches are: “(i) avoid degradation of ecosystem, (ii) minimize the risk of irreversible change to natural assemblages of species and ecosystem processes; (iii) obtain and maintain long-term socioeconomic benefits without compromising the ecosystem, and (iv) generate knowledge of ecosystem processes sufficient to understand the likely consequences of human actions” (Pikitch et al., 2004).

Different models are available to reach these purposes and they can be classified considering the kind of management answer they can generate or considering their complexity (Hollowed et al., 2000; Plágányi, 2007). Regarding management perspectives, ecosystem models can be grouped in: (i) conceptual: aimed to developing knowledge about the processes occurring within the ecosystem considered, (ii) strategic: focused on the development long-term advice, linked to policy goals, and (iii) tactical: directed to the production of short-term advice linked to operational objectives (FAO, 2008; Plagányi et al., 2014). Most of ecosystem models answer conceptual and strategic questions, but the necessity to develop tactical strategies, influencing daily fishing activity, is becoming a primary need for fisheries management (Plagányi et al., 2014).

Taking in account complexity, ecosystem models can be grouped in (Hollowed et al., 2000; Plagányi, 2007):

- i. Extensions of single-species assessment models (ESAM)
- ii. Dynamic multi-species models or Minimum realistic models (MRM)
- iii. Dynamic system models
- iv. Whole of ecosystem models

Extensions of single-species assessment models (ESAM) represent the simplest multi-species approach, because they expand single-species assessment models incorporating only few additional interactions (e.g. Livingston and Method, 1998; Hollow et al., 2000; Tjelmeland and Lindstrøm, 2005). Features of these models are the capability to include predation in a simple way, e.g. modelling it as an alternative fishing fleet (e.g. Plagányi, 2004), and the possibility to model functional predator responses either using simply formulations, e.g. Lotka-Volterra-type (e.g. Hilborn, 1990), or more complex expressions.

On the other side of the spectrum, more complex models are included in the class of dynamic system and whole of ecosystem models. These include approaches taking into account all trophic levels of the ecosystem considered, from primary producers to top predators. Some of the most famous ecosystem models, e.g. ECOPATH with ECOSIM (EwE) (Pauly et al., 2000) and ATLANTIS (Fulton, 2001; Fulton et al., 2004c), are included in these groups.

Ecopath with Ecosim (EwE) is composed by three components: i) Ecopath, a static, mass-balanced snapshot of the system ii) Ecosim, a time dynamic simulation module for policy exploration and iii) Ecospace, a spatial and temporal dynamic module primarily designed for exploring impact and placement of protected areas. The EwE suite can be

used to solve ecological problems, to evaluate the effects of the fishing activity on the ecosystem, to analyse management options, to test the effects of marine protected areas and to evaluate the consequences of environmental variations (Pauly et al., 2000). These features, together with the fact that Ecopath is freely available and has a handy interface, have contributed to its diffusion. Limits of this method are represented by the enormous request of information and the scarce ability in evaluating uncertainty among data (Plagányi and Butterworth, 2004). Anyway efforts have been undertaken to include a Monte Carlo approach within the model (Kavanagh et al., 2004).

ATLANTIS (Fulton et al., 2004c) probably represents the most powerful tool for developing an ecosystem approach to fisheries and is also appropriate for elaborating management strategy evaluation (MSE) studies (Plagányi et al., 2007). ATLANTIS is built to represent each part of the ecosystem in exam: biophysical processes, as well as socioeconomic aspects, industry, assessment and management of the resources, as well as their monitoring. Users can choose the level of complexity, starting from only few groups with simple interactions to more complex models including social and economic aspects. Notwithstanding the multiple functions of Atlantis, this approach has to be used with caution because the level of complexity and the non-linear calculations can produce results distant from the reality (Fulton et al., 2004b).

Other models belonging to this group, but less widespread are represented by OSMOSE (Object-oriented Simulator of Marine ecOSystem Exploitation) (Shin and Cury, 2001; Shin et al., 2004), SEPODYM/SEAPODYM (Spatial Environmental POpulation DYnamics Model) (Bertignac et al., 1998; Lehodey et al., 1998; Lehodey, 2001; Lehodey et al., 2003), IGBEM (Integrated Generic Bay Ecosystem Model) (Fulton et al., 2004a).

Minimum Realistic Models (MRM) gather a group of models characterized by the representation of the most important interactions among a restricted number of important species. The first MRM was developed by Punt and Butterworth (1995), in the form of a model to investigate how predation by seals influenced the stocks of hake living off the South African west coast. A restricted but essential number of functional groups were taken in account: two hake species, seals, a mixed group of fish predated either by hake or seals and also exploited by the fishery and a hake fishery, as suggested by the MRM's philosophy. The advantages of this method are: the use of a dynamic model to describe the seal population and an age-structured population model for hake, the inclusion of cannibalism and predation relationships, the fact that it explicitly

accounts for uncertainty and it is aimed to management issues. This methodology found success among researchers and a number of different models have been developed, e.g. Danielsson et al. (1997), Hvingel and Kingsley (2006), Kinzey and Punt (2009), Blamey (2010).

GADGET (Globally applicable Area-Disaggregated General Ecosystem Toolbox - <http://www.hafro.is/gadget>; Begley, 2005) is also part of MRM's. Inspired by MULTSPEC (Bogstad et al., 1997) and BORMICON (Stefánsson and Palsson, 1998), GADGET is a very flexible framework, aimed at evaluating the interactions between species and the effect of fishing activity above them. It allows the representation of populations by species, size class, age class and it can also take into account different areas and time steps; moreover it incorporates a statistical frame. Its principal limit is the necessity to have enough data to describe feeding relationships, for this reason it is used principally in the North Sea area where these information are available (Taylor et al., 2007; Hanneson et al., 2008).

Multi-species Virtual Population Analysis (MSVPA; Sparre, 1991; Magnússon, 1995) is also included in the MRM class. It provides estimates of fishing and predation mortalities for the species considered, using commercial fisheries catch-at-age and fish stomach-content data as input. This method too requires stomach-content data and this represents its biggest limit. Recently, attempts at developing multispecies statistical catch-at-age models have been pursued: Multi-species Statistical Models (MSM). These are characterised by the inclusion of predator-prey dynamics, thus changes in prey populations affect predator populations and *vice versa*; statistical methods for parameter estimation are included. Jurado-Molina et al. (2005) present an example of this approach.

Dynamic multi-species models also include a wide variety of less diffuse models, e.g. BORMICON (BOReal Migration and CONsumption model) (Stefánsson and Palsson, 1998), CCLAMLR predator-prey models (e.g. Butterworth and Thomson, 1995; Thomson et al., 2000).

Whenever the aim of a study is to answer focused management questions and simpler approaches, such as MRMs and Model of Intermediate Complexity for Ecosystem assessments (MICE; Plagányi et al., 2014), are applicable, it is preferable to develop these kinds of models. They have the benefit of being less data-hungry, they require reduced calculation times and are very flexible: model structures will be those most suitable for the data available and the desired outputs (Fulton et al., 2011).

MICE represent a group of models taking in account a restricted number of species, fundamental to describe the crucial relationships of the ecosystem in exam. Their primary aim is to answer specific tactical management questions (e.g. gear restrictions, seasonal closures, etc.), incorporating the best characteristics of single-species models and the capability to estimate parameters using standard statistical methods. MICE are similar to MRMs, except for the fact that MRMs are not necessarily focused on answering ecosystem problems, the main objective of MICE approaches (Plagányi et al., 2014).

Considering the aim of this research, that is to develop an ecosystem approach to fisheries to evaluate management scenarios for hake and Norway lobster living in the central Adriatic Sea, and the fact that models providing tactical decisions are less diffused but extremely necessary, this study focuses its attention on the development of a MICE.

The MICE approach developed for this study is explained in detail in Chapter 5.

1.4.1. Ecosystem approach to fisheries in Mediterranean Sea

The Mediterranean basin represents a suitable area to develop ecosystem approaches to fishery: different implementations have been carried out during the last two decades.

The most employed methodology is represented by Ecopath with Ecosim (EwE): it has been extensively used in different countries, such as France, Italy, Spain and Greece. France realized EwE models for different ecosystems, from coastal zones (e.g. Leloup et al., 2008) to estuaries (e.g. Rybarczyk and Elkaïm, 2003) and lakes (e.g. Reyes-Marchant et al., 1993), whereas in Spain EwE models are related mainly to marine ecosystems (e.g. Sánchez and Olaso, 2004; Coll et al., 2006; Torres et al., 2013), as well as in Greece (e.g. Piroddi et al. 2010; Moutopoulos et al., 2013). A number of EwE approaches have been realized in Italy and some specifically within the Adriatic Sea (e.g. Carrer and Opitz, 1999; Brando et al., 2004; Libralato et al., 2002; Coll et al., 2007; Coll et al., 2010; Fouzai et al., 2012). For example Coll et al. (2007) developed a complete EwE model to describe the structures and functioning of the food webs characterizing the north and central Adriatic Sea and to evaluate the impact of fishing activity on the entire ecosystem during the 1990s. The results highlighted important features of the area in exam, e.g. the relevant production of plankton by pelagic and benthic organisms, the role of keystone species of low and medium trophic levels (i.e.

benthic invertebrates, zooplankton and anchovy), the importance of microbial food webs. Fishing activity resulted as severely impacting the principal elements of the ecosystem, particularly small pelagic species, that represent the key elements for the Adriatic environment. This, together with changes in oceanographic conditions and other anthropogenic interferences, contributed to modifying the structure and functioning of this ecosystem.

Subsequently, Fouzai et al. (2012) expanded this model to include Ecospace, and this allowed to examine the effects of the creation of marine protected areas within the Adriatic sea, specifically one in the Pomo pit area and the other one northwards. Different scenarios of provisional closing to fishing activity and decrease of fishing effort for both demersal and pelagic fleets were taken in account and resulted in beneficial effects for a lot of commercial species.

Recently, attempts to developing an Individual-based model (IBM) were presented by Zavatarelli and collaborators within the Perseus framework (EU project PERSEUS, <http://www.perseus-net.eu/>). In particular, an OSMOSE (Object-oriented Simulator of Marine ecOSystems Exploitation) approach for the Adriatic Sea was developed. OSMOSE belongs to the class of Dynamic System Models and is characterized by the possibility of representing the dynamics of the species considered, taking in account their spatial movements, and depicting the connection between predators and their prey using size-based opportunistic relationships. Spatial movements of biomass and functional groups are described coupled the Princeton Ocean Model (POM; Blumberg and Mellor, 1987), that is a physical oceanographic model describing circulation dynamics, with the Biogeochemical Flux Model (BFM; Vichi et al., 2007), a model for simulating the dynamics of the pelagic environment in the marine ecosystem. These models were then integrated within the OSMOSE framework, taking into account 11 commercial species, e.g. European pilchard, European anchovy, horse mackerel, etc., and related data from 1990 to 2000. Results of this study highlighted the fact that the model seemed to work well estimating the biomass evolution of the species in exam, but some disagreement between observed and modelled values are shown, suggesting the need of some adjustments (EU project PERSEUS).

1.5 Aims and objectives

In line with an ecosystem approach to fisheries, the main aim of this study is to construct a Model of Intermediate Complexity for Ecosystem assessments (MICE) for use in developing an ecosystem-cognisant approach to evaluating different management scenarios for the hake and Norway lobster bottom trawl fishery in the central Adriatic Sea.

Chapter 2 introduces a series of important concepts related to the preparation of the data required for subsequent steps of the study. In particular, the fact that the study area is only a part of the entire management area (GSA 17), has required that official data collected for the Adriatic Sea (catches, landings, discards, trawl surveys) be subdivided according to the area of interest. Italian landings and discards data for both target species were thus scaled to the study area using information coming from the Vessel Monitoring System (VMS). In addition more complex single species stock assessment methods applied to the target species, as well as the MICE model, also needed information coming from fishery independent methods, represented by scientific surveys. VMS and scientific surveys are the objects of Chapter 2.

The target species of this study are then tackled in two separate chapters: Chapter 3 for European hake and Chapter 4 for Norway lobster. Each of these chapters contains information about distribution and biology of the species target, as well as the single-species stock assessment models used to evaluate the state of these resources in the study area.

Chapter 5 represents the fulcrum of the study; here all the steps required to develop the MICE model are explained in detail. The chapter starts with a description of the conceptual MICE model, where the importance of considering the prey of the target species (the predators) is pointed out. The construction of the model is then described in a stepwise manner finishing with the description of the management scenarios tested. Considering that the effects of the new EU discard ban (EC, 1380/2013) are evaluated, a paragraph is dedicated to the survival probability of discards. Finally, predator and prey dynamics are put together to test the different management options.

Conclusions, as well as, improvements and pitfalls of this study are discussed in chapter 6.

CHAPTER 2 – Data preparation

A number of data sets were shared by the various sections of this work and were prepared using the same methods across sections. To avoid unnecessary repetition these data sets and the methods functional to their use within both single-species assessments and the MICE model are described in this section.

2.1 The Data Collection Framework

The Data Collection Framework (DCF) was established by the European Union (EU) in 2000 and reformed in 2008 (EC 1543/2000; EC 199/2008; EC 665/2008). It establishes the collection and management of a wide range of fisheries data essential for producing management advice. Each country belonging to the European Union has to establish a National Program for the collection of data requested by the DCF program.

DCF requires both data pertaining to the fishing activity and data from scientific surveys, e.g. MEDITS survey (see section 2.3). Fishing data consists of information strictly related to the fishing activity (e.g. number of vessels, fishing days), biological data (e.g. length frequency distribution of landings and discards, growth parameters, age structure of the exploited population) and economic variables. This study takes in account biological data in particular, with the aim of: i) evaluating the length composition of the most important commercial species, defined target species, ii) estimating the biomass at sea of these target species, iii) determining relevant aspects of their biology, e.g. parameters from the length-weight relationship, growth parameters, sex ratios, and iii) estimating the impact of the fishing activity using specific indicators (EC 949/2008).

Collection of biological data foresees both on board activities and laboratory procedures. Activity on board is carried out by observers, technical staff in charge of monitoring fishing operations; more specifically they have to collect data regarding the position and duration of hauls, as well as record the length composition of the target species and, activity of particular relevance, report discards. The term ‘discards’ is referred to the part of the catch that is returned to sea, dead or alive, for one reason or another (FAO, 1996). Reasons for discarding can include, for example, the achievement of the fishing quota, catching undersized individuals, as well as illegal species or species with no commercial value (Kelleher, 2005). Usually, information about discards

is scarce for reasons related to insufficient attention in sampling this part of catches, especially in less recent years, and because, overall, Mediterranean fisheries discard very low amounts of individuals. These reasons highlight the importance of collecting information about discard (i.e. amount of discarded species, species composition of discard, length compositions of discard).

Landings are the portion of catches landed and sold. Data regarding landings too are collected under the DCF and are analysed both on board, using the same procedure explained for discard, and in the laboratory. Laboratory activities foresee the monthly sampling of a commercial fishing box for each target species following a predetermined procedure: 1) selection a representative sample, 2) measurement of all individuals included in the sample towards the generation of length frequency distributions (LFD), 3) record biological parameters (e.g. individual weight, sex and maturity if possible) on a sub-sample of the box, and 4) where relevant (teleost species), extract otoliths for age determination.

Landings quantities are also needed, by fishing gear, region, GSAs, month, etc. Government institutions provide to fulfil this task, together with the collection of the requested economic variables.

In the case of countries including more than one GSA, as is Italy, biological sampling is carried out by the different scientific units operating within each GSA. Italian data from GSA 17 are collected by the CNR-ISMAR Ancona, while Croatian data are collected by the Croatian Institute of Oceanography and Fisheries (IOF) in Split.

Croatia joined the European Union in 2013, however data from previous years are available owing to the fact that the Croatian government had established a data collection system similar to the one requested by the EU.

All the data described above are sent to European Commission annually; their uses include stock assessments for the provision of management advice.

Here, a general explanations about the origin of data used in this study was given. However, each of the following chapters include a data section given more details about the data employed for developing each step of this study.

2.2 The Vessel monitoring system (VMS)

The Satellite-based Vessel Monitoring System (VMS), also known as “blue box”, is a system that keeps track of fishing vessels and transmits information on vessel position, speed and heading periodically and automatically. All the fishing vessels with a Length Overall (LOA) ≥ 12 meter have to be equipped with VMS, as requested by European Regulation (EC) No 1224/2009.

VMS was first introduced in 2006 and represented an innovation in fisheries science, since it allows the collection of spatial information about fishing activity, without any interference from the fishermen, to be used both for monitoring fishing vessels and for research purposes (Bertrand et al., 2007; Deng et al., 2005).

The collection of these data prompted the development of platforms necessary for their analysis, such as the VMStools package (Hintzen et al. 2012). Unfortunately, this package was set up to analyse data organized as requested by ICES and this setting resulted to no particular use for investigating data coming from the Mediterranean sea, which are multi-gear and multi-species (Russo et al., 2014a). This factor favoured the development of a VMS package specific to process Mediterranean data, VMSbase (Russo et al., 2014a).

VMSbase allows the processing of data from both VMS and logbooks. Logbooks are electronic devices in which masters of EU fishing vessels with LOA ≥ 12 meter have to report information about fishing operations, notably landings of each fished species (EU 404/2011). Data from logbooks are stored in an SQL database, that it easily connected to VMSbase from the R platform. VMSbase allows the visualization of information through plots, also including accessory information requested by the user (e.g. bathymetry, GSA border, etc.) in the graphical outputs. The usefulness of this tool is already confirmed by recent approaches carried out in the Adriatic sea (Scarcella et al., 2014) and in the Strait of Sicily (Russo et al., 2014b), that investigated relationship between fishing effort and resource abundance.

The utility of this tool was also proven in this study, in which VMS data were used to characterize the behavior of Italian fishermen within the study area. In particular the activity of bottom trawlers was considered, since represents the main gear exploiting hake and Norway lobster in the study area. The principal aim of this part of work was to estimate a proportion of species-specific effort exerted in the study area in order to use it to scale landings for the whole GSA 17 to the study area only, this was not possible

before the development of this technology because catch data were collected by harbour without any specific geographical information on the area, and also to investigate the distribution of the exploitation pattern within the study area to facilitate the possible application of spatial management measures (not tested within this study). The workflow foresaw, firstly the identification of different fishing grounds based on bathymetry and the territorial and extraterritorial border lines within the study area, second fishermen behaviour was investigated based upon the time spent by fishermen within each of these fishing grounds (Fig. 2.1). This was translated into a fishing pattern (FP) for each fishing ground (Fig. 2.1). Fishermen were found to concentrate their activity close to the Italian coast (fishing patterns 5 and 8) and in the western Pomo/Jabuka pit (fishing patterns 1, 2, 3 and 6), but the percentage of fishing activity occurring in the eastern part of the study area (fishing patterns 7 and 10) was also relevant (Fig. 2.1).

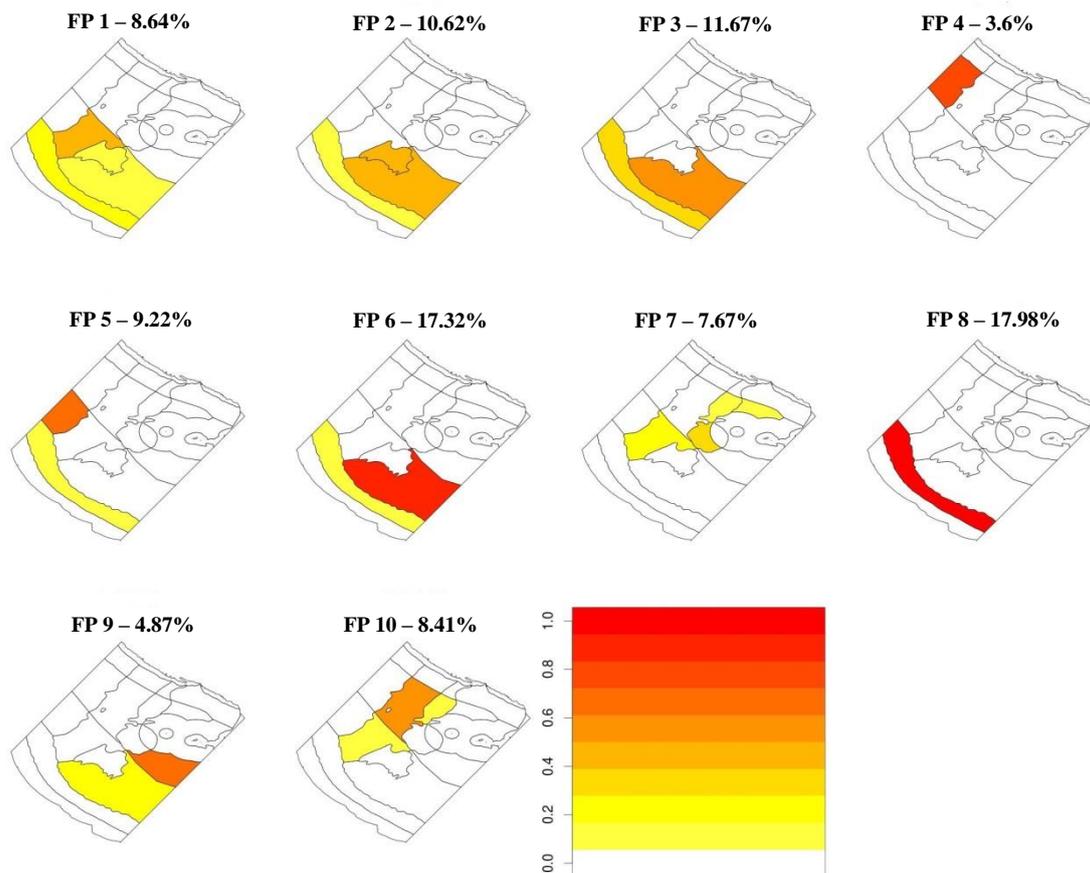


Fig. 2.1 Characterisation of fishing patterns (FP) in each fishing ground within the study area using VMS data. Source: VMS data (Russo et al., in preparation)

It was also possible to investigate the role of season in driving fishing patterns. Only the fishing patterns accounting for percentages greater than 5% were considered and this resulted in a higher exploitation of the study area in spring and autumn (Fig. 2.2).

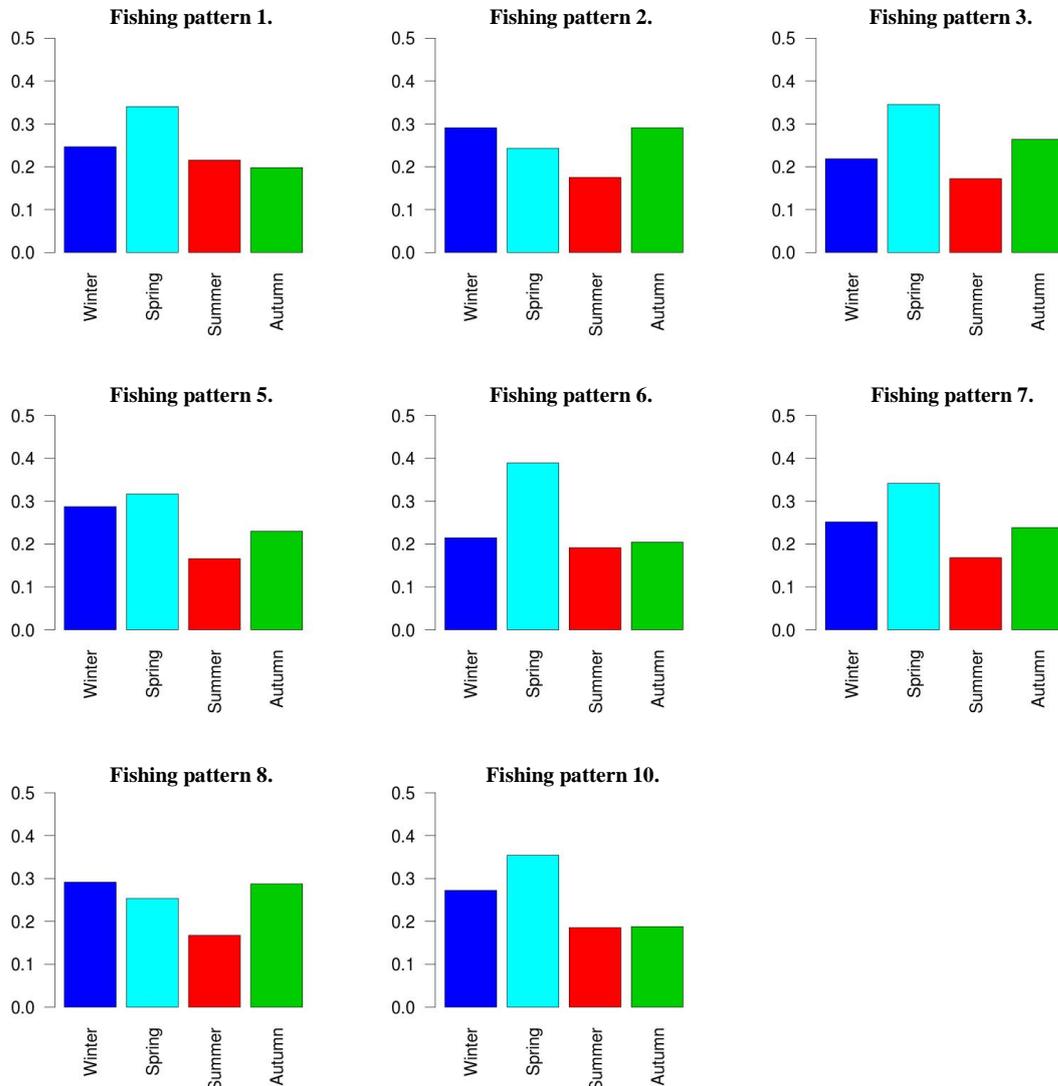


Fig. 2.2 Seasonal exploitation for each fishing pattern with a percentage higher than 5%. Source: VMS data (Russo et al., in preparation)

The final step of this analysis was directed towards the estimation of fishing effort, in number of fishing hours, for the study area and for each year considered in this study (2006 – 2013) (Fig. 2.3). The study area resulted as being exploited mainly in the last most recent years, while 2006 and 2008 showed the lowest exploitation both for the study area and the whole GSA 17 (Table 2.1). The study area accounted for *ca.* 30% of the total fishing effort of GSA 17; yearly values were used to scale annual Italian total landings into annual landings for the study area alone.

Table 2.1. Yearly fishing effort (number of fishing hours) for GSA 17 and the study area, and estimation of the percentage of effort allocated in the study area alone.

Years	2006	2007	2008	2009	2010	2011	2012	2013
Fishing hours GSA 17	66504	150417	57436	82204	142727	105208	161212	188420
Fishing hours study area	206525	461130	195004	264931	464467	324495	450840	487706
Percentage fishing hours Study area/fishing hours GSA 17	32.20	32.62	29.45	31.03	30.73	32.42	35.76	38.63

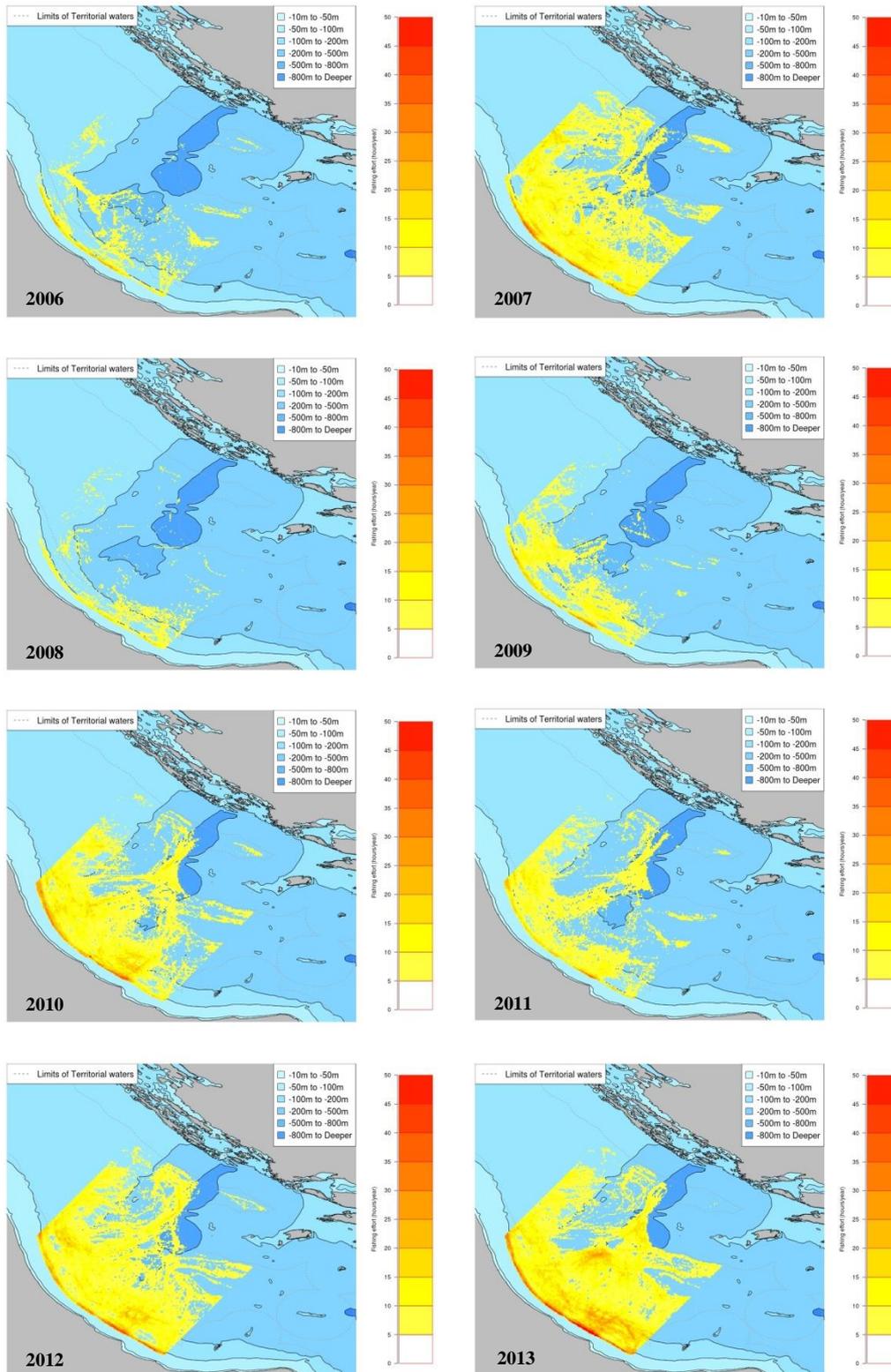


Fig. 2.3 Fishing effort (number of fishing hours) for the study area from 2006 to 2013. Source: VMS data (Russo et al., in preparation)

2.3 Scientific surveys

Stock assessment makes use of both direct (fishery independent) and indirect (fishery-dependent) methods for collecting data regarding different portions of the populations at sea. Indirect methods involve information from the commercial fishing activity, whereas direct methods comprise data collected during scientific surveys and providing estimates, independent of fishing activity, of abundance at sea and demography of the resources into the sea. Direct methods are characterized by the use of standardised sampling methods, towards the analysis of trends in the population without the influence of fishing practices. Moreover information from scientific surveys is essential within stock assessment methods, since it is used for tuning the assessment model to the perceived total abundance at sea and improve the reliability of results.

Scientific surveys are set up based on the specific resources investigated. For example, in the Adriatic Sea different surveys are carried out: the MEDITS survey is a trawl survey with the objective of gathering information on the state of the main demersal stocks, the SOLEMON survey is beam trawl survey with the principal aim of investigating flatfish resources and sole in particular, MEDIAS is an echo-survey to assess the abundance of small pelagic stocks, the underwater TV survey (UWTV) is a camera survey with the aim of investigating the population of Norway lobster in the Pomo/Jabuka pit area. Some of these surveys, i.e. MEDITS and MEDIAS, are included in the DCF framework.

The Adriatic sea has been covered by many scientific surveys. The oldest survey was the Expedition Hvar (1948 – 1949); this was followed by other surveys which didn't cover areas or periods relevant to this study.

The first systematic seasonal survey, the GRUND (GRUpo Nazionale Demersali or Pipeta Expedition at the beginning of the time series) survey, started in 1982 with the aim of monitoring the demersal communities of the Adriatic Sea. The sampling procedure foresaw two surveys using a commercial net, one in spring the other in autumn. In 1994, a European spring/summer survey, the MEDITS survey, started, and thus GRUND was carried out only in the autumn/winter period up to 2007 when it ceased. The longest time series is represented by the Italian and extraterritorial autumn/winter survey, while Croatia waters were sampled sporadically. Over the years the survey scheme was modified; of particular relevance was that in 2000 the net was increased in size due to a change in engine power of the vessel performing the survey; it

is thus preferable to split the Italian GRUND for GSA 17 into two surveys: one from 1982 to 1999 and the other from 2000 to 2007. The abundance indices for hake and Norway lobster in the last year for the GRUND, 2007, are mapped out in Figure 2.4.

The MEDITS (MEDiterranean International Trawl Survey) survey is an extensive trawl survey carried out by all European countries of the Mediterranean since 1994 and funded by the European Union. Italy has participated from the beginning, while Croatia, Albania and Slovenia joined the programme in 1996. The aim of this survey is to obtain a snapshot of fish and crustacean populations living at sea; for this reason a common sampling gear able to work in all areas and with low selectivity is used. The sampling protocol is shared by all participating countries (Bertrand et al., 2002). Stations were selected on the basis of a stratified scheme with random selection of stations in every stratum (10-50m; 50-100m; 100-200m; 200-500m and over 500m), the number of stations in each stratum is proportional to the surface area of the stratum. This survey takes place every year in spring. The most recent abundance index maps for hake and Norway lobster are shown in Figure 2.5.

Details of the specific survey data employed in this study are given in Chapter 3 for hake and Chapter 4 for Norway lobster.

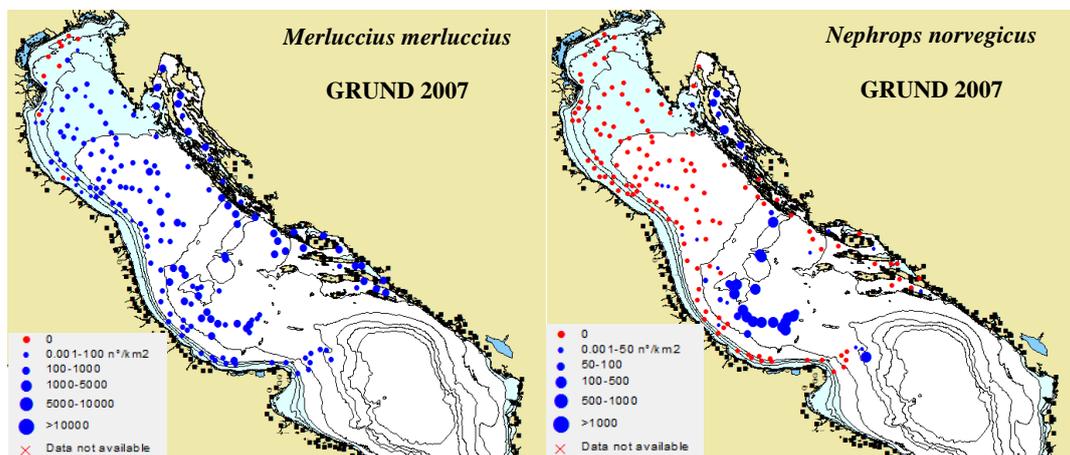


Fig. 2.4 Maps of abundance (N/km²) of hake (*Merluccius merluccius*) and Norway lobster (*Nephrops norvegicus*) from GRUND survey 2007.

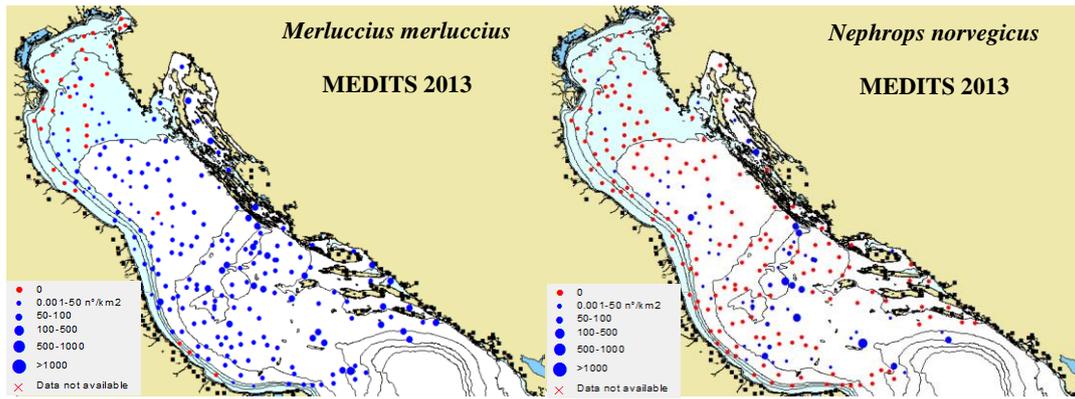


Fig. 2.5 Maps of abundance (N/km²) of hake (*Merluccius merluccius*) and Norway lobster (*Nephrops norvegicus*) from MEDITS survey 2013.

CHAPTER 3 – European hake

European hake, *Merluccius merluccius* (Linnaeus, 1758) (Fig. 3.1), is the most important demersal species in the Adriatic Sea in terms of both catches and commercial value (IREPA, 2012; UNEP-MAP-RAC/SPA, 2014). It is distributed from the north-eastern Atlantic (Norway to Mauritania) to the entire Mediterranean and along the southern coast of the Black Sea (Jardas, 1996; Relini et al., 1999) (Fig. 3.1). In the Adriatic Sea, with the exception of a small area northern of the Po river, European hake is found from several meters depth in coastal areas to the 800 m of the south Adriatic Pit (Kirinčić and Lepetić, 1955; Županović and Jardas, 1986; Ungaro et al., 1993; Jukić et al., 1999).

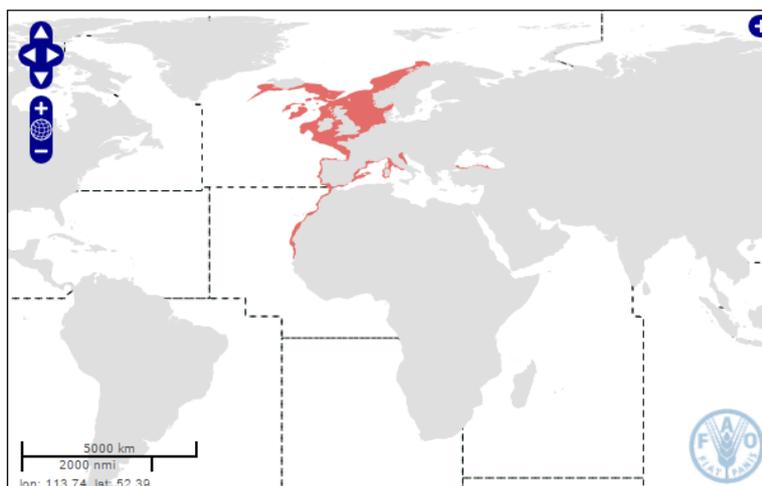


Fig.3.1 Geographic distribution of European hake, *Merluccius merluccius*. Source: FAO, 2005

<http://www.fao.org/fishery/species/2238/en>

3.1 Hake in the Adriatic Sea

3.1.1 Species description

Merluccius merluccius is a Gadiform fish of the Merlucciidae family (Fig. 3.2).

Taxonomy:
Phylum *Chordata*
Class *Actinopterygii*
Order *Gadiformes*
Suborder *Gadoidei*
Family *Merlucciidae*
Subfamily *Merlucciinae*
Genus *Merluccius*
Species *M. merluccius*

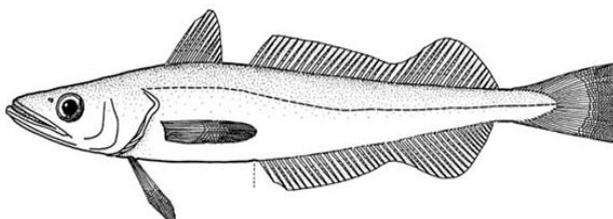


Fig. 3.2 *Merluccius merluccius* (Linnaeus, 1758). Source: FAO, 2005

<http://www.fao.org/fishery/species/2238/en>

Compared to other hake species, *M. merluccius* has a longer and rather slender body, with its widest part located behind the head. It is characterized by a large mouth, two dorsal fins (one short and triangular, and the second elongated) and one anal fin similar in shape and size to the second dorsal fin; the ventral fins are placed anteriorly to the pectorals, and the caudal fin is cut in a straight line. Coloration is dark grey dorsally and lighter laterally, whereas the belly is whitish (Relini et al., 1999).

Genetic studies show the presence of different populations between Atlantic and Mediterranean, and within the Mediterranean three lineages have been identified: western, central and eastern Mediterranean (Cimmaruta et al., 2005; Milano et al., 2014). One single population is described for the Adriatic Sea and also confirmed by studies on the vertebral count (Maurin, 1965; Piccinetti and Piccinetti- Manfrin, 1971), as well as by the genetic results of the MAREA StockMed project (Fiorentino et al., 2014).

3.1.2 Habitat and behavior

European hake is a nectobenthonic species (Carpentieri et al., 2005; Mahe et al., 2007). It does not show sediment preference, although in the Adriatic Sea the densest population was found on fine and tenacious clayey substrata and muddy bottoms (Karlovać, 1959).

In the Adriatic Sea the most abundant population is located at depths between 100 and 200 m, specifically in the area of the Pomo/Jabuka Pits, where catches are mainly composed of juveniles (Ghirardelli, 1959; Županović, 1968; Jukić and Arneri, 1984; Flamigni, 1983; Giovanardi and Rizzoli, 1984; Bello et al., 1986; Županović and Jardas, 1989; Ungaro et al., 1993; Vrgoč, 2000). This area is considered a nursery ground for this species (Županović and Jardas, 1986; Mediterranean Sensitive Habitats, 2013).

Hake performs migrations. Migrations to the more shallow coastal waters of Croatian channels occur in spring during the spawning season (details about spawning are given in section 3.1.4), whereas in winter adults, together with juveniles, move to deeper waters of the central Adriatic in search of food (Županović and Jardas, 1989). Diurnal migrations are associated to feeding: during the day they lie on the bottom and move to higher strata at night, in search for food. This pattern of diurnal and seasonal migrations appears to considerably affect catches, generating the highest catches in the first haul after sunrise (Županović, 1968). Moreover, catches appear to increase a few years after the ingression of more saline, warmer waters from the Mediterranean basin: these are

thought to trigger an increase in primary production (Buljan, 1953, 1957; Zore-Armanda, 1963, 1969, 1984), enhancing the survival probability of larvae and postlarvae (Županović, 1985) which ultimately have the effect of enhancing catches.

3.1.3 Age determination

Otoliths (ear bones) are commonly used to determine age in individuals of teleost fishes. Three pairs of otoliths exist, the largest being the *sagittae*, (Fig. 3.3). In hake these have a complex macrostructure, probably due to the long spawning season and their migration patterns. These life history events such as spawning and migrations result in the deposition of several translucent and opaque rings per year making their interpretation difficult.

Despite the progress made in recent years, an accurate and agreed methodology for ageing of hake *sagittae* has yet to be developed (De Pontual et al., 2006; Piñeiro et al., 2007).

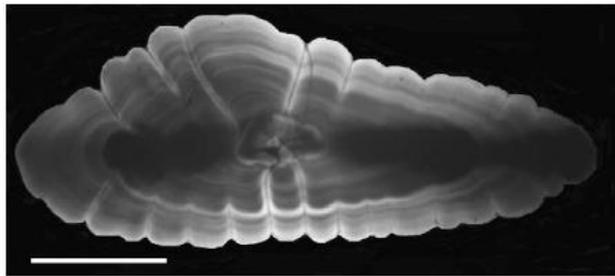


Fig. 3.3 Frontal section of the *sagitta* of *Merluccius merluccius*. Source Belcari et al., 2006

3.1.4 Growth, size and sexual maturity

Literature reports maximum total lengths for the Adriatic of 107 cm (Grubisić, 1959); however, catches are usually composed of individuals from 10 cm to 60 cm (Vrgoč et al., 2004).

European hake is a long-lived species that, in the Mediterranean, can live more than 25 years (Vitale et al., in press). Despite this, the exploited population in the Adriatic Sea is mainly constituted by individuals of 0, 1 and 2 years of age, with a maximum age of 8 years (Ungaro et al., 2001; Vrgoč et al., 2004).

Females attain larger sizes than males, whose growth generally slows down after reaching sexual maturity (3 - 4 years old) (Vrgoč et al., 2004). Consequently, males are better represented in the smaller length classes, whereas the larger sizes comprise mostly females. In the northern and central Adriatic Sea in particular, females dominate

the population from the length of 30-33 cm and Vrgoč (2000) observed that trawl catches over 38-40 cm are mainly composed by females.

Hake growth is a debated point. As stated in the previous paragraph, there is no agreement on the ageing methodology, and this has produced various sets of von Bertalanffy growth parameters than can cause uncertainty in the definition of growth patterns for this species. Literature referred to the central and eastern Mediterranean sea mostly reports von Bertalanffy k parameters (an indication of the growth rate) close to 0.1 y^{-1} (e.g. Papaconstantinou and Stergiou, 1995; Fiorentino et al., 2000; Vrgoč, 2000), highlighting a slower growth compared to k parameters coming from the western Mediterranean and the Atlantic Ocean which are close to 0.2 y^{-1} (e.g. Alemany and Oliver, 1995; Garcia-Rodriguez and Esteban, 2002). Recent tagging studies, carried out in the Gulf of Lions, support the thesis that hake is a fast growing species (Mellon et al., 2010) and this theory has also been followed for producing current management advice (e.g. hake stock assessments presented at the GFCM 2014). However, Mellon et al. (2010) also highlighted the fact that European hake grow faster in the Atlantic than in the Mediterranean and differences between these two stocks are also supported by genetic variations between the Atlantic and Mediterranean hake populations, as well as by the fact that environmental factors, such as temperature and food availability, can influence the growth pattern of this species (Cimmaruta et al., 2005). Moreover, a recent work by Vitale et al. (in press) has demonstrated a much higher longevity of hake, suggesting that the issue of the description of the growth of hake it is still open. Considering these observations, and pending a decision regarding hake growth in the Adriatic Sea, for this study we selected a set of growth parameters coming specifically from the study area (Table 3.1). These growth parameters support the slow growth theory which also provides a more conservative perception of the situation.

Spawning is another debated point, since hake spawn throughout the year in the Adriatic Sea with different intensities and peaks in summer and winter (Karlovać, 1965; Županović, 1968; Županović and Jardas 1986, 1989; Jukić and Piccinetti, 1981; Ungaro et al., 1993). The earliest spawning occurs in winter in the deeper waters of the Pomo/Jabuka Pits. Then, as spring and summer approach, spawning occurs in progressively shallower waters. Recruitment does not seem to be strictly related to the parental stock size (Alegria Hernandez and Jukić, 1992). It has two peaks, one in spring and second in summer, linked to the intensity of the spawning occurring in the central Adriatic Sea (Županović and Jardas, 1989). Hake larvae have been found from October

to June, with a peak between January and February (Karlovać, 1965). Larvae and postlarvae have mainly been reported between 40 m and 200 m depth, and particularly concentrated between 50 m and 100 m in the Adriatic Sea. In the Pomo Pit, hake at a length of 16 mm and an age of approximately 40 days change from the pelagic to the demersal phase, close to the area of concentration of juveniles (Arneri and Morales Nin, 2000).

Sexual maturity is reached at lengths between 20 cm and 28 cm for males and between 23 cm and 33 cm for females.

3.1.5 Food

Hake is a night predator (Hickling, 1927; Casey and Pereiro, 1995; Bozzano et al., 2005). Juvenile hake (< 14 cm TL) prefer crustaceans but, as they grow, they start feeding on small and medium-sized fish and cephalopods, and adults exhibit cannibalistic behaviour (Karlovać, 1959; Jukić, 1975; Bozzano et al., 2005; Stagioni et al., 2011).

Studies on the diet of hake in the Adriatic Sea report *Sardina pilchardus*, *Engraulis encrasicolus*, *Scomber scombrus*, *Boops boops*, *Trachurus spp.* and *Sprattus sprattus* as main fish prey (Karlovać, 1959; Županovic, 1968; Stagioni et al., 2011). *Maurolicus muelleri* is the only fish species eaten by juveniles, particularly in the Pomo Pit area (Frogliia, 1973). A wide variety of crustacean species are reported as prey (Karlovać, 1959; Jukić, 1975; Bozzano et al., 2005; Stagioni et al., 2011), with decapods and benthic species being particularly relevant in the Adriatic Sea (e.g. *Processa sp.*, *Solenocera membranacea*, *Alpheus glaber*, *Munida intermedia*) (Karlovać, 1959; Jardas, 1976). Juvenile hake prefer Euphasiaca, Mysidiacea and Amphipoda (Frogliia, 1973). The presence of this kind of crustacean in the diet of smaller hake has also been observed in other areas, e.g. *Meganyctiphanes norvegica* is also reported in the northern Atlantic (Hickling, 1970), and pelagic crustaceans are also consumed off the Levantine coasts of Spain (Larrañeta, 1970). Cephalopoda are reported in smaller percentages and the most represented species for the Pomo Pit area are *Alloteuthis subulata* and *Sepiola sp.* The consumption of other classes, for example, Polychaeta and Echinodermata are negligible and traces of unidentified species have also been found.

3.1.6 Predators

The literature reports scarce information on predators for hake. The only species mentioned as hake predators are some Gadidae (e.g. *Gadus morhua*, *Merlangius merlangus*) in Norway (Bergstad, 1991; Hislop et al., 1991), Rajidae (e.g. *Raja Clavata*) in the UK (Holden et al., 1974), and Carangidae and Congridae in the Mediterranean (Casadevall and Matallanas, 1990; Matallanas et al., 1995). In the Adriatic Sea the only reported hake predators are *Trachurus mediterraneus* (feeding on hake juveniles) and *Scyliorhinus caninula* (Šantić et al., 2003; 2012).

3.1.7 Economic importance and fishing methods

The hake stock in the Adriatic Sea is shared by Italy, Slovenia, Croatia (Yugoslavia before 1992), Serbia, Montenegro and Albania; Italy takes the lion's share, at 70% of total Adriatic catches. Total commercial catch has fluctuated throughout the years, attaining a peak of 9433 tonnes in the mid 1980s; in 2013 total catch was over 3000 tonnes (Fig. 3.4). Based on our estimates, 30% of Adriatic hake catches come from the Pomo/Jabuka pits and they mainly comprise juveniles (< 30 cm TL; details are given in paragraph 3.2.1).

Bottom, otter, trawls are the main gear used to fish hake in the northern central Adriatic Sea, but Croatia also has an important long - line fishery targeting larger individuals (Vrgoč et al., 2004). Italy has an important fleet of long-liners operating mainly in southern Adriatic which occasionally fish in the northern part.

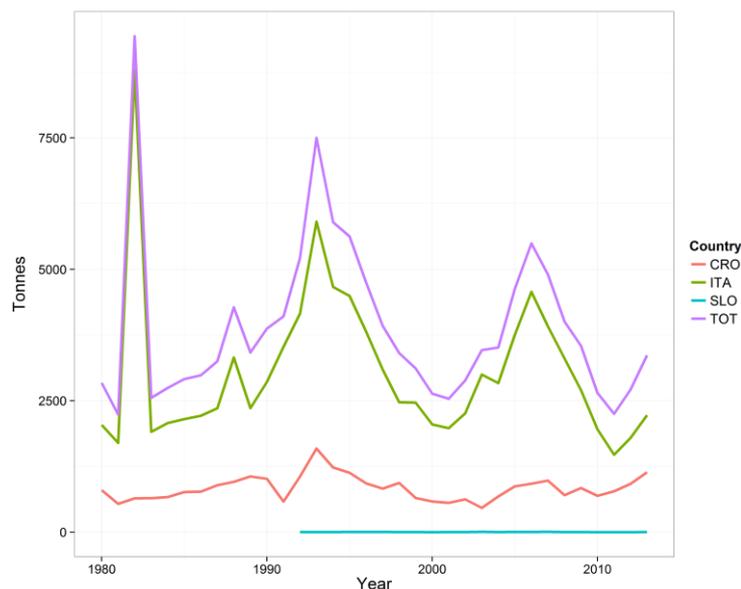


Fig. 3.4 Catches of hake for the northern and central Adriatic Sea by year and country: CRO (Croatia, Yugoslavia before 1993), ITA (Italy), SLO (Slovenia), TOT (all country). Source: FishStatJ, 2015.

3.2 Stock assessment

3.2.1 Data

Hake is considered as a single stock in the entire Adriatic Sea (Maurin, 1965; Piccinetti and Piccinetti- Manfrin, 1971; Fiorentino et al., 2014), although for management purposes it has been split into two stocks, one inhabiting the northern and central Adriatic Sea (GSA 17) and the other one living the southern Adriatic (GSA 18), according to the FAO Geographical Sub Areas (GSA). The study area is located within GSA 17 and includes the Pomo/Jabuka pits (Fig. 1.4); which is the main nursery and spawning area for hake in GSA 17.

The study area is exploited only by a part of the Adriatic trawl fleet. For this reason catch data were calculated only considering the fishing harbours known to exploit it: Ancona, San Benedetto, Martinsicuro, Giulianova, Pescara and Termoli for the Italian side and Split and Šibenik for the Croatian side (Fig. 1.4). Commercial length frequency distributions (LFDs) were obtained from DCF samples from San Benedetto and Giulianova between 2006 and 2013. Considering the peculiarity of the Pomo/Jabuka pits and assuming Italian and Croatian trawl fleets to have the same selectivity, Italian LFDs were applied to Croatian catches. LFDs are available both for landings and discards, they are expressed in total length (TL, cm) and individuals larger than 40 cm TL were grouped into one final length class forming a so-called “plus group”.

The time series considered in this study goes from 2006 to 2013. Input data for the stock assessment are summarized in the following sections:

- Growth

Considering the available literature and the biological data coming from CNR-ISMAR Ancona, the growth parameters listed in Table 3.1 were selected.

Tab. 3.1 Von Bertalanffy Growth Function (VBGF) for hake. Notes: L_{inf} – asymptotic length at which growth is zero, k – growth rate, t_0 – age at which the organisms would have had zero size, a – y-intercept of length-weight relationship, b – slope of length-weight relationship.

Parameter	Value	Source
L_{inf} (cm)	92.83	Alegria-Hernandez and Jukić, 1990
k y^{-1}	0.067	Alegria-Hernandez and Jukić, 1990
t_0	-0.629	Alegria-Hernandez and Jukić, 1990
a	0.01	Arneri et al., 2006
b	2.88	Arneri et al., 2006

- Mean weight at length

The mean weight at length was derived from biological samples of catches. It represents an essential information for estimating biomass and abundance of the stock in consideration.

Tab. 3.2 Weight-at-length in kg per year.

TL cm	Year								
	2006	2007	2008	2009	2010	2011	2012	2013	
6	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	
8	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	
10	0.008	0.008	0.008	0.008	0.008	0.009	0.008	0.008	
12	0.013	0.013	0.013	0.013	0.013	0.013	0.013	0.013	
14	0.021	0.021	0.021	0.021	0.020	0.020	0.020	0.021	
16	0.030	0.031	0.030	0.031	0.031	0.032	0.030	0.031	
18	0.041	0.043	0.042	0.043	0.044	0.042	0.047	0.042	
20	0.057	0.061	0.059	0.060	0.061	0.058	0.067	0.060	
22	0.079	0.080	0.079	0.080	0.080	0.076	0.083	0.081	
24	0.099	0.102	0.101	0.103	0.104	0.104	0.105	0.104	
26	0.123	0.133	0.128	0.130	0.132	0.131	0.136	0.131	
28	0.155	0.162	0.159	0.162	0.165	0.166	0.170	0.159	
30	0.198	0.210	0.204	0.203	0.202	0.208	0.202	0.195	
32	0.239	0.251	0.245	0.248	0.251	0.250	0.257	0.246	
34	0.237	0.295	0.266	0.287	0.308	0.307	0.309	0.309	
36	0.254	0.343	0.298	0.327	0.355	0.351	0.343	0.371	
38	0.260	0.340	0.419	0.425	0.414	0.437	0.406	0.398	
40+	0.571	0.573	0.573	0.579	0.567	0.592	0.518	0.592	

- Catches

Catches include hake fished in the study area only. Italian landings for the entire GSA 17 were split using VMS data (details are given in section 2.2) whereas for Croatia it was assumed that 40% of total Croatian landings were caught in the study area (N. Vrgoč, pers. comm.) and this proportion was applied to derive landings for all years. In 2012 and 2013 Italian DCF sampling of catches reported discards. To estimate discards when data were not collected (2006-2011), a proportional value was added to the landings of each year for which discards were not quantified. Assuming Italian and Croatian fleets have the same

selectivity, the Italian discard ratio was also applied to Croatian landings for each year.

The Italian catches estimated for the study area exhibit a fluctuating decreasing trend, last peak of the considered time series is reported in 2006, after this year a continuous decreasing trend to 2011 is described, followed by an increase in 2012 and 2013. Croatian catches appear to have been low and stable throughout the years, with a slight increase in recent years (Fig 3.5)

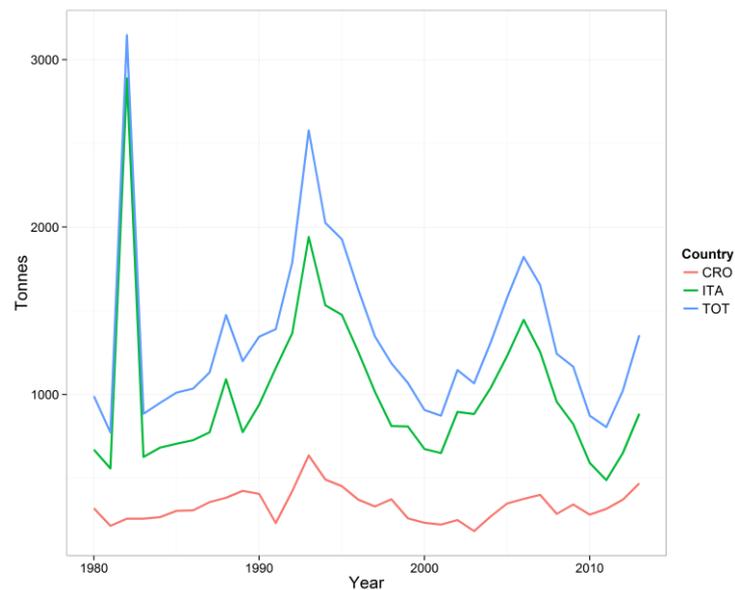


Fig. 3.5 Estimated catches for hake in the study area from 1980 to 2013: total (TOT, blue line); Croatian (CRO, pink line) and Italian catches (ITA, green line).

- Length frequency distributions

The LFD of the catches considered in this study describe a continuous decreasing trend over the years, with 2006 being the most abundant year (Fig. 3.6). Examining the shape of the LFD in the various years, the first three years (2006, 2007 and 2008) show an almost unimodal distribution with peaks between 16 cm and 24 cm TL; from 2009, LFDs appear to be more fragmented with multiple peaks. Larger individuals (> 36 cm) are the least represented for all the time series considered and particularly in 2006 and 2007.

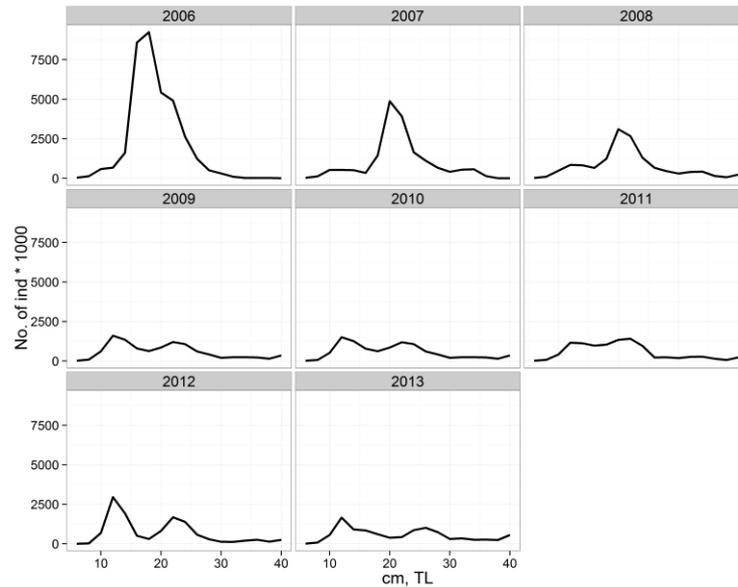


Fig. 3.6 Length Frequency Distributions (LFD) of European hake catches in the study area for years from 2006 to 2013.

- Natural mortality and maturity

Natural mortality (M) was estimated using PRODBIOM (Abella et al., 1997; 1998) (Tab. 3.3): a methodology that allows the estimation of a natural mortality vector at age starting from growth information (Tab. 3.1). Growth information is essential for the calculation of overall biomass losses and overall production in the unfished population, and the rate at which these are balanced correspond to the M at age. PRODBIOM is developed in such a way as to allow a natural mortality vector by length to be extracted (Tab. 3.3).

Table 3.3 also reports the maturity vector, representing the proportion of mature individuals per length class, by length considered in the study (Vrgoč et al., 2004).

Tab. 3.3 Natural mortality vector (M) by length obtained using Prodbiom (Abella et al., 1997; 1998) and the proportion of individuals mature at each length (Mat).

Length (cm. - TL)	M (yr ⁻¹)	Mat
6	0.759	0
8	0.759	0
10	0.759	0
12	0.759	0
14	0.386	0
16	0.386	0
18	0.386	0
20	0.386	0.5
22	0.263	0.5
24	0.263	0.5
26	0.263	0.5
28	0.219	1
30	0.219	1
32	0.219	1
34	0.195	1
36	0.195	1
38	0.195	1
40+	0.181	1

- Survey data

Survey data were obtained from the GRUND survey (see section 2.3) and the MEDiterranean International Trawl Survey (MEDITS, Bertrand et al., 2002; see section 2.3).

The GRUND survey was a national trawl survey aimed at monitoring demersal communities and occurred between years 1982 and 2007. Years considered in this study go from 1992 to 2007 (except for 1999) and only Italian indices were taken into account, since they constitute the longest and more continuous time series for this survey (Fig. 3.7). GRUND indices fluctuate over the years, with an important peak in 1994 and another, smaller, one in 2005.

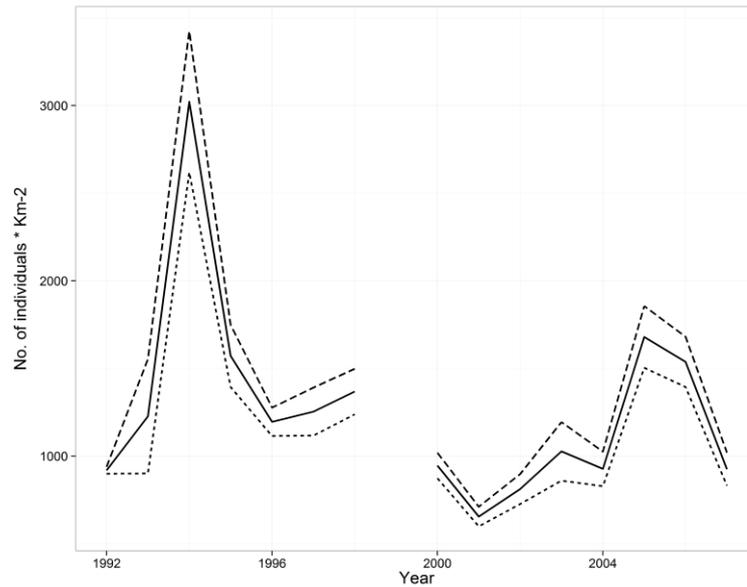


Fig. 3.7 Hake – abundance indices from the GRUND survey for 1992 - 2007: dashed lines represent value \pm CV.

The MEDITS survey is a European standardized trawl survey started in 1994 with the aim of collecting data on demersal communities towards the description of their distribution and demographic structure.

Both yearly abundance indices and absolute abundances derived from the MEDITS survey were used in this study. Absolute abundance was estimated by scaling the survey abundance indices ($N \cdot km^{-2}$; Fig. 3.8) to the study area (23,855 km^2). Relative abundance indices were used to develop the SS3 model (see section 3.2.4), while the absolute abundances were required by the Mark 3 model (see section 3.2.3). These tuning indices have different time series: relative abundance indices generated by the survey were considered from 1992 and reveal a decreasing trend over the time series, while absolute abundances were calculated only for years from 2006 to 2013 (Fig. 3.8).

LFDs from MEDITS survey were also available for each year (Fig. 3.9). They show unimodal distributions with peaks corresponding to the smaller length classes (Fig. 3.9). The most represented lengths were 10 cm and 12 cm, except for 2009 and 2010 for which the most abundant length classes were 14 cm and 16 cm. 2007, 2009 and 2013 show a more fragmented length frequency distribution.

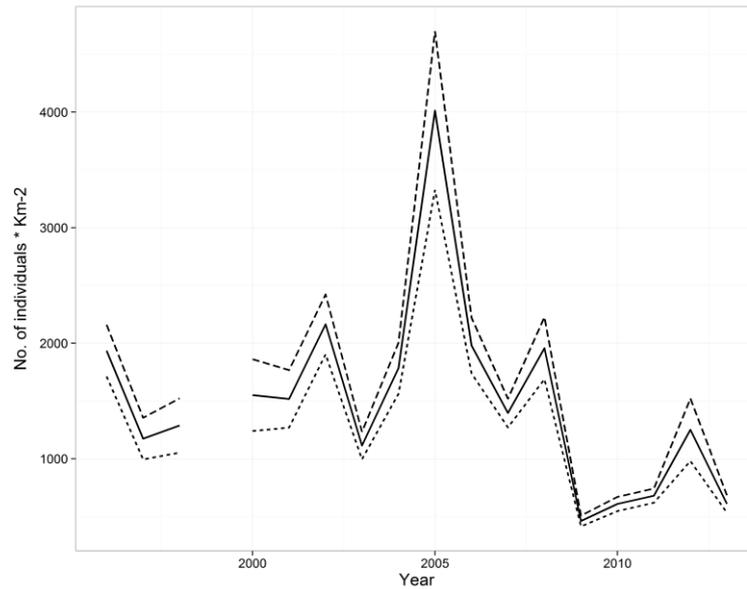


Fig. 3.8 Hake – index of abundance from the MEDITS survey for 1996- 2013: dashed lines represent value \pm CV.

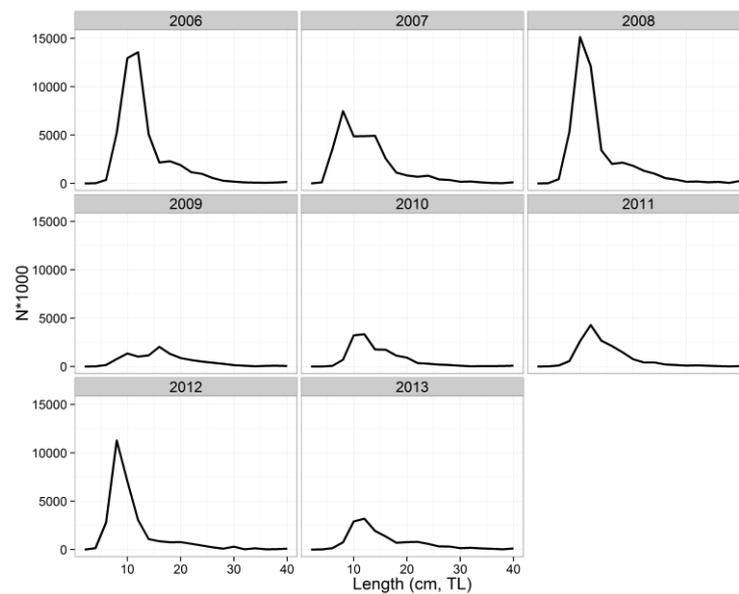


Fig. 3.9 Hake length frequency distributions (LFD) from the MEDITS survey for 2006 - 2013.

3.2.2 Length Cohort Analysis

A Length Cohort Analysis (LCA) was developed using the VIT software (Leonart and Salat, 1992, 1997). VIT performs a virtual population analysis (VPA) using catch data, structured by age or size, and some auxiliary parameters, reconstructing the population

backwards under the assumption of a steady state and estimating fishing mortality (F). The model allows the use of data coming from multiple gear fisheries.

The steady state assumption implies a state of equilibrium, that is that biomass gains are compensated by the losses, therefore each year is processed independently. Considering that neither recruitment nor mortality are constant, this assumption is limiting and it has to be considered when interpreting results (Leonart and Salat, 1992, 1997). However, quantitative estimates are considered valid when the model is employed with short time series of more than one year and resulting parameters do not show relevant variations (Rätz et al., 2010).

In this case the reason for choosing an LCA was linked mainly to (i) the short times series of data available, and (ii) the lack of an age determination procedure. The process starts by using the Baranov catch equation (Eq. 3.1) to calculate the number of individuals of the most recent size class (N_{i+1}) (Eq.3.2). Then with Pope's equation (Eq. 3.3) the number of individuals in the previous class (N_i) is calculated, while the fishing mortality (F_i) is estimated by solving the catch equation for F . The process continues backwards until the entire population is reconstructed.

$$C_i = \frac{F_i}{Z_i} N_i (1 - e^{-Z_i \Delta t_1}) \quad (\text{Eq. 3.1})$$

$$N_{i+1} = N_i e^{-Z_i \Delta t_1} \quad (\text{Eq. 3.2})$$

$$N_i = N_{i+1} e^{M \Delta t_i} + C_i e^{\frac{N}{2} \Delta t_1} \quad (\text{Eq. 3.3})$$

where C_i is the catch in numbers of individuals per length class i , F_i and Z_i are the fishing and the total mortality for class i respectively and M is natural mortality.

Tables 3.1 and 3.3 and Figs. 3.5 and 3.6 summarize parameters and data used in this assessment.

The estimated total biomass shows a fluctuating decreasing trend to 2011, followed by a steep increase reaching a maximum value of 2876 tonnes in 2013 (Fig. 3.10 – red line). Accordingly, fishing mortality, represented by the mean of fishing mortality values overall length classes (F_{bar}), follows a decreasing trend: the estimated F_{bar} value for 2006 being 1.04 yr^{-1} , corresponding to the maximum value of the time series, and reaching a minimum of 0.38 yr^{-1} in 2013 (Fig. 3.10 – blue line). Nevertheless, catches increased in 2012 and 2013 (Fig. 3.5), without reaching values as high as 2006, the number of fished individuals resulted relatively low compared to the previous years

(Fig. 3.6), supporting the increase of abundance shown in 2013, and probably also due to the mechanism of balance of the VIT model.

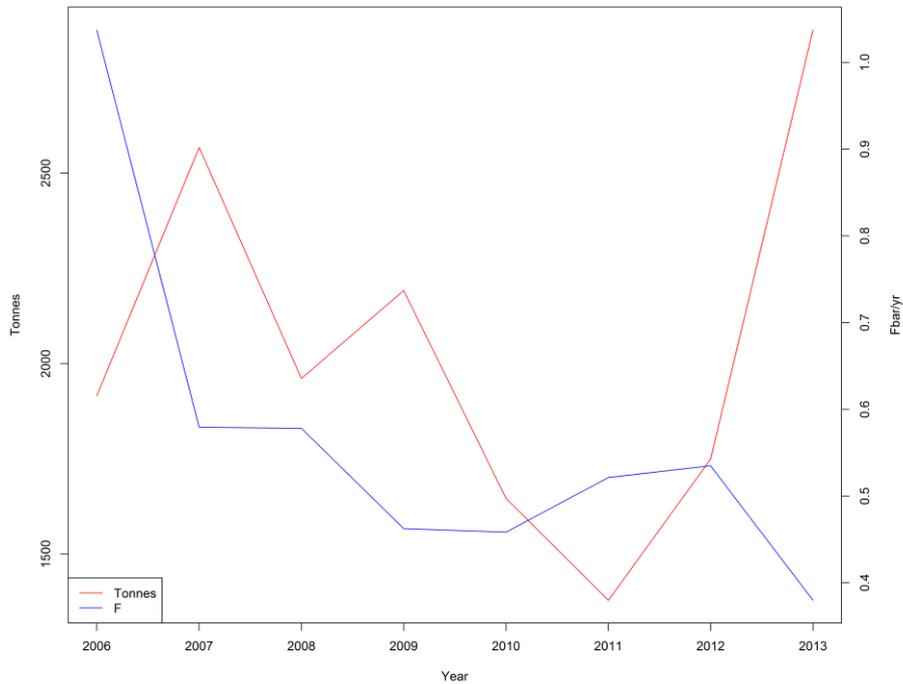


Fig. 3.10 Hake biomass (red line) and mean fishing mortality (yr^{-1} , blue line) estimated by LCA.

3.2.3 Statistical catch at length model

Statistical catch at age or length (SCAA) models represent improvements of VPA approaches. These models are characterized by the fact that they compute calculations using a forward procedure, estimate initial parameters (i.e. abundance at age (or length), recruitment fishing mortality, selectivity), as well as errors in catch at age data, producing more accurate results, especially of the more recent years.

Here, a statistical catch-at-length stock assessment method including all the features listed above was developed using ADMB (Automatic Differentiation Model Builder, Fournier et al., 2013) and R 3.1.1 (R Core Team, 2014). This model is hereon referred to as “Mark 3” and the entire code is reported in Appendix A.

Mark 3 is custom-coded model, flexible to the data available and to the desired outputs. For this study, a format including all the information listed in section 3.2.1 (with the exception of the GRUND survey), and resulting in the outputs necessary to construct the MICE model described in Chapter 5 was chosen. Following an analysis of the input data, the choice was made to fit total catch abundance and catch at length composition

separately. A lognormal distribution was assumed for catch abundance and a multinomial one for catch at length composition.

A transition matrix, T_{ij} , (Eq. 3.4; Punt and Kennedy, 1997; Starr et al., 1999, Hillary, 2011) is needed to develop a length-based stock assessment model. The transition matrix, T_{ij} , is used to describe the movement of animals through different length classes and time, as well as to define the appropriate length bins to be used in subsequent steps. Length bins are the new length classes defined by the use of T_{ij} and reported in Table 3.4

$$T_{ij} = \frac{\mu[G(l_t, \tau, \theta) \cap \lambda_j]}{\mu[G(l_t, \tau, \theta)]} \quad (\text{Eq. 3.4})$$

where T_{ij} defines the probability of an animal in length class λ_i growing into length class λ_j after time τ , μ represents Lebesgue measure (a standard approach to assign a measure to a given subset of n-dimensional Euclidean space, in this case it helps to effectively define interval size), G is the growth increment, θ represents the von Bertalanffy parameters (k and L_{inf}), and l_t is the length at time t .

The growth increment, G , expresses the increase in length of an animal from the time t_0 to time τ (Hillary, 2011):

$$G(l_t, \tau, \theta) = (l_{inf} - l_t)(1 - \exp[-kt]) \quad (\text{Eq. 3.5})$$

The growth parameters required for this calculation are summarized in Tab. 3.1. The resulting transition matrix is shown in Tab. 3.4.

Tab. 3.4 Transition matrix and length bins for a statistical catch-at-length assessment of *Merluccius merluccius*

cm	6	14	20	22	26	28	30	32	34	36	38	40+
6	0	0.823	0.177	0	0	0	0	0	0	0	0	0
14	0	0	0.131	0.735	0.135	0	0	0	0	0	0	0
20	0	0	0	0	0.698	0.302	0	0	0	0	0	0
22	0	0	0	0	0	0.400	0.551	0.049	0	0	0	0
26	0	0	0	0	0	0	0	1	0	0	0	0
28	0	0	0	0	0	0	0	0.004	0.996	0	0	0
30	0	0	0	0	0	0	0	0	0.106	0.894	0	0
32	0	0	0	0	0	0	0	0	0	0.207	0.793	0
34	0	0	0	0	0	0	0	0	0	0	0.309	0.691
36	0	0	0	0	0	0	0	0	0	0	0	1
38	0	0	0	0	0	0	0	0	0	0	0	1
40+	0	0	0	0	0	0	0	0	0	0	0	1

Once the transition matrix was defined, an initialization process was carried out. Firstly, input data (e.g. survey and catch LFDs) were analysed in order to adequately fix parameters describing both fishery (F_{sel}) and survey selectivities (S_{sel}). These values, together with a starting value for recruitment, corresponding to the number of individuals in the first length bin ($logRec$), and for the abundance by length bin ($logStartN$) constitute the *.pin* file needed to start the model.

In addition to the *.pin* file, ADMB requires two additional files: a *.dat* file, containing all the data, and a *.tpl* file, containing the assessment model. Both files are reported in Appendix A.

The *.tpl* file, essential to run the assessment, comprises different sections:

1. the DATA_SECTION describes and summarizes the data used in the model
2. the PARAMETER_SECTION describes the structure of both initial and estimated parameters
3. the PROCEDURE_SECTION lists the functions used in the model
4. the REPORT_SECTION gives indications to generate the report containing the results
5. all the functions used for the assessment model are reported after the REPORT_SECTION
6. Finally, the GLOBAL_SECTION, that reports the output files.

This assessment allowed us to estimate the mean values of fishing mortality per year (F_{bar}) and the stock abundance for each length bin and year ($N_{(t,l)}$), along with recruitment (R) and spawning stock biomass (SSB). Catches-at-length (C) were also recalculated, as well as survey abundances ($U_{(t,l)}$).

ADMB fits the model to data by minimizing an objective function (f) and thus estimates the parameters of the model. It employs a negative log-likelihood for fitting to data, though this can be set to any function that should be minimized. In this case the objective function value was composed by the catch abundance (f_c) and its length bin frequencies (f_{clf}), the survey abundance (f_s) and its prior catchability (p_q).

Uncertainty was given by the Monte Carlo Markov Chain (MCMC), a stochastic simulation technique allowing the generation of fair samples from a prior distributions.

Once the assessment and the MCMC process have been carried out, results can be examined. Figures were obtained using R.

The stock of hake inhabiting the study area decreases along the considered time series, with important troughs in 2009 and 2013 (22174 individuals; Fig. 3.11 – left hand side).

Fishing mortality follows a fluctuating decreasing trend over the years (Fig. 3.11 – right hand side), with the highest value in 2006 ($F_{bar} = 1.36$), and the lowest in 2011 ($F_{bar} = 0.734$). The highest F_{bar} value corresponds to the highest abundance, this is probably due by the fact that MEDITS survey reveals a high abundance in 2006 considering the time series in exam (2006 – 2013; Fig. 3.8), but at the same time catch (Fig. 3.5) and number of fished individuals were the highest compared to the following years (Fig. 3.6), suggesting the need for an high stock to support the high fishing effort. In the following years a strong reduction of catches occurred, particularly in 2011. The MEDITS survey too highlighted a decrease in the estimated abundance, particularly for 2009 and 2010, supporting the reduction in both fishing mortality and stock abundance. Finally, the MEDITS survey showed an increase in 2012, also evident in the Mark 3 results, whereas 2013 was characterized by a new decline of survey abundance and an increase in catch causing decreasing stock estimates. Fishing mortality estimates in 2013 were similar to those of 2012, but with a larger uncertainty. Overall, uncertainty is greater in most recent years (Fig. 3.11).

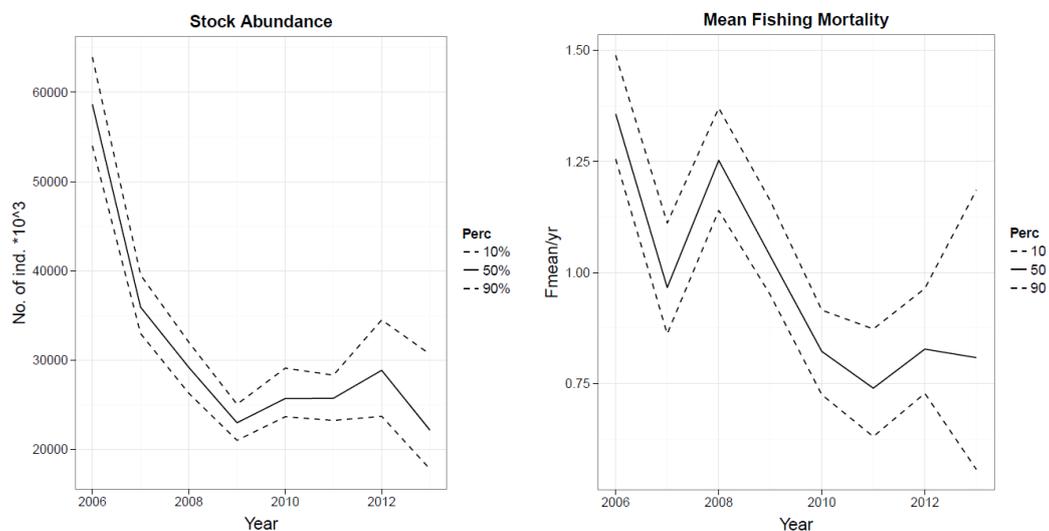


Fig. 3.11. Mark 3 model results - Abundance and mean fishing mortality per year for European hake inhabiting the study area. Upper and lower dashed lines represent the first and third quartiles (10th and 90th percentiles), solid line is the median value.

Spawning stock biomass (SSB) and abundance of recruits were also estimated (Fig. 3.12). SSB decreases from a median value of 932 tonnes in 2006 to 370 tonnes in 2010; after that it increases, reaching 578 tonnes in 2013 (Fig. 3.12 – left side). The abundance of recruits exhibits a fluctuating decreasing trend, with the highest value in 2006

($27924 \cdot 10^{-3}$ individuals) and the lowest in 2013 ($8563 \cdot 10^{-3}$ individuals) (Fig. 3.12 – right hand side). Mark 3 results support the theory that the number of recruits is not related to parental stock size (section 3.1.4), since the trend of recruits is decreasing over the years and does not reflect the trend of the spawning stock biomass. Moreover, recruitment seems to be mainly influenced by environmental variables, i.e. temperature, bottom currents and food availability (Druon et al., 2015). Finally, owing to the fact that the study area represents a nursery ground for hake, mortality is likely to have the greatest effect on hake recruits, since juveniles comprise the largest portion of the stock.

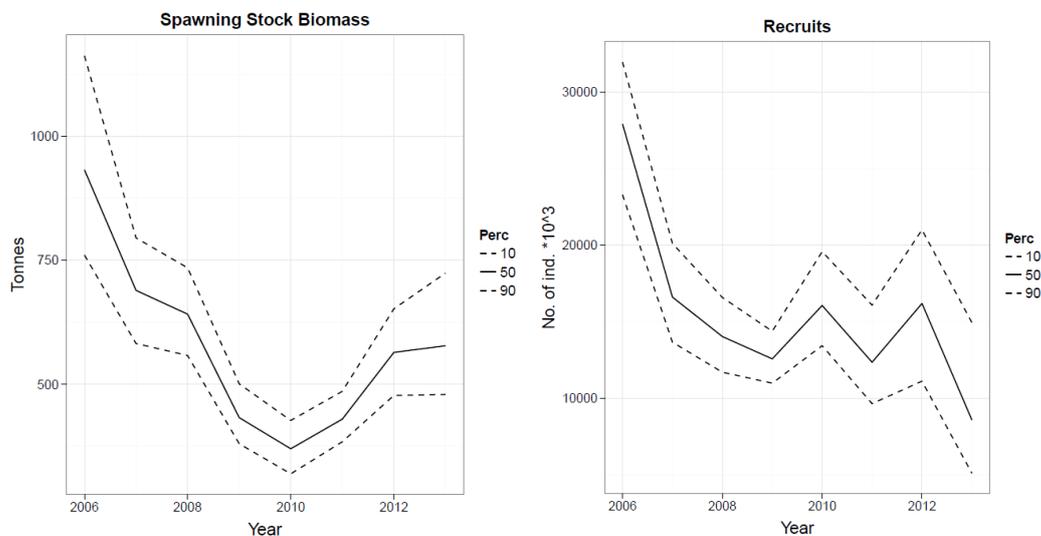


Figure 3.12. Mark 3 model results – Spawning stock biomass (SSB) (left) and recruit abundance (right) per year for European hake inhabiting the study area. Upper and lower dashed lines represent the first and third quartiles (10th and 90th percentiles), solid line is the median value.

The spawning potential ratio (SPR) is an index that describes how fishing mortality influences the capacity of each recruit to become a spawner (Mace and Sissenwine, 1993). It compares the spawning capacity of a fished stock (SPR_{cur}) to the spawning capacity of an unfished stock (SPR_0). As expected for this area, the SPR ratio is quite low, close to 0.1, highlighting the prevalence of juveniles in the study area and the high fishing pressure on these individuals (Fig. 3.13).

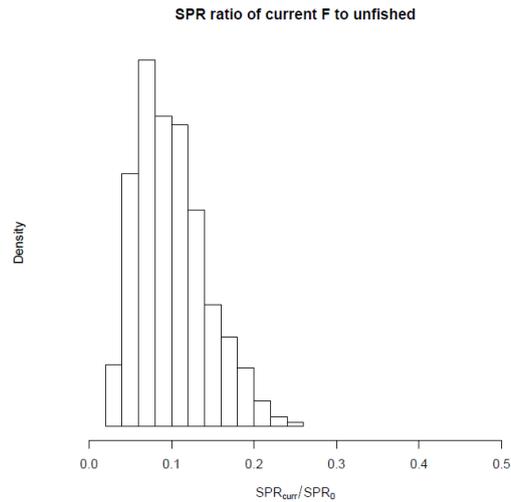


Fig. 3.13 Mark 3 model results – Spawning potential ratio SPR_{curr}/SPR_0 .

Survey catchability was analyzed by comparing prior and posterior survey catchabilities (q_{surv}) (Fig. 3.14). Results show that the posterior distribution of the q_{surv} parameter estimated by the assessment is quite different from the prior distribution which was assumed to have a normal distribution with mean = 0.9 and standard deviation = 0.1. This difference highlights that the MEDITS survey in reality fished less animals than those assumed by the prior (posterior $\mu = 0.7$), indicating that there are more fish in the sea than those captured by the survey. Thus, total abundance is not set only on the informative prior for q_{surv} , but the data too contain information.

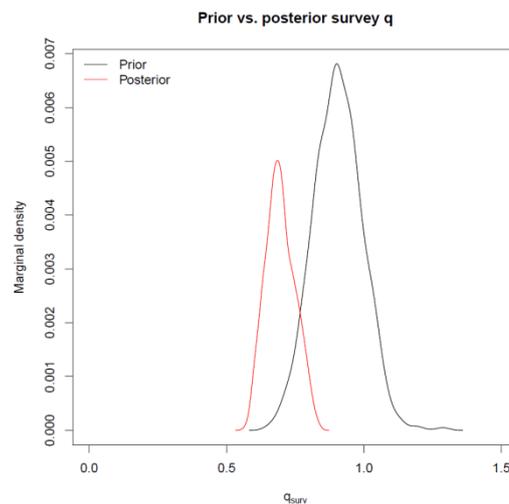


Fig.3.14. Mark 3 model results – Survey catchability profile: posterior (red line), and prior (black line) distributions of q_{surv} .

Model fitting was also examined. Firstly, observed and estimated survey data were compared (Fig. 3.15 – left hand side): estimated data (lines) show smoother trends than

those observed (dots), but the peak in 2008 that was not estimated. Also, LFDs do not agree perfectly (Fig. 3.15, right side). This is especially true in 2007 and 2008 when estimated LFDs (pink line) show a greater number of individuals in the first length bins compared to those observed (blue line). However the proportion of juveniles is consistently higher than that of adults a larger who nevertheless show an increase in 2009, 2010 and 2013. Anyhow, fitting can be considered quite good: the noisy input data in a relatively short time series makes it difficult to obtain better estimates.

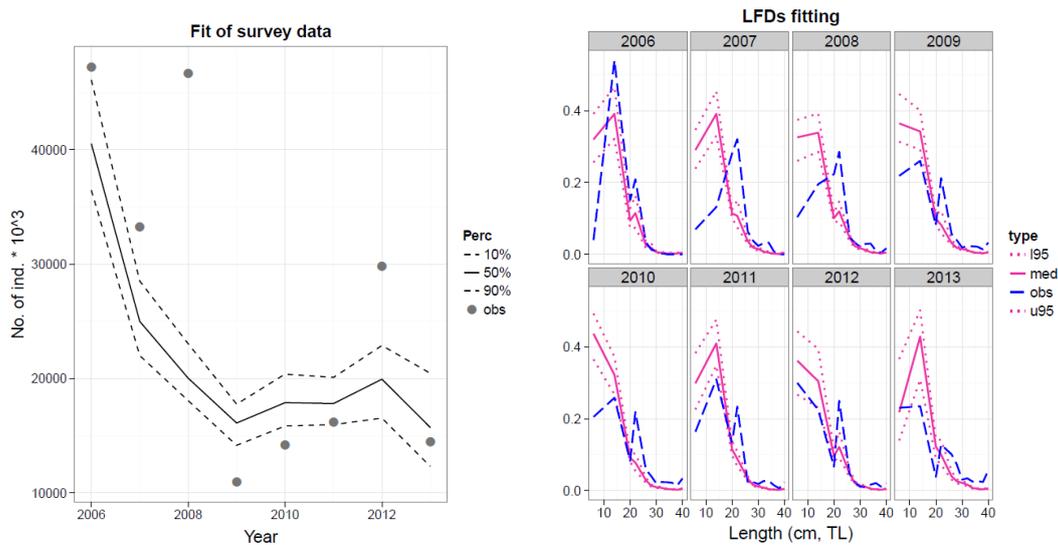


Fig. 3.15. Mark 3 model results – Fitting of data. Left: observed (dots) vs. estimated (lines: median (solid line) and first and third quartiles (upper and lower dashed lines)) survey abundance. Right: observed length frequency distribution of catches (blue line) vs. estimated (pink lines: solid represents the median and dashed lines the first and third quartiles) length frequency distribution of the stock.

3.2.4 Stock synthesis

Stock synthesis 3 (SS3; Method and Wetzel, 2013) is a statistical framework able to reconstruct population dynamics using either age or length composition data. It is designed to include different information from fishery and survey data, as well as to consider different subareas within the same stock. Selectivity can be modeled by age and/or length. SS3 is based on ADMB C++ software, allowing to easily work with large databases, as well as to simultaneously estimate a number of parameters. SS3 also includes a management part, where estimated parameters and their uncertainty can be propagated into the future to simulate different catch scenarios.

Here we chose to use a length structured SS3 model using all the information available for the stock of hake in the study area. Thus, the time series of the assessment was

extended from 1980 to 2013. Landings data for years prior to 2006 were derived from the FishStatJ (2015) database and were scaled to the study area according to the VMS data for the most recent years for Italian landings and using the value of 40% for Croatian landings as suggested by Vrgoč (pers. comm.) (Fig. 3.5). Moreover, the possibility of considering multiple fleets was used; thus Italian and Croatian commercial information were kept separate.

Two sources of survey data were used: GRUND and MEDITS surveys. The GRUND survey was only used as index of abundance for the years 1992 – 1998 and 2000 – 2007 (Fig. 3.7). Whereas, the MEDITS survey was used as an index of abundance (Fig. 3.8), for 1996 – 1998 and 2000 – 2013, and as length composition for 2006 – 2013 (Fig. 3.10) – 1999 is missing because the conflict within Balkans required an interruption in fishing activity.

Input data are summarized in figure 3.16.

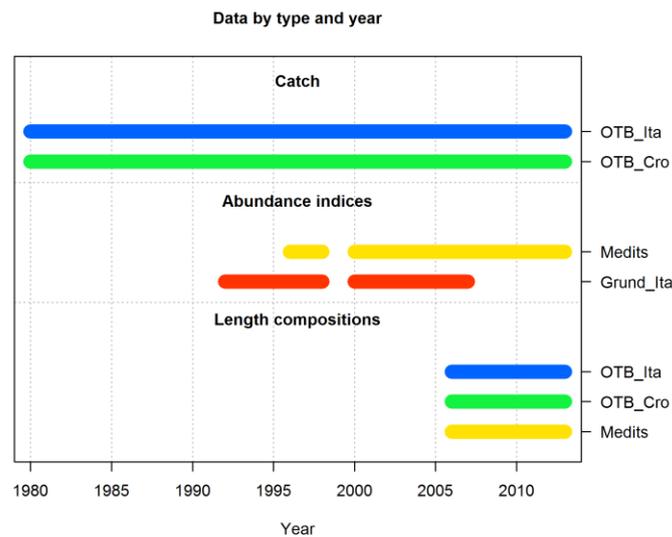


Fig. 3.16 Summary of input data used in the Stock Synthesis assessment. Catch data are divided in Italian (OTB_Ita) and Croatian (OTB_Cro) bottom trawl; abundances indices include estimate from MEDITS (Medits) and GRUND (GRUND_Ita) surveys. Length compositions are represented by the number of individuals per length class within Italian catch (OTB_Ita), Croatian catch (OTB_Ita) and MEDITS survey (Medits).

Growth (Table 3.1) and natural mortality (Table 3.3) information was the same used for the other assessments. Information about the fecundity relationship and stock recruitment relationship were also included.

One of the most important advantages of SS3 is the possibility of estimating selectivity choosing the most appropriate model from a wide set of choices. Selectivity can be

modeled by age and/or length; in this case length-based selectivities were set. Based on the features characterizing bottom trawl selectivity and the length composition exploited by this gear, a double normal selectivity for both Italian and Croatian fishery was chosen (Figure 3.17).

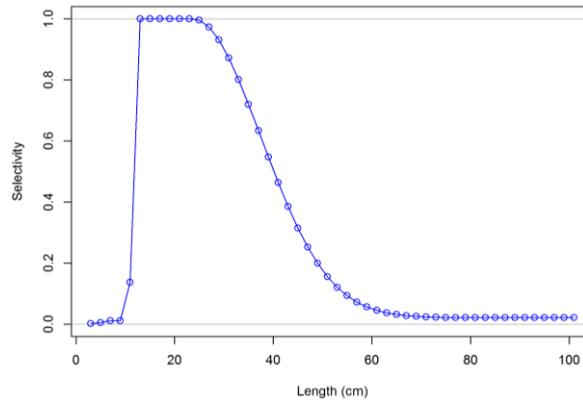


Fig. 3.17 Estimated length-based selectivity for Italian and Croatian bottom trawl.

Considering that the GRUND survey used a net similar to the commercial one, a double normal selectivity was assumed for that too (Fig. 3.18). A cubic spline selectivity was assumed for the MEDITS survey, since this type of selectivity better suited to the smaller mesh size used in this survey (Fig. 3.19). These models allow to shape the selectivity curve closer to the length frequency distributions, favoring a better fitting particularly when LFDs are noisy, as in this case.

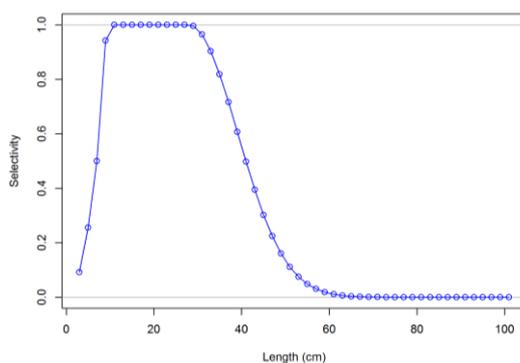


Fig. 3.18 Estimated length-based selectivity for the Grund survey.

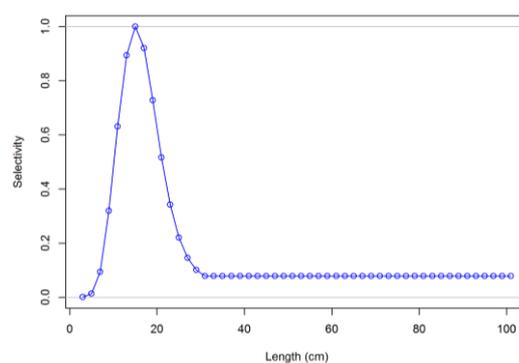


Fig. 3.19 Estimated length-based selectivity for the Medits survey.

Estimated stock biomass decreases continuously along the time series reaching the minimum value of 5730 tonnes in 2013 (Fig. 3.20), accordingly fishing mortality

describes a continuous increasing trend reaching the maximum value of 1.34 in 2013 and recording the peak of catches in 1982 estimating a value of 0.47 (Fig. 3.21). Fishing mortality is also reported by fleet (Fig. 3.22), clearly showing that the stock is mainly exploited by Italy although Croatia has increased its fishing activity in recent years.

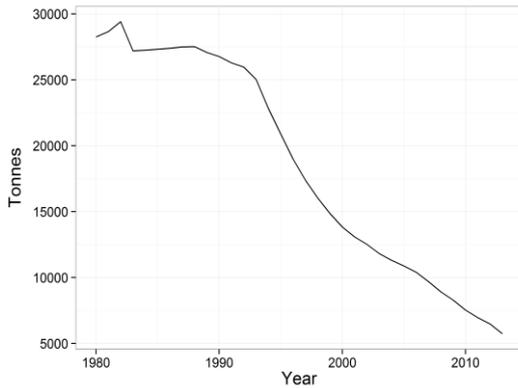


Fig. 3.20 Hake in the study area, SS3 – estimated stock biomass.

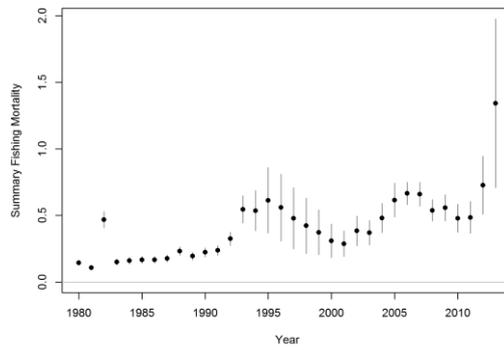


Fig. 3.21 Hake in the study area, SS3 – total fishing mortality, represent 25% and 95% percentiles.

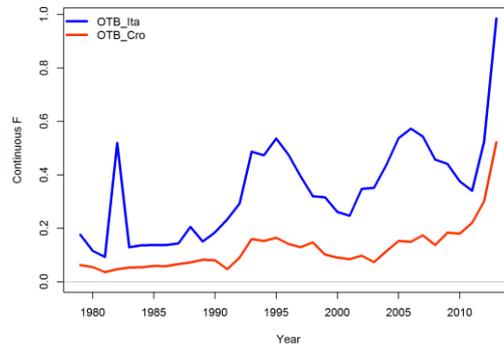


Fig. 3.22 Hake in the study area, SS3 – total fishing mortality by fleet where the Italian trawl fleet is represented by the blue line and the Croatian one by the red.

Estimated spawning stock biomass (SSB) shows a decreasing trend over the years (Fig. 3.23), whereas recruitment is initially quite stable and starts to fluctuate from 1996 when more information is included in the model, with a peak of recruits in 2005 and a trough in 2009 (Fig. 3.24).

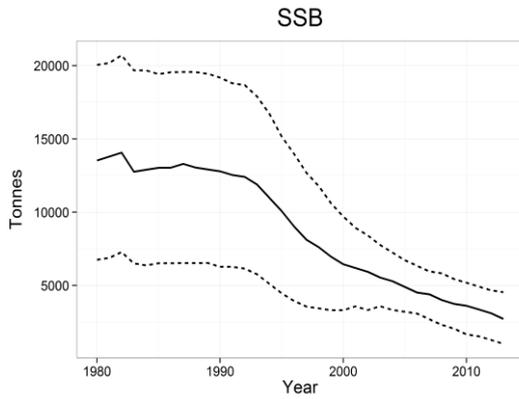


Fig. 3.23 Hake in the study area, SS3 – estimated spawning biomass, upper and lower lines correspond to the 25% and 95% percentiles.

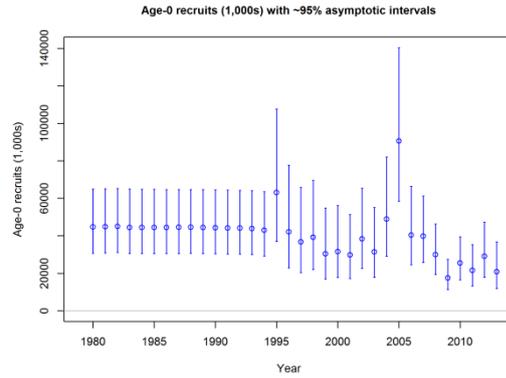


Fig. 3.24 Hake in the study area, SS3 – estimated recruits; bars represent 25% and 95% percentiles.

The fitting between observed and estimated length frequency distributions for each fleet (MEDITS survey, Italian bottom trawlers and Croatian bottom trawlers) is shown in figure 3.25. The best fitting was obtained for the MEDITS survey, since LFDs are more stable over the years, whereas LFDs coming from the fishing activity present bimodal distributions with differences among years. Residuals are low and do not present particular trends, except for the fact that they are equal for Italy and Croatia since same LFDs were assumed (Fig. 3.26).

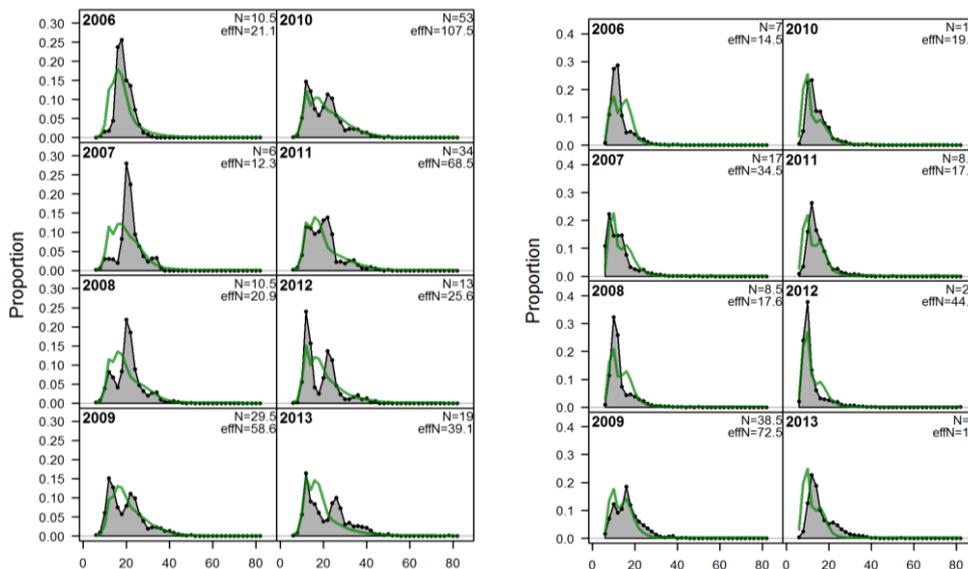


Fig. 3.25 Hake in the study area, SS3 – Length frequency distributions: observed (grey) vs estimated (green) for the MEDITS survey (left), Italy and Croatia (right).

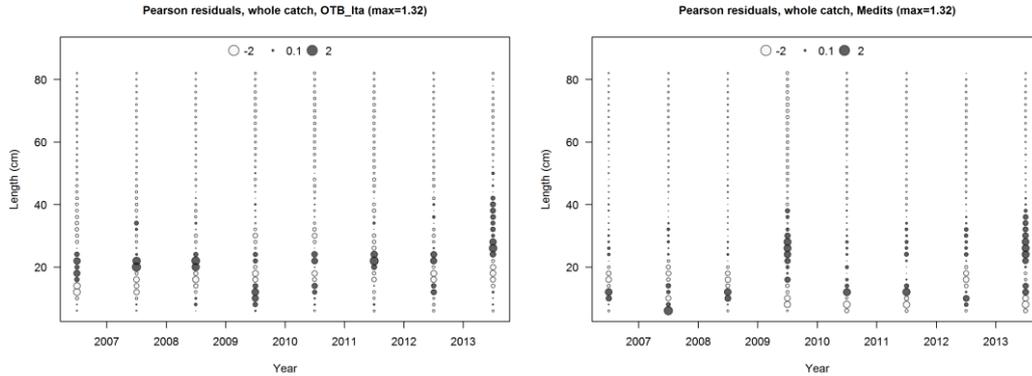


Fig. 3.26 Hake in the study area – Residuals for Italian and Croatian LFDs (left) and for the MEDITS survey LFDs (right)

Fitting of the survey indices is also estimated (Fig. 3.27). SS3 seems to work quite well with the survey indices, although it is not able to record large peaks or decreases, e.g. the 1994 peak and the 2000 and 2001 decreases in the GRUND survey are not tracked (Fig. 3.27 left). With the exception of the peaks in abundance in 2005 and 2008, the fluctuating trend of the MEDITS survey is estimated well (Fig. 3.27 right).

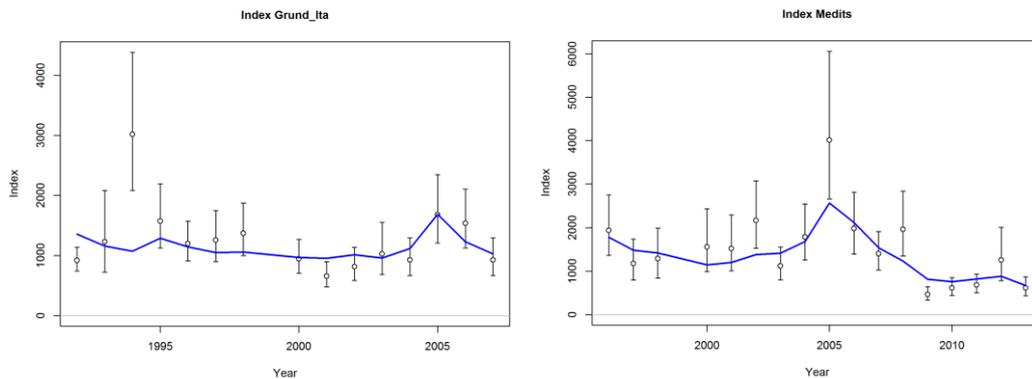


Fig. 3.27 Hake in the study area – Fitting of survey indices: GRUND (left) and MEDITS (right); bars represent 25% and 95% percentiles.

3.2.5 Comparison of stock assessments

The stock of European hake in the study area presents a concerning situation: all models describe decreasing trends with a more optimistic situation traced by the VIT model, in which the stock is estimated to increase from 2011 (Fig. 3.28 – top).

Trends in fishing mortality are quite different among models (Fig. 3.28 – bottom). The general trend is a decreasing one, with the Mark 3 model estimating higher mortalities, except for 2013 when the highest value emerges from the SS3 model. This is in agreement with the abundance estimates.

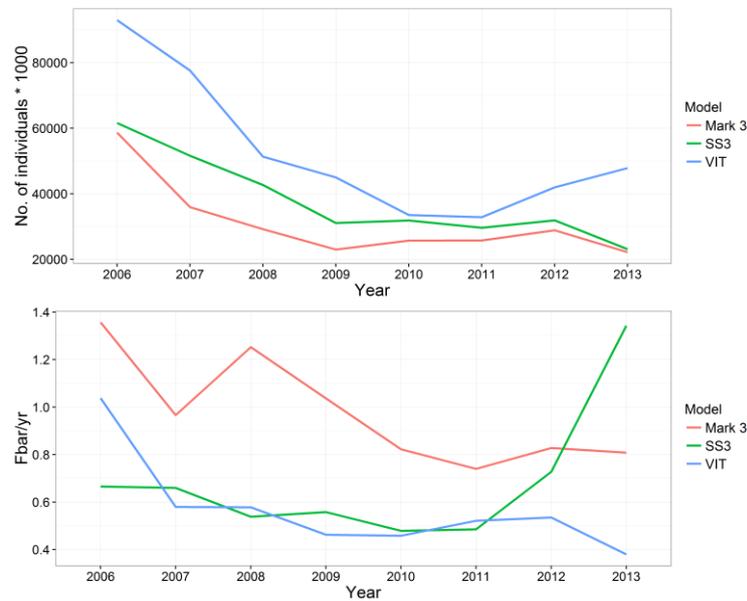


Fig. 3.28. Comparison of stock assessment results: total abundance by year (top) and mean fishing mortalities (F_{bar}) by year (bottom) estimated by the Mark 3 (pink), SS3 (green) and VIT (blue) models.

Despite an overall decrease in fishing mortality over the years, it is still high enough to prevent a recovery of the stock. Moreover, fishing activity insists mainly on juvenile individuals (Figs. 3.6). Thus, a state of overexploitation for hake in the study area is depicted by all the models. These results are in agreement with the latest hake stock assessment in the northern and central Adriatic Sea (GFCM, 2014). The fishing mortalities estimated by all models are comparable to those reported in the literature (Vrgoč et al., 2004).

The results highlight the existing differences among the models used. Firstly, complexity has to be taken in account. VIT is the simplest model concerning both input data and calculations. Mark 3 is of intermediate complexity with relatively complex population dynamics and the requirement for information from multiple sources. SS3 is by far the most complex model of the three: it allows the inclusion of all the available information about the stock in exam regardless of the length of the time series, and mixing age- and length-structures. Moreover, a lot of accessory information is required, e.g. detailed information about maturity and fecundity, and stock-recruitment parameters (including steepness) which are sometimes difficult to find. SS3 yields a wide set of outputs which are exhaustive, but can be hard to understand for non-expert users.

Model complexity results in different amounts of data being considered in each assessment. Certainly the more data available, the more accurate the estimates obtained. However data quality has to be considered: poor quality input data will generate less meaningful results (Method and Wetzel, 2013). This fact supports results obtained by the SS3 model, in which only “truthful” and available data were considered. However differences in abundance estimates are mainly given by model calculations. VIT performs a backward calculation from the last length class using Pope’s approximation and assuming a steady state, whereas Mark 3 and SS3 compute forward calculations within a dynamic framework. More specifically, Mark 3 computes abundance considering the survival probability and the transition matrix resulting in a truly length based approach. SS3 is more similar to other statistical catch-at-age models and length data, if available, are translated into age data using a sophisticated slicing method; this model, though takes advantage of all available data to tune the model (Method and Wetzel, 2013). These differences are reflected in the abundance estimates: VIT probably estimated higher values because each year is individually computed assuming a state of equilibrium, and this can yield misleading estimates. However, it describes a generally decreasing trend, as do Mark 3 and SS3. Mark 3 is likely the model that performs better, since estimates are obtained using length based dynamics only. Whereas SS3 gives accurate estimates since more information are included, but calculations are strictly related to age composition, that can be problematic for hake. Fishing mortality estimates also highlight differences among models. VIT derives F by the solution of the Baranov catch equation for F (Lleonart and Salat, 1992; 1997), whereas Mark 3 estimates F combining selectivity functions and natural mortality by length. VIT and Mark 3 models work using a length structure, whereas SS3 calculates F values as a vector by age. SS3 estimates initial values using Pope’s approximation, these are then used to adjust the continuous F values to closely approximate the observed catch (Method and Wetzel, 2013). Considering this, Mark 3 seems to give the best estimates taking in account both length composition and selectivity, whereas values from SS3 are strongly influenced by age composition and this can be the reason for the difference in trends. Fishing rates obtained by the VIT model are affected by the steady state approach, however their trend is quite similar to the Mark 3 model except for years 2008 and 2013 and estimates are obviously lower considering the higher estimates of abundance.

Another point of difference between models is the inclusion of selectivity, which is represented in Mark 3 and SS3 models but not in the VIT. Selectivity in stock assessment models is interpreted as the probability that a fish of a given age/size will be caught by the gear if it is available (i.e. classical “net selectivity”) combined with the probability that a fish will be available to the fishing gear (i.e. “availability”) (Maunder et al., 2014; Punt et al., 2014). Selectivity is affected by different factors, e.g. fishing gear characteristics, fish behaviour, spatial heterogeneity in the distribution of different sizes/ages of fish and the spatial distribution of the sampling and the fishing. Consequently, models including selectivity are more informative than simpler models and are able to estimate stock size more reliably (CAPAM workshop, 2013). Considering that selectivity is influenced by various factors resulting in different selectivity forms, SS3 presents a wide choice of selectivity options, whereas Mark 3 offers the possibility to code in different selectivity models. In the case of European hake for example, a double normal configuration was chosen to model the selectivity of Italian and Croatian fisheries and the GRUND survey, whereas a more complicated form, the cubic spline selectivity, was chosen for the MEDITS survey, since its LFDs showed a complicated distribution over the years. These selectivity shapes were used in the SS3 model and resulted in a rather good fitting between observed and estimated LFDs. The Mark 3 model, on the other hand, used a lognormal distribution to model the fishery selectivity and a multinomial distribution for the MEDITS survey; the fitting in this case resulted acceptable. Input data are noisy, making it difficult to achieve optimal fitting and suggesting more investigation regarding this point is required.

In this chapter an evaluation of different stock assessment models was carried out. Owing to the fact that they take into account a wide range of information, SS3 and Mark 3 are regarded as the best models for the assessment of this species and the production of results useful for suggesting management strategies. Moreover, they do not assume a steady state (which represents the main limitation of the VIT model) and they can be developed both using age- and length-structures. However, SS3 presents the disadvantage of not being a purely length based model, since even in the presence of length structured input data, most of the results are obtained by developing age dynamics, e.g. the fishing mortality estimates. Mark 3, on the other hand, is purely length-based, as well as not being a prepackaged model, thus can be adapted to any situation required. Mark 3 seems to be the best model when the evaluation is not the only end, i.e. when outputs from the assessment model are fed into other models.

Finally, VIT has the advantage that it allows a stock assessment even if the available data time series are short. This model can be run through a practical interface, reducing required computing and coding capabilities (Leonart and Salat, 1992, 1997). On the other hand, the assumption of a steady state has various implications (e.g. strong inter-annual variations in the estimated fishing mortality, especially in years when the age composition shows strong year-class effects) that suggest this model should only be used to draw qualitative conclusions; quantitative estimations should be carefully interpreted and only in the presence of short time series (Rätz et al., 2010).

The MICE model, presented in Chapter 5, was carried out using the outputs of VIT model; this choice was supported by the fact that MICE approach was to be developed, therefore the simplest data represented the best choice to start the model and results from VIT were well adapted to this necessity. However, improvements of this work foresee the use of complex stock assessment models to describe the predator dynamics within the MICE model and the comparison of results.

CHAPTER 4 – Norway lobster

Norway lobster, *Nephrops norvegicus* (Linnaeus, 1758) (Fig. 4.1), is one of the most important crustacean species in the Adriatic Sea, where it ranks first by value and second by weight among the exploited crustaceans. It is distributed throughout the eastern Atlantic region, from Iceland to south Atlantic coast of Morocco; in the western and central basin of the Mediterranean west of 25° E, the Baltic Sea, the Bosphorus and the Black Sea.

In the Adriatic Sea, *Nephrops* occurs on muddy (silty-clay) grounds at depths from around 30 m to over 400 m (Artegiani et al., 1979; Wieckzorek et al., 1999), with important concentrations occurring around 70 m depth off Ancona, around 220 m depth in the Pomo pit and in the Velebit Channel, Kvarner and Kvarnerić region along the Croatian coast (Karlovać, 1953; Crnković, 1964, 1965; IMBC et al., 1994; Froglija and Gramitto, 1981, 1986, 1988; Froglija et al., 1997).

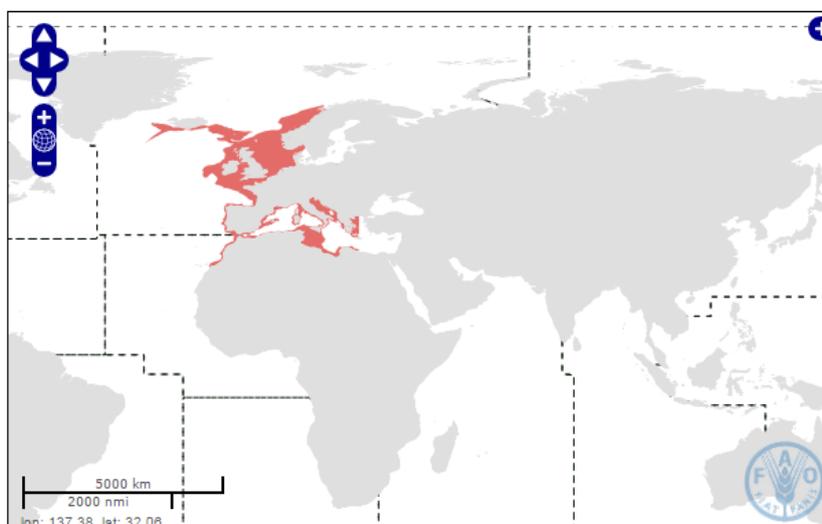


Fig. 4.1 Geographic distribution of Norway lobster, *Nephrops norvegicus*. Source: FAO, 1991 (<http://www.fao.org/fishery/species/2647/en>)

4.1 Norway lobster in the Adriatic Sea

4.1.1 Species description

Nephrops norvegicus (Fig. 4.2) is a crustacean belonging to Nephropoidea group, order Decapoda, infraorder Astacidea, family Nephropidae.

Taxonomy:
 Phylum *Arthropoda*
 Class *Malacostraca*
 Order *Decapoda*
 Suborder *Pleocyemata*
 Family *Nephropidae*
 Genus *Nephrops*
 Species *N. norvegicus*

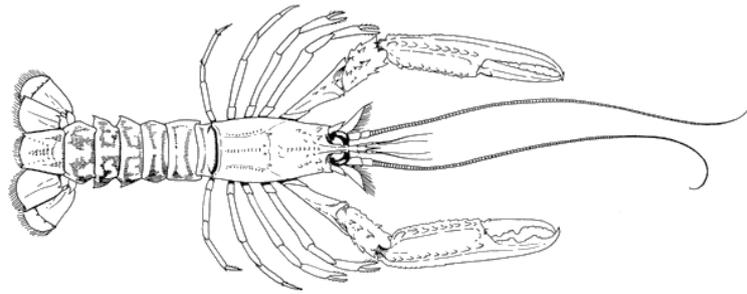


Fig. 4.2 *Nephrops norvegicus* (Linnaeus, 1758). Source: FAO, 1991
<http://www.fao.org/fishery/species/2647/en>

Its body is totally covered by a hard structure, the exoskeleton, and is divided into segments, or somites. Somites are grouped into two main parts: the cephalothorax, separated internally into cephalon (that includes head and the firsts 5 somites), thorax (including somites 6-13), and the pleon. Each somite of the cephalon has a pair of appendages with sensory and feeding functions (eyes, antennules, antennae, manibles, maxillules and maxillae), whereas those situated on the thorax are feeding appendages (maxillipeds), chelipeds (the first pereopods) and walking legs (all the others pereopods). The pleon is the posterior part of the body and it is composed by a series of movable somites or pleomeres bearing pleopods and ending with the telson, or tail fan, a false somite bearing the anus antero-ventrally (Stachowitsch, 1992). Pleopods are designed to create a current for locomotion and chemical communication; they also serve as egg-brooding structures in females (Atema and Voigt, 1995). Locomotion is obtained mostly by walking rather than swimming (Fisher et al., 1987).

The cephalon and thorax, together known as the cephalothorax, are covered by the carapace, a rigid structure that laterally protects the branchial chambers (Glaessner, 1969; Stachowitsch, 1992). Frontally, the carapace ends with the rostrum, a median anterior prolongation that extends between the eyes. The thorax represents the ventral part of the body and it is composed by segments, called sternites. Female thorax is characterized by the thelycum, located between pereopods 4 and 5. This is a pouch-like accessory copulatory structure needed to store the sperm packets (spermatophores) before use at the right time. With the exception of the first, all other female pleopods facilitate the attachment of eggs after spawning. The male copulatory organs are represented by the first and second pairs of pleopods: the first one is used to transfer sperm from the male gonoduct to the female thelycum, the second one is like the others but with an additional article, the appendix masculine, a hard, elongate and paddle-like

flap, arising from the base of the endopod. This appendix is needed for copulating or sperm transfer (Stachowitsch, 1992).

4.1.2 Habitat

The geographic distribution of *Nephrops* is highly discontinuous because heavily dependent upon sediment composition which should be muddy and preferably medium-grained (~ 40% of clay and silt) (Farmer, 1975; Afonso-Dias, 1998; Bell et al., 2006). Within this type of sediment, *Nephrops* build burrows. Burrows can be simple U-shaped tubes, ~ 30 cm deep into the sediment, or complex galleries with multiple entrances. The density of burrows can be used as an index of abundance (Bell et al., 2006). Importantly, there seems to be a stock-specificity to the relationship between burrow density and sediment composition which has been found to hold true over time (Campbell et al., 2009).

This, added to the fact that *Nephrops* is sedentary (Chapman and Rice, 1971), means that this species is generally characterised by spatially segregated populations (or stocks) with little or no exchange between them (Bell et al., 2006). This heterogeneity in distribution is also present within smaller areas, giving rise to smaller “subpopulations” or “stocklets” with different population densities, sizes, sex compositions, growth rates, sizes at first maturity, etc. (Maynou and Sardà, 1997; Bell et al., 2006).

Of interest to this study is the fact that differences in *Nephrops* length frequency distributions are reported between the grounds off Ancona and those in the northern Adriatic channels, and the Pomo/Jabuka Pits (Karlovać, 1953; Crnković, 1964, 1965, 1970; Jukić, 1974; Froglija and Gramitto, 1981, 1988, Županović and Jardas, 1989, IMBC et al., 1994).

Numerous studies carried out in GSA 17 have highlighted that Norway lobster has different growth rates and sizes at first maturity depending on the portion of GSA 17 considered (Fig. 4.3). The MEDISEH project (Mediterranean Sensitive Habitats, 2013) used Zero Inflated General Additive Modelling to identify one prevalent nursery area (R1) and four prevalent spawning grounds (S1 – S4) in GSA 17 (Fig. 4.4). The Pomo/Jabuka pit area is of particular interest as it was identified as both a nursery area (R1) and a spawning ground (S1; Fig. 4.4).

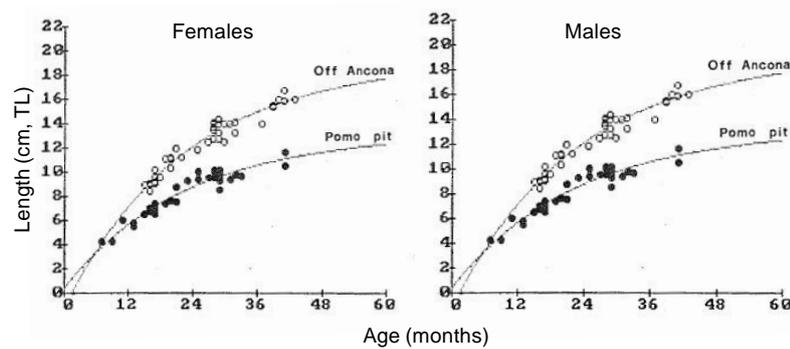


Fig. 4.3. Von Bertalanffy growth curves for female (left) and male (right) *Nephrops* in the Pomo/Jabuka pit and off Ancona (modified from Froglija and Gramitto, 1988)

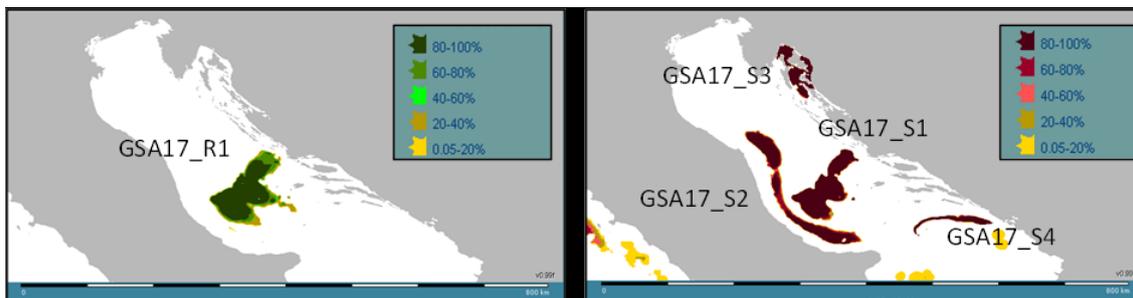


Fig. 4.4. Position of persistent nursery (left) and spawning areas (right) of Norway lobster in GSA 17 as identified by the MEDISEH project (source: Mediterranean Sensitive Habitats, 2013)

The reality is that the individuals characterising the so-called nursery area in Fig. 4.4 are unlikely to be true recruits as the Pomo/Jabuka pit area, for reasons related to its geography, morphology and oceanography, is likely to be inhabited by a very dense “subpopulation” of smaller animals with slower growth rates (see section 4.1.4) (Froglija and Gramitto, 1981; Froglija and Gramitto, 1988; IMBC et al., 1994). As a result the Pomo/Jabuka pit “subpopulation” should likely be considered as separate from the other grounds off the eastern Italian coast south of Ancona (S2, Fig. 4.34 Froglija and Gramitto, 1981; Froglija and Gramitto, 1988; IMBC et al., 1994) and in the northern Croatian channels (S3, Fig. 4.4; Vrgoč et al., 2004). The fact that genetic analyses have not revealed differences between the “Ancona subpopulation” and the “Pomo/Jabuka subpopulation” that went beyond the population level allows the inference that the differences are mainly due to environmental effects (Mantovani and Scali, 1992). More specifically, the slower growth rates in the Pomo/Jabuka pit compared to elsewhere have been attributed to a combination of density-dependent effects of mean size and lack of food (Wieczorek et al., 1999). Alternatively or cumulatively, the small sizes in the Pomo/Jabuka pit could be due to the effect of the fishery as suggested by Abello et al. (2002) for *Nephrops* in the Mediterranean.

These differences should be taken into consideration when assessing the *Nephrops* population in GSA 17 as it appears that treating it as one single stock unit may be questionable and could lead to an inaccurate and imprecise evaluation of the status of the resource. The north-east Atlantic *Nephrops* stocks, for example, are managed by Total Allowable Catch (TAC) advised annually by ICES (ICES, 2003): although TACs are delivered for aggregated areas, all advice is based on small Management Areas taking into account the poor connectivity between stocks and the possibility of different life history characteristics.

4.1.3 Burrowing and emergence behaviour

Nephrops are bottom-dwellers, building complex burrows in muddy sediments, emergence from which varies with time of day, season, animal size, sex, and reproductive status (Froglia, 1972; Atkinson and Naylor, 1976; Naylor and Atkinson, 1976; Aréchiga et al., 1980; Chapman, 1980; Froglia and Gramitto, 1986; Tuck et al., 2000). Emergence patterns follow diel and seasonal patterns. Diel patterns of peak emergence have been reported to differ according to depth as follows (Bell et al., 2007):

- Shallow depths (< 30 – 40m): one peak during night time
- Intermediate depths (40 – 100m): two peaks one at dawn and one at dusk
- Deep waters (>100m): one peak during day time

The regulatory mechanisms driving these diurnal emergence patterns are yet to be pinpointed, but are believed to be entirely exogenous, from light to hydrodynamics to predation (Bell et al., 2007; Aguzzi and Sardà, 2008; Aguzzi et al. 2008, 2009).

Seasonal patterns are also present and most important for females who do not leave their burrows during the egg-bearing period; the emergence of both sexes is more sporadic in winter (Marrs et al., 2000; Bell et al., 2007). Accordingly, in the Adriatic Sea the peak of *Nephrops* catches is reported in spring and the minimum in winter (Wieckzorek et al., 1999). Juveniles tend to spend more time in their burrows. Burrows usually host one individuals, but newly settled post-larvae and early juveniles can live in association with larger animals (Tuck et al., 1994).

Hypoxic conditions can negatively influence the natural emergence patterns causing mass mortalities. Hypoxic events were observed in the Adriatic and Kattegat Sea (Froglia and Gramitto, 1982; Bagge, 1988; Hallbäck and Ulmestrand, 1990). When oxygen concentration falls below about 50% saturation, *Nephrops* are forced to stay outside of their burrows in search for oxygen (Bagge and Munch-Petersen, 1976).

Moderate hypoxia (< 30% O₂ saturation) causes a reduction in motility and promotes an unnatural position with raised legs to increase oxygen uptake. Juveniles are more sensitive to hypoxia than adults, a reduction of oxygen availability below about 25% saturation for 24 hours can be lethal (Eriksson and Baden, 1977). Hypoxic events also cause a higher mortality to fishing, since during low oxygen events, *Nephrops* are much more vulnerable to trawling: they cause an increase in catch rates giving the false impression that stock density is increasing. If severe hypoxic events come in succession, an entire population of *Nephrops* can be wiped out, requiring years to re-build the pre-hypoxia state (Hallbäck and Ulmestrand, 1990; ICES, 1990).

This all means that the fishery exploits the population selectively and in a different manner according to sex and environmental conditions. These factors all affect the availability of *Nephrops* to trawls, their absolute catches and the sex ratio of animals caught. Thus, care has to be taken when using trawl surveys to generate abundance indices: a good estimate of population density based on catchability can only be obtained if the trawl surveys are scrupulously carried out at specific times of the day and under the same conditions of time and season from year to year (Aguzzi and Sardà, 2008). An alternative would be to carry out surveys based on methods that are independent of the emergence behaviour of the animal: underwater TV (UWTV) surveys counting burrow openings are the most common of these methods (Marrs et al., 2000).

4.1.4 Growth, size and sexual maturity

Norway lobster is characterised by discontinuous growth with moults interspersed by intermoult periods and growth only occurring during the latter period. *Nephrops* thus grows by the combined effect of moult frequency and size increment at moult, processes that have different frequencies at different stages of life. Juveniles in the benthic stage and up to the autumn of their first year of life, grow rapidly moulting once per month (Conan, 1978). After the onset of sexual maturity, moults diminish to 1-2 per year in males (usually in late winter or spring, and in late summer or autumn) and 0-1 in females (in late winter or spring, after the hatchings of the eggs) (e.g. Hillis, 1971; Farmer, 1973; Charuau, 1975; Conan, 1975, 1978; Sardà, 1991; Talidec and Reyss, 1993). This is reflected in different growth rates according to stage and sex: when immature, males and females have a similar growth patterns and similar growth curves; following sexual maturity, females grow considerably slower than males resulting in

smaller females with flatter growth curves compared to those of males (Fig. 4.3) (Frogliola and Gramitto, 1988; Vrgoč et al., 2004; Bell et al. 2007). The largest size classes of commercial *Nephrops* are thus composed mostly by males, whereas the smallest size classes comprise both sexes in more or less equal numbers.

It should be noted that, due to the lack of a reliable method for the determination of *Nephrops* age, its growth curves have to be established using indirect methods. These indirect methods rely either on the progression of modes in length-frequency distributions, or on tagging animals or on captivity experiments; all alternatives have some shortcomings (Mytilineou et al., 1998; Ulmestrand and Eggert, 2001; Bell et al., 2007). The commonly used Von Bertalanffy growth function, in the case of *Nephrops* thus appears to have some shortcomings related to the shape of the growth curve at different life stages, in particular for females. This has, for example, prompted the ICES Working Group on *Nephrops* to assess the species using a “combined” growth curve for females whereby the growth of immature females (up to the size at 50% maturity) is represented by the male growth curve while that of mature females by the female growth curve (Bell et al., 2007). This is of particular relevance for a species that lacks a routine age-determination method whose assessment may require the conversion of catches at length into catches at age based on the assumed Von Bertalanffy growth function (Bell et al. 2007, Dobby and Hillary, 2008). In this work we have only used truly length-based models and have assumed the Von Bertalanffy growth function to be an acceptable approximation of *Nephrops* growth; nevertheless these issues need to be borne in mind when interpreting the results.

Fisher et al. (1987) observed a maximum total length of 24 cm for Norway lobster, but larger individuals have been reported in the Adriatic Sea (e.g. 26.5 cm of total length (TL) in the northern Adriatic channels Crnković (1965)).

The size at 50% of maturity (L_{50}) is known for most of *Nephrops* stocks. This is estimated easily for females since ovary maturation stage is visible macroscopically. For males this is harder involving either a) the determination of the presence of spermatophores in the *vasa deferentia*, or b) the determination of a size in which allometric changes occur in the morphology of the appendix masculine and the cutter claw (McQuaid, 2002). In the shallow depths of north-western and northern Europe, females mature between 23 and 30 mm of carapace length (CL) and around 30-36 mm of CL in the deep waters of Portugal and in the Mediterranean Sea. The corresponding

age at 50% of maturity is around 3-4 years (Bell et al., 1996); 2-3 years for the Adriatic Sea (Frogliia and Gramitto, 1981, Orsi Relini et al., 1998).

Hatching and spawning periods, and length of egg incubation vary with latitude, whereas the breeding cycle changes from annual to biannual as one moves from south to north. In the Mediterranean, the reproduction cycle is annual (Frogliia and Gramitto, 1981; Bailey, 1984; Sardà, 1991; Redant, 1994). It starts in winter or in spring when mating takes place, then during spring or summer the ovaries mature and in late summer or early autumn egg-laying takes place. Immediately after spawning, berried females retreat into their burrows, waiting for the next hatching period in late winter or early spring. Briefly after hatching, females moult and mate again, starting a new cycle.

The length of the larval period depends on temperature and has been reported to last from 3 weeks (at 18°C) and 7 weeks (at 8°C) (Farmer, 1975; Orsi Relini et al., 1998; Dickey-Collas et al., 2000). Not much is known for the Adriatic Sea, especially in the Pomo/Jabuka pit. Once larvae are ready to settle, success is dependent upon the presence of suitable sediment and some sort of retention mechanism (Hill and White, 1990; Bailey et al., 1995). For example the combination of both factors is thought to favour dense *Nephrops* populations in the western Irish Sea, the Kattegat and Skagerrak, the Minches and the Pomo/Jabuka pit (Bailey et al., 1995; Brown et al., 1995; Hill et al., 1996, 1997; Øresland, 1998). The management implications of these retention areas become very important in depleted or overexploited situations (Bell et al., 2007) and in areas where little information exists on larval dynamics.

Potential fecundity (i.e. the number of eggs in the ovary) is exponentially associated to female body size, and increments from 600-1200 oocytes in females of 25 mm CL, to 3200-4800 oocytes in females of 45 mm CL. Effective fecundity (i.e. the numbers of eggs close to hatching – stage D) is considerably lower than potential fecundity in all *Nephrops* stocks, but the level of egg loss differs broadly between areas. In the Mediterranean, the loss of eggs from ovaries at stage D is around 40-50% (Gramitto and Frogliia, 1980; Mori et al., 1998). The main causes are extrusion failure, failure to adhere to the pleopods, unsuccessful embryonic development, predation and cannibalism (de Figueiredo and Nunes, 1965; Morizur et al., 1981).

4.1.5 Food

Nephrops are “*opportunistic predators and scavengers*” (Thomas and Davidson, 1962), leaving their burrows to feed at times of low light intensity and remaining in their

vicinity (Bell et al., 2007; Johnson et al., 2013). Feeding studies to ascertain the diet of *Nephrops* are fraught with difficulties related to the fact that this species uses its mouthparts and gastric mill to grind food, making it very difficult to identify stomach contents (Wieczorek et al., 1999; Bell et al., 2007). Nevertheless, a number of studies have been carried out, revealing a non-selective feeding pattern and a diet heavily dependent upon prey abundance rather than composition (Bell et al., 2007). Overall, at lower taxonomic resolutions, diet appears to be fairly consistent among areas, comprising crustaceans, polychaetes and some echinoderms and fish, in varying proportions depending on the existing prey community (Andersen, 1962; Thomas and Davidson, 1962; Fontaine, 1967; Fontaine and Warluzel, 1969; Lagardère, 1977; Gual-Frau and Gallardo-Cabello, 1988; Cristo, 1998; Cristo and Cartes, 1998; Wieczorek et al., 1999; Parslow-Williams et al., 2002; Bell et al., 2007). Suspension feeding (material $\leq 200 \mu\text{m}$; Loo et al., 1993) has been reported by several authors and is thought to be a mechanism of sustenance for berried females, who do not leave their burrows (Bell et al., 2007). Cannibalism has been found to occur at rather high levels (16% in fed *Nephrops* and 36% in starved *Nephrops*) in the laboratory (Sardà and Valladares, 1990); it has not been confirmed in the wild but has been postulated as a regulating factor for recruitment of juveniles to the stock in overcrowded conditions (Bell et al., 2007). Males and females are reported to have very similar diets and feeding patterns (Mytilineou et al., 1992). The prey diversity, especially from one area to another (Wieczorek et al., 1999), proves that *Nephrops* is a non-selective feeder heavily depending on prey availability/abundance rather than preference and reflecting the differences in benthic assemblages (Chapman and Rice, 1971; Chapman et al., 1975). *Nephrops* stomachs present the lowest fullness in summertime, when gonads grow intensively occupying most of the body cavity (Wieczorek et al., 1999).

The feeding pattern of *Nephrops* in the Adriatic Sea is described in detail in Wieczorek et al. (1999). They examined 2123 stomachs coming from the area “off Ancona” and the “Pomo/Jabuka Pits area”. Stomach contents comprised small pieces of both hard and soft parts of prey finely fragmented by manipulation, mastication and the action of gastric mill. Thus, the identification of prey species was complicated, however most of the food was classified at least to family and often genus and species level.

The great part of the diet of *Nephrops* consisted of crustaceans and fish. In particular, *Liocarcinus depurator* was the most important species for the Ancona ground, replaced by *Munida intermedia* in the Pomo ground. *Goneplax rhomboides* was a common

species for both grounds. Regarding Brachyura, *Monodaeus couchii* was observed only in the Pomo pit samples, whereas *Inachus sp.* occurred in only one sample of Ancona area. Natant decapods were principally represented by *Solenocera membrabacea*, *Alpheus glaber* and *Processa sp.* Crustaceans belonging to the Ostracoda, Copepoda, Stomatopoda, Mysidacea, Cumacea, Tanaidacea, Isopoda, Amphipoda and Euphasiacea were observed with less frequency. Only *Natatolana borealis* (Isopoda) assumed an important role in the diet of *Nephrops* living in the Pomo Pits and this is postulated to be an effect of discards.

Remains of Pisces were found in *Nephrops* from both the Ancona and Pomo pit grounds. *Sardina pilchardus* and *Engraulis encrasicolus* were the most abundant for the Ancona area. *Maurolicus muelleri*, *Gadiculus argenteus* and *Lepidopus caudatus* were found only in samples coming from the Pomo pits. The Gobiidae were well represented in the stomach contents of *Nephrops*; it was possible to identify the genera *Pomatoschistus*, for the Ancona grounds, and *Lesuerigobius*, in both areas. Other common species were *Cepola rubescens* and *Callionymus maculatus*, *Arnoglossus laterna* was found only in one sample from the Ancona ground.

Mollusca were also present, especially in the diet of small *Nephrops*, mainly *Turritella sp.*, *Alvania sp.*, *Nucula sp.*, *Phaxas adriaticus*, *Solenocurtus scopula* and the family Cardiidae. Scaphopoda were found in individuals from the Ancona ground, whereas Thecosomata were present in Pomo Pit samples only. Cephalopods were only identified when remains of beaks or sucker rings were found; *Ilex coindetii* and *Alloteuthis sp.* were recognized. Polychaeta also has to be mentioned, the most important taxa being *Glycera sp.*, *Nephtys sp.*, *Aphroditidae* and *Hyalinoecia tubicola*, with the latter taxa occurring in both areas, and by *Sigalionidae*, *Eunicidae*, *Sternaspis scutata* and *Pectinaria sp.* occurring only in the samples from Ancona.

Very small numbers of Hydrozoa, Bryozoa, Ophiuroidea and Holothuroidea were found infrequently in *Nephrops* stomachs in the Adriatic and ingestion of Foraminifera is regarded as incidental.

4.1.6 Predators

Contrary to *Nephrops* in its northernmost distribution where it has been reported to be predated upon mainly by cod, *Gadus morhua*, and other demersal fish species as well as possibly cephalopods (Armstrong et al., 1982, 1991; Lordan et al., 1998; Johnson et al., 2013), information on predation in its southernmost distribution is scarce. Many studies

on the diets of predatory fishes have failed to report *Nephrops* e.g. Serrano et al. (2003) on the Bay of Biscay. This lack of predation has been attributed to an interaction between the unavailability of the species owing to its burrowing behaviour, and the large and spiny bodies of adult *Nephrops* (Johnson et al., 2013). Nevertheless, early accounts of predation in the Adriatic Sea indicate anglerfish (*Lophius* spp.), elasmobranchs, hake (*Merluccius merluccius*), weevers (*Trachinus* spp.), gurnards (*Trigla* spp.), scorpionfish (*Scorpaena* spp.), poor cod (*Trisopterus minutus capelanus*), crabs (*Liocarcinus* sp.) and the musky octopus (*Eledone moschata*) as possible predators, but very little information is available (Farmer, 1975; Planas and Vives, 1952; Politou and Papaconstantinou, 1994). Past studies found a high percentage of stomachs of the lesser spotty dogfish (*Scyliorhinus canicula*) and the thornback ray (*Raja clavata*) to contain *Nephrops* (Thomas, 1965). The hypothesis of elasmobranch predation on *Nephrops* is of interest especially owing to the strong decrease of sharks and rays in the Adriatic Sea in the past few decades, which is attributed to bottom trawling (Ferretti et al., 2013).

4.1.7 Fishing methods

Nephrops is mainly fished by otter trawl gears. In Europe at least three type of trawlers are reported (Sardà, 1998); they differ in net size and proportions, width of mouth opening and size of otter doors. Italian fishing vessels use the smallest net type (Sardà, 1998; Maynou et al., 2003). Codend mesh size is 50 mm for diamond mesh or 40 mm for square mesh areas according to EC Regulation 1967/2006, in the past Italy and Greece trawlers used smaller meshes (28-32 mm) (Sardà, 1998; Maynou et al., 2003).

Baited traps and trammel nets are also used, particularly in northern Europe (e.g. Faeroe Island, UK, Scotland) and in some areas of the northern Aegean and Adriatic Sea, where trawling is forbidden, e.g. baited traps in the northern-eastern Adriatic channels (Maynou et al., 2003; Vrgoč et al., 2004). These gears sample different portions of the population: trawls will only catch individuals when they happen to be outside of their burrows, whilst the bait in traps entices animals out of their burrows meaning they can also catch berried females for example (Morello et al., 2009).

The rate of discarding of undersized or poor quality (soft post-moult) *Nephrops* can be quite high in some areas of northern Europe. Discarded individuals have a high mortality rate, around 75% (Sangster et al., 1997), that can increase in the Kattegat and Skagerrak area where discarded animals are subjected to low salinity surface waters

(Harris and Ulmestrand, 2004). When discarded individuals are left on deck for a long time, mortality rate reaches 100%. Discard rates of Norway lobster in the Adriatic Sea are negligible, since also small sizes have a considerable commercial value (Wieczorek et al., 1999).

The Norway lobster stock in the Adriatic Sea is shared by Italy and Croatia (Yugoslavia before 1992); Italy is the country that mainly exploits this stock, accounting for the 70% of total Adriatic catches (Fig. 4.5). Total commercial catch has fluctuated throughout the years, attaining a peak of 2530 tonnes in 1992 and a minimum value of 764 tonnes in 2002; post-2002 catches increased again attaining a new peak in 2005 (2195 tonnes), followed by a declining trend with 867 tonnes recorded for 2014 (Fig. 4.5).

Based on our estimates, 30% of Italian Adriatic Norway lobster catches come from the Pomo/Jabuka pits, whereas Croatian Norway lobster catches are principally derived by this area (85%; N. Vrgoč; pers.comm.).

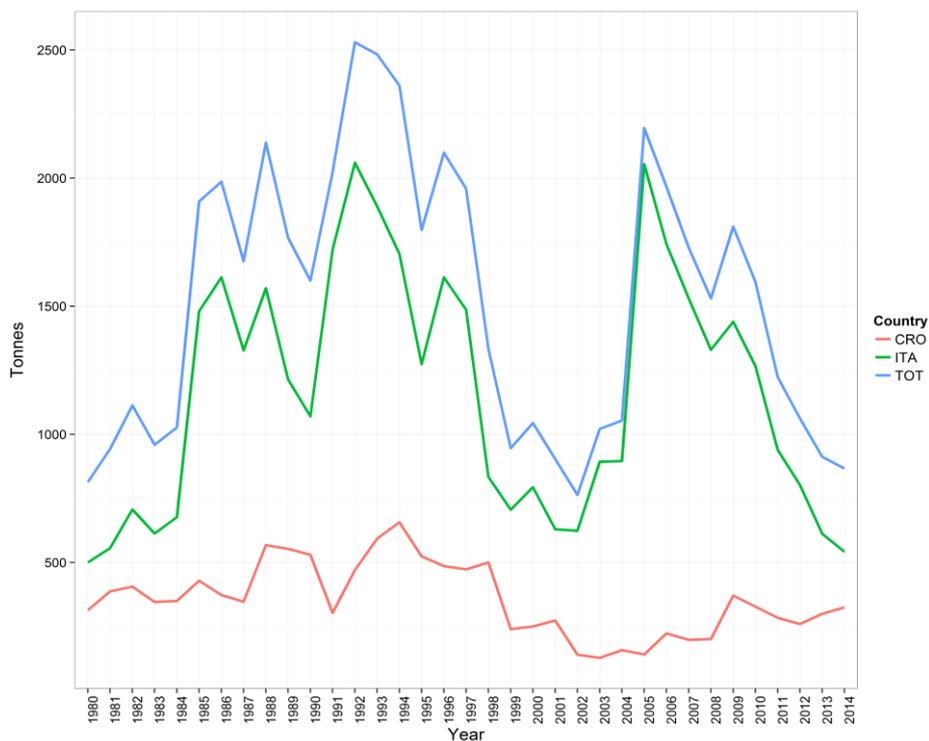


Fig. 4.5 Catches of Norway lobster for the northern and central Adriatic Sea by year and country: CRO (Croatia), ITA (Italy) and TOT (all country). Source: FishStatJ, 2015.

4.2 Stock assessment methods

4.2.1 Data

The assessment of *Nephrops* populations is fraught with difficulties: 1) their burrowing behaviour and emergence patterns (individuals only leave their burrows to feed and mate) heavily influence their availability to fishing gear and this varies according to sex and season, 2) there is a marked sexual dimorphism in growth parameters, 3) they are characterised by discontinuous growth which occurs only during moulting, making accurate age determination impossible. In the Adriatic Sea, they are the target of two fleets, the Italian and Croatian trawling fleets. For these reasons, the classical stock assessment methods based on the use of age classes are poorly successful, highlighting the need for explicitly length-based methods which consider length classes directly as well as treating sexes separately, yielding fleet-based results and using all data available regardless of the duration of the time series. Here two approaches have been tested: a simple length cohort analysis (LCA; section 4.2.2) and a more structured and detailed model, CASAL (Bull et al., 2012; see section 4.2.3).

Data used to develop these approaches refer to the study area only and they have been scaled using the same methodology employed for hake (Chapter 3): catches were calculated considering the fishing harbours known to exploit the study area (Ancona, San Benedetto, Martinsicuro, Giulianova, Pescara and Termoli for the Italian side and Split and Šibenik for the Croatian side; Fig. 1.4) and commercial length frequency distributions (LFDs) were obtained from DCF samples from San Benedetto and Giulianova between 2006 and 2013. Considering the peculiarity of the Pomo/Jabuka pits and assuming Italian and Croatian trawl fleets to have the same selectivity, Italian LFDs were applied to Croatian catches. LFDs are available both for landings and discards, they are expressed in terms carapace length (CL, mm) and individuals larger than 40 mm CL were grouped into one final length class forming a so-called “plus group”.

Input data used for developing the stock assessment models are summarised hereunder:

- Growth

Table 4.1 summarises the parameters describing the growth of Norway lobster and selected by literature. Sex is considered within the CASAL assessment,

whereas VIT does not permit to include data separated by sex, thus the average value of each single parameter was included.

Tab. 4.1 Von Bertalanffy Growth Function (VBGF) for Norway lobster. Notes: L_{inf} – asymptotic length at which growth is zero, k – growth rate, t_0 – age at which the organisms would have had zero size, a – y-intercept of length-weight relationship, b – slope of length-weight relationship.

Parameter	Value	Sex	Source
$L_{inf} (mm)$	59.0	M	Frogliia and Gramitto, 1988
$k y^{-1}$	0.324	M	Frogliia and Gramitto, 1988
t_0	-0.16	M	Frogliia and Gramitto, 1988
a	0.000246	M	Frogliia and Gramitto, 1981
b	3.28	M	Frogliia and Gramitto, 1981
$L_{inf} (mm)$	41.7	F	Frogliia and Gramitto, 1988
$k y^{-1}$	0.528	F	Frogliia and Gramitto, 1988
t_0	-0.02	F	Frogliia and Gramitto, 1988
a	0.000489	F	Frogliia and Gramitto, 1981
b	3.07	F	Frogliia and Gramitto, 1981

- Catches

Catches include Norway lobster fished in the study area only. Italian landings for the entire GSA 17 were split using VMS data (details are given in section 2.2) whereas for Croatia it was assumed that 85% of total Croatian landings were caught in the study area (N. Vrgoč, pers. comm.) and this proportion was applied to derive landings for all years. In 2011, 2012 and 2013 Italian DCF sampling of catches reported discards. To estimate discards when data were not collected (2006-2010), a proportional value was added to the landings of each year for which discards were not quantified. Assuming Italian and Croatian fleets have the same selectivity, the Italian discard ratio was also applied to Croatian landings for each year.

Figure 4.6 represents estimated catches within the study area; a generally increasing trend is shown to 1993, when the highest value of 1128 tonnes was recorded: catches decreased to reach the minimum value of 325 tonnes in 2002. During these years Italy and Croatia accounted for similar values, while from 2003, Italy increased its catches to 678 tonnes in 2005. The years following present a continuous decreasing trend. Croatia, on the contrary, shows an increasing trend in catches from 2003 to 2014, accounting for lower values

compared to those from Italy, with the exception of the two most recent years. LCA takes in account years from 2006 to 2013 only, while CASAL considers a longer time series, from 1985 to 2014. Moreover, CASAL, being a more structured method, allowed for the use of data organised by time step (details are given in section 4.2.3); catches were thus split into two time steps and are shown in figure 4.7 for Italy and figure 4.8 for Croatia.

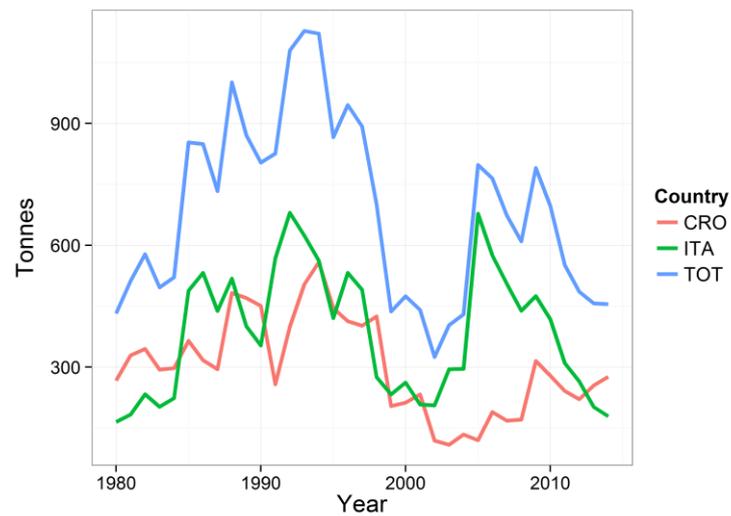


Fig. 4.6 Estimated catches for Norway lobster in the study area from 1980 to 2014: total (TOT, blue line); Croatian (CRO, pink line; before 1993 data refers to Yugoslavia) and Italian catches (ITA, green line).

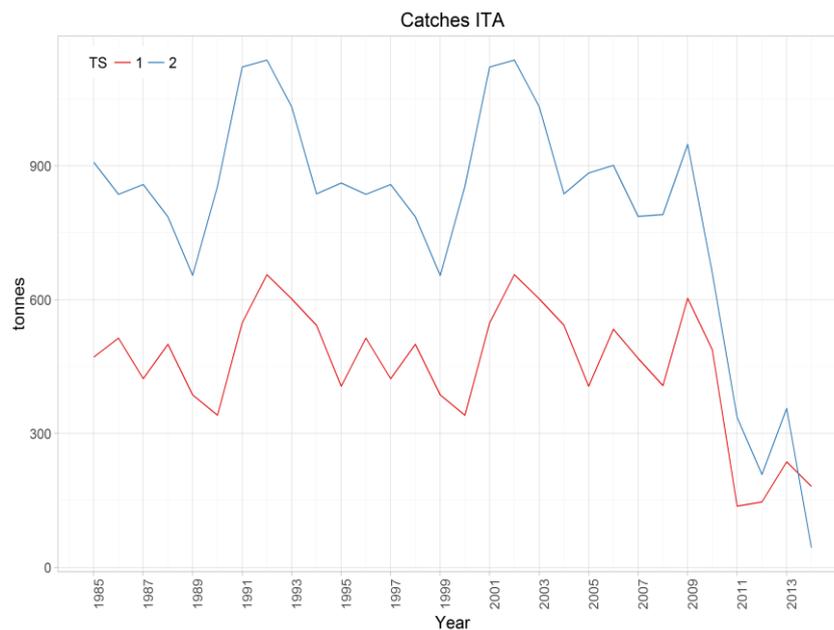


Fig. 4.7 Italian estimated catches for Norway lobster in the study area from 1985 to 2014: time step 1 (red line) and time step 2 (blue line).

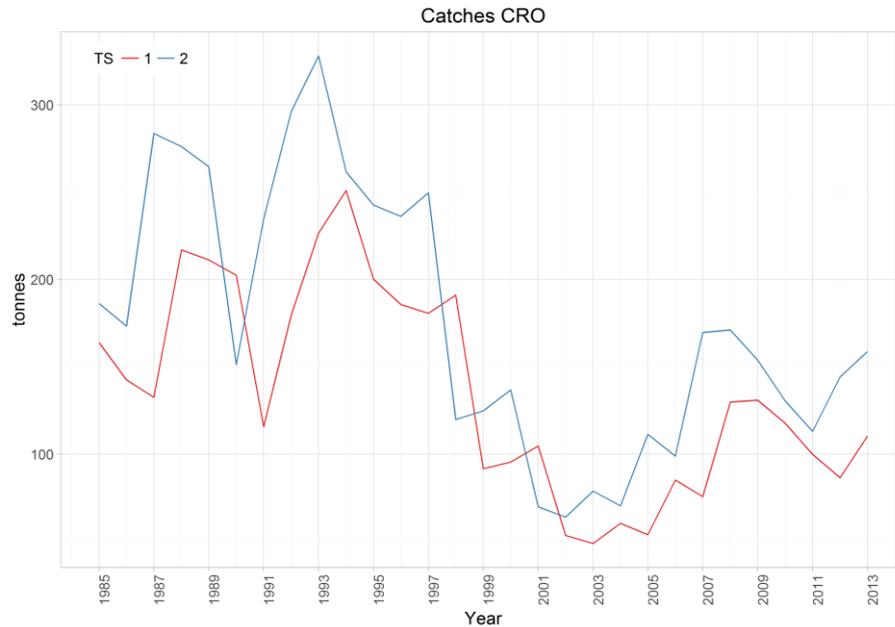


Fig. 4.8 Croatian estimated catches for Norway lobster in the study area from 1985 to 2014: time step 1 (red line) and time step 2 (blue line).

- Length Frequency distributions

The LFD of the catches considered in this study describe a continuous decreasing trend over the years, with 2006 being the most abundant year (Fig. 4.9). LFDs present a non-uniform distribution among years, their shape is mainly unimodal but peaks are different among years (Fig. 4.9). More specifically, in 2008 and 2009 larger individuals were found compared to previous and following years. These distributions have to be interpreted with attention: as mentioned previously, the Norway lobster stock living in the Pomo Pit area comprises smaller individuals compared to the stock located off Ancona and considering that LFDs were subdivided between areas (study area and outside the study area) using landing harbours only some mismatches may have resulted. This fact is suggestive of the use of georeferenced data, i.e. VMS and logbooks, to split LFDs between areas; this work is in progress and until proper data will not be available, this is the best possible partitioning.

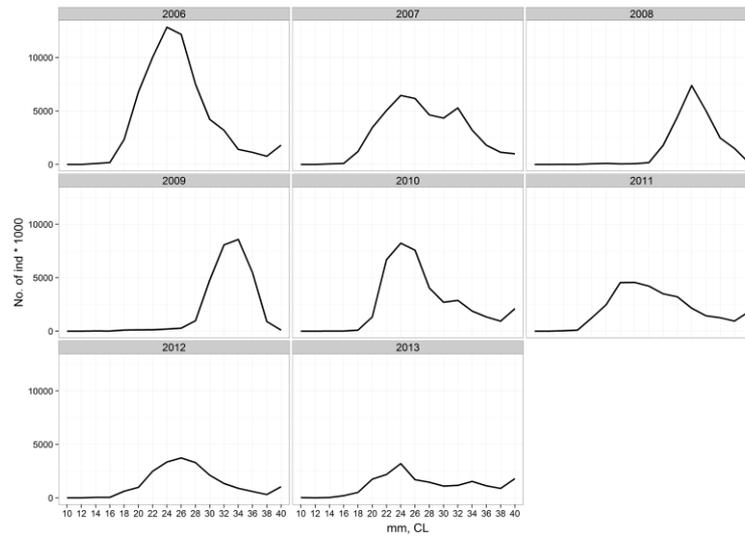


Fig. 4.9 Length Frequency Distributions (LFD) of Norway lobster catches in the study area for years from 2006 to 2013.

LFDs structured by sex and time step are used for developing the CASAL model (Figs. 4.10 and 4.11). VIT requires the number of individuals by length classes, whereas CASAL needs proportions by length class only. Moreover the plus group used in CASAL was larger (60+ mm, CL).

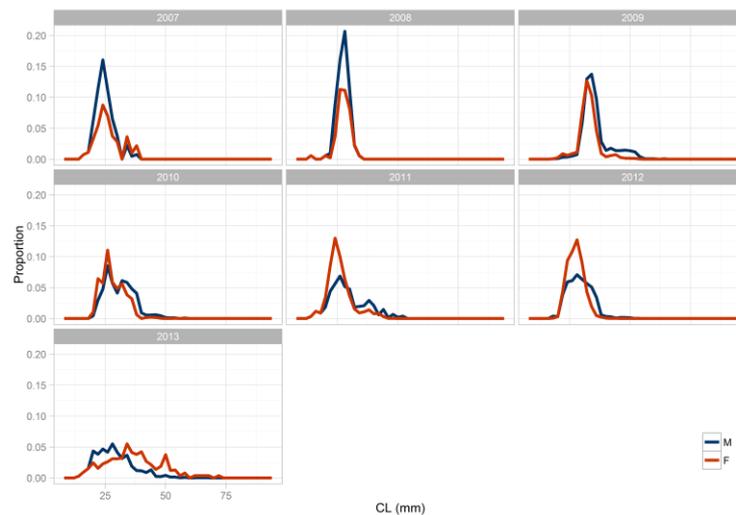


Fig. 4.10 Length Frequency Distributions (LFD) of Norway lobster catches for time step 1 within the study area for the years included in the CASAL model (2007-2013) and divided by sex: female (red) and male (blue).

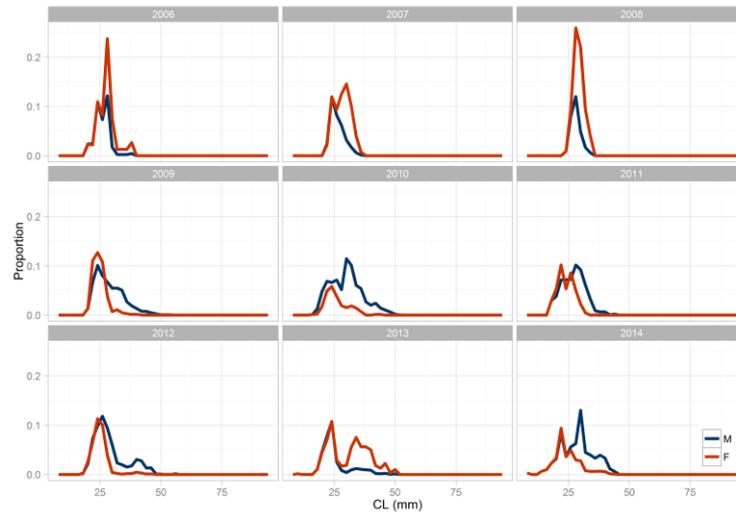


Fig. 4.11 Length Frequency Distributions (LFD) of Norway lobster catches for time step 2 within the study area for the years included in the CASAL model (2007-2013) and divided by sex: female (red) and male (blue).

- Natural mortality and maturity

Natural mortality (M) accounts for the rate of mortality of a given species due to all causes except fishing. M can be a scalar, meaning that the same constant value is applied to all lengths or ages, or a vector, allowing to model natural mortality by length or age. The most common option for the Norway lobster assessment is the use of scalar natural mortality, and if sexes are considered the M value for females is assumed to be lower than that of males, since females spend more time in burrows decreasing their probability of dying of natural causes (Morizur, 1982; ICES, 1994; Dobby and Hillary, 2008). A constant natural mortality over length classes and years of 0.3yr^{-1} was assumed for the VIT assessment (Marrs et al., 2000; Table 4.2) since sex was not considered.

A vector of the proportion of mature individuals at length was used and this was time invariant (Table 4.2) (Froglia and Gramitto, 1981; Vrgoč et al., 2004).

Tab. 4.2 Natural mortality (M) at length and the proportion of mature individuals at length (Mat).

Length (mm. - CL)	M (yr^{-1})	Mat
10 - 20	0.3	0
22- 28	0.3	0.5
≥ 36	0.3	1

CASAL model, on the other hand, was developed using a vector of natural mortality calculated using PRODBIOM (Abella et al., 1997; 1998) (Table 4.3). PRODBIOM is able to calculate a value of M at length or age considering the growth features of the species in exam; this method was initially developed for demersal fish species but in recent years it has also been used in the assessment of some crustacean species (.g. pink shrimp in GSA 12 and red shrimp in GSA 19, GFCM, 2014) and is tested here for *Nephrops*.

Tab. 4.3 Natural mortality vector (M) at length obtained using Prodbiom (Abella et al., 1997; 1998).

Length (mm, CL)	M males (yr ⁻¹)	M female (yr ⁻¹)
4	1.26	1.26
6	1.14	1.14
8	1.01	1.01
10	0.89	0.89
12	0.76	0.76
14	0.65	0.65
16	0.55	0.55
18	0.48	0.48
20	0.44	0.44
22	0.41	0.41
24	0.39	0.39
26	0.36	0.36
28	0.34	0.29
30	0.32	0.27
32	0.31	0.26
34	0.30	0.25
36	0.28	0.23
38	0.27	0.22
40	0.26	0.21
42	0.25	0.20
44	0.25	0.20
46	0.24	0.19
48	0.23	0.18
50	0.22	0.17
52	0.21	0.16
54	0.21	0.16
56	0.21	0.16
58	0.21	0.16
60+	0.21	0.16

- Survey data

Survey data for the tuning were obtained from the GRUND survey (see section 2.3) and the MEDiterranean International Trawl Survey (MEDITS, Bertrand et al., 2002; see section 2.3).

Two series were considered for the GRUND survey. The first one, “GRUND”, includes time series for Italian and Croatian stations separately from 2000 to 2007 (Fig. 4.12) and the second, “GRUND 2”, comprises the Italian side only from 1985 to 1998 with notable gaps in 1986, 1987, 1989 and 1990 (Fig. 4.13). GRUND describes a general increasing trend, with the highest values in 2005 for both Italy and Croatia, and the lowest values in 2002 for Italy and 2004 for Croatia. GRUND 2 includes less recent years and presents a more fluctuating, although generally decreasing, trend; the highest biomass is reported for 1991, whereas the lowest biomass was recorded in 1998.

More recent abundance estimates (1996 – 2014) come from the MEDITS survey and are available for Croatia and Italy separately (Fig. 4.14). Both Italy and Croatia reveal a decreasing trend over the considered time series; Italy accounted for the highest abundance in 1997 and the lowest in 2013. The highest abundance for Croatia was observed in 1996, and the lowest in 2011.



Fig. 4.12 Norway lobster – index of absolute abundance from the GRUND survey for 2000 - 2007.

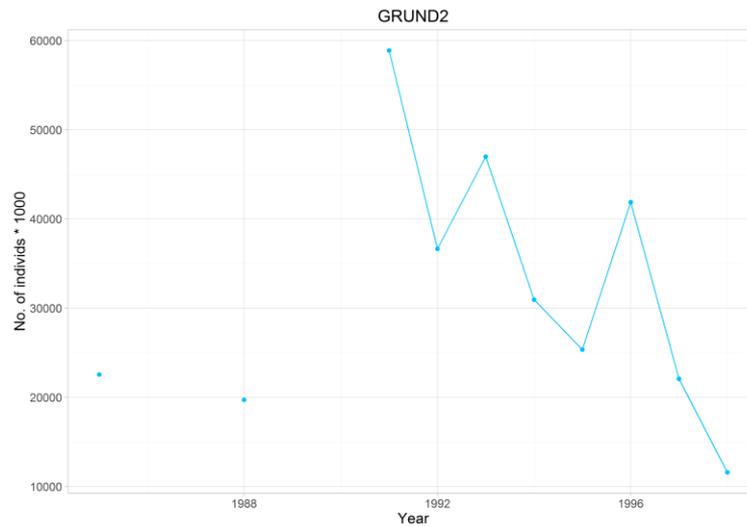


Fig. 4.13 Norway lobster – index of absolute abundance from the Italian GRUND survey for 1985 – 1998 (GRUND 2), except years 1986, 1987, 1989 and 1990.



Fig. 4.14 Norway lobster – index of absolute abundance from MEDITS survey for years from 1996 to 2014 for both Croatia (pink line) and Italy (blue line).

Length frequency distributions derived from the survey were also included in the CASAL model; for the GRUND survey, LFDs were available only for 2003 and 2005 – 2007 for the Italian side (Fig. 4.15) and for years 2004, 2005 and 2007 for the Croatian side (Fig. 4.16). The population described by the GRUND survey includes mainly small animals between 15 mm and 40 mm (CL), bigger sizes are principally represented by males (Figs. 4.15 and 4.16).

In the case of the MEDITS survey, LFDs of males and females were more similar, and highlighted the fact that the population in the study area was mainly

composed by small individuals. LFDs underline also a strong decrease over the years (Fig. 4.17 – Italian Medits; fig. 4.18 - Croatian Medits).

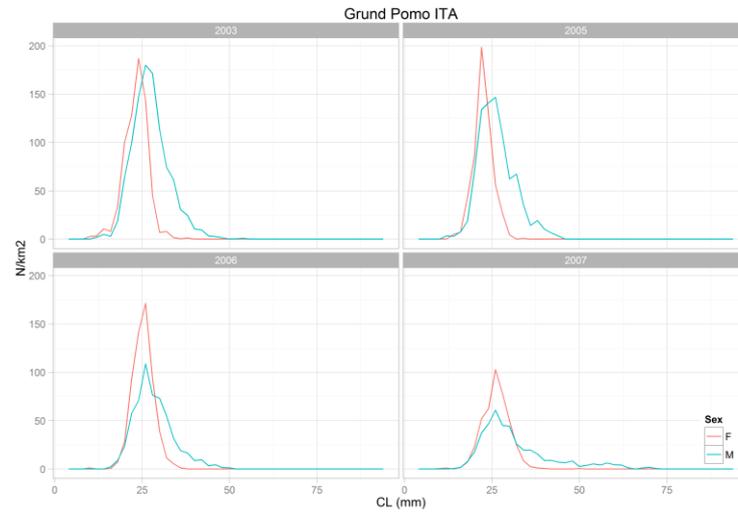


Fig. 4.15 Norway lobster length frequency distributions (LFD) from the GRUND survey for Italy for 2003, 2004, 2006 and 2007. Colours represent sex: female, pink line, and male, blue line.

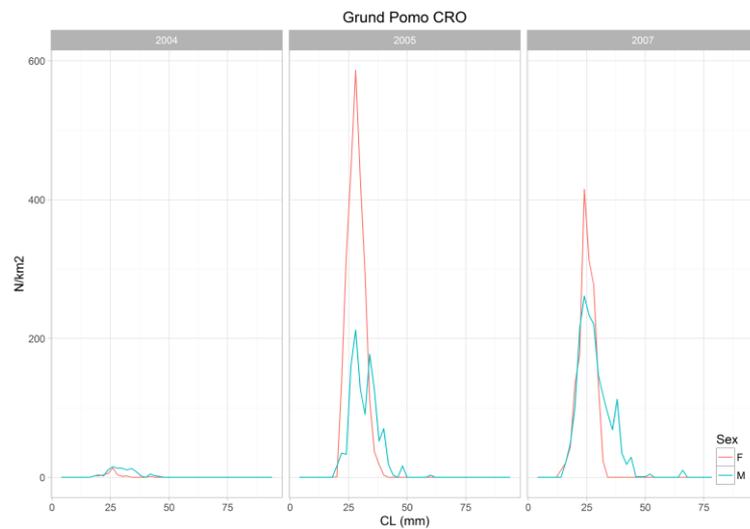


Fig. 4.16 Norway lobster length frequency distributions (LFD) from the GRUND survey for Croatia for 2004, 2005 and 2007. Colours represent sex: female, pink line, and male, blue line.

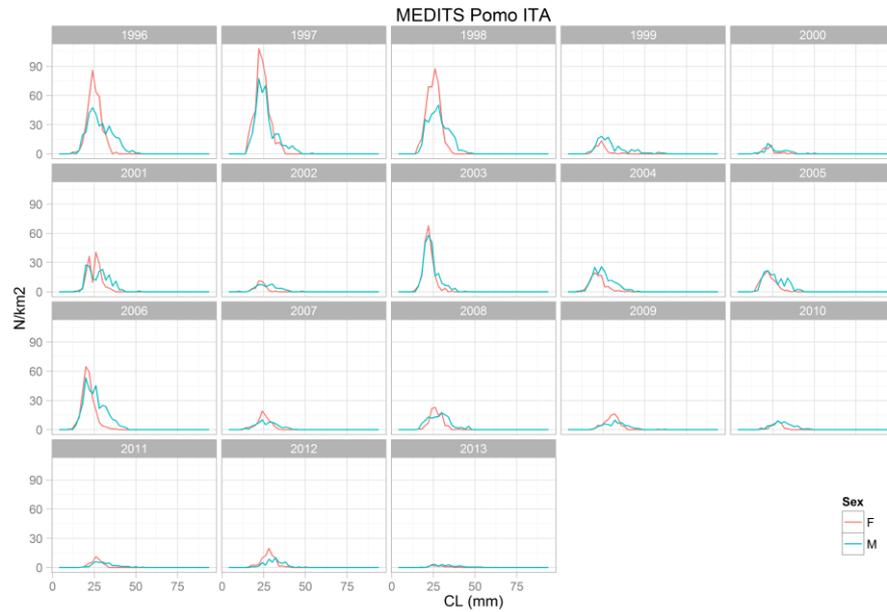


Fig. 4.17 Norway lobster length frequency distributions (LFD) from the MEDITS survey for Italy from 1996 to 2013. Colours represent sex: female, pink line, and male, blue line.

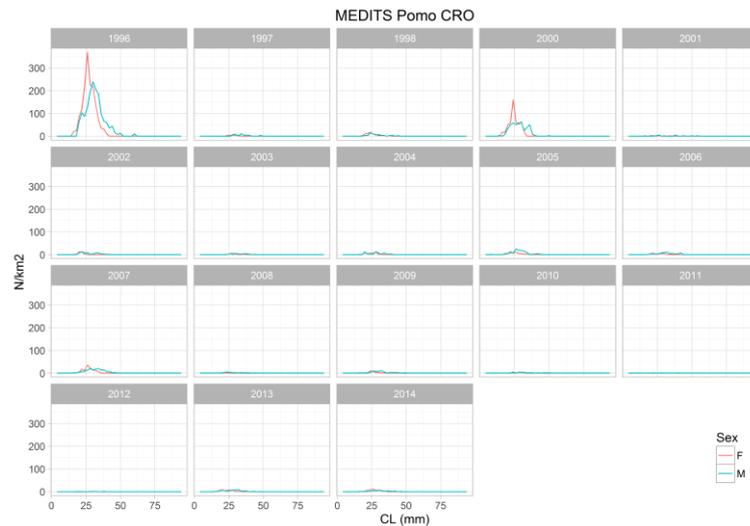


Fig. 4.18 Norway lobster length frequency distributions (LFD) from the MEDITS survey for Croatia from 1996 to 2014. Colours represent sex: female, pink line, and male, blue line.

4.2.2 Length Cohort Analysis

A Length Cohort Analysis (LCA) was developed using the VIT software (Leonart and Salat, 1992, 1997) for Norway lobster too. VIT performs a virtual population analysis (VPA) using catch data, structured by age or size, and some auxiliary parameters, reconstructing the population backwards under the assumption of a steady state and estimating fishing mortality (F). See section 3.2.2 for more specifications.

The reasons for choosing a LCA were mainly linked to the facts that (i) for crustaceans age determination is not available, and (ii) the short times series of catch-at-length data

available. Input data for this analysis are presented in tables 4.1 and 4.2 and figures 4.6 and 4.9.

The results for Norway lobster indicate a rather stable biomass over the years, with a minimum of 639 t in 2008 and a maximum of 1163 t in 2010, 1124 t are recorded in 2013 (Fig. 4.19 – red line). Fishing mortality, represented by the average overall length classes F_{bar} , shows a fluctuating trend increasing from 0.69 yr⁻¹ in 2006 to 0.92 yr⁻¹ in 2009, then decreasing to its lowest value in 2013 (F_{bar} = 0.37 yr⁻¹) (Fig. 4.5 – blue line). Results are in agreement with the fluctuating trend shown by catches (Fig. 4.6) and the MEDITS trend (Fig. 4.14).

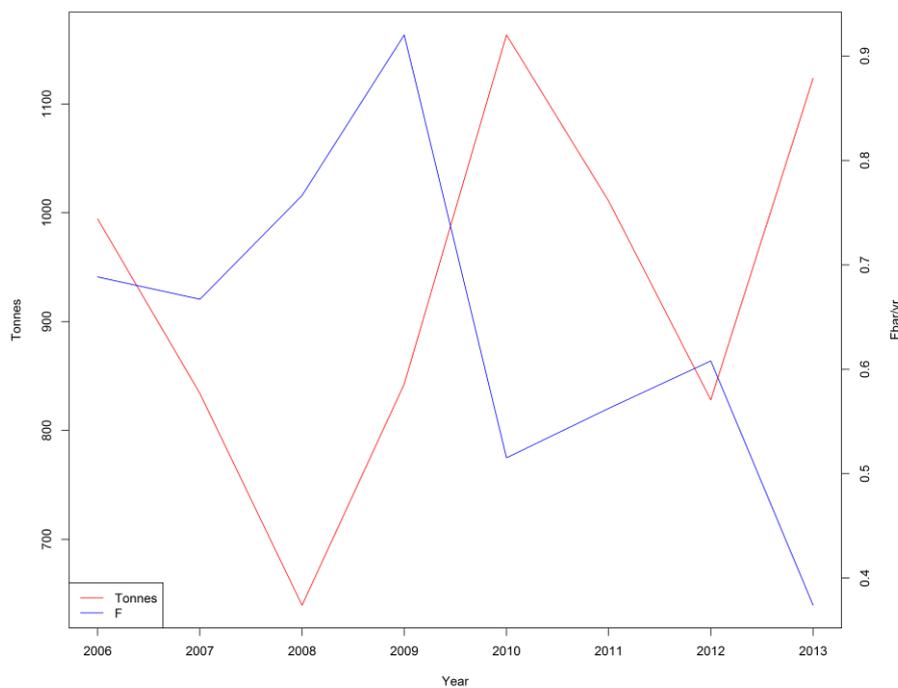


Fig. 4.19 Norway lobster biomass (red line) and mean fishing mortality (yr⁻¹, blue line) estimated by LCA.

4.2.3 CASAL

CASAL is a very flexible platform which allows the specification of complex models, both single and multi-species, taking into account numerous variables and using information by length directly without slicing it into ages. It can generate point estimates of the main parameters of interest as well as likelihood profiles and Bayesian posterior distributions, and can project stock status into the future as well as calculate outputs of interest to management e.g. F_{max} , $F_{0.1}$, MSY (Bull et al., 2012).

The main difference between an age-based and a size-based model lies in the way growth is specified. In a size-based model growth is the process by which fish move between subsequent size classes. In CASAL growth can be specified in three different ways: (i) the Francis parameterisation (Francis, 1988) which makes use of growth increments from the von Bertalanffy growth function, (ii) an alternative Francis parameterisation with exponential decay and (iii) a fixed user-defined transition matrix. Here the first option was selected, since it represents the ‘basic’ model in which the von Bertalanffy growth function, estimated for *Nephrops* residing in the Pomo pit (Table 4.1) in this case, were used as fixed input parameters within the CASAL model described below

Model structure reflected the seasonal patterns in Norway lobster sex ratio, related to moulting and reproductive behaviour. The dynamics of the *Nephrops* population in the Pomo pit were thus partitioned into two separate time steps:

- Time step (TS) 1: from April to July inclusive, reflecting periods of the year when both sexes are relatively equally available to the fishery, and
- Time step (TS) 2: from August to March when mature egg-bearing females are far less available than males.

Adoption of these time steps has meant that the model year runs from April to March, i.e. we have a split year situation.

Sex was included in the model partition to allow for different availability of the two sexes.

The *Nephrops* stock in the study area extends from international waters into the Croatian territorial sea. Two distinct fisheries, Italy and Croatia, operate here and, given that the species does not migrate, it was decided to consider the two areas as separate. Data, collated by sex, year, time step and area, are summarized in Table 4.4 and details are presented in section 4.2.1.

The model was run over the period April 1985 to March 2014 (model years 1985 - 2013), with model year labelled by the calendar year that it starts in.

Table 4.4. Data available for Norway lobster assessment in the study area. Years represent overall year range, but data may not be available for all intermediate years.

	Italian area	Croatian area
Landings	Time step 1 (1985-2013)	Time step 1 (1985-2013)
	Step 2 (1985-2013)	Time step 2 (1985-2013)
Length frequency of commercial catches	Time step 1 (2007-2013)	Used Italian data
	Time step 2 (2006-2013)	Used Italian data
Surveys	MEDITS (1996-2013)	MEDITS (1997-2013)
	GRUND (2000-2007)	GRUND (2001-2007)
	GRUND2 (1985-1998)	
Length frequency of survey catches	MEDITS (1996-2013)	MEDITS (1996-2013)
	GRUND (2000-2007)	GRUND (2004-2007)
	GRUND2 (1993-1998)	
Growth	From Froglija and Gramitto 1988	
Maturity	From Froglija and Gramitto 1981	
Length weight relationship	From Froglija and Gramitto 1988	
Natural mortality	Calculated with PRODBIOM (Abella et al., 1997)	

The annual cycle of processes applied within the population model according to each TS are summarized in Table 4.5 and Fig. 4.20.

Table 4.5. Annual cycle of the population model for the study area, showing the processes taking place at each time step, their sequence within each time step, and the available observations. Fishing and natural mortality that occur together within a time step occur after all other processes, with 50% of the natural mortality for that time step occurring before and 50% after the fishing mortality.

Time step	Period	Process	Proportion in time step
1	April - July	Growth	
		Natural mortality	0.333
		Fishing mortality	From landings
2	August - March	Recruitment	1
		Maturation	1
		Natural mortality	0.667
		Fishing mortality	From landings

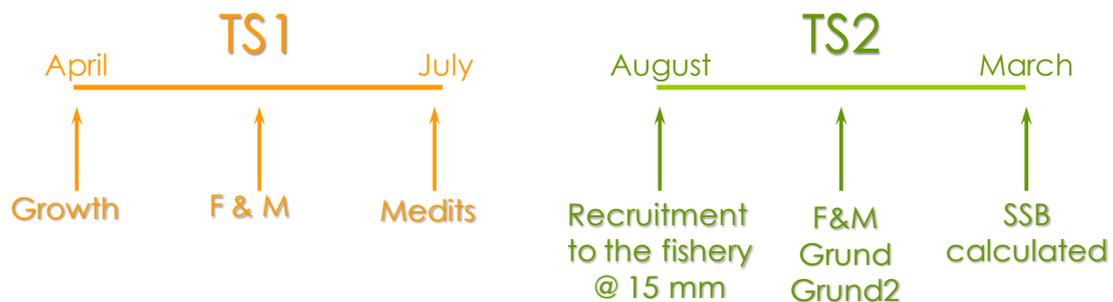


Fig. 4.20. Depiction of the annual cycle of the CASAL *Nephrops* population model for the study area, showing the timing of the processes captured within each time step (TS) of the model.

Italian landings data were allocated to time step and area on the basis of analysis of VMS data examining the distribution of fishing effort and landings, and applying the patterns to historical years (see section 2.2). Croatian landings data were allocated to time step and area applying the seasonal pattern in catch observed for fishery Zones C and D in 2008 - 2010 to all previous years. Commercial fishery and trawl survey selectivities were assumed to be the same in the two areas, but varied between time step and survey (although the selectivity was assumed to remain constant between the earlier GRUND 2 and later GRUND surveys). No commercial sampling data (length frequency distributions) were available for the Croatian fishery and were thus assumed to be the same as those of the Italian fishery.

A single recruitment index was estimated and applied to both areas, with the proportion of total recruits going to each area estimated within the model and assumed constant over time. Growth was fixed on the basis of data contained in Froglija and Gramitto

(1988). Natural mortality was applied as a vector by length, calculated by sex using PRODBIOM (Abella et al., 1997) and derived from the von Bertalanffy growth function and the length-weight relationship.

Selectivity in stock assessment models is expressed as the probability that a fish of a given age/size will be caught by the gear if it is available combined with the probability that a fish will be available to the fishing gear (Maunder et al., 2014; Punt et al., 2014). CASAL takes into account selectivity using a capped logistic selectivity for males, that is a logistic selectivity allowing a maximum selectivity other than 1, and double normal selectivity for females, that is a distribution describing also a declining right limb (Fig. 4.23); these models allow to represent differences in overall catchability between the sexes, and reduced availability of mature (larger) females while ovigerous. The length frequency data showed evidence that the GRUND survey was not catching large males (Figs. 4.15 and 4.16) (which were caught by the commercial fishery; figs. 4.10 and 4.11), implying reduced availability to the survey (potentially related to specific spatial targeting by the fishery versus the random sampling scheme of the scientific survey). A double normal selectivity was therefore also applied for males in the GRUND survey.

Fits and key parameter estimates (Table 4.6) show that the model estimates an SSB_0 (the spawning stock biomass that would exist if no fishing occurred) for the study area of 15900 tonnes, with SSB_{2013} estimates at 5200 tonnes, i.e. 33% of SSB_0 . The model estimates that 83% of the recruitment (in numbers) occurs in the Italian (and extraterritorial) area. Fits to the survey indices were variable (Fig. 4.21), and the model estimated a general declining biomass trajectory, with short term increases associated with strong recruitment in the late 1980s and mid 2000s (Fig. 4.22). The exploitation rate (catch / SSB) increased slowly during the 1980s, remained stable during the 1990s, but increased and became more variable during the 2000s (Fig. 4.22).

Table 4.6. Key estimated parameters from the CASAL *Nephrops* model in the study area.

Parameter	Estimate
SSB_0	15895.3 tonnes
SSB_{2013}	5206.53 tonnes
SSB_{2013}/SSB_0	0.3275
Proportion recruitment to Italian area	0.834471
Survey q values	
GRUND	0.148257
GRUND2	0.115953
MEDITS	0.0248663
MSY (max. ann. sustainable catch)	630 tonnes
B_{MSY}	10327.55 tonnes

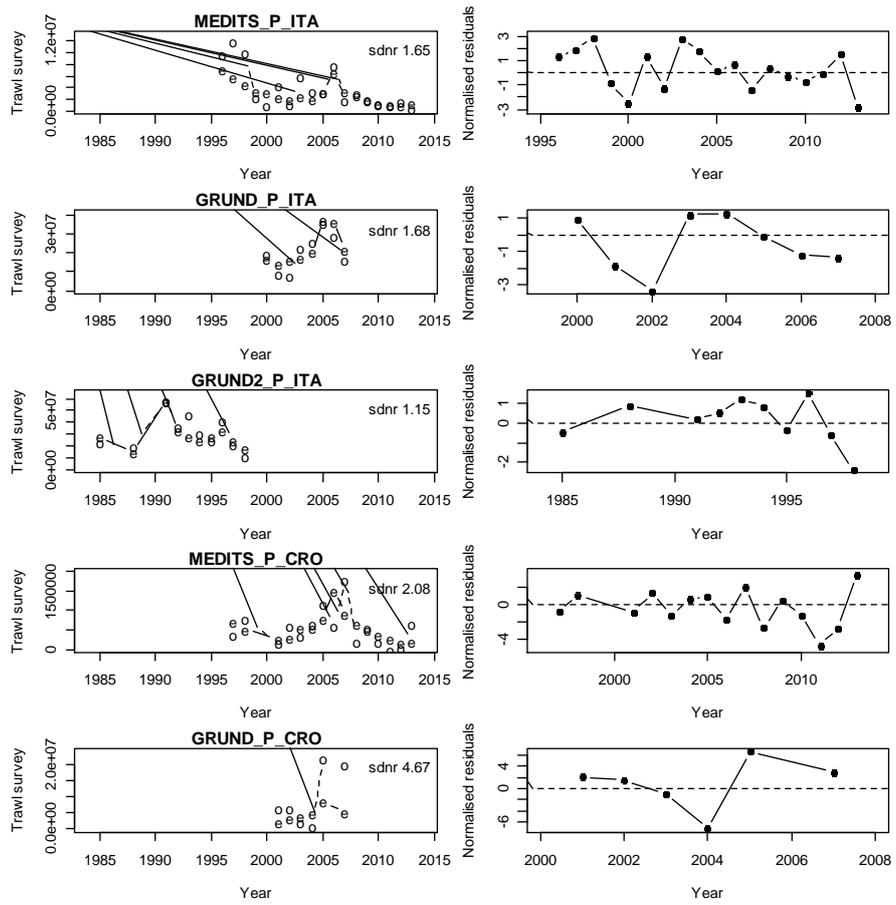


Fig. 4.21. Fits to trawl survey indices (left column) and normalised residuals (right column) for each survey for the study area.

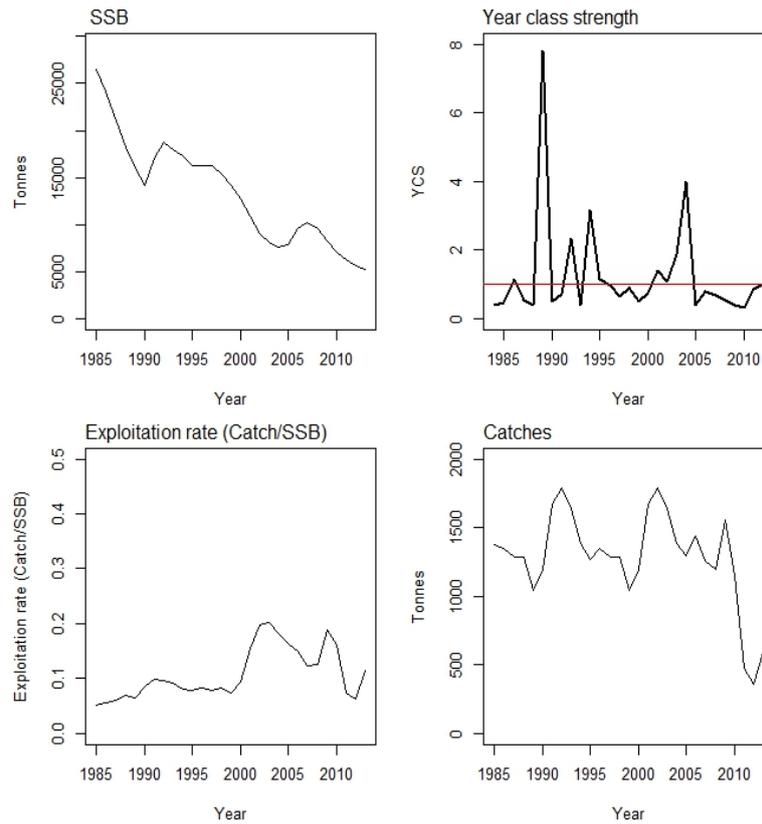


Fig. 4.22. Trajectory of estimated spawning stock biomass (SSB)(top left), year class strength (YCS)(top right) and exploitation rate (catch / SSB)(bottom left) and catches (bottom right) for *Nephrops* in the study area.

Estimated selectivities (Fig. 4.23) follow expected patterns, in that male availability was considerably higher than females during time step 2. Average fits to the length distributions were good (Figs. 4.24 and 4.25), but fits to individual samples were more variable (Figs. 4.24 to 4.34).

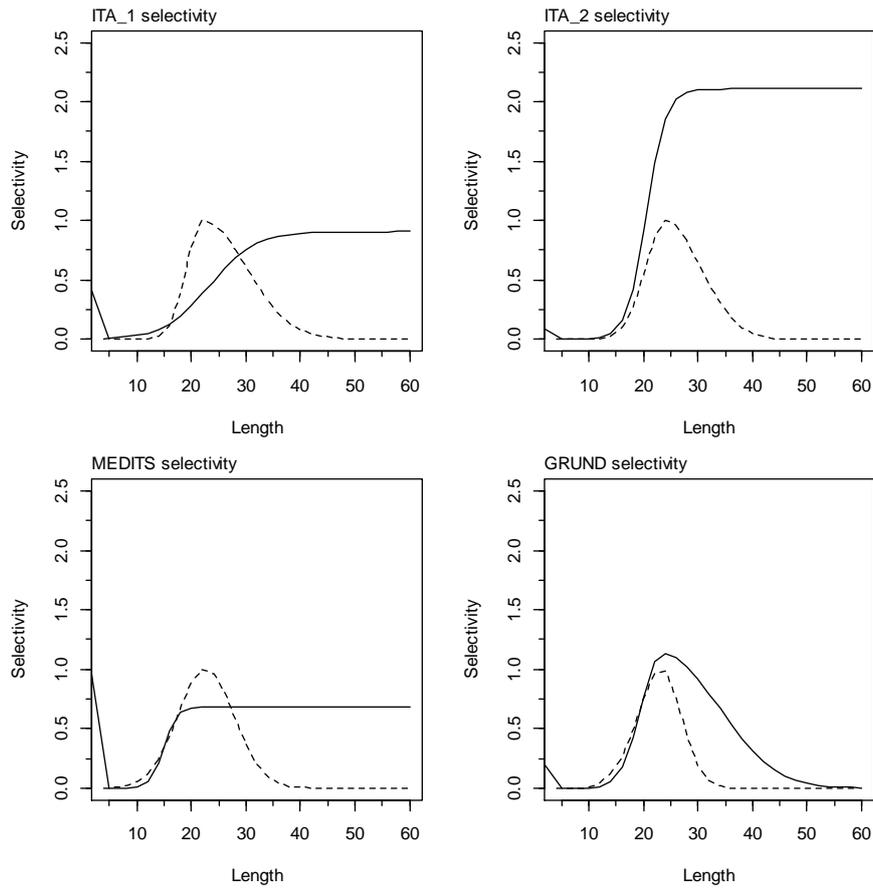


Fig. 4.23. Fishery and survey selectivity curves for fleets and surveys considered: commercial trawl fleet in time step 1 (ITA_1, top left), commercial trawl fleet in time step 2 (ITA_2, top right), MEDITS in time step 1 (bottom left) and GRUND in time step 2 (= GRUND2 survey, bottom right) surveys. Solid line – males, dotted line – females.

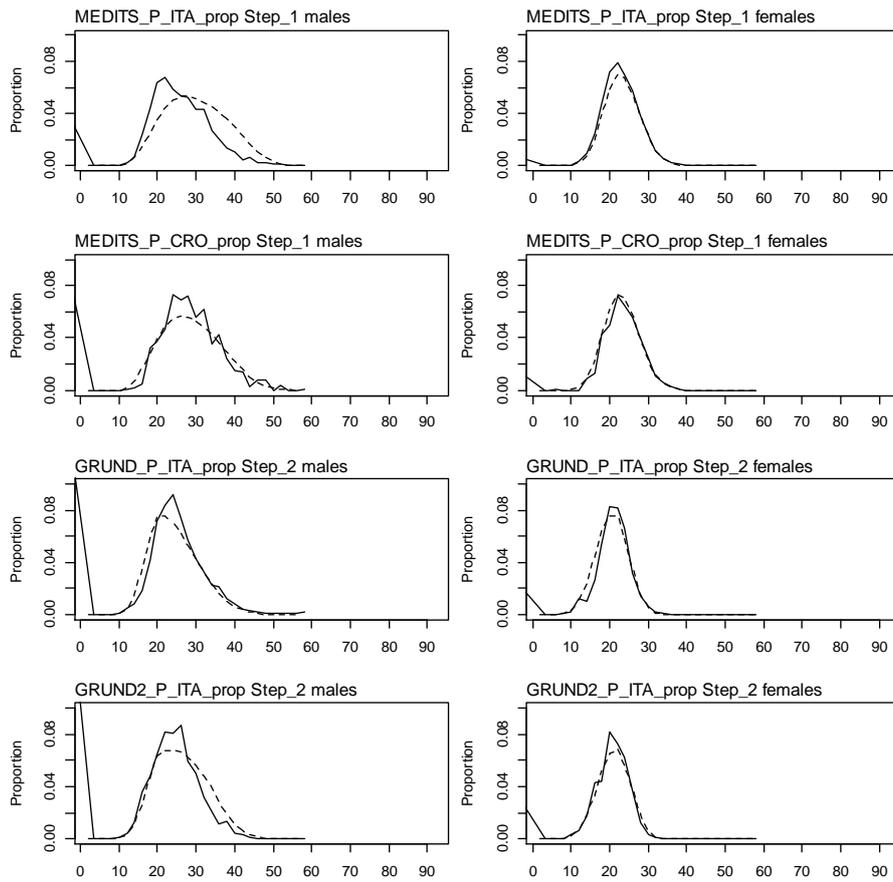


Fig. 4.24. Average observed (solid line) and fitted (dashed line) length frequency distributions for MEDITS (Italian and Croatian areas), GRUND (Italian area) and GRUND2 (Italian area) survey length frequency samples for the study area.

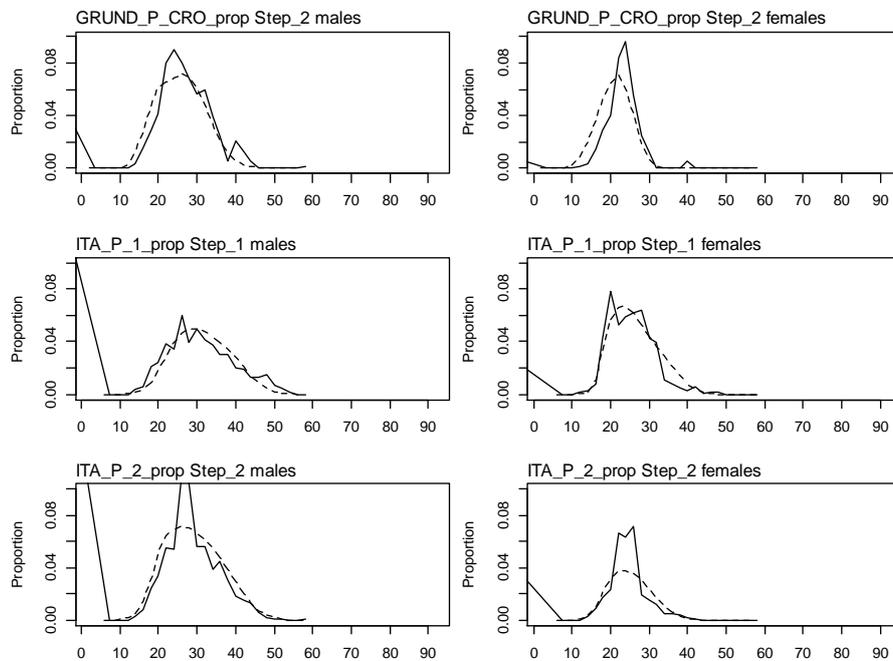


Fig. 4.25. Average observed (solid line) and fitted (dashed line) length frequency distributions for GRUND (Croatian area) survey and Italian commercial fishery length frequency samples for the study area.

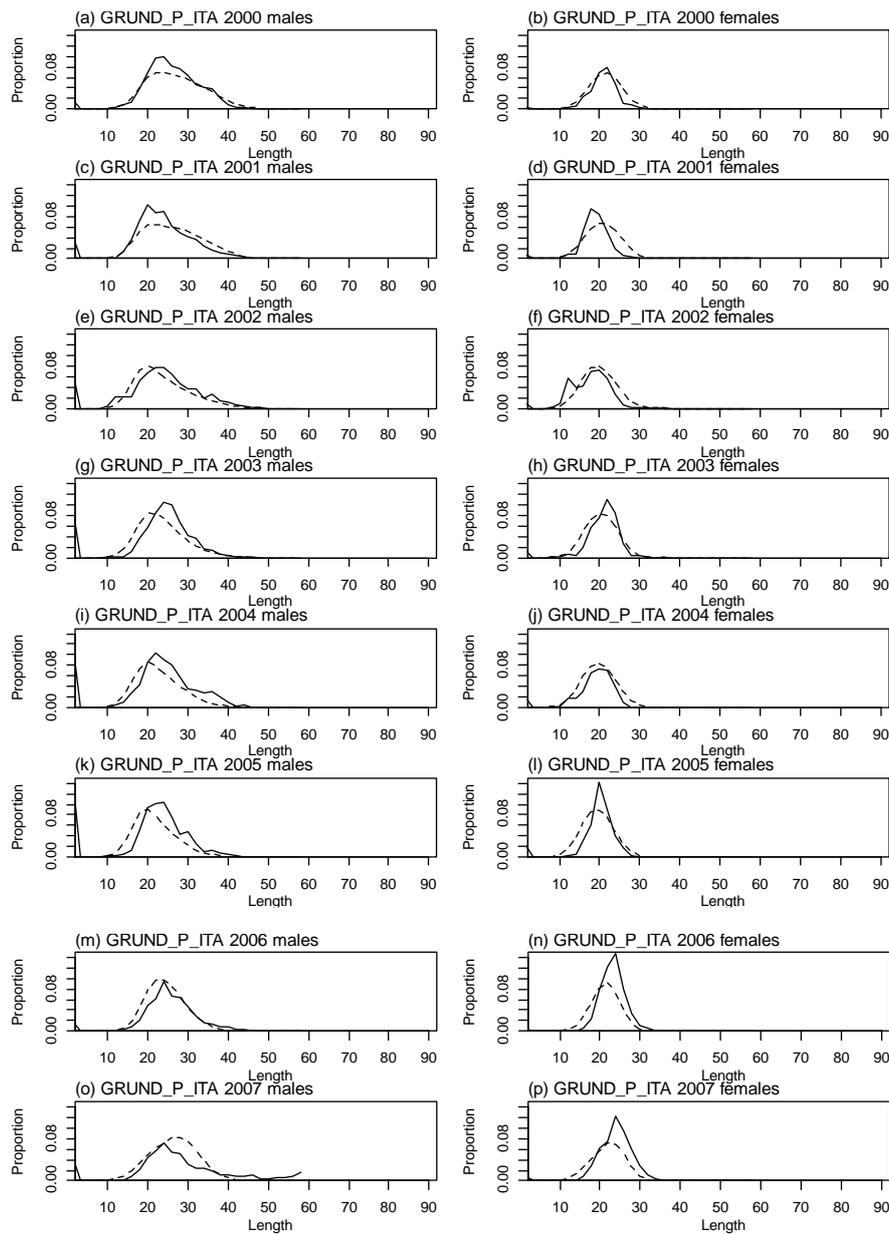


Fig. 4.26. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, GRUND survey (Italian area).

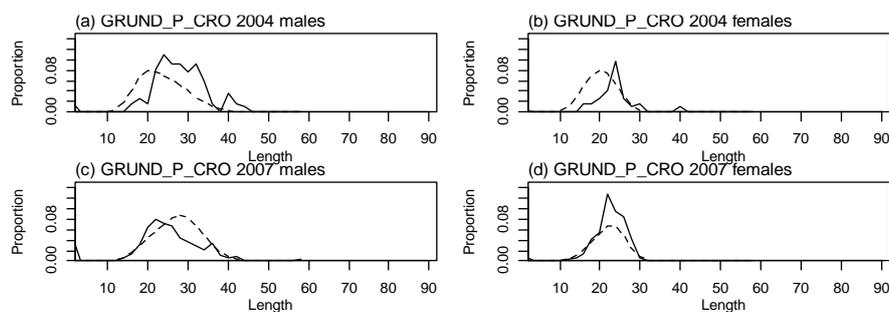


Fig. 4.27. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, GRUND survey (Croatian area).

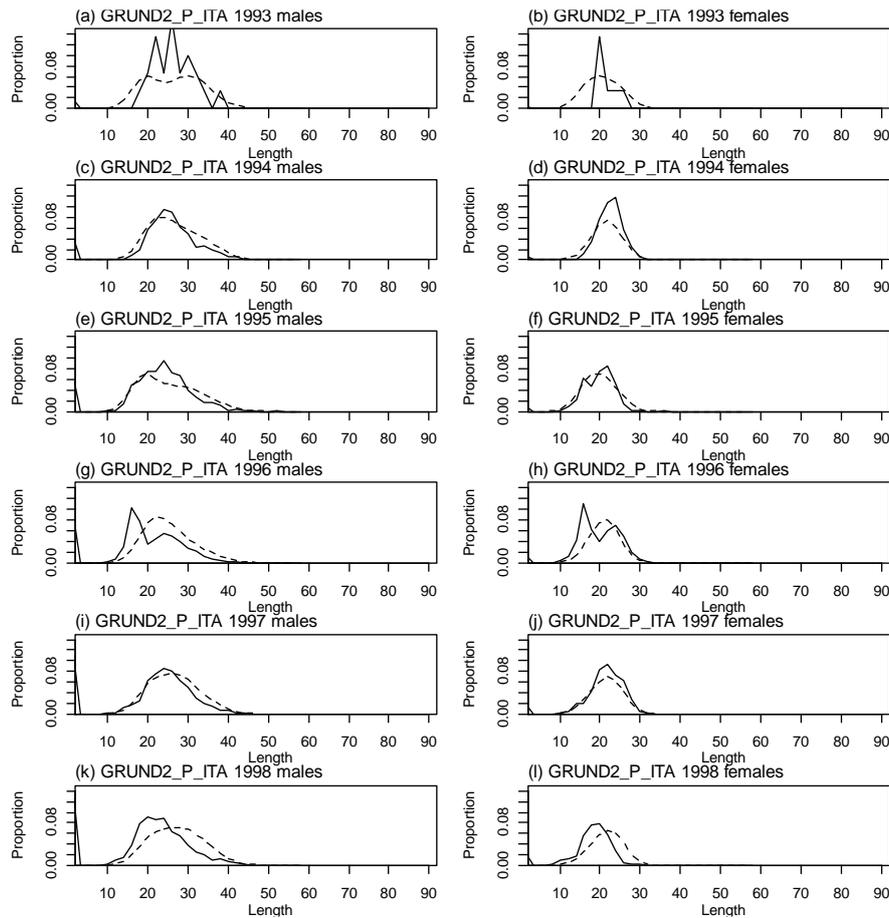


Fig. 4.28. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, GRUND2 survey (Italian area).

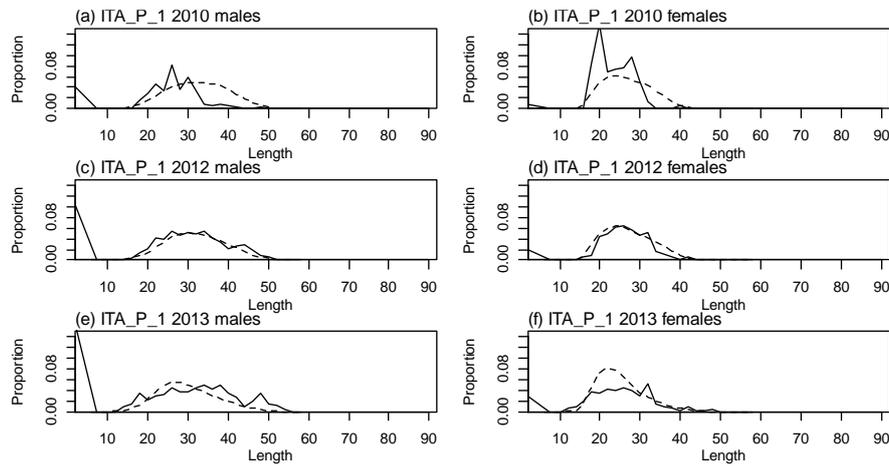


Fig. 4.29. Observed (solid line) and fitted (dashed line) length frequency distributions for commercial catch length frequency samples in time step 1 (Italian area).

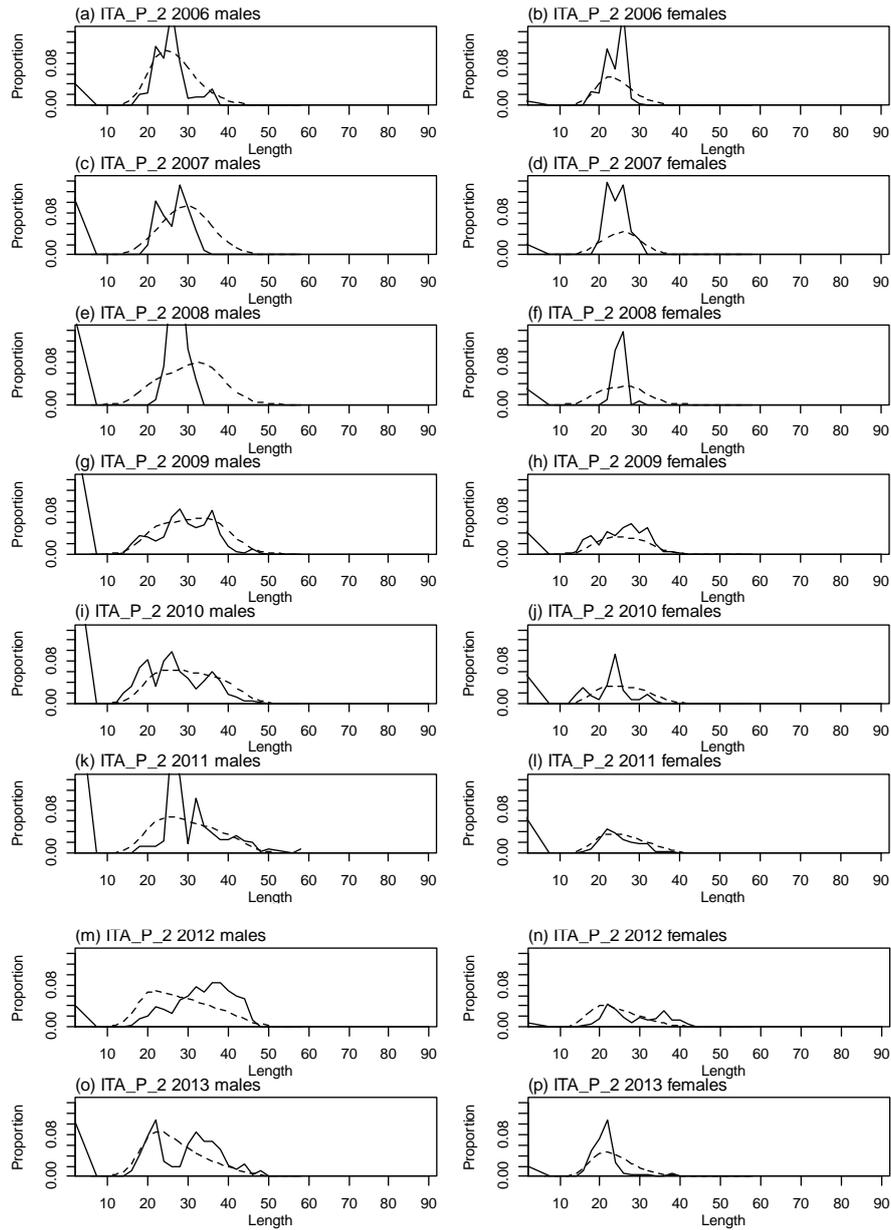


Fig. 4.30. Observed (solid line) and fitted (dashed line) length frequency distributions for commercial catch length frequency samples in time step 2 (Italian area).

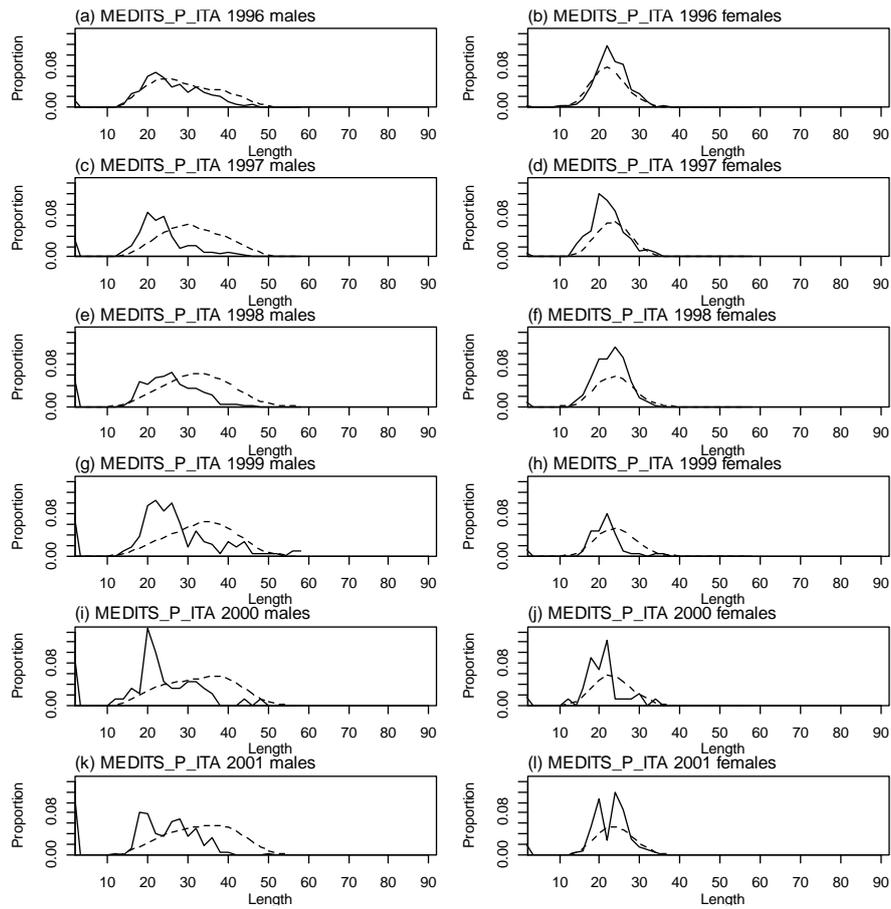


Fig. 4.31. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, MEDITS survey (1996-2001; Italian area).

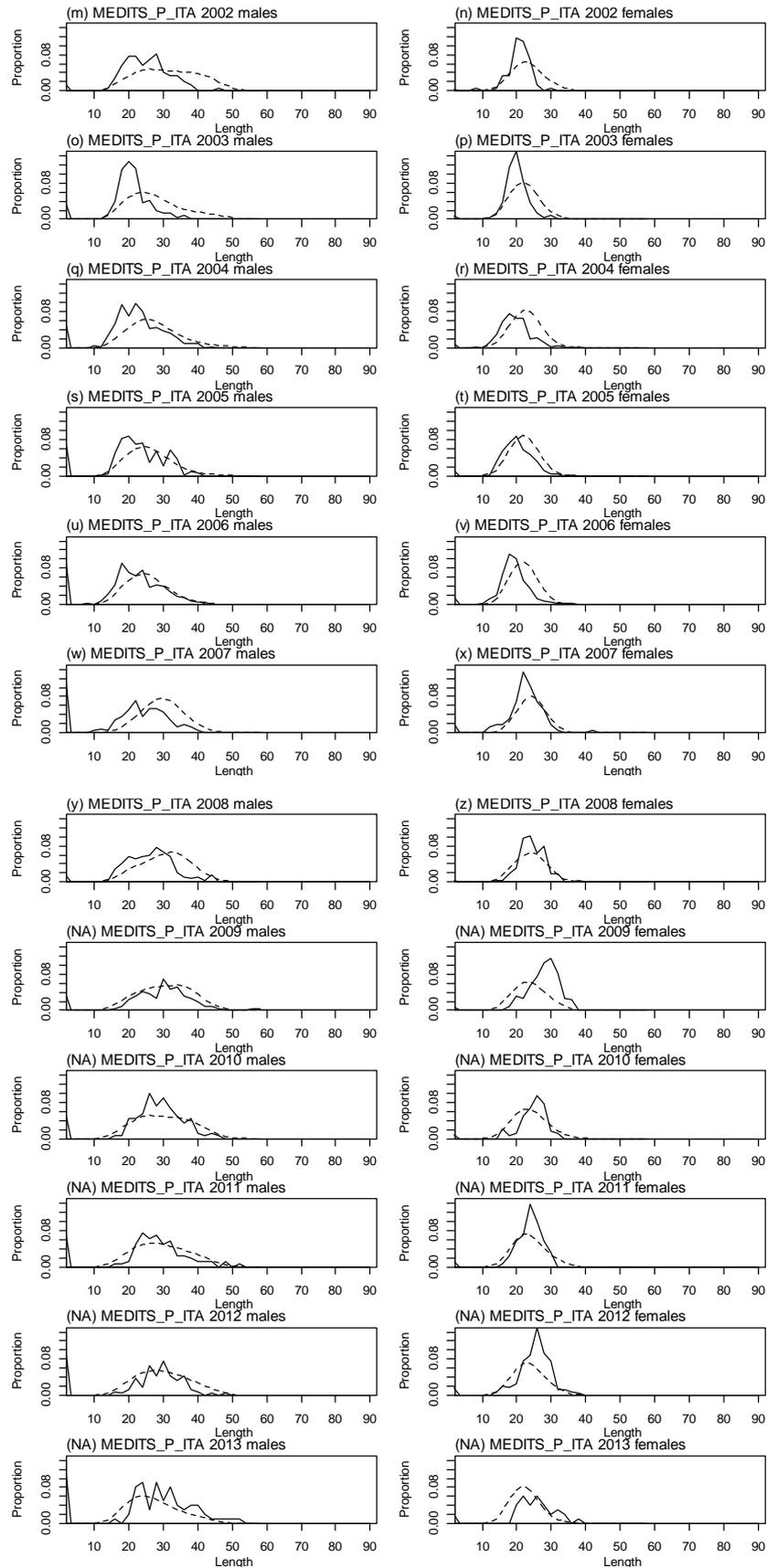


Fig. 4.32. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, MEDITS survey (2002-2013; Italian area).

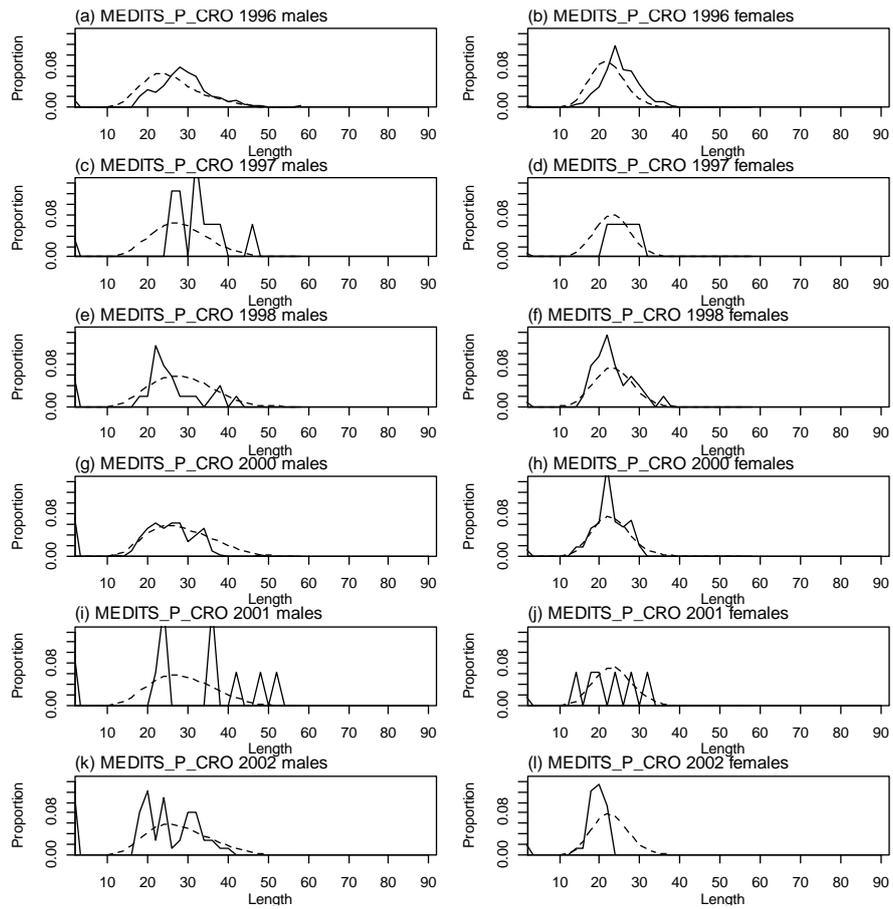


Fig. 4.33. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, MEDITS survey (1996-2002; Croatian area).

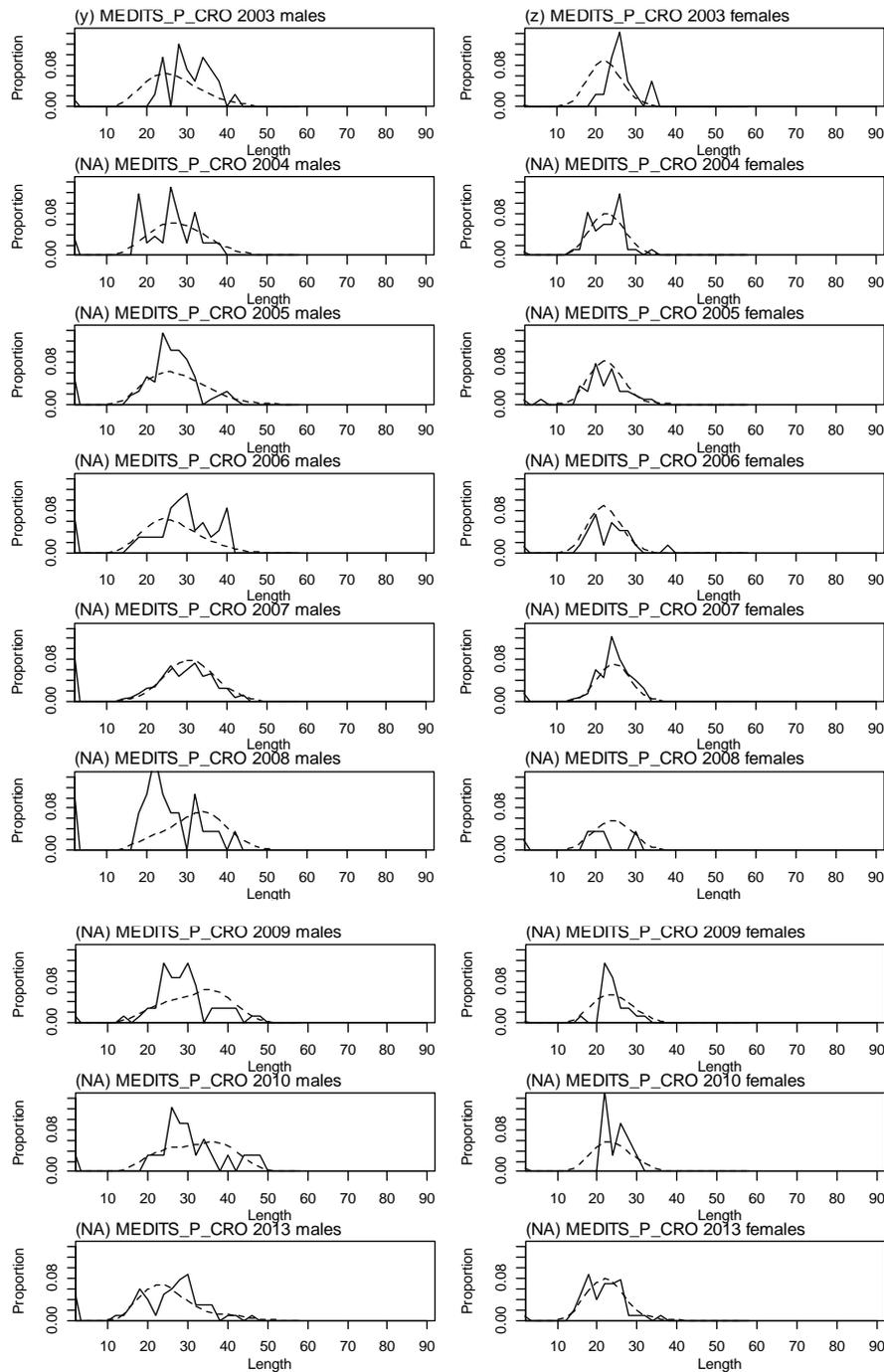


Fig. 4.34. Observed (solid line) and fitted (dashed line) length frequency distributions for survey length frequency samples, MEDITS survey (2003-2013; Croatian area).

The likelihood profile for SSB_0 showed a clear minimum at about 16000 tonnes, and was “U” shaped (Fig. 4.35). There was some conflict between the data sets, which warrants further investigation.

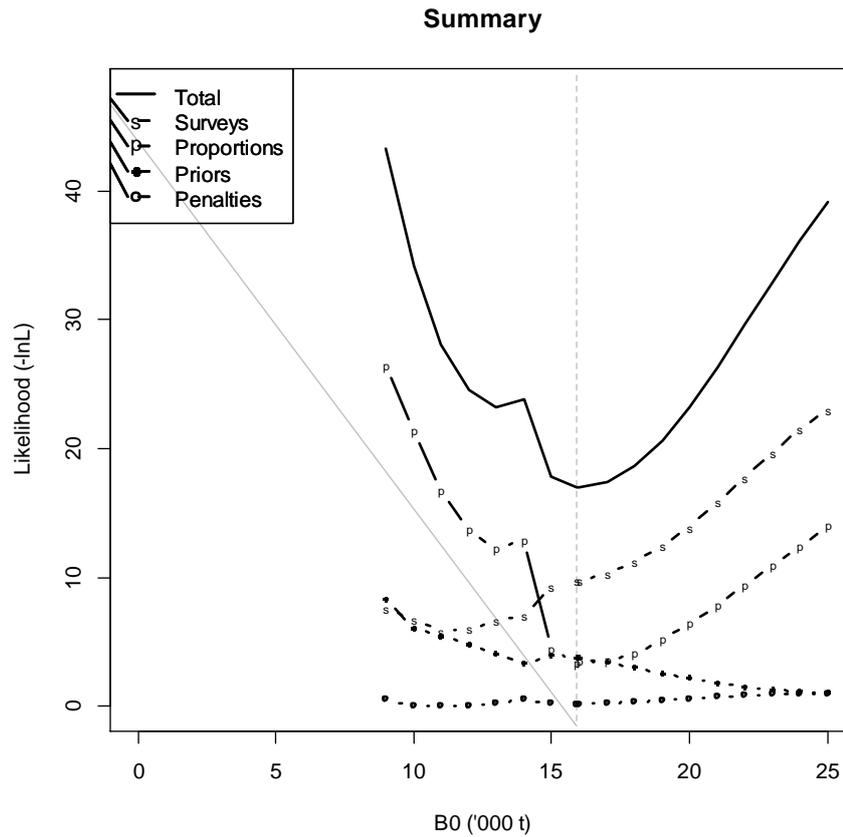


Figure 4.35. Likelihood profiles for *Nephrops* in the study area when B_0 is fixed in the model. Figure shows the overall profile, and contributions from the surveys, proportions at length, priors and penalties. Vertical dashed line represents maximum posterior densities (MPD).

Annual F_{bar} (20 – 40mm CL) as estimated from model outputs (Fig. 4.36): for the whole study area it shows a period of low stable exploitation up until the end of the 1990s, followed by a period of higher more variable exploitation (Fig. 4.36, black line). The pattern in the Italian area matches the overall pattern well (Fig. 4.36, blue line), while the exploitation in the Croatian area appears to have increased rapidly in the most recent years (Fig. 4.36, red line). Plots of exploitation against biomass (Figs. 4.37 to 4.39) suggest F_{bar} increased gradually as biomass declined, but became higher and more variable once biomass fell below a particular level. The high estimated exploitation in the Croatian area in 2013 is associated with a low biomass (Fig. 4.39).

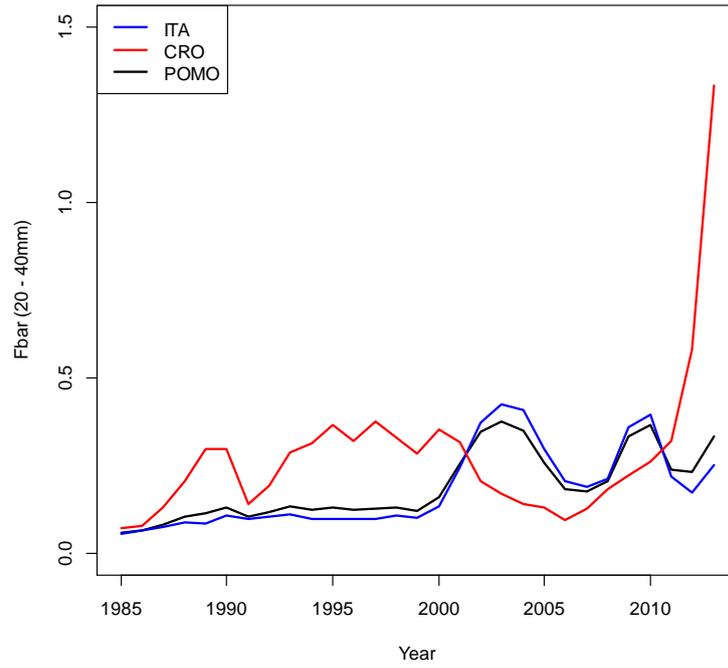


Fig. 4.36. Plot of estimated F_{bar} (20 – 40 mm) over the modelled period 1985 to 2013, for the whole stock, and Italian and Croatian fleets separately.

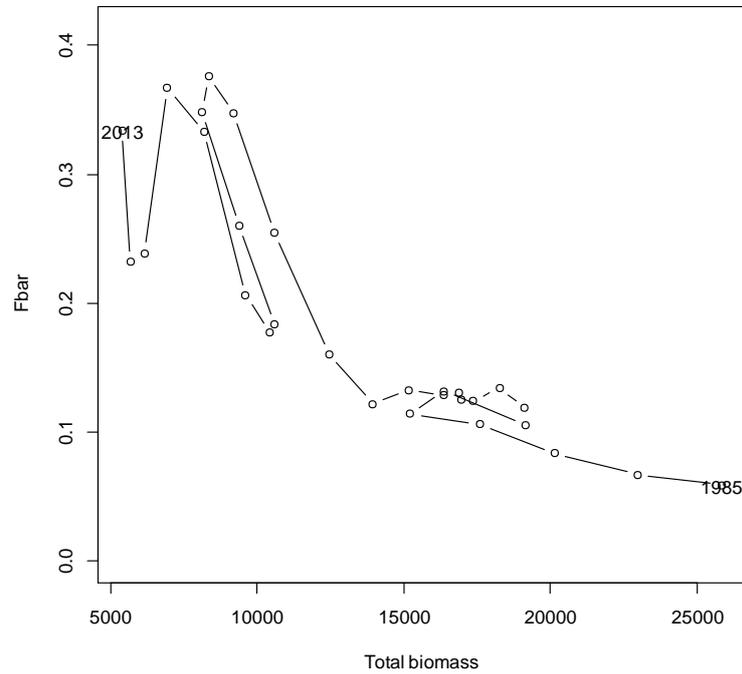


Fig. 4.37. Plot of estimated F_{bar} (20 – 40 mm) against total stock biomass for the whole study area population over the modelled period 1985 to 2013.

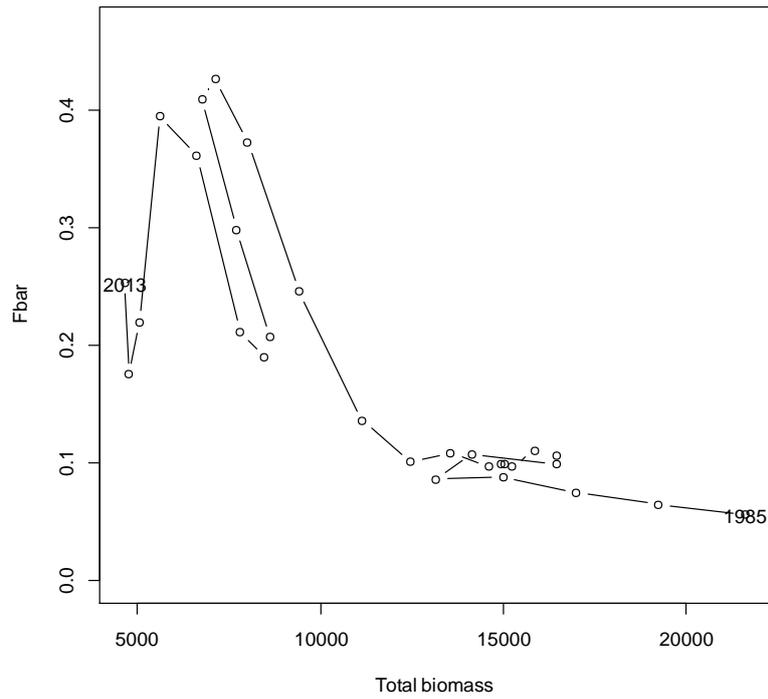


Fig. 4.38. Plot of estimated F_{bar} (20 – 40 mm) against total stock biomass for the Italian/international portion of the study area over the modelled period 1985 to 2013.

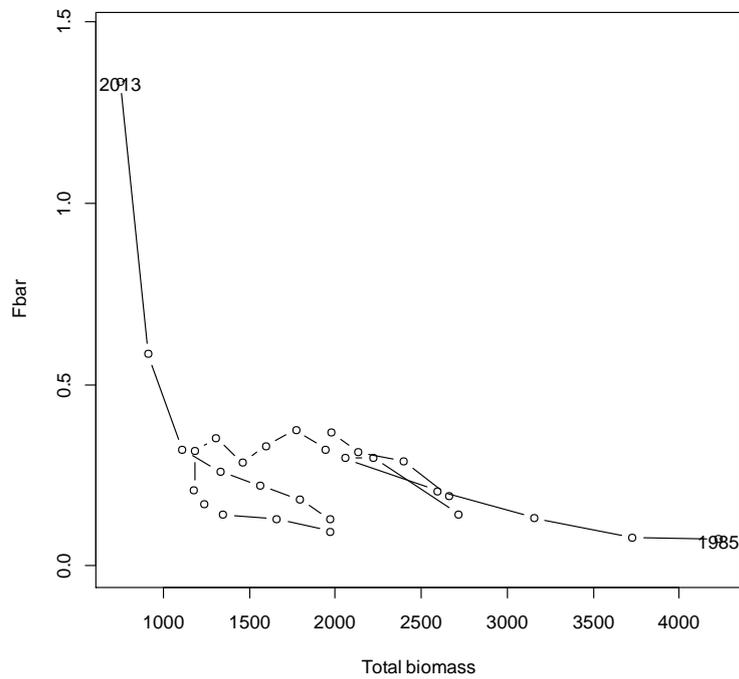


Fig. 4.39. Plot of estimated F_{bar} (20 – 40 mm) against total stock biomass for the Croatian portion of the study area over the modelled period 1985 to 2013.

4.2.4 Comparison of stock assessments

The stock of Norway lobster in the study area presents an uncertain situation, since model results show quite different estimations. CASAL shows a more optimistic trend, accounting for higher values compared to those estimated by the VIT model. However, CASAL *Nephrops* abundance decreases continuously from 2006 to 2011, with the lowest value (304409 individuals) in 2011, to be followed by an increase to 2013 when 425908 individuals were estimated (Fig. 4.40 – top). The VIT on the other hand presents a more stable situation but lower values: *Nephrops* abundance fluctuates between 95092 individuals in 2006 and 67606 individuals in 2013 (Fig. 4.40 – top). A generally decreasing trend is depicted for the fishing mortality rates calculated by the VIT model, whereas the opposite trend is described by CASAL (Fig. 4.40 – bottom). VIT estimates a maximum value of 0.92 yr^{-1} in 2009 and a minimum value of 0.37 yr^{-1} in 2013, whereas CASAL the maximum and minimum estimated by CASAL are 0.6 yr^{-1} in 2010 and 0.29 yr^{-1} in 2007, respectively (Fig. 4.40 – bottom).

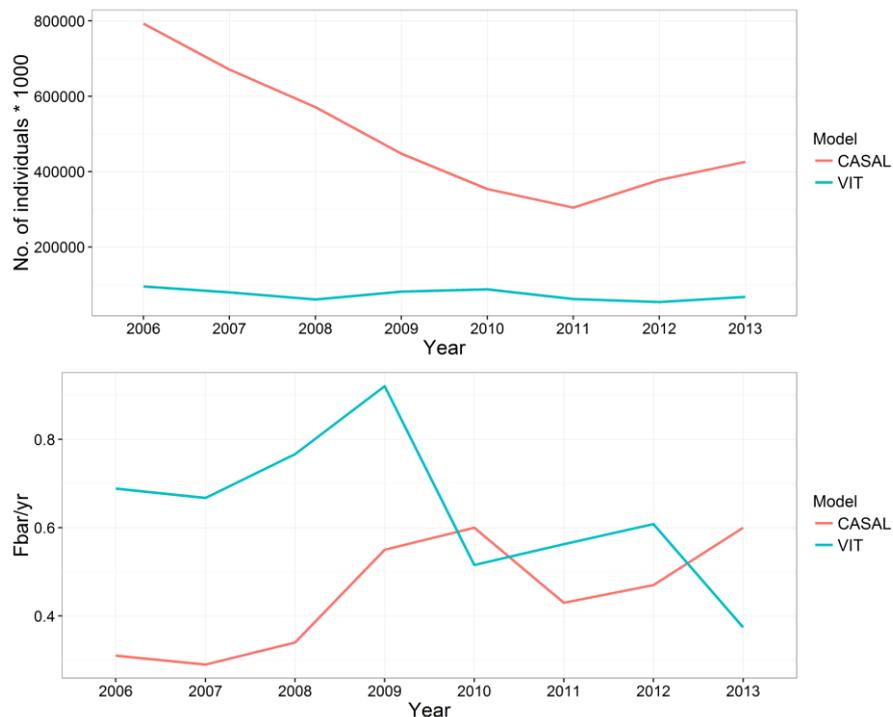


Fig. 4.40. Comparison of stock assessment results: total abundance by year (top) and mean fishing mortality (F_{bar}) by year (bottom) estimated by CASAL (pink line) and VIT (blue) models.

No comparison is available with official assessment results because this species has not been assessed annually in the Adriatic Sea. The most recent formal Norway lobster stock assessment in northern and central Adriatic sea dates back to the 2009 General

Fisheries Commission for the Mediterranean and the Black Sea working group (GFCM, 2009), but only Italian data were taken in account. This stock assessment was carried out using the VIT model, that estimated fishing mortality rates between 0.69 yr^{-1} and 0.77 yr^{-1} for females and between 0.87 yr^{-1} and 0.96 yr^{-1} for males, supporting the VIT estimates of this study. The stock was defined in overexploitation, meaning that fishing mortality exceeded the sustainable fishing rate ($F_{0.1}$, a more conservative measure based on yield-per-recruit analyses) of 0.25 yr^{-1} for females and 0.20 yr^{-1} for males.

More recent attempts to assess the stock of Norway lobster were carried out by the Scientific, Technical and Economic Committee for Fisheries (STECF) EWG 15-16 in 2015 but did not produce usable results, since no agreement was reached among experts regarding the procedure to follow for the production of an effective assessment that takes all the issues related to this species into account (STECF, 2015).

Here, two stock assessment models were tested: one simple length cohort analysis, carried out with VIT, and a more complex one, CASAL. Complexity is the main difference between these two models, given by both the data and the calculations. VIT is the simplest model: it requires only few data about the fishing activity and the growth of the species in exam, and estimates (e.g. abundance, biomass, fishing mortality) are given using a backward calculation from the last length class based on the Pope's approximation and assuming a steady state. CASAL, on the other hand, is much more complex: it can assume an age- or size-structure, allowing great flexibility in describing population dynamics, estimating parameters and model outputs. Here, the CASAL model used was length-based and divided in two time steps (TS1 April – July and TS2 August – March) based on the biological features of this particular species. Moreover, information from the scientific surveys MEDITS and GRUND were also taken in account. The inclusion of more biological detail into a single species stock assessment allows to better describe the biological dynamics of the species in exam, resulting in more realistic estimates (Kuparinen et al., 2012). This is the case of CASAL. However data quality has to be considered: poor quality input data will generate less meaningful results (Methot and Wetzel, 2013). Further, in the case of CASAL, more assumptions were made compared to the VIT model.

Differences between models are also given by natural mortality, since a scalar value of 0.3 yr^{-1} was used for the VIT assessment, whereas a vector by length and sex was employed for the CASAL model. Natural mortality is one of the most influent

parameters in determining stock dynamics, but it is difficult to estimate (Cotter et al., 2004). Often natural mortality is assumed constant (Patterson et al., 2001; Cotter et al., 2004; Gislason et al., 2010) and in many cases is assumed equal to values found in literature for the same species or similar ones (Kuparinen et al., 2012). In this case, the scalar value was derived from literature (Marrs et al., 2000), whereas the vector was calculated (PRODBIOM; Abella et al., 1997; 1998). The use of lower M rates will generate higher estimates of fishing mortality, implying higher exploitation rates, as in the case of the VIT model. CASAL, employs a vector in which the mortality rates of the smaller length classes are high (ca. 1.00 yr^{-1}) and those for the larger length classes considerably lower (ca. 0.2 yr^{-1}); the overall value is around 0.35 yr^{-1} , very close to the natural mortality rate of the VIT model. Despite the resulting natural mortality rates being similar, estimates of both abundance and fishing mortality are very different between models suggesting that more investigations on the performance of scalar vs. vector natural mortality would be required.

VIT and CASAL are truly length-based models, however the fishing mortality trends they describe are different: generally decreasing for VIT and generally increasing for CASAL. Computations are different; as explained in sections 3.2.2 and 3.2.5, VIT derives F by the solution of the Baranov catch equation for F (Leonart and Salat, 1992; 1997), whereas CASAL uses the *instantaneous mortality* formulation (Bull et al., 2012). The *instantaneous mortality* is estimated as an exploitation rate and this value is valid in the case that only one fishery is considered and selectivity reaches the maximum of 1. Otherwise, and as in this case, the exploitation rate is split between the fisheries included in the model as equivalent fishing mortalities. These observations seem to support the fishing mortality rates obtained by CASAL, however this aspect should be explored further particularly in connection with the analysis of natural mortality.

Selectivity is included in CASAL; this fact, as already explained for hake (section 3.2.5), makes results from this method more accurate (CAPAM workshop, 2013). Within the CASAL framework, selectivity is assumed equal for the surveys and the commercial fisheries, but different among sexes. VIT is not able to take into account selectivity when a length cohort analysis is performed, as in this case. Thus VIT, by not estimating selectivity, assumes that all the larger individuals are taken by the fishery. CASAL, on the other hand, accounts for the fact that larger individuals may be able to escape fishing for some reason or other; e.g. the double normal selectivity assumed for females allows for the fact that in certain times of the year large females are not caught.

Considering the results of the stock assessments presented here, the status of the stock of Norway lobster within the study area is unclear: VIT describes a stable trend, while results from CASAL are more fluctuating, thus suggesting this resource should be managed with caution until new and more precise evaluations will be carried out. This conclusion is also shared by the literature and the outcomes of international meetings.

The VIT model was the preferred choice for inclusion in the MICE model (Chapter 5): simplicity was preferred over complexity (see chapter 6). The development of a more complex model, such as CASAL, was important and will be considered in future developments of this study.

CHAPTER 5 – MICE

5.1 Conceptual MICE model

Previous chapters have highlighted the importance of the study area with respect to the entire Adriatic ecosystem, underlining its significant role for two of the most important commercial species in the Adriatic Sea, European hake and Norway lobster.

As highlighted in chapters 3 and 4, these species appear in a concerning status. Considering they share same habitat and consume similar prey, the application of an Ecosystem Approach to Fisheries (EAF; or ecosystem based fisheries management, EBFM) is strongly advisable.

EBFM and EAF have the aim of protecting ecosystems from major degradation and irreversible change, as well as broadening knowledges on the role of human activities in ecosystem dynamics (Garcia et al., 2003; Pikitch et al., 2004). This latter part provides the drive to take in account non-commercial species crucial to describe the ecosystem under exam, with the aim of identifying the best management measures for protecting both target species and the ecosystem more in general while allowing a sustainable fishing activity. Among the different models available to reach the purposes of an EAF approach (section 1.4), a Model of Intermediate Complexity for Ecosystem Assessment (MICE; Plagányi et al., 2014) was chosen for this study. This chapter explains, in detail, the development of a MICE approach for the study area.

The core MICE philosophy foresees that only a limited number of components (species or functional units) describing the ecosystem in exam and fundamental for testing specific management questions be accounted for.

The model (figure 5.1) represents the interaction between the trawl fishery, the two target species (Norway lobster and European hake, also defined “predators”) and their prey. Both species are separated into small and large, allowing us to emphasize the important role of the Pomo Pit as a nursery area for hake and have a better understanding of their diet. Predator species do not compete with each other, but are both affected by the same fishing activity as they are principally caught by bottom-trawl nets (Vrgoč et al., 2004), i.e. they are subjected to technical interactions. The two predators share most of the prey, principally crustacean and fish species, that have been grouped into several groups considering common growth features, thus maintaining the

MICE philosophy of keeping things simple. Discard, representing fished individuals returning, dead or alive, into the sea (FAO, 1996), is also taken in account, since it is relevant for both the diet of Norway lobster and management priorities in the area.

The aims of this model are:

1. To investigate how the dynamics of predators and prey influence each other;
2. To examine how the fishery may have the power to modify their interactions indirectly, as well as directly, further impacting the hake and Norway lobster stocks in the study area;
3. To explore how different management scenarios influence the predator-prey system. In particular, investigating the controversial institution of a discard ban imposed by EC Regulation No. 1380/2013 (see section 5.4).

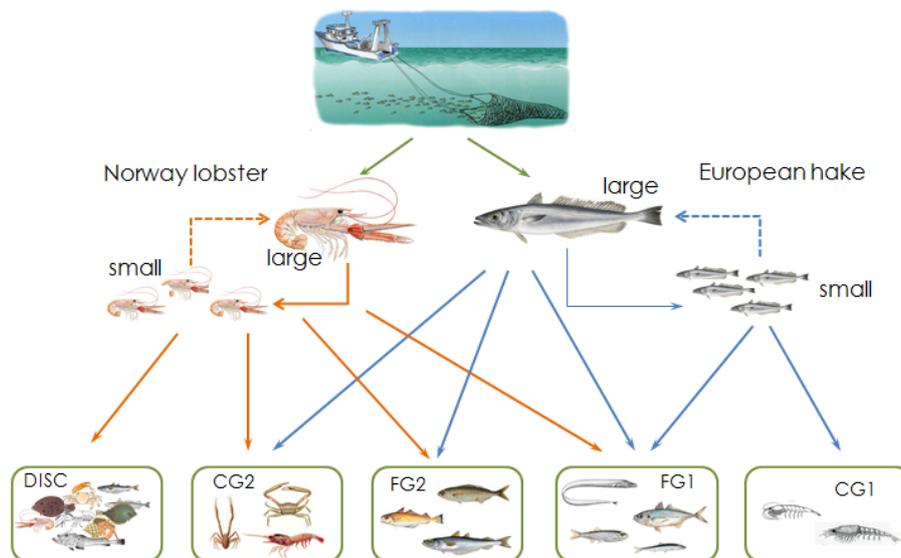


Fig. 5.1. Conceptual model for the MICE of the Central Adriatic Sea. Prey groups are: CG2, crustacean group 2; FG2, fish group 2; FG1, fishing group 1; CG1, crustacean group 1; discards (DISC). Solid lines represent direct effects, dotted lines represent feedbacks.

The MICE model was developed in a step-wise manner. Steps are strictly critically connected, sometimes in a woven way involving multiple iterations of the same process; the understanding of the work is facilitated by a flow chart (Fig. 5.2).

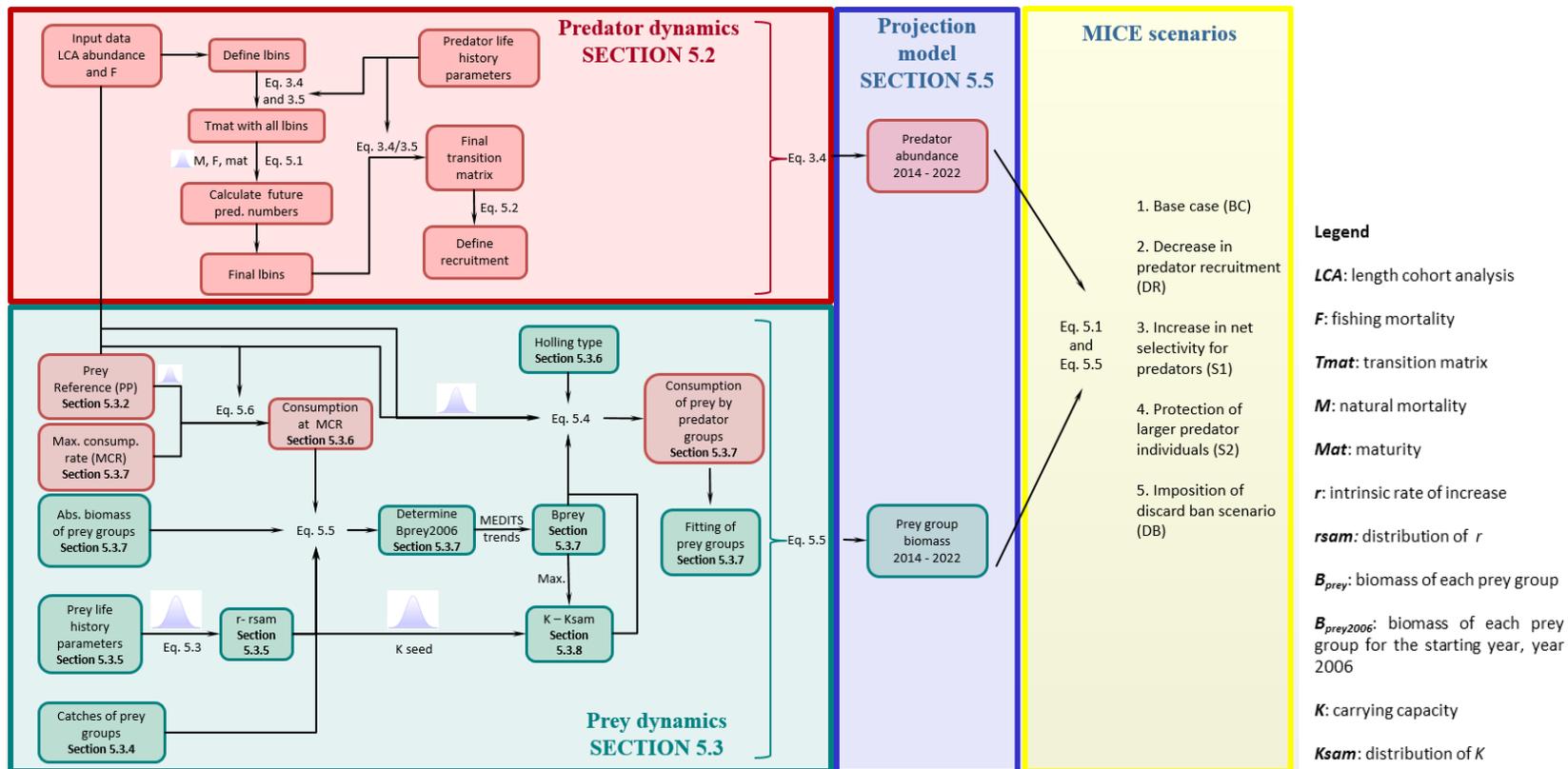


Fig. 5.2 Flow chart summarising the steps adopted to run the MICE model and derive future abundances of predators and prey under different management scenarios. Red boxes represent predator dynamics, whereas green boxes represent prey group dynamics. Predator and prey dynamics are linked in the projection model, blue box, representing the last step of the MICE model.

5.2 Predator dynamics

The dynamics of predator species, hake and Norway lobster, are projected into the future (2013-2022) using a length-based approach to estimate the number of predators in each length bin, $N_{t+\tau,l}$, over the years:

$$N_{t+\tau,l} = \sum_{j=1}^P N_{t,j} T_{i,j} \pi_{t,j}^S \quad (\text{Eq. 5.1})$$

where $N_{t+\tau,l}$ is the number of predators in length bin, l , in years $t+\tau$ (where $\tau = 1$ year), $N_{t,j}$ is the number of predators in length bin j , $T_{j,l}$ is the length-transition matrix, $\pi_{t,j}^S$ is the survival probability of an animal of length j from time t to $t+\tau$ (given by $\exp(-Z_{t,j})$ where Z is total mortality, i.e. the sum of natural mortality (M) and fishing mortality (F) (Table 5.1), estimated by VPA, by length bin), and P is the number of the MCMC iterations. The initial input value for $N_{t,j}$ (i.e. for 2013) is represented by the number of individuals per length class j resulting from the VIT run of 2013 (Table 5.1).

Tab. 5.1 MICE input predator data: output data from the VIT assessment model for 2013. Abundance in number of individuals $\cdot 10^3$ and fishing mortality (F), and natural mortality (M) by length bin.

European hake				Norway lobster			
Length bin cm, TL	Abundance	F _{bar}	M	Length bin mm, CL	Abundance	F	M
6 - 13	25347	0.125	0.759	10 - 23	35160	0.163	0.3
14 - 19	9671	0.256	0.386	24 - 31	15074	0.527	0.3
20 - 21	2398	0.168	0.386	32 - 33	3090	0.413	0.3
22 - 25	3944	0.354	0.263	34 - 37	5076	0.571	0.3
26 - 27	1428	0.747	0.263	38 - 39	2003	0.485	0.3
28 - 29	1082	0.711	0.219	40+	7203	0.274	0.3
30 - 31	869	0.369	0.219				
32 - 33	720	0.501	0.219				
34 - 35	586	0.454	0.195				
36 - 37	468	0.595	0.195				
38 - 39	353	0.718	0.195				
40+	984	0.6	0.181				

The transition matrix, $T_{i,j}$, describes the probability that a given animal will grow (transition) from length class, j , to the following one, l , within a lapse of time τ , where $\tau = 1$ year (Eq. 3.4), considering the growth increment calculated using von Bertalanffy growth parameters (Eq. 3.5). Given this, the transition matrix was first run to define the length bins to be used in the projection model and then was run again to obtain the

probability that a given individual will transition into the next length bin one year later. For hake this process was done within the Mark 3 model (Section 3.2.3). Resulting length bins for each predator species are shown in table 5.1.

Recruitment was assumed to correspond to the abundance of the first length bin, l_1 . More specifically, recruitment is assumed to be equal to the number of individuals of the first length bin in the first year, R_{t,l_1} , and is projected into the following years, R_{t+1,l_1} , by adding or removing a random value drawn from a normal distribution with mean zero and variance, σ , 0.5:

$$R_{t+1,l_1} = R_{t,l_1} e^{N(0,\sigma_R^2) - \sigma_R^2/2} \quad (\text{Eq. 5.2})$$

where $N(0,\sigma_R^2)$ stands for the normal distribution and $-\sigma_R^2/2$ represents a correction term accounting for lognormal errors specific to recruitment time series (Haltuch et al., 2008; Haddon, 2011).

5.3 Prey groups dynamics

5.3.1 Definition of prey groups

To adequately describe the subset of the central Adriatic Sea ecosystem model, it was necessary to take the prey of the target species into account. A review of the information contained in the published literature regarding the feeding ecology and behaviour of hake and Norway lobster in the Pomo Pit was carried out to select the appropriate species to be included in the model. The diet of Norway lobster was derived from Wieczorek et al. (1999), that of small hake from Froggia (1973), whilst Karlovac (1959) and Jardas (1976) were found to contain the best information on the diet of large hake. Based on feeding information, Norway lobster too were divided into small (≤ 29 mm, CL) and large (≥ 30 mm, CL) and this was mainly because of cannibalism. The diets of the two *Nephrops* groups were quite similar, consuming principally crustaceans (e.g. *Munida intermedia*, *Natatolana borealis*, *Goneplax rhomboids*) and fish (e.g. *Maurolicus muelleri*, *Gadiculus argenteus*, *Lesueurigobius spp.*), whereas Mollusca and Cephalopoda are less important. Small hake (< 14 cm, TL) prefer crustaceans, in particular Mysidacea and Euphausiacea, whereas large hake (≥ 14 cm, TL) prefer fish, such as *Trachurus spp.*, *Boops boops*, *Engraulis encrasicolus*.

Prey species were pooled into prey groups according to similarities in their life history characteristics and the role they play in the ecosystem (Table 5.2):

- Fish group 1 (FG1), includes mostly pelagic species, characterised by a fast growth and high natural mortality, e.g. *Engraulis encrasicolus*, *Sardina pilchardus*, *Gadiculus argenteus*
- Fish group 2 (FG2), comprises mainly demersal species, characterised by a slower growth and low natural mortality, e.g. *Boops boops*, *Trisopterus minutus capellanus*, *Micromesistius poutassou*
- Crustacean group 1 (CG1), includes the benthopelagic species, above all *Lophogaster typicus* and *Nyctiphanes couchii*
- Crustacean group 2 (CG2), comprises benthic crustacean species, e.g. *Solenocera membranacea*, *Processa mediterranea*, *Chlorotocus crassicornis*, *Alpheus glaber*.

To take into account the possibility of cannibalism, a hake group and a Norway lobster group (representing small individuals of each species predated upon by larger ones of the same species) were also included and modelled within the predator dynamics described in equation 5.1. This was done by calculating an extra mortality term, predation natural mortality (M_{pred}), and including it within the survival term which becomes:

$$\pi_{t,j}^S = \exp^{-(M+M_{pred}+(F*selectivity))}$$

Discard, as source of food, was also taken in account. Norway lobster is a scavenger and a sedentary species, presumably prefer prey close to its burrows, making sinking discard an easy and important source of food for this species (Wieczorek et al., 1999; Bozzano and Sardà, 2002; Castro et al., 2005). Thus, a group for discard (DISC), consumed by Norway lobster only, was also included (see section 5.3.2).

Table 5.2. Composition of the four prey groups and their presence (marked by an x) in the diet of the four groups of predator species.

Prey species/Predators	Juvenile hake	Adult hake	small N. lobster	large N. lobster
FISH GROUP 1 (FG1)				
<i>Alosa fallax</i>		x		
<i>Argentina sphyraena</i>		x		
<i>Chlorophthalmus agassizi</i>		x		
<i>Engraulis encrasicolus</i>		x	x	x
<i>Gadiculus argenteus</i>		x	x	x
<i>Lepidopus caudatus</i>		x	x	x
<i>Maurollicus muelleri</i>	x		x	x
<i>Sardina pilchardus</i>		x		
<i>Sprattus sprattus</i>		x		
<i>Tachurus mediterraneus</i>		x		
<i>Trachurus trachurs</i>		x		
FISH GROUP 2 (FG2)				
<i>Arnoglossus laterna</i>		x		
<i>Boops boops</i>		x		
<i>Citharus linguatula</i>		x		
<i>Gobius niger</i>		x		
<i>Lesueurigobius friesii</i>		x	x	x
<i>Merlangius merlangus</i>		x		
<i>Merluccius merluccius</i>		x		
<i>Micromesistius poutassou</i>		x		
<i>Mullus barbatus</i>		x		
<i>Scorpaena notata</i>		x		
<i>Spicara maena</i>		x		
<i>Spicara smaris</i>		x		
<i>Trigla lyra</i>		x		
<i>Trisopterus minutus capelanus</i>		x		
CRUSTACEAN GROUP 1 (CG 1)				
<i>Lophogaster typicus</i>	x	x		
<i>Meganyctiphanes norvegica</i>	x		x	
CRUSTACEAN GROUP 2 (CG 2)				
<i>Alpheus glaber</i>		x	x	
<i>Chlorotocus crassicornis</i>		x		
<i>Goneplax rhomboides</i>			x	x
<i>Monodaesus couchii</i>			x	x
<i>Munida intermedia</i>		x	x	x
<i>Nephrops norvegicus</i>			x	x
<i>Processa mediterranea</i>		x	x	x
<i>Solenocera membranacea</i>		x		x

5.3.2 Prey preferences

Prey preference probability is a measure of which prey is favoured by which predator and its estimation is a focal point when joining predator and prey groups. If the number of stomach samples examined and the percentage composition of the different prey groups is known, the Dirichlet probability distribution, that is a multivariate probability distributions often used as prior of unknown distributions (Gelman et al., 2004), can be used to calculate the prey preference probability for any predator. This can be expressed as follows:

$$p(p_i) \sim Dir(\alpha_i + N_i) \quad (\text{Eq. 5.3})$$

where i is the prey group, p_i is the estimated percentage composition of any prey group in the stomach content, Dir is the Dirichlet distribution, α_i is the prior distribution of the prey group i (set at $\alpha_i = 0.5$ to be non-informative) and N_i is the number of samples in which prey group i was observed. This method is basic and assumes that the samples were independently taken and prey composition can be conflated with preference; uncertainty was incorporated by including a vector of 1000 p_p estimates propagated as follows.

Prey preferences were estimated for each predator and prey group. Two sets of prey preference probabilities were computed, one considering discards (Fig. 5.3A) and one not taking discards into account (Fig. 5.3B).

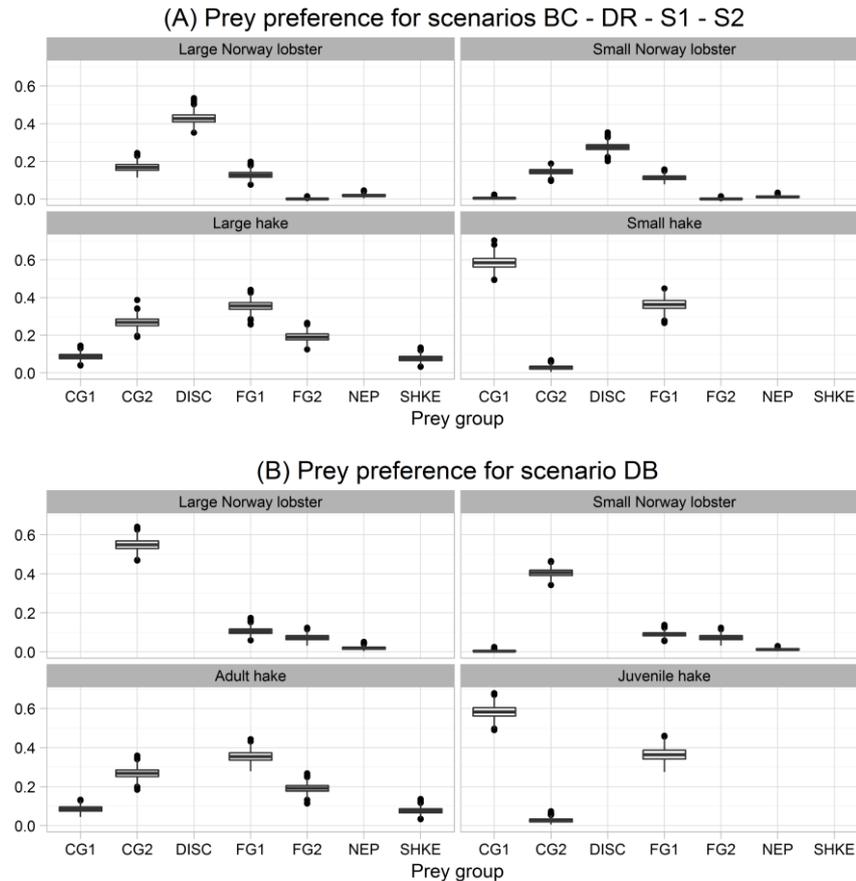


Fig. 5.3 Estimated prey preference probabilities for the predator groups: large Norway lobster, small Norway lobster, large hake and small hake for (A) the base case (BC), decrease in recruitment (DR), increase in net selectivity (S1) and protection of larger individuals (S2) scenarios, and (B) the discard ban (DB) scenario. Prey groups are as follows: CG1 (crustacean group 1), CG2 (crustacean group 2), DISC (discard), FG1 (fish group 1), FG2 (fish group 2), NEP (Norway lobster), SHKE (small hake). Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

In the presence of discards (Fig. 5.3A), discards themselves represent the favourite prey of Norway lobster, followed by benthic crustaceans (CG2) and fish group 1 (FG1). Fish group 2 (FG2) and crustacean group 1 (CG1) are consumed in small percentages, with CG1 eaten only by small Norway lobster. In the absence of discards, Norway lobster increase their preference for prey groups CG2 and FG1 (Fig. 5.3B). Hake do not consume discards, thus their diet is not influenced by its presence or absence (Fig. 5.3A and B). Small hake prefer small pelagic crustaceans (CG1), followed by FG1 and a small percentage of CG2. Instead, the favourite prey of large hake is FG1, followed by CG2, FG2 and CG1.

Cannibalism is not preponderant for these species, however hake is the predator group that accounts for the highest prevalence of this feeding behaviour. Direct trophic

interactions between hake and Norway lobster do not occur, the two species simply share the same food items and for this reason can be modelled as (implicit) competitors.

5.3.3 Biomass of prey groups

Estimates of prey group biomass, as well the definition of their life history parameters (see section 5.3.5), are of primary importance to proceed towards the application of the MICE model.

Biomass information was principally obtained from the MEDITS survey and integrated with other sources when species in exam were not accurately sampled by this survey. This was the case of small pelagic species, anchovy and sardine, in FG1, for which biomass data derived from the results of the stock assessment presented at GFCM in 2014 were scaled to the study area and then added to the species revealed by the MEDITS survey.

Biomass of benthic crustacean species, CG2, were also estimated from data collected by Šimunović (1997) and Gramitto (unpublished data) and assumed to reflect the biomass at the start year (2006) of this work.

Absolute biomass with corresponding coefficients of variation (CV) are summarised in table 5.3. Information for CG1 prey group were derived exclusively from MEDITS survey and only for years 2006, 2011 and 2013.

Table 5.3 Biomass (in tonnes) and coefficients of variation in brackets for each prey group and available year.

	FG1	FG2	CG1	CG2
2006	340276 (0.12)	1258 (0.25)	0.03 (1.01)	227 (0.01)
2007	277024 (0.08)	1107 (0.23)		
2008	238029 (0.09)	2018 (0.31)		
2009	216641 (0.08)	1673 (0.36)		
2010	220501 (0.09)	1530 (0.22)		
2011	249480 (0.1)	1564 (0.26)	0.03 (0.96)	
2012	218504 (0.16)	3551 (0.29)		
2013	236089 (0.17)	4333 (0.2)	0.16 (1.08)	

5.3.4 Catches of prey groups

Catches are composed by landings and discards. Discards are not negligible in Mediterranean trawl fisheries and for this reason they are taken in account in this study (more information about discards is given in section 5.4).

Information about discards was obtained from data collected by DCF (see section 2.1) sampling in 2011, 2012 and 2013 and from literature for those species not included in these samplings.

Small benthic crustacean species (CG2) are not included in DCF discard. Proportions of discards for these species were obtained from the scientific survey carried out by CNR-ISMAR Ancona in 1997 and 1998 and aimed at studying the discard composition in the Pomo Pit area. These proportions were then applied to the class of ‘undetermined discard’, containing a mix of non-target species, included in the DCF sampling to estimate the discard biomass of benthic crustacean species in years 2011, 2012 and 2013. Once the biomass of discarded CG2 was defined, it was possible to calculate the percentage of CG2 on the overall discard. The most discarded species of CG2 is *Munida intermedia*, whereas other species (e.g. *Alpheus glaber*, *Goneplax rhomboids*, *Processa spp.*) accounted for very low discard rates.

CG1 does not appear in either landings or discards, whereas FG1 and FG2 constitute the bigger part of discards. Species belonging to these latter groups were present in the DCF samples (years 2011, 2012 and 2013), allowing the calculation of the discard percentage of these prey groups on overall discards. The most discarded species of FG1 and FG2 are *Engraulis encrasicolus*, *Sardina pilchardus*, *Mullus barbatus*, *Micromesistius poutassou*.

Percentage composition of discards by prey groups is shown in table 5.4.

Tab. 5.4 Estimated percentage composition of discards.

FG1	FG2	CG1	CG2
51.30%	10.94%	0	26.61%

Then the overall discard ratio for years 2011, 2012 and 2013 was estimated at 1.41%, 1.58 and 10.36%, respectively. The increase in discard ratio is probably due to improvements in monitoring, however it has been chosen to use the mean value of 4.45%.

Discard estimates were essential for the calculation of the total catch of prey groups, as well as to model the discard ban scenario.

Regarding landings, the IREPA database provided official Italian landings for FG1 and FG2, whereas Croatian landings were provided by FishStatJ (2015). These values are referred to the entire GSA 17. Data were scaled to the study area using VMS data for the Italian side, whereas Croatian landings were reduced to 30%, corresponding to the effort (fishing days) exerted in the study area (zone C of Croatian fishing zones) with respect to the overall area (PHARE, 2005). Once total landings for the study area were determined, discard amounts for each year were calculated using the mean value of 4.45%. The resulting discard amount was split among prey groups considering the percentage shown in Table 5.4 and the corresponding values were added to the landings to obtain catches of prey groups (Table 5.5).

Table 5.5 Estimated catches, in tonnes, for each prey group and year.

Year	2006	2007	2008	2009	2010	2011	2012	2013
FG1	24737	23870	20136	26257	25962	27978	34905	34313
FG2	2488	2275	1923	1898	1764	2007	1966	2172
CG2	314	301	254	325	320	346	426	421

5.3.5 Intrinsic rate of increase

The intrinsic rate of increase, r , describes how fast a population grows; the higher the r value, the faster the population grows. To estimate r it is essential to know the life history parameters for each prey group. These were mainly taken from FishBase (Froese and Pauly, 2015) and the literature. Growth parameters for each prey group are summarised in table 5.6, whereas relative references are included in Appendix B.

Table 5.6. Life history parameters for the four main prey groups. Lengths are in cm of total length (TL) for FG1 (fish group 1) and FG2 (fish group 2), mm of total length (TL) for CG1 (crustacean group 1) and in mm of carapace length (CL) for CG2 (crustacean group 2). Notes: L_{inf} – asymptotic length at which growth is zero, k – growth rate, t_0 – age at which the organisms would have had zero size, a – y-intercept of length-weight relationship, b – slope of length-weight relationship, M_{low} – lowest natural mortality estimate, M_{high} – highest natural mortality estimate, A_{max} – maximum age, Lm_{50} – length at 50% maturity, Am_{50} – age at 50% maturity, Am_{95} – age at 95% maturity, h_{low} – lowest estimate of the steepness of the stock-recruitment relationship, h_{high} – highest estimate of the steepness of the stock-recruitment relationship.

	L_{inf}	k	t_0	a	b	M_{low}	M_{high}	A_{max}	Lm_{50}	Am_{50}	Am_{95}	h_{low}	h_{high}
FG1	23.37	0.35	-0.704	0.01	3	0.61	2.31	6	12	1.5	2	0.34	0.71
FG2	47.51	0.31	-1.06	0.005	3.032	0.2	0.6	8	13	1.5	2.5	0.31	0.81
CG1	34.62	0.04	8 (L_0)	0.03	2.8	1.25	1.9	2.5	22.5	0.8	1	0.2	0.3
CG2	24.95	0.52	-0.44	0.0002	3.37	1	2	3	10	0.5	1	0.2	0.4

Prey dynamics were described using a modified biomass dynamic model (Eq. 5.5), in which r represents a key parameter. To estimate r , the Euler-Lotka equation was used (Fisher, 1930):

$$\sum_{a=1}^{\infty} e^{-ra} w_a m_a \pi_a \alpha = 1 \quad (\text{Eq. 5.3})$$

where a is the age or length, w_a is the weight-at-age or weight-at-length, m_a is the relative fecundity of females, π_a is the survival probability to length a for females, and α is the maximum number of recruits-per spawner.

The equation was implemented in R and all variables listed in table 5.6 were used to solve equation 5.3 for r ; results are shown in figure 5.4. FG1 is the prey group growing fastest ($r = 0.53 \text{ yr}^{-1}$), followed by FG2 ($r = 0.38 \text{ yr}^{-1}$) and CG2 ($r = 0.29 \text{ yr}^{-1}$), whereas CG1 ($r = 0.22 \text{ yr}^{-1}$) is the slowest prey group.

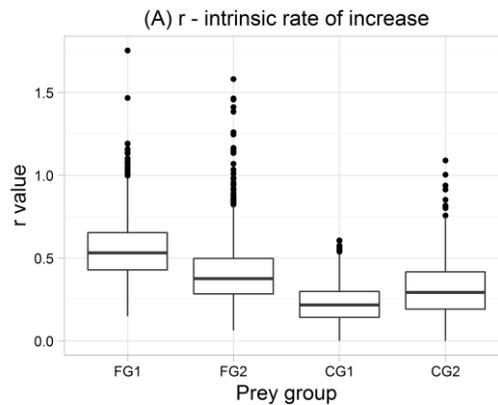


Fig. 5.4 Estimated intrinsic rate of increase, r (yr^{-1}), for each prey group: FG1 (fish group 1), FG2 (fish group 2), CG1 (crustacean group 1) and CG2 (crustacean group 2). Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

5.3.6 Prey-predator functional response

Estimating the rate at which a predator obtains its prey (i.e. the functional response) is central for the MICE approach. Different models can be used to estimate this value, the most common being the Holling Type II and III responses (Holling, 1959a; b); the outcomes of using one or the other were evaluated using the MICE model. In the Holling Type II the rate of predation increases with prey density to reach a maximum and stable value, modelled using an asymptote. The Holling Type III describes the rate of feeding as a sigmoid where the rate of feeding decreases at low and at high prey densities. These predator functional responses were modelled using the following equation:

$$\Phi_{P,p} = \chi_P \bar{N}_l \varphi_{P,p} \frac{(B_p/K_p)^n}{\mu_p^n + (B_p/K_p)^n} \quad (\text{Eq. 5.4})$$

where ϕ is the consumption (in tonnes) of prey group p by predator group P , χ_P the maximum consumption rate (yr^{-1}) of the predator P , N_l is the abundance summed over length (l) of predator group P , $\varphi_{P,p}$ is the relative preference of predator group P for prey group p , μ describes the so-called “half-saturation” level (the prey biomass level at which predation consumption is half the maximum) which helps define the rate at which overall predation declines with reduced prey biomass and it assumed equal to 0.5, B_p is the biomass of the prey group, K is the carrying capacity of the prey group and n is the Holling Type exponent ($n=1$ indicates the Holling Type II, $n=2$ the Holling Type III). Both models estimated similar ϕ values for each predator and, reflecting the shape of the Holling functional response curves, these similarities were more marked at the extremes of the biomass range. In light of this, the results presented hereafter assume an underlying Holling Type II relationship.

5.3.7 Fitting of prey group biomass

Biomass of prey groups entering in the MICE model were calibrated to the predator-prey dynamics for years preceding the projections (2006-2013). This process was done by developing the biomass dynamic equation:

$$B_{y+1,p} = B_{y,p} + r_p + B_{y,p} \left(1 - \frac{B_{y,p}}{K_p}\right) - \sum_{j=1}^{n_p} \Phi_{P,y} - C_{p,y} \quad (\text{Eq. 5.5})$$

where $B_{y,p}$ is the biomass of prey p in year y , r_p the intrinsic rate of increase of prey p , K_p is the carrying capacity of prey p , n_p is the number of predator groups, $\Phi_{P,y}$ is the consumption (in tonnes) of prey p by predator P in year y and $C_{p,y}$ denotes the relevant commercial catches of prey group p in year y . The above equation is the core of the model: it covers the reproductive, density-dependent, predator consumption and harvesting dynamics of each prey and predator group and, to the extent feasible, each component is based on data-driven estimates with uncertainty included.

Before developing equation 5.5, different steps were carried out.

1. Estimation of the maximum consumption of prey groups.

The maximum consumption of each prey group by each predator was estimated developing equation 5.4 at the maximum consumption rate, that is:

$$\Phi_{P,p} = \chi_P \bar{N}_l \varphi_{P,p} \quad (\text{Eq. 5.6})$$

N_l and $\varphi_{P,p}$ were already mentioned and estimated, whereas the calculation of the rate of food that a given species can eat if their prey are infinitively available, χ_P or the

maximum consumption rate, needs to be clarified. This was determined as 4% of the body wet weight individual⁻¹ day⁻¹ for hake (Cartes et al., 2004; Carpentieri et al., 2008) and 0.5g individual⁻¹ day⁻¹ for Norway lobster (Sardà and Vallarades, 1990).

2. Development of the biomass dynamic equation considering the maximum consumption rate.

Once ϕ at the maximum consumption rate is estimated and catches of prey groups are known (section 5.3.4), it was possible to develop equation 5.5 at the maximum consumption rate, using the maximum value of biomass of each prey group as a proxy of their carrying capacity, K . This process allowed to determine a biomass value for each prey group at the starting year (2006), $B_{prey,2006}$, which would be able to support both catches and consumption of each prey group through to 2013.

3. Definition of prey group biomass time series starting from $B_{prey,2006}$ and following the MEDITS trend.

The biomass of prey groups, B_p , was then recalculated, starting from $B_{prey,2006}$ and following trends revealed by MEDITS survey (Fig. 5.5). For those prey groups, such as CG1 and CG2, for which the MEDITS survey did not describe a specific trend, the overall trend of demersal fish (FG2 and hake) was assumed to be representative (Fig. 5.5).

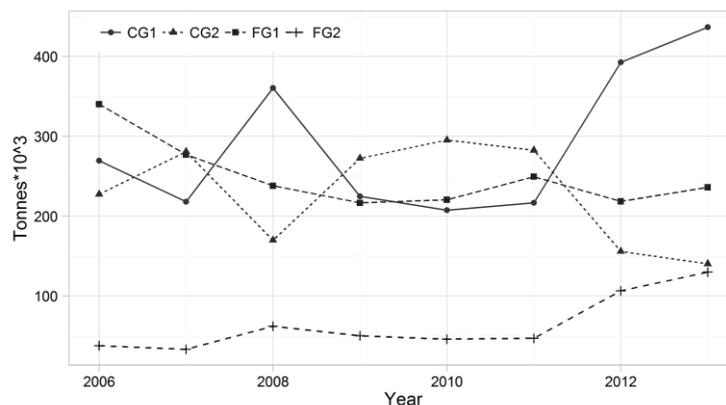


Figure 5.5. Estimated biomass for each prey group: crustacean group 1 (GC1), crustacean group 2 (CG2), fish group 1 (FG1) and fish group 2 (FG2). Kendall's robust line-fit method (Sen, 1968) was used to investigate trends in prey group biomass estimates: CG1 ($p > 0.0624$) and CG2 ($p > 0.844$) had non-significant trends, FG1 ($p > 0.0234$) had a significant decreasing trend, and FG2 ($p > 0.0141$) a significant increasing trend.

4. Estimation of the functional predator response.

Once prey biomass was defined, the functional predator response (Eq. 5.4) was fully developed, using the prey group biomass estimated in point 3 for B_p and the maximum value of B_p of each prey group as a proxy for K . Thus the consumption of each prey group by each predator, Φ , for years from 2006 to 2013 was estimated.

5. Fitting of prey groups.

Finally, all the information was used to fully develop equation 5.5 and thus estimate the biomass of prey groups for 2013, corresponding to the first year of the MICE projection model. Figure 5.6 shows the result of this tuning process, comparing estimated results (pink lines) with observed values for the MEDITS survey (blue points). As expected, the best fits were obtained for the prey groups with the best information, FG1 and FG2, whereas for the groups with uncertain input data, CG1 and CG2, biomass estimates differed from the original data describing more stable trends.

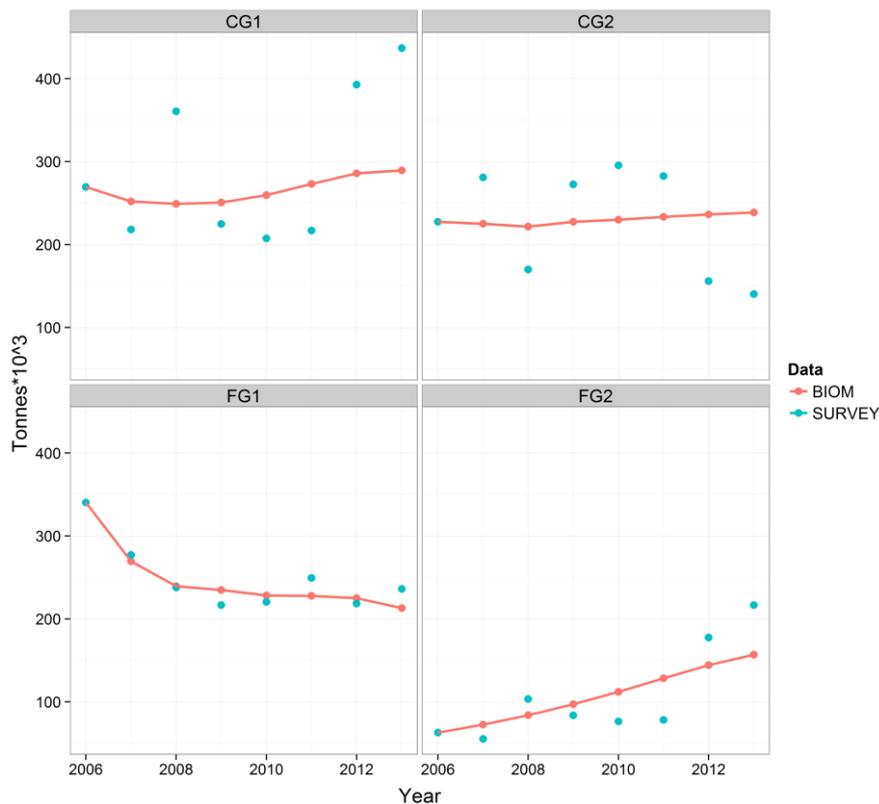


Fig. 5.6 Prey biomass from the fitting procedure. SURVEY points represent the biomass value derived from the MEDITS survey for prey groups CG1 (crustacean group 1), CG2 (crustacean group 2), FG1 (fish group 1) and FG2 (fish group 2); BIOM lines depict the prey group biomass estimated by the model, considering the prey and predator dynamics.

5.3.8 Carrying capacity

The carrying capacity, K , represents the maximum long-term biomass value that a given species can reach in a given environment. Estimates of this value are difficult to find in the literature and, given the noisy and short time-series of abundance for these species, it was very hard to estimate directly and unambiguously. In view of this and the scarcity of the information available, a value of K was computed for each prey group (K_p) while considering the negative correlation very often observed between the intrinsic rate of increase, r_p , and carrying capacity. This was done to preserve the variation in the individual parameters themselves as well as the negative correlation between them to generate a joint distribution for r_p and K_p . Wherever possible, direct estimation is preferable, but until available data become informative enough, this method provides a usable alternative that attempts to describe the key statistical relationship (covariance) of these two vital parameters.

To estimate K_p , a starting value, K_{init} , is needed; this is represented by the highest value of biomass for each prey group, also used to calibrate prey groups in section 5.3.7. The negative correlation between r and K is described by the generation of random values from a uniform distribution with a negative range: -0.5 and -0.9. The standard deviation was determined assuming (i) K_{init} , and (ii) its coefficient of variation to be equal to those derived from the MEDITS survey, or the other considered surveys, for the same years of K_{init} (Table 5.7). The distribution of K_p was calculated using the bivariate normal distribution with 1000 iterations (Fig. 5.7). The principle is that in the absence of clear information on K_p , it is precautionary to take this kind of “minimum likely value” approach; the true value may well be higher, but this approach will hopefully avoid overly-optimistic estimates being used.

Table 5.7 K_{init} value (in tonnes) and coefficient of variation (CV) for each prey group

	CG1	CG2	FG1	FG2
K_{init}	436708	295341	340276	129998
CV	1.08	0.88	0.12	0.2

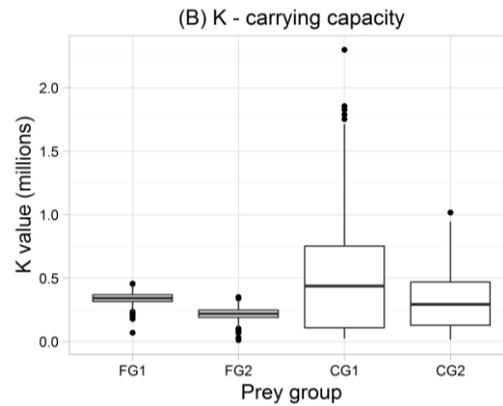


Fig. 5.7 Estimated carrying capacity, K (millions of tonnes), for each prey group: FG1 (fish group 1), FG2 (fish group 2), CG1 (crustacean group 1), CG2 (crustacean group 2). Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

5.4 Discards and survival probability

In the European Union, discards represent a debated point since the European Commission issued a controversial regulation, EC Regulation No. 1380/2013, that foresees a ban on discarding, (a.k.a. landing obligations). This regulation predicts that in the Mediterranean, from 2017 (or 2019 in some cases), all catches of species subject to catch limits and/or minimum landing sizes should be retained and landed. This decision is considered controversial for a number of ecological and economic reasons. From an ecological perspective, if on one hand discards represent a waste of natural resources, on the other, the return of this organic material represents energy re-entering into the sea, supporting secondary production and energy recycle (Coll et al., 2008; Libralato et al., 2008). Moreover discards can be an important source of food for some species (e.g. invertebrates, marine turtles, marine seabirds; Tomas et al., 2002; Bozzano and Sardà, 2002; Bicknell et al., 2013), and some species do not necessarily die in the process thus decreasing the effects of fishing mortality and favouring biodiversity (Sardà et al., 2013). From an economic point of view, the discard ban may increase operational costs of fishing activity, since fishermen will be employed to manipulate, store and land products of low value, and this can favour the creation of new markets for fishmeal or black markets, increasing the depletion of these stocks (Sardà et al., 2013). Considering these controversies, the inclusion of a scenario simulating the discard ban is of particular importance.

To create the discard ban (DB) scenario, the fate of discards once they returned to sea was taken into account. Under normal fishing practice, where a portion of catch is discarded because undersized or undesirable (i.e. in scenarios BC, DR, S1 and S2), a certain proportion of caught target species and prey groups are returned to sea. This was simulated assuming that these animals would if (i) dead, sink into the sea and be available as food for scavenger species, or, if (ii) alive, re-enter both the pool of available prey biomass and the landings of the same year. To represent this, a prey group for discards (DISC) was created, which was specific for Norway lobster. On the contrary, in the event of a discard ban (scenario DB), none of these animals would return to sea, adding to the landings of the year in which they were caught. The simulations assume perfect compliance to the discard ban rule.

To include discards within the MICE model, survival probabilities of discarded species are needed. These were drawn from the literature and refer to the species (or similar) included in the predator or prey groups. According to the legislation governing the discard ban (EC, No. 1380/2013), this applies only to species with a minimum landing size, and in our case it translates into the target species and the fish prey groups, FG1 and FG2. To make this tractable within the structure of the model, target species and prey groups were treated differently: target species were manipulated in terms of F and prey groups in terms of biomass.

More specifically, as suggested by fishermen, hake was considered not to survive capture at all (i.e. 100% of hake in landings and discards are dead). Instead, survival probability for Norway lobster has been reported in literature; Castro et al. (2003) observed 35% survival for individuals released after capture. Consequently, the fishing mortality of *Nephrops* > 24 mm CL in the discards was decreased by 35% for all scenario except for the discard ban scenario (DB). Species belonging to FG1 have been found not to survive catch (Depestele et al., 2014) so, for each simulated year (2014–2022), the discard amount was added to the FG1 biomass in all scenarios except DB. Prey group FG2 has an average discard survival probability of 36.76% (Depestele et al., 2014; Benoît et al., 2010, 2012). In this case 36.76% of the discard was added, for each projected year (2014–2022), both to the catches and to the biomass of this prey group.

In the discard ban scenario (DB), discards of the target species and prey groups FG1 and FG2 were landed.

5.5 Projection MICE model

Prey and predator dynamics were connected and projected 10 years into the future using the biomass dynamic equation (Eq. 5.5) with the aim of testing different management scenarios:

1. Base case (BC): the continuation of the present situation where the fishery operates normally and discards undersized and undesirable catch;
2. Decrease in recruitment by 50% (DR), to test the effect of a reduction of young individuals entering in the populations;
3. Increase in net selectivity for smaller individuals (S1): in this scenario F values estimated from the predator single species stock assessments for the length classes lower than the minimum landing size ($>10 < 24$ mm carapace length for Norway lobster and $> 6 < 20$ cm total length for hake) were reduced by 50%, simulating an increase in mesh size;
4. Protection of larger individuals (S2): F values estimated from the predator single species stock assessments for the length classes ≥ 24 mm for Norway lobster and ≥ 26 cm for hake was reduced by 50%, simulating a change in fishing area towards the protection of large reproducers or a change in gear (e.g. traps or longlines);
5. The imposition of a discard ban (DB) as specified by Reg. (EC) No.1380/2013.

In this step equation 5.5 was developed taking in account the uncertainty: the model was run including 1000 iterations and incorporating vectors of carrying capacity (K , section 5.3.8), prey preference (p_{pref} , section 5.3.2) and intrinsic rate of increase (r , section 5.3.5) of the same length of iterations. Prey preferences including discards were taken in account for simulating scenarios BC, DR, S1 and S2 (Fig. 5.3 A), whereas prey preferences without discards were used for developing scenario DB (Fig.5.3 B).

Results are discussed comparing scenarios DR, S1, S2, DB with the base case (BC) one. Considering the target species, the base case scenario (BC) and scenario S1 behave really similarly, showing a slight increase over the projected period for both abundance and spawning stock abundance (SSA) of predator species (Fig. 5.8); this increase is reflected only in the smaller length classes (Fig. 5.9).

The scenario simulating a decrease in recruitment by 50% in the first year (DR scenario) produces the worst situation, inducing a reduction in the estimated abundance of both

target species (Fig. 5.8 A and B), that extends to all projected years with important consequences for the spawning stock abundance, which decreases from 2017 for hake and from 2016 for Norway lobster (Fig. 5.8 C and D). This scenario results in a marked decrease in the abundance of all length bins of both species compared to the BC (Fig. 5.9).

The protection of larger individuals (S2) appears to be particularly important, since stock abundance of both target species increases (Fig. 5.8 A and B), particularly of the larger length bins (Fig. 5.9). Consequently, spawning stock abundance shows a positive trend over the projected years (Fig. 5.8 C and D). Contrary to expectation, this measure has little effect on the cannibalistic relationship of both predators: no change is evident compared to the base case in the abundance of the smaller portion of either hake or Norway lobster (Fig. 5.9).

The discard ban scenario (DB) does not appear to improve predator species, particularly Norway lobster abundance decreases immediately in 2014 to then follow a stable trend to 2022 (Fig. 5.8 B), whereas for hake the trend is very similar to the BC scenario. Moreover, the spawning stock abundance does not increase over the years, rather it decreases for Norway lobster (Fig. 5.8 C and D).

Figure 5.10 shows the results for prey groups. As for predators, scenarios BC and S1 describe similar results, depicting a continuous decreasing trend for FG1, CG1 and CG2, whereas FG2 presents a slight increasing trend. The DR scenario depicts the most favourable situation, since the decrease in FG1 is slower than in the base case scenario accounting for higher value (Fig. 5.10 A), FG2 increases markedly (Fig. 5.10 B) and CG1 and CG2 stay approximately stable after an initial decrease (Fig. 5.10 C and D). Scenario S2 results in visible differences compared to the base case scenario; FG1, CG1 and CG2 decrease continuously to 2022, accounting for lower values with respect to BC, particularly CG2 (Fig. 5.10 C). FG2 shows an increasing trend to 2018, followed by a decreasing trend that accounts for lower values compared to the base (Fig 5.10 B). The DB scenario describes a trend similar to the BC scenario for FG1 and CG1 (Fig. 5.10 A and V), whereas that for FG2 almost identical to the one resulting from scenario S2 (Fig. 5.10 B); CG2 follows a marked continuous decreasing trend to 2022 (Fig. 5.10).

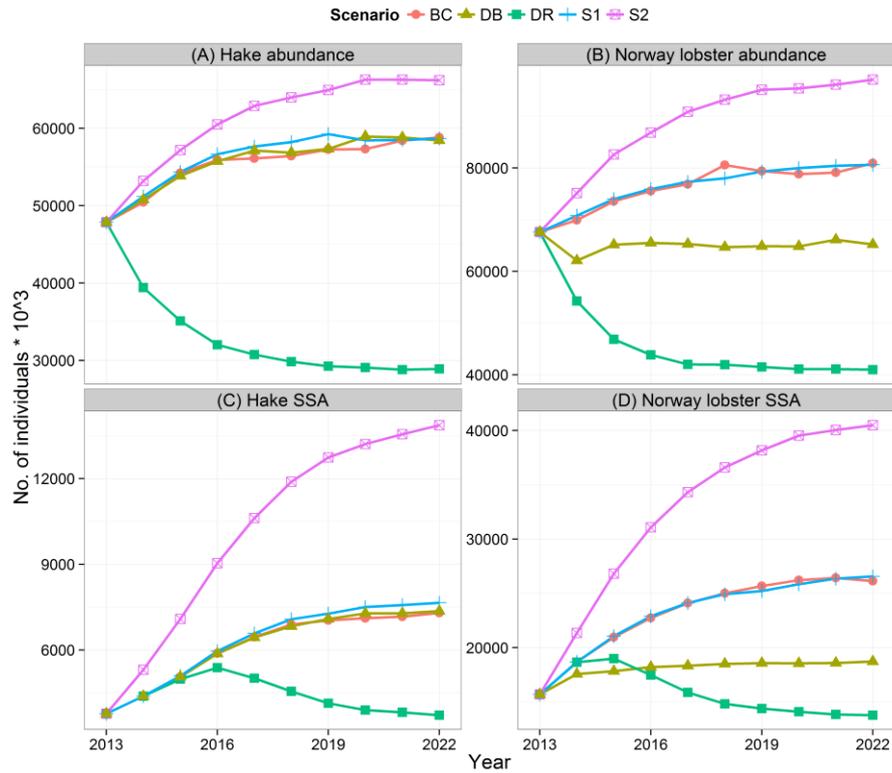


Fig. 5.8 MICE model results – Abundance and Spawning Stock Abundance (SSA) summaries per year for hake (A and C) and Norway lobster (B and D) for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals and DB – the discard ban scenario. Note that in the hake base case (BC) SSA is overlaid by the discard ban scenario (DB). These plots were obtained by summing the estimated abundance of all length bins for each predator and scenario, and plotting the 50% quantile.

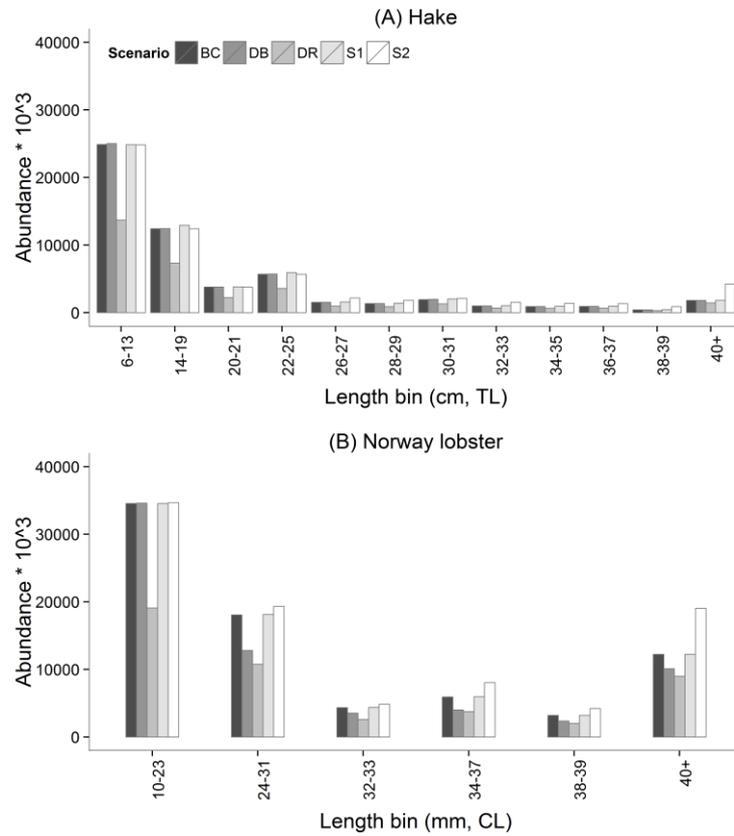


Fig. 5.9 MICE model results – Length frequency distributions averaged over the years (2013–2022) for (A) hake and (B) Norway lobster for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals, and DB – the discard ban scenario. For each predator and length bin, these plots were obtained by calculating the average estimated abundance for all years and plotting the 50% quantile.

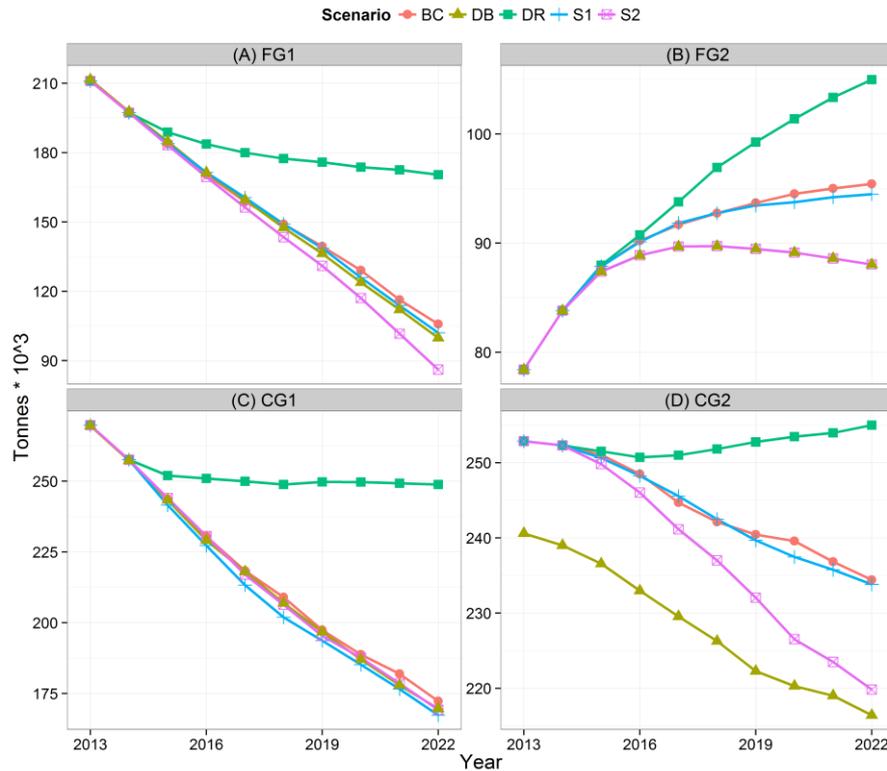


Fig. 5.10 MICE model results – Biomass summaries for the four prey groups: (A) FG1 (fish group 1), (B) FG2 (fish group 2), (C) CG1 (crustacean group 1), and (D) CG2 (crustacean group 2), for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals, and DB – the discard ban scenario. For each prey group and scenario, these plots show the 50% quantile of the estimated biomass.

Figures 5.8 and 5.10 present the results considering the 50% quantile, derived from iterations, with the aim of giving a better understanding of the outcomes. However stock abundance of target species with uncertainty included is showed in figures 5.11 and 5.12, and spawning stock biomass is reported in figure 5.13 for hake and figure 5.14 for Norway lobster. Biomass of prey groups were also estimated including uncertainty and results are represented in figure 5.15. These figures highlight the fact that uncertainty increases predictions approaching the year 2022 and confidence intervals are larger for prey group estimates for which different sources of uncertainty r_p , K_p , p_{pref} are included. The scenarios associated with the lowest levels of uncertainty are scenarios DR and DB. Finally, table 5.8 summarises predictions in terms of their probability of increase or decrease with respect to the first projection year (2013). Probabilities are reported for the middle of the time series in exam, year 2017, and at the end of the projected years, 2022, and they highlight scenario S2 as the best option for predators, whereas scenario DR represents the best option for prey groups.

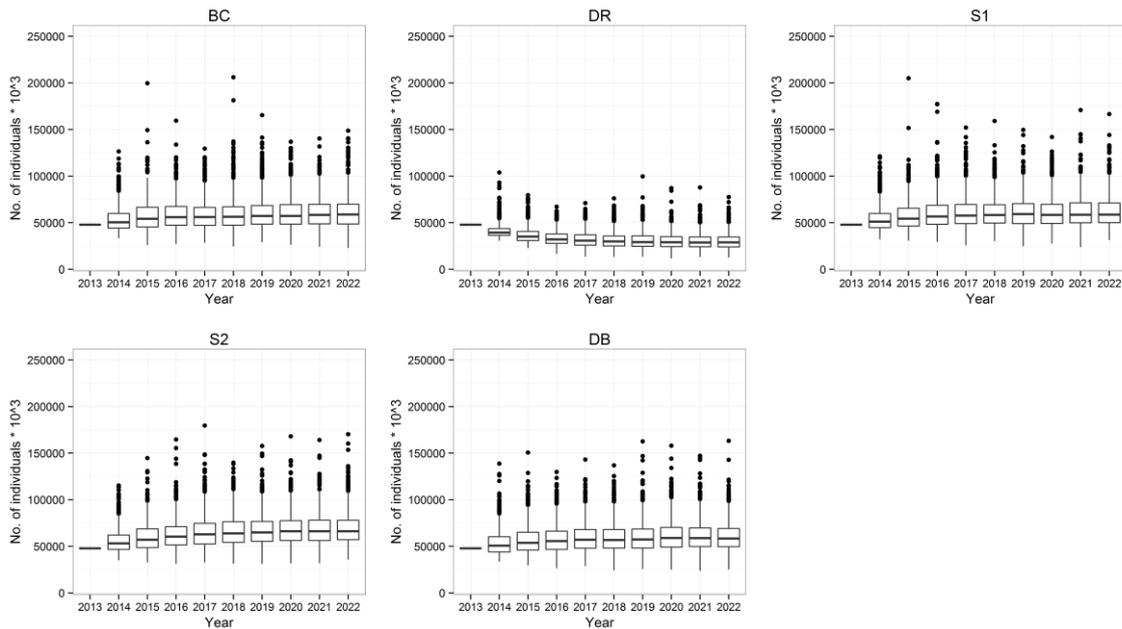


Figure 5.11. MICE model results - Abundance per year for hake for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals and DB – the discard ban scenario. Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

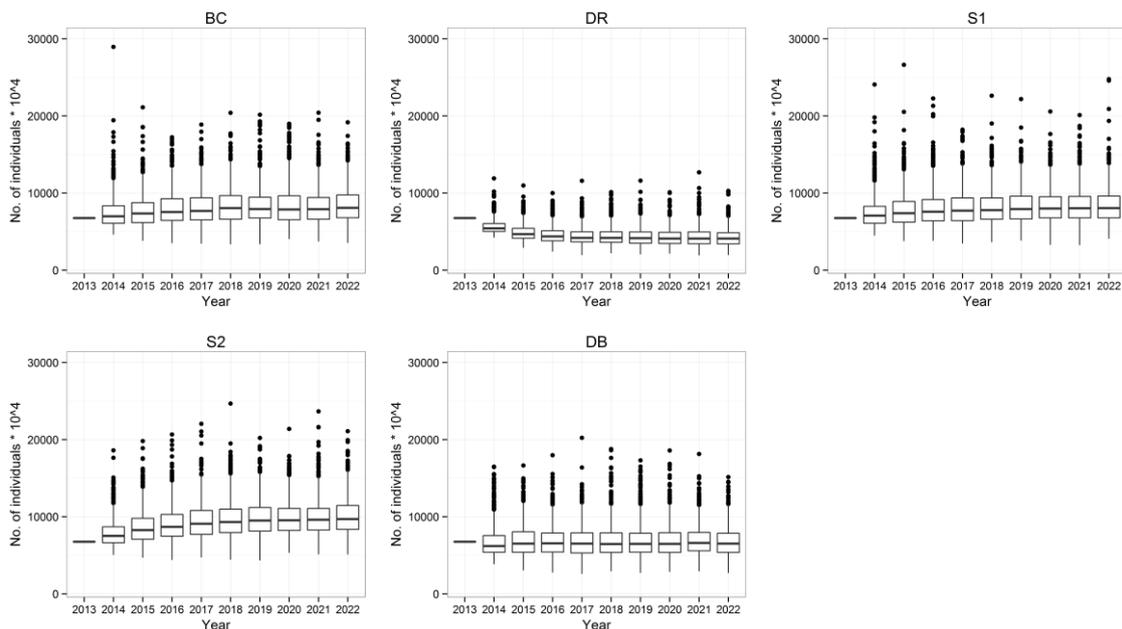


Figure 5.12. MICE model results – Norway lobster abundance per year for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals and DB – the discard ban scenario. Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

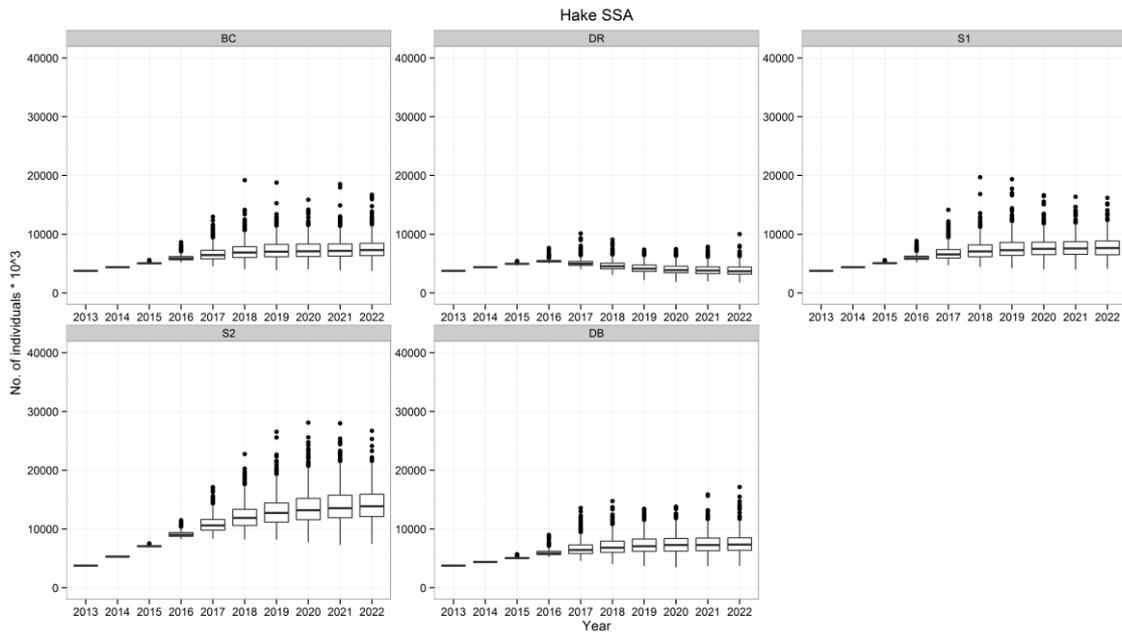


Figure 5.13. MICE model results – Hake spawning stock abundance (SSA) per year for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals and DB – the discard ban scenario. Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

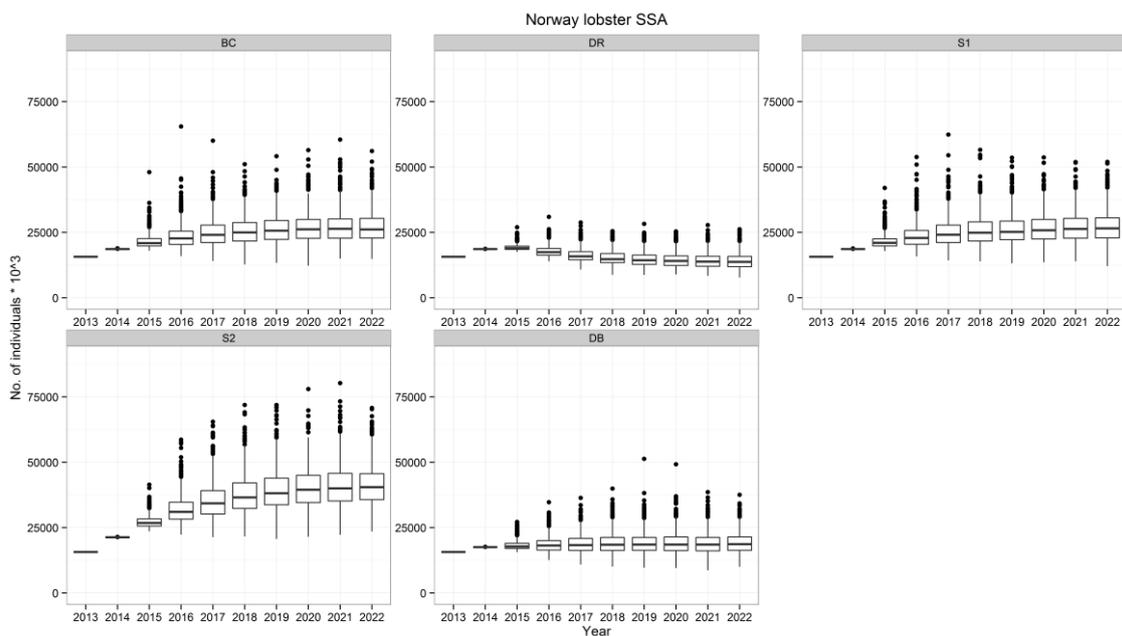


Figure 5.14 MICE model results – Norway lobster spawning stock abundance (SSA) per year for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals and DB – the discard ban scenario. Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value and points are outliers.

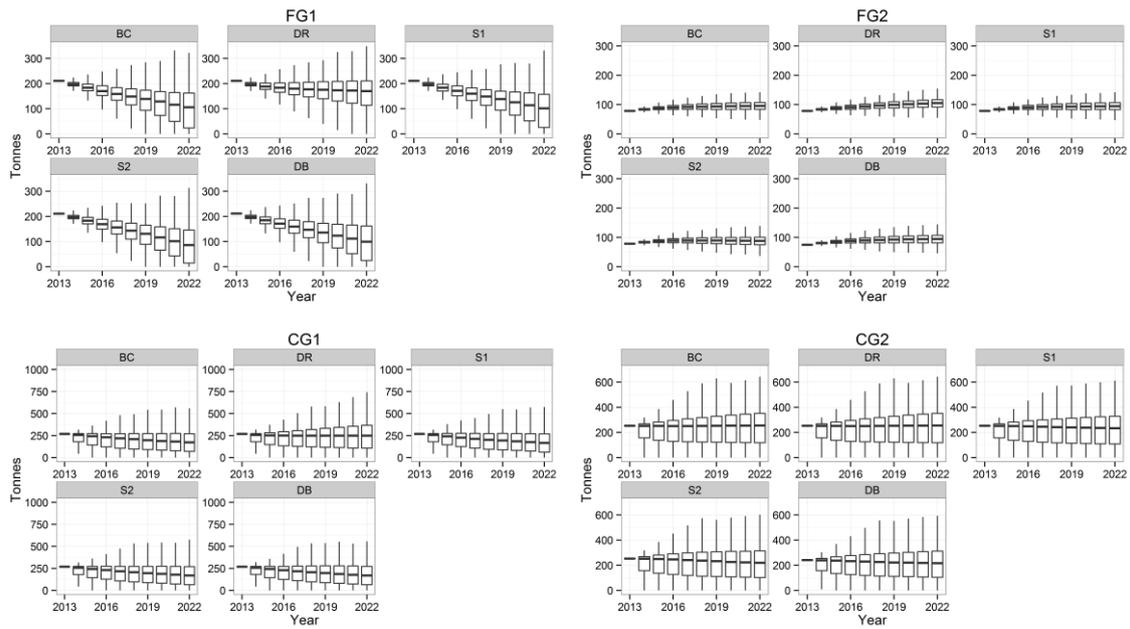


Figure 5.15 MICE model results - Biomass for the four prey groups: (A) FG1 (fish group 1), (B) FG2 (fish group 2), (C) CG1 (crustacean group 1), and (D) CG2 (crustacean group 2), for the different scenarios: BC – base case, DR – a decrease in recruitment by 50%, S1 – increase in net selectivity for smaller individuals, S2 – protection of larger individuals, and DB – the discard ban scenario. Upper and lower horizontal lines represent the first and third quartiles (25th and 75th percentiles), bold line is the median value, whiskers extend to the maximum and minimum value.

Table 5.8. Probability that the predicted abundance and spawning stock abundance (SSA) of predators and the total biomass of prey half way through (2017), and the end of the projection period (2022) will have increased (> 0.5) or decreased (< 0.5) with respect to the starting biomass (2013). Probabilities were calculated taking into account the variability associated to the predictions (i.e. resulting from 1000 iterations).

<i>Scenario</i>	<i>Hake abundance</i>		<i>Norway lobster abundance</i>		<i>Hake SSA</i>		<i>Norway lobster SSA</i>		<i>FG1</i>		<i>FG2</i>		<i>CG1</i>		<i>CG2</i>	
	2017	2022	2017	2022	2017	2022	2017	2022	2017	2022	2017	2022	2017	2022	2017	2022
<i>Base Case (BC)</i>	0.73	0.77	0.69	0.76	1.00	1.00	0.99	1.00	0.08	0.06	0.86	0.82	0.26	0.25	0.46	0.45
<i>Decrease Recruitment (DR)</i>	0.05	0.03	0.04	0.03	1.00	0.48	0.53	0.26	0.18	0.25	0.90	0.91	0.41	0.45	0.49	0.51
<i>Selectivity 1 (S1)</i>	0.77	0.80	0.69	0.75	1.00	1.00	0.99	1.00	0.06	0.05	0.86	0.81	0.27	0.25	0.47	0.45
<i>Selectivity 2 (S2)</i>	0.87	0.94	0.90	0.96	1.00	1.00	1.00	1.00	0.06	0.04	0.82	0.70	0.26	0.25	0.45	0.42
<i>Discard Ban (DB)</i>	0.75	0.80	0.45	0.45	1.00	1.00	0.81	0.80	0.08	0.05	0.88	0.85	0.27	0.26	0.46	0.45

The MICE approach has been useful to test different management options impacting both target species, hake and Norway lobster, and the other species, i.e. prey, living in the study area.

Results support the scenario simulating the protection of adults (S2), since it appears to produce the most beneficial results for both predator species in terms of spawning stock abundance (SSA) and adult size. The direct consequence of this was a visible decrease in all prey groups compared to the base case. This was particularly true for FG1, FG2 and CG2, all targeted by large hake and large Norway lobster, and less so for CG1, the main prey of small hake. Nevertheless, decreases in prey group over the projected period, were not so relevant enough to consider not supporting this management option. Management measures directed towards reaching these results could entail the creation of a trawling ban within the study area, the use of technical measures for improving selectivity of fishing gear, for example the use of flexible grids in front of the cod-end (Sardà et al., 2006; Bahamon et al., 2007), as well as the use of more selective fishing gear such as longlines and baited traps (Santos et al., 2002; Morello et al., 2009). Regarding the trawling ban option, the biological importance of the study area is also acknowledged by the Italian legislation that determined a temporary closure of the Pomo/Jabuka pits to bottom trawls from 26 July 2015 to 26 July 2016 (D.M. 3/07/2015); results of this measure will be verified years to come.

Regarding the remaining scenarios, the base case scenario describes a rather stable situation, for both predators and prey species, and for this reason it can easily shift to having negative consequences. This is supported by the fact that a decrease in recruitment by 50% represents the worst situation for both predator species that decrease consistently in projected years. This scenario has a tangible influence on prey groups as well. The projected trends of all prey groups improve compared to the base case, consistent with a decrease in their predators. Efforts should thus be directed towards avoiding this situation, to the extent possible: one that can easily arise either as a consequence of adverse environmental conditions affecting larval and juvenile phases or when stocks are highly exploited at young ages and individuals are not allowed grow to adult sizes. Particularly in the Pomo/Jabuka pits where the bottom trawl fishery can heavily affect juvenile hake, this can be obtained by closing the area to bottom trawling, especially at times of high abundance of hake juveniles (spring and autumn; Vrgoč et al., 2004).

The scenario investigating an increase in net selectivity for small predators showed modest beneficial effects resulting in only a slight increase in the number of small individuals of both predators. Finally, the imposition of the discard ban scenario was tested, but no improvements for either predators or prey were verified. In particular, Norway lobster (small and large) and prey groups FG2 and CG2 decreased with respect to BC. CG2 showed the most marked decrease, since it represents food for both predators and includes most of the discarded species in this area. Thus, the absence of discards drives Norway lobster, in particular, to increase the consumption on these live prey leading to a strong decrease of this group. Moreover, the discard proportion in the Adriatic bottom trawl catch is quite low and this is one of the reasons why this measure is unlikely to result in beneficial effects. The possibility of negative consequences of a discard ban should be carefully assessed, as already mentioned in section 5.4.

This study allowed us to pinpoint at least one management option for protecting different levels of the ecosystem in exam. Moreover, the study also highlights the importance of taking in account predation, since appears to be the main factor regulating the biomass of the prey groups; this is not surprising as they mainly comprise species not targeted by the fishery. Similar conclusions are drawn in other studies, e.g. Punt and Butterworth (1995), Livingston and Jurado-Molina (2000), and Overholtz et al. (2008), in which predation substantially affects prey biomass.

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CHAPTER 6 – Conclusions

The main aim of this study was to develop a Model of Intermediate Complexity for Ecosystem assessments (MICE; Plagányi et al., 2014) towards evaluating different scenarios for the management of the European hake and Norway lobster bottom trawl fishery in the central Adriatic Sea. These two species thus represent the target species, as well as the predators, of this study; they are two of the most important species fished by the bottom trawl fishery, accounting for both highest landings and commercial value among demersal species in the area.

The study area is located in the central Adriatic Sea and includes the Pomo/Jabuka pits, the deepest part of the central and northern Adriatic Sea, and takes in account the fishing activity of the principal harbours exploiting this zone at depths greater than 100 m. This area represents an important zone both economically and biologically. Economically because a great part of the catches of GSA 17 come from this area and they account for an high commercial value, whereas biologically because it represents a nursery ground for hake and hosts a distinctive population of Norway lobster. Moreover, thanks to the peculiar circulation of the Adriatic Sea, upwelling phenomena occur in this area allowing the formation of a rich planktonic community that supports a richness in pelagic and demersal resources (Adriamed, 2006). This richness in species, as well as the significant importance of the area for the target species of this study and the considerable exploitation of this zone by fishing activity, make it an interesting place to test multispecies management alternatives.

Definition of management alternatives to apply in a multispecies context is one of the key objectives of ecosystem-based fisheries management (EBFM) and an ecosystem approach to fisheries (EAF). In particular, these approaches include the protection of ecosystems from majored degradation and irreversible change, as well as the broadening of our knowledge on the role of human activities in ecosystem dynamics (Garcia et al., 2003; Pikitch et al., 2004).

Different models are available to reach EAF purposes, here the choice was made to develop a MICE approach, since it is well adapted to test specific management questions, as required by this study, and accounts for an intermediate complexity. MICE represents a group of models taking in account a restricted number of species, fundamental to describe the crucial relationships of the ecosystem in exam. Their

primary aim is to answer specific tactical management questions (e.g. gear restrictions, seasonal closures, etc.), incorporating the best characteristics of single-species models and the capability to estimate parameters using standard statistical methods.

In this case, the MICE model was developed in a step-wise manner. Firstly, a conceptual model was defined: this represents the interaction between the trawl fishery, the two target species (Norway lobster and European hake, also defined “predators”) and their prey (grouped in four meaningful groups: mostly pelagic fish species – FG1; mainly demersal fish species – FG2; crustacean benthopelagic species - CG1; benthic crustacean species – CG2). Discards were also considered, representing a source of food for Norway lobster and being important in terms of management options. Secondly, management scenarios to be tested were determined: (i) base case (BC), that is the investigation of the effects of the continuation of the present situation, (ii) the examination of the effects of a recruitment reduction of predators by 50% (DR), (iii) the impact of an increase in net selectivity for smaller individuals (S1), (iv) the effect of a protection of larger individuals (S2) and (v) the impact of the imposition of the discard ban (Reg. EC No.1380/2013).

Finally, with the conceptual model and the desired outputs at hand, it was possible to develop the dynamics of each single functional unit, which were then joined within the MICE model and projected into the future (from 2013 to 2022) for the evaluation of the different management strategies selected.

Regarding predator dynamics, it first of all necessary to evaluate their status applying single species stock assessments and producing the input values (i.e. fishing mortality rates and stock abundance at length) for the MICE. For hake three single species models were compared: a length cohort analysis (LCA with VIT (Lleonart and Salat, 1992; 1997)), a statistical catch at length model (Mark3) and an integrated analysis (SS3; Methot and Wetzel, 2013). Results seem to favour estimates produced by the Mark3 method, since it is a purely length based model, more appropriate to describe the length structure dynamics of hake. Moreover, being a statistical catch at length, it produces more accurate estimates compared to the VIT analysis, that it is too a truly length based model but is based on an assumption of steady state which can generate biased estimates. SS3 has to be mentioned; this method belongs to the set of models performing an integrated analysis and thus able to include a wide variety of input data, with different structures. This model, however, is not a purely length based model, making other methods more suitable to describe length based dynamics at hand.

Actually SS3 is one of the most used stock assessment models, especially outside Europe (e.g. Helu et al., 2000; Shoho et al., 2010; Cope, 2013).

For the stock assessment of Norway lobster two models were compared: a simple length cohort analysis (LCA with VIT (Lleonart and Salat, 1992; 1997)) and CASAL (Bull et al., 2012). Both VIT and CASAL are purely length based models, but VIT has the limit of assuming a steady state, whereas CASAL performs an integrated analysis which takes care of this problem. CASAL seems to give more reliable estimates since it include a larger amount of data that better describe the specific biological features of this species, i.e. sex ratio related to moulting and reproductive behaviour. CASAL is a widely used method, mainly in the southern hemisphere (New Zealand and Australia) (e.g. Hillary et al, 2006; Candy and Constable, 2008; Cordue, 2014).

The MICE model was develop using results from VIT assessments for both hake and Norway lobster. The reasons for choosing this assessment and not the others are two: 1) the VIT outputs represented the least complex inputs for the MICE model, satisfying the underlying MICE philosophy which embraces simplicity; 2) the investigation of a number of more complex stock assessment method (Mark 3, SS3, CASAL) is an important part of this study. The aim was to test possible improvements to single species models for two important species whose assessments to date has not been ideal. Nevertheless, the development of these models requires a considerable amount of time, as does the development of a MICE model. The VIT assessment, on the other hand is rather quick and the use of its results allowed the implementation of the MICE model to be more expedite. The more complex new single species approaches, Mark 3 and CASAL in particular, seem to perform better than VIT, probably giving more reliable estimates; their outputs are being tailored for the MICE model and will be included in future developments of this study.

The inclusion of prey species within the model allowed us to investigate the effects of predation. Predation is a fundamental aspect of multispecies models. When predators are more generalist, as in this case, prey items can be partitioned into meaningful groups, with the net effect of reducing model complexity and calculations. In support of this, Yodzis (1998) demonstrated that when the weakest trophic relationships within an ecosystem were removed from a model, predictions did not undergo substantial changes; the contrary is true if important links were removed.

Moreover, predation appears to be the main factor regulating the biomass of the prey groups; this is not surprising as they mainly comprise species not targeted by the

fishery. Similar conclusions are drawn in other studies, e.g. Punt and Butterworth (1995) showed the importance of taking into account all the important predator-prey interactions within the model, including predation and explained 90% of hake mortality in this way; Livingston and Jurado-Molina (2000) observed the influence of predation in limiting recruitment of pollock species, making the use of different fishing strategies almost not useless. We are not able to see more bottom-up type dynamics as we have not parameterised them given the lack the available data to do so (e.g. primary production, nutrients). We are aware of the importance of exploring and understanding such processes. The main issue, and one not at all specific to this example system, is that obtaining data to estimate these processes is far more difficult than collecting data on the top-down dynamics such as predation uptake and diet preference. The next step will thus be to incorporate such feedbacks as a function of the effect of prey groups in terms of biomass (and accounting for predator prey preference) on predator somatic growth and/o reproductive success. This is truly in line MICE philosophy where the representation of predator-prey interdependencies is simplified to what consumption affects (e.g. the effect of prey biomass on growth, reproduction or survival) rather than delving into the bioenergetics associated to consumption for which we have no supporting data (Plagányi et al., 2014).

Finally, predator and prey dynamics were joined within the MICE model and projected into the future under different management scenarios. The base case scenario describes a rather stable status quo situation, for both predator and prey species, and for this reason it can easily shift to negative consequences. A possible decrease in recruitment of predators by 50%, easily caused by adverse environmental conditions affecting larval and/or juvenile phases or when stocks are highly exploited and individuals cannot grow to adult sizes, represents the worst situation for both predator species. Efforts should thus be directed towards avoiding this situation. The protection of adults appears to be the best management option, producing the most beneficial results for both predator species in terms of spawning stock abundance (SSA) and adult size. Under this scenario, prey groups showed a visible decrease compared to the base case scenario but this was not so relevant enough to discard the option. The management strategies available to act upon these results are the creation of a trawling ban in the Pomo area, as well as the use of flexible grids in front of the cod-end (Sardà et al., 2006; Bahamon et al., 2007) and the use of more selective fishing gear such as longlines and baited traps

(Santos et al., 2002; Morello et al., 2009). The former of these two options has recently been put in place for a trial period of one year.

Finally, neither an increase in net selectivity for small predators nor a discard ban scenario showed modest tangible (if any in the case of the discard ban) beneficial effects on predator or prey groups. In particular, under a discard ban scenario, Norway lobster and the most consumed prey groups (FG2 and CG2) decreased with respect to the base case. This may have the net effects of inducing a possible reduction of biodiversity, possibly causing modifications of the trophic interactions characterising the impacted communities (e.g. shortening of food chains) (Groenewold and Fonds, 2000), altering benthic communities and reducing additional food sources for birds and turtles (Tomás et al., 2002; Suuronen and Erikson, 2010; Bicknell et al., 2013; Depesstele et al., 2014). This would add to the possible economic effects of a discard ban e.g. the possible creation of new markets (e.g. fishmeal), inducing fishermen to increase catches of undersized or illegal and non-commercial species, thus increasing the fishing mortality in particular on juvenile fish (Sardà et al., 2013; Bellido Millán et al., 2014).

This MICE application has demonstrated a capacity for producing valuable management options to avoid ecosystem degradation sustaining the well-being of marine ecosystems and the fisheries they support, that is the crucial objective of an ecosystem approach to fisheries (Garcia et al., 2003; Pikitch et al., 2004). Other ecosystem models were tested in the Adriatic Sea, particularly whole-of-ecosystem models constructed to evaluate fisheries impacts and they do not portray a hopeful future for the Adriatic Sea, which has been reported as having possibly been subject to ecosystem over-fishing in the past 30 years (Coll et al., 2007; Libralato et al., 2008; Coll et al., 2010a). These studies demonstrated the overall depletion of the Adriatic Sea ecosystem that caused important changes in the structure and functioning of this ecosystem, e.g. the increase of small and fast-growing organisms versus large and slow-growing organisms. In particular, the depletion of the Adriatic Sea ecosystem was caused by an increase in fishing activity in recent years, together with environmental changes, such as the increase of the water temperature. The overall depletion of the Adriatic Sea was further confirmed upon comparison with other 19 ecosystems (Coll et al., 2010b; Link et al., 2010). The importance of appropriate management of the Pomo/Jabuka Pit area is also highlighted (central Adriatic; Fouzai et al., 2012), especially in view of this area's status as a

nursery ground for European hake (Županović and Jardas, 1986; Druon et al., 2015), one of the most important demersal species of the Adriatic Sea.

Moreover, this MICE model highlights the role of multispecies models in complementing single-species models in terms of simulating alternative management options and evaluating associated trade-offs, especially when taking trophic interactions into account. By utilising all available data within a rigorous framework that accounts for the associated uncertainty, this approach represents a small step forward in terms of advancing an ecosystem approach to fisheries.

Improvements and future perspectives of this model are foreseen and they include: (i) the expansion of the modelled area to the entire Adriatic Sea, (ii) the integration of new and more accurate single-species stock assessments, taking into consideration the different growth dynamics in different areas, as well as data from additional sources (e.g. abundance indices from Underwater TV survey for Norway lobster, Martinelli et al., 2013; spatial effort data to be used for splitting catches by area with VMS data, Russo et al., 2011); (iii) the incorporation of prey-predator feedbacks, (iv) the inclusion of better estimates of prey biomass and an investigation of the use of additional forms of the predator functional response, e.g. Holling type III, predator interference, Hassell-Varley; and (v) the inclusion of environmental variables, e.g. temperature, oxygen and proxies for water replenishment/renewal in the Pomo/Jabuka Pits (Artegiani et al., 1997a; b) to understand whether these processes underlie hydrographic (Marini et al., 2006) and biological variations of importance for this Adriatic system.

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Appendix A

The basic equations to pursue the stock assessment of hake with the Mark3 model are listed below.

The codes for the Mark 3 assessment are also reported. The dat.file includes the input data used, and the pin.file comprises the starting values obtained by the initialization process. The tpl.file contains the actual ADMB assessment code.

Equations

Spawning stock biomass (*SSB*):

$$SSB = mat_l * N_l * w_l$$

where mat_l represents the maturity vector by length bin (l), N_l the number of individuals in each length bin (l) and w_l the mean weight of each length bin (l).

Recruitment (R):

$$R = e^{\log R_l}$$

where $\log R_l$ represents the logarithm of the number of individuals contained in the first length bin of each considered year divided by the survey selectivity, $selsurv$, for the first length bin.

The survey selectivity is assumed to be logistic:

$$selsurv = \frac{1}{(1 + 19 * e^{(\theta_1 - n_l)}) / (\theta_2 - \theta_1)}$$

where

θ_1 = length at 50% selectivity

θ_2 = length at 95% selectivity

n_l = number of length bins

Fishing mortality by year and length bin ($F_{t,l}$) and survival rates by year and length bin ($S_{t,l}$) are calculated as follows:

$$F_{t,l} = e^{\log F_t} * self_l$$

$$S_{t,l} = e^{-(F_{t,l} + M_l)}$$

where $\log F_t$ are the starting values for fishing mortality for each year, derived from the mean value among length bins of the ratio between the number of individuals in the catches and the number of individuals in the survey. M_l is natural mortality at length and

$self$ is the selectivity for the commercial fishery, which is assumed to be a double normal function:

$$self_l = 2^{-[(l-\lambda)/\sigma_L]^2}; l_0 < l \leq \lambda$$

$$self_l = 2^{-[(l-\lambda)/\sigma_U]^2}; l > \lambda$$

Where:

l = length bin

λ = length bin at maximum selection (selectivity parameter 1)

σ_L = rate at which selectivity decays (selectivity parameter 2)

σ_U = rate at which selectivity reaches the maximum (selectivity parameter 3)

Survey abundance by length ($UI_{t,l}$) is given by:

$$UI_{t,l} = e^{\log qsurv} * N_{t,l} * (S_{t,l})^{fsurv}$$

where $UI_{t,l}$ represents the number of fish caught by the survey by length bin (l) and year (t), $\log qsurv$ represents the starting value for the survey catchability, assumed to be 0.9, $N_{t,l}$ is the number of individuals by length and year within the stock, $S_{t,l}$ is the survival rate for each length bin and year and $fsurv$ is the fraction of year gone by when survey starts and here the survey is assumed to start at the beginning of the year.

Catches ($C_{t,l}$), by year t and length bin l , are estimated as follows:

$$C_{t,l} = \frac{F_{t,l}}{F_{t,l} + M_{t,l}} * ((1 - N_{t,l}) * S_{t,l})$$

where $F_{t,l}$ represents the fishing mortality by year and length bin, $M_{t,l}$ the natural mortality by year and length bin, $N_{t,l}$ the number of individuals in the stock by year and length bin and $S_{t,l}$ the survival probability by year and length bin.

Stock abundance by year and length bin ($N_{t,l}$):

$$N_{t,l} = N_{t-1,j} * \gamma_{j,l} * S_{t-1,j}$$

where $N_{t-1,j}$ represents the number of individuals in the previous year ($t-1$) of a given length (j), $\gamma_{j,l}$ represents the transition matrix from length j in year $t-1$ to length l in year t ; l starts at the second length bin and $S_{t-1,j}$ is the survival probability of the previous year ($t-1$) by length (j). See section 3.2.3 for the equation for $\gamma_{j,l}$

Codes for Mark 3 assessment.

```
// ADMB DAT.file for M. merluccius stock assessment model MARK3
```

```
// :: MARK 3 similar to SS
```

```
// R. Hillary and S. Angelini (2014)
```

```
##### length: 6 - 40+ # years: 2006 2013
```

```
# lbins:6 14 20 22 26 28 30 32 34 36 38 40
```

```
# no. of length bins
```

```
12
```

```
# min and max years
```

```
2006
```

```
2013
```

```
# survey min and max years
```

```
2006
```

```
2013
```

```
# fraction of year gone when survey starts
```

```
0.
```

```
# transition matrix
```

0	0.82	0.18	0	0	0	0	0	0	0	0	0
0	0	0.13	0.73	0.13	0	0	0	0	0	0	0
0	0	0	0	0.70	0.30	0	0	0	0	0	0
0	0	0	0	0	0.40	0.55	0.05	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0.00	1.00	0	0	0
0	0	0	0	0	0	0	0	0.11	0.89	0	0
0	0	0	0	0	0	0	0	0	0.21	0.79	0
0	0	0	0	0	0	0	0	0	0	0.31	0.69
0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	1

```
# maturity ogive
```

```
0
```

```
0
```

```
0.5
```

```
0.5
```

```
0.5
```

```
1
```

```
1
1
1
1
1
1
1
# M
0.759
0.386
0.386
0.263
0.263
0.219
0.219
0.219
0.195
0.195
0.195
0.181
# observation error for catch data (CV)
0.1
# observation error for survey data (CV)
0.25
# effective sample size of catch length frequency data
10
# prior mean for survey catchability (muq)
0.9
# prior CV for survey catchability (cvq)
0.1
##### total catches in numbers (thousand)
36018.2634
17351.49757
13904.89474
10659.83113
10322.20466
10132.55077
12244.60648
10062.31741
##### catch length frequencies
0.04 0.54 0.15 0.21 0.03 0.01 0.01 0.00 0.00 0.00 0.00 0.00
```

0.07	0.13	0.28	0.32	0.06	0.04	0.02	0.03	0.03	0.01	0.00	0.00
0.10	0.20	0.22	0.29	0.05	0.03	0.02	0.03	0.03	0.01	0.00	0.02
0.22	0.26	0.08	0.21	0.06	0.04	0.02	0.02	0.02	0.02	0.01	0.03
0.20	0.26	0.08	0.22	0.06	0.04	0.02	0.02	0.02	0.02	0.01	0.03
0.16	0.31	0.13	0.23	0.02	0.02	0.02	0.03	0.03	0.01	0.01	0.02
0.30	0.22	0.07	0.25	0.05	0.02	0.01	0.01	0.02	0.02	0.01	0.02
0.23	0.23	0.04	0.13	0.10	0.07	0.03	0.03	0.03	0.03	0.02	0.06

wts (weight at length in kg)

0.005	0.031	0.057	0.089	0.123	0.155	0.198	0.239	0.237	0.254	0.26	0.571
0.005	0.032	0.061	0.091	0.133	0.162	0.21	0.251	0.295	0.343	0.34	0.573
0.005	0.031	0.059	0.09	0.128	0.159	0.204	0.245	0.266	0.298	0.419	0.573
0.005	0.031	0.06	0.091	0.13	0.162	0.203	0.248	0.287	0.327	0.425	0.579
0.01	0.032	0.061	0.092	0.132	0.165	0.202	0.251	0.308	0.355	0.414	0.567
0.009	0.031	0.058	0.09	0.131	0.166	0.208	0.25	0.307	0.351	0.437	0.592
0.01	0.032	0.067	0.094	0.136	0.17	0.202	0.257	0.309	0.343	0.406	0.518
0.01	0.031	0.06	0.092	0.131	0.159	0.195	0.246	0.309	0.371	0.398	0.592

tuning (total N in 000s from MEDITS survey)

32124	9527	1888	2154	558	283	186	103	83	65	92	160
20894	8630	820	1501	417	350	178	205	103	43	35	115
33055	7598	1819	2312	554	400	178	197	116	164	53	247
3316	4495	876	1180	390	273	145	80	33	68	85	51
7352	4624	909	644	200	164	87	36	43	38	57	82
7613	6248	749	845	214	163	91	115	84	43	22	39
23110	3602	766	1203	302	191	190	179	78	70	39	113
5533	5147	741	1499	463	333	203	159	143	120	65	120

// ADMB PIN.file for *M. merluccius* stock assessment model MARK3
// :: MARK 3 similar to SS
// R. Hillary and S. Angelini (2014)
the following three values represent the fishery selectivity Fselpar
3.5
1.5
10
the following two values represent the survey selectivity Sselpar
6
4
the following eight values are logFpar
-0.6421563
-0.5794159

```
-0.3565372
-0.2528373
-0.3029269
-0.3193075
-0.3232366
-0.3337357
# the following eight values are logRpar
10.50428
10.07415
10.53286
8.233492
9.029597
9.064573
10.17495
8.745368
# the following eleven values are logNpar
9.162214
7.543063
7.675312
6.324655
5.645761
5.22565
4.631578
4.421836
4.178992
4.521452
5.07381
0.9 # qpar
# the following two values are logsdpar
-2.995732
-2.995732
```

```
// ADMB TPL file for M. merluccius stock assessment model MARK3
// :: MARK 3 similar to SS
// R. Hillary and S. Angelini (2014)
```

DATA_SECTION //this section describes the structure of the data in your model

```
init_int nlength
init_int minyr
init_int maxyr
init_int sminyr
init_int smaxyr
init_number fsurv
init_matrix Gamma(1,nlength,1,nlength)
init_vector mat(1,nlength)
init_vector M(1,nlength)
init_number cvC
init_number cvS
init_number neff // effective sample size of catch length frequency data
number sdC
number sdS
// The escape sequence (!!) can be used to include one line of
// the user's code into the DATA_SECTION or PARAMETER_SECTION
!!sdC=sqrt(log(1.+cvC*cvC));sdS=sqrt(log(1.+cvS*cvS));
init_number muq
init_number cvq
number sdq
!!sdq=sqrt(log(1.+cvq*cvq));
init_vector ctotn(minyr,maxyr)
init_matrix clfreq(minyr,maxyr,1,nlength)
init_matrix weights(minyr,maxyr,1,nlength)
init_matrix tuning(sminyr,smaxyr,1,nlength)
```

PARAMETER_SECTION // this section is used to describe the structure of the parameters in your model

```
// double normal selectivity for fishery
init_bounded_vector Fsel(1,3,1e-2,100.) // A vector with index between 1 and 3,
// logistic selectivity for MEDITS survey
init_bounded_vector Ssel(1,2,1e-2,100.)
init_vector logFyrs(minyr,maxyr) // it means that we'll have a vector of eight values, since we
have eight years
```

```

init_vector logRec(minyr,maxyr) // it means that we'll have a vector of eight values, since we
have eight years
init_vector logStartN(1,nlength-1) // it's a vector of eleven values, since the lengths are 12
init_number logqsurv
init_number logsdsurv //log-scale total SD for the survey :-)

vector self(1,nlength)
//vector selsurv(1,nlength)
vector sdvec(1,2)

sdreport_vector SSB(minyr,maxyr)
sdreport_vector Fbar(minyr,maxyr)
sdreport_vector R(minyr,maxyr)
sdreport_vector chat(minyr,maxyr) // model-predicted total catches
matrix F(minyr,maxyr,1,nlength)
matrix S(minyr,maxyr,1,nlength)
matrix N(minyr,maxyr,1,nlength)
matrix U1(minyr,maxyr,1,nlength)
matrix C(minyr,maxyr,1,nlength)
matrix phat(minyr,maxyr,1,nlength) // model-predicted catch length frequencies
number psum // useful later on
// These values participate to evaluate the objective function
number f_c
number f_clf
number f_s
number p_q
objective_function_value f

```

PROCEDURE_SECTION //model calculations

```

get_mortality_and_survival_rates();
get_numbers_at_length();
get_catch_data();
get_survey_at_length();
calculate_report_vars();
evaluate_the_objective_function();
if (mceval_phase())
{
  write_mcmc();
}

```

```

REPORT_SECTION // This section shows how to generate a report of ADMB program
report << "Likelihoods" << endl; // to skip a line after writing the object, it needs to include the
stream manipulator 'endl' at the end of the line
report << "f, f_c, f_clf, f_s, p_q" << endl;
report << f << endl;
report << f_c << endl;
report << f_clf << endl;
report << f_s << endl;
report << p_q << endl;
report << "Sigma parameters logsigmaU1" << endl;
report << logsdsurv << endl;
report << "Selectivities self, selsurv" << endl;
report << self << endl;
//report << selsurv << endl;
report << "Annual F multiplier from logFyrs" << endl;
report << mfexp(logFyrs) << endl << endl;
report << "Estimated total numbers in catch" << endl;
report << chat << endl << endl;
report << "Estimated length frequency in the catch" << endl;
report << phat << endl << endl;
report << "Estimated survey" << endl;
report << U1 << endl << endl;
report << "Estimated numbers of fish" << endl;
report << N << endl << endl;
report << "Estimated fishing mortality" << endl;
report << F << endl << endl;
report << "Estimated Fbar" << endl;
report << Fbar << endl << endl;
report << "Estimated SSB" << endl;
report << SSB << endl << endl;

```

```

FUNCTION dnorm(const dvariable& x, const dvariable& mu, const dvariable& sd)
return 0.5 * (log(2*M_PI*sd*sd) + square(x-mu)/(sd*sd));

```

```

FUNCTION get_mortality_and_survival_rates

```

```

// Calculate selectivity from sel_coeffs
// fishery: double normal
double ltmp;
for (int l=1; l<=nlength; l++) {

```

```

    ltmp = double(l);
    if(ltmp < Fsel(1)) {
        self(l) = pow(2,-square((ltmp-Fsel(1))/Fsel(2)));
    } else {
        self(l) = pow(2,-square((ltmp-Fsel(1))/Fsel(3)));
    }
}
F = outer_prod(mfexp(logFyrs),self); //the mfexp function is the exponential function
for (int t=minyr; t<=maxyr; t++)
    //Fbar(t) = mean(row(F,t)(2,8));
    Fbar(t) = mean(row(F,t));
for (int l=1; l<=nlength; l++)
    S = mfexp(-(F+M(l)));

```

FUNCTION get_numbers_at_length

```

for (int t=minyr; t<=maxyr; t++) // first length bin of each year
    N(t,1) = mfexp(logRec(t));
for (int l=2; l<=nlength; l++) // from the second length bins
    N(minyr,l) = mfexp(logStartN(l-1)); // logstartN(l-1) means the length before

for (int t=minyr+1; t<=maxyr; t++) {
    for (int l=2; l<=nlength; l++) {
        N(t,l) = 0.;
        for(int k=1; k<=nlength; k++) {
            N(t,l) += N(t-1,k) * Gamma(k,l) * S(t-1,k); // N per year and length is N times
transition matrix times survival rates
        }
    }
}

```

FUNCTION get_catch_data

```

// catch-at-length first
for (int l=1; l<=nlength; l++)
    C = elem_prod(elem_div(F,(F+M(l))), elem_prod(1-S,N)); // efficient way to multiply and divide
matrices :-)
// total catch in numbers
for(int t=minyr;t<=maxyr;t++) {
    chat(t) = 0.;
    for(int l=1;l<=nlength;l++) chat(t) += C(t,l);
}

```

```
// get catch proportions
for(int t=minyr;t<=maxyr;t++) {
    psum = 0.;
    for(int l=1;l<=nlength;l++) psum += C(t,l);
    for(int l=1;l<=nlength;l++) phat(t,l) = C(t,l)/psum;
}
```

FUNCTION `get_survey_at_length`

```
//for (int l=1; l<=nlength; l++)
    //selsurv(l)=1./(1.+mfexp(-Ssel(1)*double(l)+Ssel(2)));
// need total kgs of fish from numbers in 1000s
for (int t=sminyr; t<=smaxyr; t++)
    for (int l=1; l<=nlength; l++)
        U1(t,l) = mfexp(logqsurv) * N(t,l) * pow(S(t,l),fsurv);
```

FUNCTION `calculate_report_vars`

```
SSB = mat * trans(elem_prod(N, weights)); // trans means transforme (transpose so swap rows
with columns)
R = mfexp(logRec);
```

FUNCTION `evaluate_the_objective_function`

```
f_c = 0.0;
f_clf = 0.0;
f_s = 0.0;
p_q = 0.0;
// Commercial total catch-in-numbers
sdvec(1) = sdC;
for (int t=minyr; t<=maxyr; t++)
    f_c += dnorm(log(chat(t)), log(ctotn(t)), sdvec(1));
// commerical catch length frequencies
for (int t=minyr; t<=maxyr; t++) {
    for (int l=1; l<=nlength; l++) {
        if(phat(t,l) > 0.) f_clf -= neff * clfreq(t,l) * log(phat(t,l));
    }
}
// Survey
sdvec(2) = sqrt(square(mfexp(logsdsurv))+sdS*sdS);
for (int t=sminyr; t<=smaxyr; t++)
    for (int l=1; l<=nlength; l++)
```

```

    f_s += dnorm(log(U1(t,l)), log(tuning(t,l)),sdvec(2));
// prior for q for survey
p_q = dnorm(logqsurv,log(muq),sdq);
// Add all components
f = f_c + f_clf + f_s + p_q;

```

FUNCTION write_mcmc

```

// Likelihoods
if (mcmc_lines == 0)
{
    mcmc_like << "f_c f_clf f_s p_q" << endl;
}
mcmc_like << f << " " << f_c << " " << f_clf << " " << f_s << " " << p_q << endl;
//parms
//mcmc_par << self << logFyrs << logRec << logStartN << logqsurv << logsdsurv << endl;
mcmc_par << self << logFyrs << logRec << logStartN << " " << logqsurv << " " << logsdsurv
<< endl;
// Estimated number of fish
mcmc_N << N << endl;
// Length frequency distributions in catches
mcmc_phat << phat << endl;
// Number of individuals in the survey
mcmc_u1 << U1 << endl;
// Fbar
mcmc_f << Fbar << endl;
// Recruitment
mcmc_rec << R << endl;
// Biomass
mcmc_ssb << SSB << endl;
// Counter
mcmc_lines++;

```

GLOBALS_SECTION

```

#include "admodel.h"
int mcmc_lines = 0;
ofstream mcmc_like("like.mcmc");
ofstream mcmc_N("N.mcmc");
ofstream mcmc_phat("lfdC.mcmc");
ofstream mcmc_u1("NoIndS.mcmc");
ofstream mcmc_par("parms.mcmc");

```

```
ofstream mcmc_f("f.mcmc");  
ofstream mcmc_rec("rec.mcmc");  
ofstream mcmc_ssb("ssb.mcmc");
```


Appendix B

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