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Marine-demersal species distribution models for spatial management, assessment, and prediction in Adriatic and Ionian Seas

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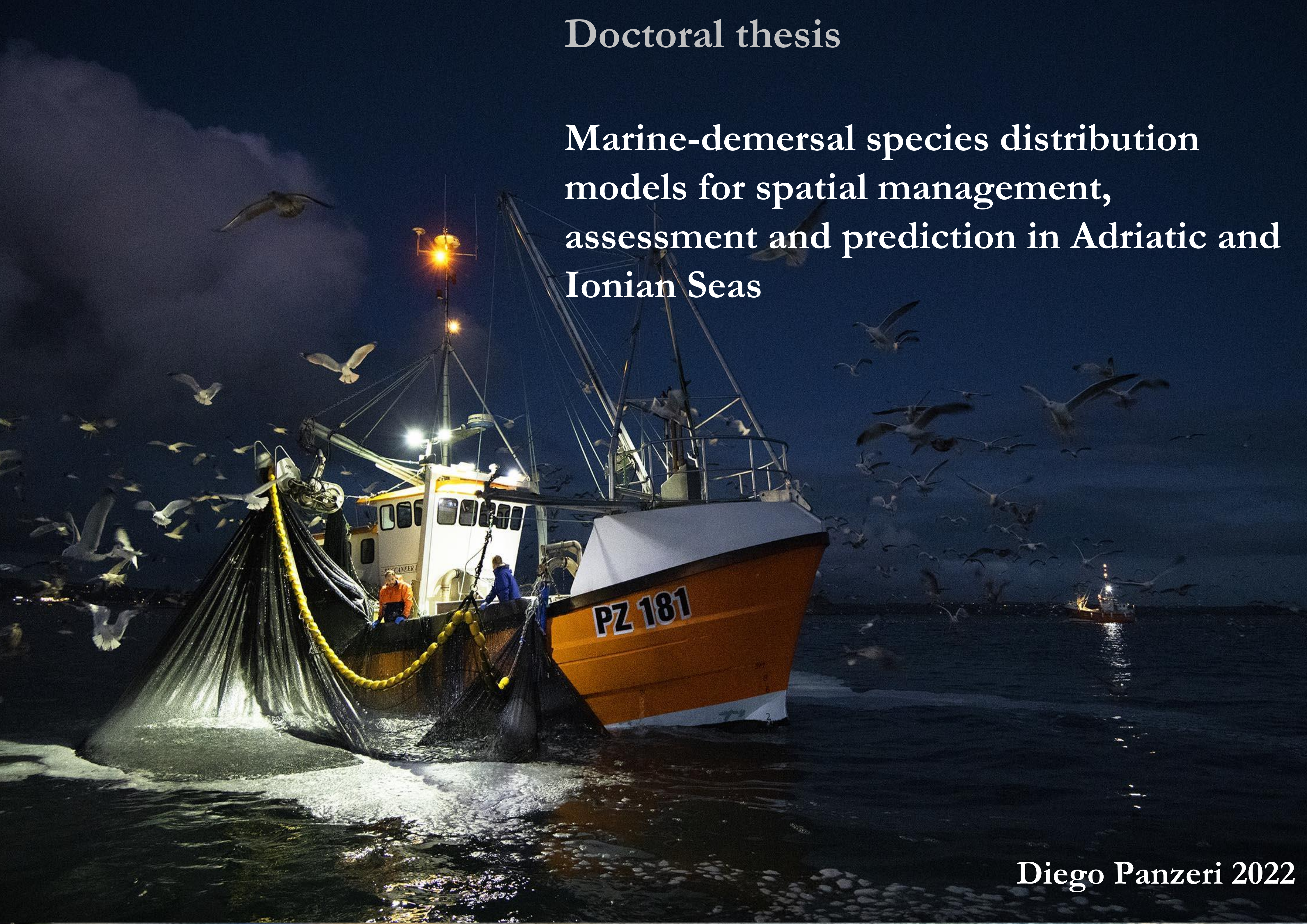

Doctoral thesis

Marine-demersal species distribution models for spatial management, assessment and prediction in Adriatic and Ionian Seas

Diego Panzeri 2022

Da piccolo, incontrai un vecchio che viveva in una casa di pietra.
Mi ricordo che mi raccontò una bella storia, dove una goccia d'acqua spruzzata dal respiro di una balena era arrivata su un gabbiano, il quale, sbattendo le ali, la trasportò fino a una nuvola e, che allora, la goccia d'acqua quando piovve, cadde, andando a nutrire gli orti della terra, gli alberi e i cespugli della foresta, per poi finire nel fiume che l'attraversava e grazie al quale i pesci avevano una dimora e gli uomini e gli altri animali potevano dissetarsi, e che questo fiume accarezzava i ciottoli e riempiva la terra per poi sfociare in mare, il luogo da cui proveniva la goccia di balena.

Sorrise e mi disse che questo è il principio della vita, della storia infinita della vita che si nutre di sé, e che tutte le gocce del mare racchiudono questo segreto così semplice e che anch'io, dopotutto, ero nato da una balena.

C.T.P.

Disse che aveva perso la voglia di studiare
Voleva solo viverlo
Per questo e per altro
Divenne mare.

Ringraziamenti

Beh, il mio è stato un dottorato unico, svoltosi durante una pandemia, almeno in buona parte. Sembrava il mondo si fosse fermato, chiuso, arginato in sé stesso e per me, era proprio il periodo peggiore, o forse no. L'inizio del percorso non è stato dei migliori. Sono stato molto tempo solo a svolgere le attività, non perché non sostenuto dal mio tutor, ma fisicamente solo a svolgerle, senza interazioni eccessive. Era come essere in un acquario, vedere il mondo da dentro, ovattato, appannato, intoccabile. Ma è passato, e tra le poche persone che ringrazio, qui di seguito, ci sono:

Un grazie a Simone, mi ha aiutato, penso ci abbia creduto, e mi ha sostenuto quando e come poteva.
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Un grazie al mio coinquilino Fabrizio per i momenti di spensieratezza durante il lockdown e le serate alla Playstation.
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E poi, un grazie a me, comunque sia andata, devo volermi bene. Il resto è una costruzione.

List of publications derived from this thesis

This Ph.D. thesis is presented following the format of a compendium of publications. It includes four publications: two already published, one under review, and one in preparation.

The list of manuscripts is here presented; organized by chapters.

CHAPTER 2: Developing spatial distribution models for demersal species by the integration of trawl survey data and relevant ocean variables. *Copernicus Marine Service Ocean State Report, Issue 5, Journal of Operational Oceanography*, 14:sup1, s114–s123; DOI: 10.1080/1755876X.2021.1946240. **Author**: Panzeri D., Bitetto I., Carlucci R., Cipriano G., Cossarini G., D'Andrea L., Masnadi F., Querin S., Reale M., Russo T., Scarcella G., Spedicato M.T., Teruzzi A., Vrgoč N., Zupa W. and Libralato S. (2021).

CHAPTER 3. Defining a procedure for integrating multiple oceanographic variables in an ensemble of marine species distribution. *International Workshop on Metrology for the Sea; Learning to Measure Sea Health Parameters (MetroSea).* IEEE. 2021, pp. 360-365, DOI: 10.1109/MetroSea52177.2021.9611559. **Author**: Panzeri D., Libralato S., Carlucci R., Cipriano G., Bitetto I., Spedicato M.T., Masnadi F., Ricci P., Scarcella G., Russo T., Zupa W., Vrgoc N., D'Andrea L., Solidoro C. (2021).

CHAPTER 4: Identifying priority areas for spatial management of mixed fisheries using an ensemble of multi-species distribution models. Submitted to*: Fish and Fisheries, under review.* **Author**: Panzeri D., Russo T., Anrneri E., Carlucci R., Cossarini G., Isailovic I., Sifner S.K, Manfredi C., Masnadi F., Reale M., Scarcella G., Solidoro C., Spedicato M.T., Nedo V., Zupa W., Libralato S.

CHAPTER 5: Future Distribution of demersal species in a warming Mediterranean sub-basin. *In prep.*

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Thesis abstract

Species distribution models (SDMs) have been widely used in ecology, especially in recent decades in the marine context - in this particular case, in fisheries science. We know that demersal species are very important for the marine ecosystem and the fishing industry and should be managed accordingly. A growing number of studies highlight the importance of spatial management for rebuilding stocks and protecting ecosystem resources and biodiversity. SDMs could assist fisheries management in spatial operations. In this study, I focused on different aspects of species distribution and defined a procedure to develop an ensemble of models combining different modeling approaches. I combined Generalized Additive Models, Random Forest, and the Gradient Boosted method for ten demersal species, two life stages (adult and juvenile fish), and two different indices such as kilograms per km^2 (kg/km^2) and number of individuals per km^2 (n/km^2). I used data from two surveys conducted in the Adriatic and Ionian Seas: Mediterranean International Trawl Survey (MEDITS) and Sole Monitoring (SOLEMON). In detail:

- In Chapter 2, I analyzed biomass indices (kg/km^2) for European hake, common sole, mantis shrimp, red mullet, and common cuttlefish using a series of generalized additive models (GAMs) with and without abiotic variables. The results show that the geostatistical model used to estimate the distribution of different demersal species based on trawl data is improved when additional environmental variables (oceanographic variables) are included.

- In Chapter 3, I analyzed the density index (n/km^2) by defining a new procedure for developing an ensemble of models that resulted from combining 5 different approaches (General Additive Models (Tweedie, Delta, and Gaussian), Random Forest, and Gradient Boosting methods). I implemented spatial training and testing datasets to evaluate the best performance of 9 models against a set of indicators. These models include various combinations of covariates, ranging from the simplest model (depth, year, and spatiotemporal variables) to the most complex model (which includes oceanographic variables and fishing effort). The results show the improvement (smaller difference between modeled and observed data) for the models with environmental variables using the European hake (*Merluccius merluccius*) in the Adriatic and Ionian Seas as an example.

- In Chapter 4, I used the ensemble of species distribution models (e-SDM) described in Chapter 3 to determine the hot spot of juvenile and adult aggregation of ten species, using density indices (n/km^2) derived from MEDITS and SOLEMON and geographic data (depth, Latitude, longitude, and month), relevant 3D oceanographic variables (temperature, salinity, chlorophyll-a, dissolved nutrients and oxygen, particulate organic carbon, pH), and fishing effort (from the vessel monitoring system).

- In Chapter 5, I extended the ensemble species distribution models (e-SDM) described in Chapter 4 to assess the future distribution of ten demersal species in the study area and to determine aggregation areas for four different scenarios (2012, 2018, 2035, and 2050) and the two life stages. I estimated projected future changes in aggregation centroids, density distributions, and centroids for the 10 species in the study area by GSA (Geographic Sub Area, 17, 18, and 19). The results allow prediction of areas gained and lost under future IPCC RCP 8.5 climate conditions and provide the basis for determining potential range shifts for the 10 species.


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Chapter 1

General Introduction

Introduction: The Mediterranean Sea

The impact of human activities, especially fishing, on the Mediterranean Sea has been significant. Stocks have collapsed, and eutrophication phenomena and invasive species have appeared throughout the basin since the 1980s (FAO, 2022). The marine ecosystem is being greatly affected, and this stress could have major impacts on species distribution and abundance, biodiversity, and ecosystem services (Pereira et al., 2010; Worm et al., 2007).

We must also consider the perspective of climate change, which is contributing to drastic changes in environmental conditions in the Mediterranean Sea (Reale et al., 2022; Solidoro et al., 2022). The impact of climate change on political and economic aspects is important, and the Intergovernmental Panel on Climate Change (IPCC, 2022) has provided much evidence over the years.
The ocean is critical to regulating the Earth's climate and sequesters about 25% of CO2 (Le Quéré et al., 2018). To assess future climate change, the IPCC proposes several scenarios for the impacts of human activities, simulating possible warming levels compared to pre-Industrial Revolution levels. The scenarios are called Representative Concentration Pathways (RCPs - +2.6 W/m2, +4.5 W/m2, +6.0 W/m2, and +8.5 W/m2), measured as radiative forcing (W/m2 - watts per m2).
These potential changes have implications for ocean circulation (Liu et al., 2017); ocean warming has been observed since the 1960s (Cheng et al., 2017), with surface temperatures increasing by about 0.7 °C from 1900 to the present (Huang et al., 2015). In addition, changes in dissolved oxygen affect global carbon and nitrogen cycles (IPCC, 2022), and global warming is the cause of ongoing deoxygenation in the open ocean (Breitburg et al., 2018). It is estimated that primary production will decline by 6% by 2100 (Kwiatkowski et al., 2017).

All of these aspects of climate change could affect marine life in the Mediterranean and consequently fisheries, for example, by altering the future distribution of resources (Moullec et al., 2019a) and the rapid spread of invasive species (Giakoumi et al., 2019; Tsirintanis et al., 2022). The Mediterranean Sea is a biodiversity hotspot where invasive species are increasing, and various management measures are still under discussion (Bahri et al., 2021), for example, for invasive species such as the silver-cheeked toadfish (*Lagocephalus sceleratus*).

The Mediterranean Sea is characterized by a long history of human pressures, with changes in ecosystem condition from the second half of the last century to the present day, largely documented by numerous studies (Coll et al., 2008; Fortibuoni et al., 2017; Piroddi et al., 2020). The basin is characterized by a multispecies fishery and only 8 species account for more than 62% of the total landings (FAO, 2022), such as the pelagic fishes sardine (*Sardina pilchardus*) and anchovy (*Engraulis encrasicolus*), and 6 demersal fish species such as European hake (*Merluccius merluccius*), deep-sea red shrimp (*Parapenaeus longirostris*), squid cuttlefish (*Sepia officinalis*), octopus (*Octopus vulgaris*), blue and red shrimp (*Aristeus antennatus*), and red mullet (*Mullus barbatus*) (Figure 1.1). The demersal species targeted by trawl gear are heavily impacted by fishing and have high fishing mortality on juveniles and a large amount of discards (Maina et al., 2018; Tsagarakis et al., 2014).

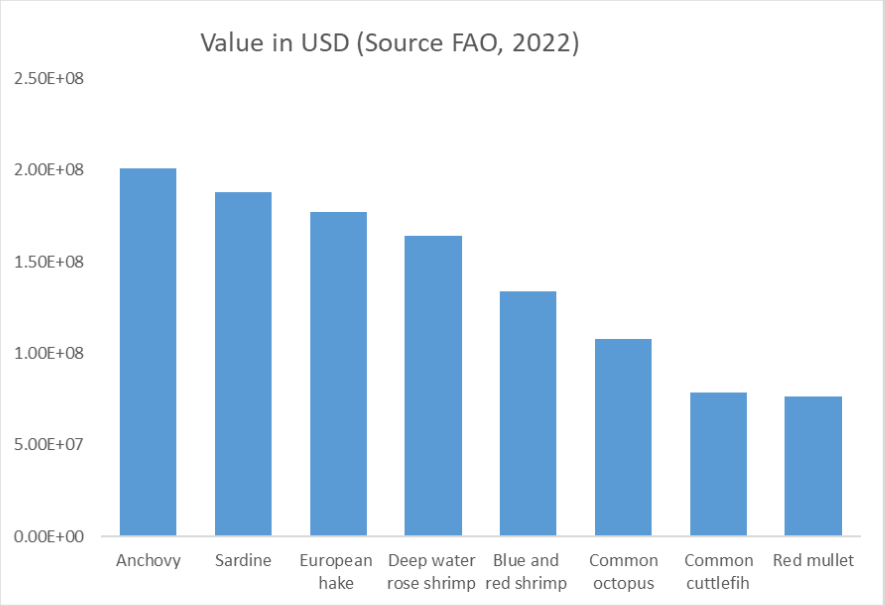

Figure 1.1: main 8 commercial species reaching over 62% of landings values in the Mediterranean Sea (6 are demersal species)

In the Mediterranean (and Balck Sea), the General Fisheries Commission for the Mediterranean and the Black Sea of the Food and Agriculture Organization (GFCM-FAO) is responsible for all marine waters, adopting binding and non-binding decisions that apply to all Mediterranean and Black Sea countries. The area of application is divided into five subregions: western, central and eastern Mediterranean, Adriatic Sea and the Black Sea.
These binding recommendations are then transposed into European Union or national legislation by all contracting parties, such as the European Union's Common Fisheries Policy (CFP), which provides for a reduction in fishing effort in European member countries from 2002.
The 23 contracting parties (EU and non EU) are: Albania, Algeria, Bulgaria, Croatia, Cyprus, Egypt, European Union, France, Greece, Israel, Italy, Lebanon, Libya, Malta, Monaco, Montenegro, Morocco, Romania, Slovenia, Spain, Syria, Tunisia, Turkey. The GFCM also includes 6 non-contracting parties: Bosnia-Herzegovina, Georgia, Jordan, Republic of Moldova, Saudi Arabia, Ukraine.
Contracting parties contribute to the GFCM budget and finance its activities. The cooperating non contracting parties are not formally affiliated with the GFCM but actively participate in the activities of the GFCM, attend the meeting of the Commission and commit to fully implement all recommendations of the GFCM.
Despite the efforts of the relevant agencies, many stocks in the Mediterranean are overfished (see Box 1), and some estimated reductions in fishing effort in 2020-2021 toward the 2026 maximum sustainable yield (MSY-see the Overview of Fishing Pressure subsection) are significant, e.g., in the Adriatic, a 12% reduction in otter trawling and a 16% reduction in beam trawling (FAO,2022).

In the face of climate change, invasive species, temperature, oxygen, and nutrient changes, and past and ongoing overfishing in the Mediterranean, resource status assessment is essential. The main assessment carried out by GFCM-FAO is based on the stock assessment method, and the number of stocks assessed has increased significantly since 2008 and will reach 62 in 2020 (FAO, 2022), covering spatial and temporal information for the entire Mediterranean Sea. In addition, the determination of the fishing footprint is carried out to assess the spatial extent of bottom fishing, taking into account the area of the seabed exploited by bottom gears in space and time, in order to identify the location and intensity of fishing activities through mapping (Amoroso et al., 2018).

At GFCM-FAO, temporal and spatial measures are also taken, such as reducing fishing pressure during the spawning season or increasing protection during the migrations of some endangered species. These measures are sometimes incorporated into multi-year plans. For example, following the concept of ecosystem approach to fisheries, GFCM-FAO has introduced the fisheries restricted areas (FRA - for the Adriatic Sea subsection of Chapter 1 Overview of fishing pressure and management regulation in the study area), established to protect essential fishing habitats (EFH) and/or vulnerable marine ecosystems (VME) in the Mediterranean Sea. A fisheries restricted area (FRA) is a geographically defined area where certain fishing activities are temporarily or permanently prohibited or restricted in order to improve exploitation patterns and conservation of certain stocks, habitats and deep-sea ecosystems. Monitoring of this area within and adjacent to it is critical and is one of the main objectives of the GFCM, which has identified in its decisions, including multi-year management plans (see next sub-section Overview of fishing pressure and management regulation in the study area) some important points for this spatial management:

1) regular collection of fishery-independent data
2) regular collection of fisheries-related data, focusing on key stocks protected by the FRA;
3) collection of socioeconomic data to assess the effects of changes in the size and composition of landings from fisheries affected by the FRA;
4) Collect local ecological knowledge from fishermen and stakeholders directly affected by the FRA;
5) Preparation of periodic assessments of the status of fisheries affected by the FRA by the existing expert.

Among others, FRAs have been established for the conservation and management of the demersal stocks, including European hake in the Jabuka/Pomo Pit (Adriatic Sea) and deepwater shrimp in the three FRAs of the Strait of Sicily.

Key GFCM management measures (GFCM Compendium, 2021b) are summarized as follows:

- Establish spatio-temporal measures, including Fisheries Restricted Areas (FRAs), to improve the status of key species and/or protect sensitive ecosystems.
- Monitoring of established FRAs.
- Mapping of FRAs established by GFCM countries within their national waters (nFRAs).
- Identify VME indicators and EFHs that will be compiled into a regional database of sensitive benthic species and habitats to support scientific advice.
- Collect information on VME indicators, habitats, and taxa through direct observations and the use of protocols for reporting encounters and trials in deep-sea bottom fisheries.
- Mapping fisheries footprints using the vessel monitoring system (VMS), automatic identification system (AIS), local ecological knowledge, and other tools.

In addition to demersal species, small pelagic species are also regulated by GFCM for all countries in the affected area (especially the Adriatic Sea), with the main objective of restoring and maintaining a stable population of exploited species by reaching the level of MSY (MSY - Schaefer, 1954). When we talk about fisheries, it is important to remember the concept of MSY, which in ecology consists in the highest theoretical equilibrium yield that can be achieved from a stock under existing environmental conditions (Fath, 2018). The concept of MSY aims to maintain the maximum growth rate of the population size so that the population can continue to be productive indefinitely despite fishing.

The yield (or catch) of an ecosystem is determined by two main factors, one is the "top-down" effect, which consists of fishing, and the other is the "bottom-up" effect, which consists of primary production (PP) (Conti et al., 2012). In addition, the recent implementation of the landing obligation for EU countries (only for European countries - European Commission EC, 2013, GFCM compendium, 2021b) aims to apply technical measures to discourage the catch of undersized commercial species, through the closure of some areas where, for example, juveniles accumulate (Hot Spot of Juvenile, see Chapter 4, Figure 4.2 - 4.3). Regulations such as the aforementioned landing requirement, seasonal closure, or mesh size are primarily based on specific assumptions, as juvenile fish are particularly vulnerable in the nursery area and reducing fishing mortality on immature fish is a prerequisite for sustainable fisheries.

The scientific community has developed the ecosystem approach to fisheries (EAF) (Sinclair & Valdimarsson, 2003), which involves managing the ecosystem rather than a single stock. The EAF is more complex and it is not clear if it works well for the single species approach, especially due to data availability (Russo et al., 2019).

The data used in the GFCM area, which consists of 23 countries (EU and non-EU), come primarily from the Data Collection Reference Framework (DCRF), i.e is the entire collection of fisheries data since 2000 based on catch and landings monitoring (https://www.fao.org/gfcm/data/dcrf/en/), including fishing effort and survey-derived fishery data, i.e., the MEDITS and SOLEMON survey data used in this work.

The effort data are derived from the vessel monitoring system (VMS) and the automatic identification system (AIS) (Zhao et al., 2014). The former is used on commercial fishing vessels with an EU license longer than 12 m to track and monitor fishing vessel activity, determine the location of the vessel at a given time, and periodically transmit this information to a shore-based monitoring station. The VMS consists essentially of an antenna and receiver (GPS), a computer (which may be built-in or provided by the user), and a transmitter and antenna suitable for communication between the vessel and the flag center. The use of VMS is mandatory and required by the European Union, where vessels are required to report catch on entry, weekly catch, transhipment, port of landing, and catch on exit.

AIS are collision avoidance devices used by vessels on board to report position, trachics and speed with high frequency radio transmission.

The AIS is not mandatory on smaller vessels (< 15m), but many use it simply for its safety benefits. It shows all other vessels in the vicinity the vessel's position and the routes these vessels are taking, reducing potential collision risks.

In recent years, private companies have developed satellites that can receive AIS, increasing its range. This has led to some confusion with VMS, leading some to believe AIS can be used for fisheries management (Fournier et al., 2018).

New strategies and a shared vision are needed to restore marine resources and promote sustainability.
One of the objectives of this work was to explore modeling approaches based on statistical methods in the field of species distribution models (SDMs) using fishery-independent data in combination with environmental variables to represent the " best' distribution of some of the main commercial demersal species in the Adriatic and Ionian Seas.

With these objectives in mind, I consider different modeling approaches, input data and scenarios under climate change conditions, map the hotspots and areas of overlap between species to understand the distribution range of these species, and consider this work as an opportunity to incorporate SDMs in the assessment of stock management in the study area and the Mediterranean Sea as a future challenge to improve spatial management in this area.

Overview of fishing pressure and management regulation in the study area

The Adriatic and Ionian Seas have a great diversity of fisheries that have developed over a long history in this area, where the exploitation of resources began a thousand years ago (Farrugio et al., 1993). In addition, the great biodiversity of the area, the high productivity and the long time series of data (Fortibuoni et al., 2017) represent important added values of the study area. It's well known that the northern and central Adriatic Sea is intensively exploited by fisheries (Fig. 1.2) and many species are overfished (Fortibuoni et al., 2017; Russo et al., 2019).

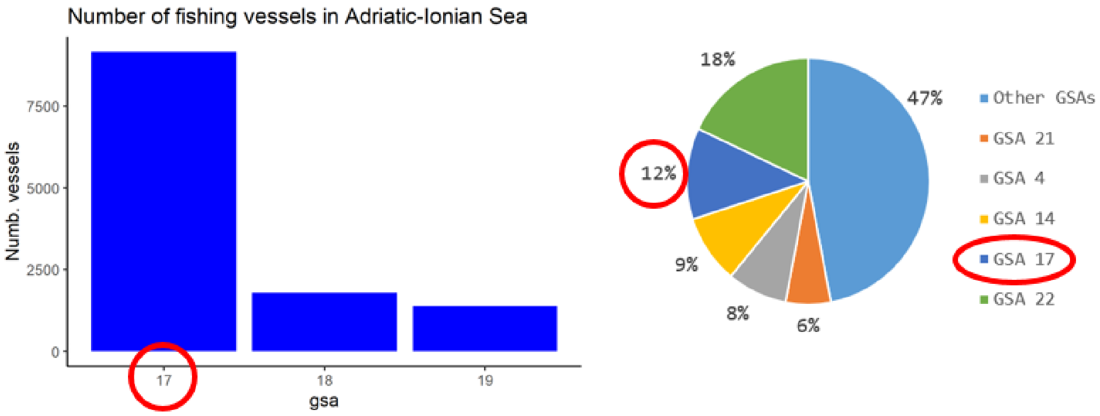

Figure 1.2: Left panel: number of fishing vessels in the three GSA belonging to the Adriatic and the Ionian Sea. Right: percentage of the total number of fishing vessels for all GSA in Mediterranean Sea. (source FAO, 2022). In red is the highlighted GSA 17.

The Adriatic Sea alone contributes 15% of the total Mediterranean catch, which ranges from 170000 to 180000 tonnes (see Fig. 1.3). Moreover, landings (in tonnes) in the Adriatic Sea are dominated by Italy - 56.8% - and Croatia - 39.1% - followed by the other Adriatic countries such as Albania (3.5%), Montenegro (0.5%) and Slovenia (0.1%) (FAO, 2022). In the Ionian Sea, particularly in GSA 19 (see Fig. 1.4), which is also referred to as the Western Ionian Sea (the others being the Southern (GSA 21) and Eastern (GSA 20) Ionian Seas), bottom shrimp fisheries for red king prawns (*Aristaemorpha foliacea*) and blue and red shrimp (*Aristeus antennatus*) are the main activities, with Italy accounting for about 58% of the total fleet (FAO, 2022). The number of vessels (Fig. 1.2) operating in the western Ionian Sea is about 1500, which represents the small number in the study area.

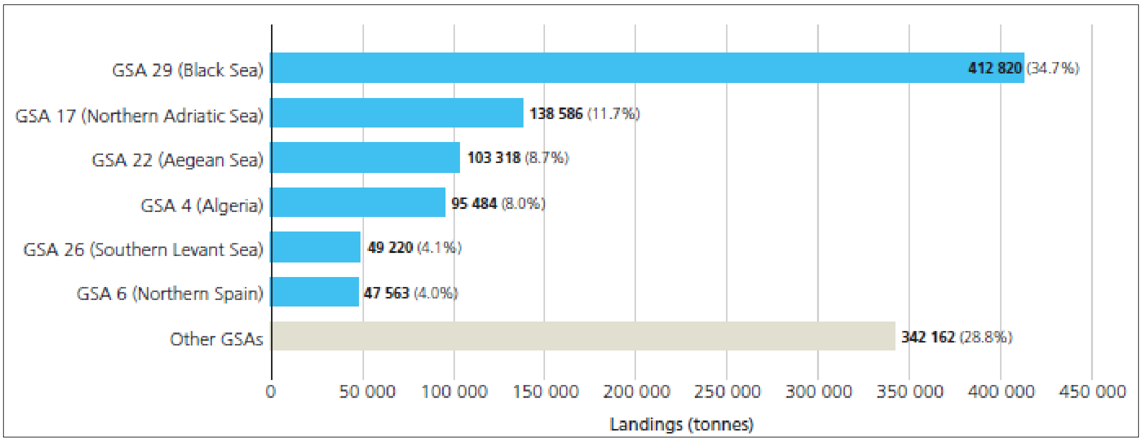

Figure 1.3: Average annual landings by GSAs for years 2016-2018. Source (FAO, 2022).

The recommendations proposed by GFCM-FAO for conservation and management measures in the study area of this work, the Adriatic and Ionian Seas, concern in particular:

Adriatic Sea (GSA 17 & 18):

The GFCM recommendation provides multi-year management plans (MMPs) for sustainable demersal fisheries that ensure consistent long-term yields within maximum sustainable yield (MSY) and low risk of stock collapse to maintain a stable fishery. For example, the Adriatic MMPs propose the following:

- Precautionary approach to fisheries management
- Ensure exploitation rates of key stocks (e.g., hake, Nephrops, or mullet) are at MSY levels by 2026
- Help eliminate discards, reduce bycatch (unwanted catch), and landings obligations
- Protect nursery and spawning areas and key fish habitat for demersal stocks

Especially considering the last point, the integration of modelling tools for the spatial distribution of species could be an important tool to highlight and assess the basic areas for some important groundfish stocks, in order to protect and conserve nursery and spawning areas that are essential for some species in the Adriatic Sea (e.g., hake, Norway lobster, or mullet).

The GFCM recommendation specifically aims to keep fishing mortality of exploited stocks within the Fmsy level (fishing mortality at MSY) and recommends numerous technical measures, such as the minimum conservation reference size for European hake, the minimum conservation reference size for deepwater red shrimp (20 mm carapace length - CL) or Norway lobster (70 mm total length -TL), and for red mullet (11 cm TL) and sole (20 cm TL). In addition, as mentioned above, the GFCM recommends the establishment of FRA and the conservation and monitoring of the current Jabuka/Pomo pit, which also proposes a new possible FRA in the southern part of the Adriatic Sea (GFCM Compendium, 2021b).

Regulation of FRA in the Jabuka/Pomo Pit was adopted by a GFCM recommendation in 2017 and made permanent by another GFCM recommendation in 2021, which includes regulations for bottom fishing and pelagic fishing throughout the year in the core area, and spatial and temporal restrictions in the other adjacent areas

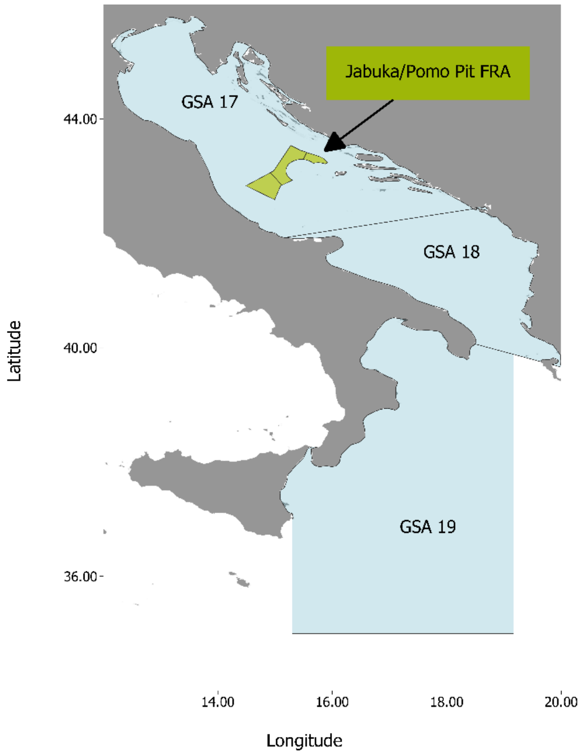

Figure 1.4: Jabuka/Pomo Pit FRA in the center of the Adriatic Sea, in the GSA 17. In light blue, the area of study corresponds to the GSA 17, 18, and 19.

The decision to establish the FRA in the Jabuka/Pomo Pit area was due to the critical situation of Norway lobster and European hake catches, which had declined until 2015, before the closure (see Box 1). After the defined period, in 2016, there was a visible increase in catches in the Pomo Pit area, which is considered by GFCM-FAO as a "win-win" situation for marine biodiversity restoration and benefits for fishermen (FAO, 2020b). Currently, 138 vessels (63 Croatian and 75 Italian) operate in the area where fishing is restricted. Another FRA is located in the Bari canyon (see Fig. 4.4, chap. 4) in the southern Adriatic Sea, where fishermen and researchers hope to achieve similar results (FAO, 2022).

Table 1.1: percentage of the fleet segment in the different subregions of the Mediterranean Sea (source FAO, 2022)

Fleet segment group	*West Med (%)*	*Central Med (%)*	*Adriatic Sea (%)*	*Eastern Med (%)*
Smale scale vessels	73.8	86.8	78.2	86
Trawlers and beam trawlers	10.8	5.0	13.1	5.7
Purse seiners and pelagic trawlers	13.1	2.8	3.0	3.2
Other fleet segments	2.3	5.3	5.6	5.1
Total	**100**	**99**	**100**	**100**

Ionian Sea (GSA 19-20-21):
The GFCM recommendation establishes an MMPs for sustainable demersal fisheries, particularly red king prawns and blue and red shrimp, that ensure consistent yields over the long term at maximum sustainable yield (MSY) and low risk of stock collapse to maintain a stable fishery. Some examples of recommendations include:

- the MMPs should maintain fishing mortality at MSY levels for key species (*Aristeus antennatus* and *Aristaemorpha foliacea*)
- Develop a future management plan to reduce the risk that, in the absence of a meaningful scientific assessment, management of the stock will remain sustainable.
- Address illegal, unreported, and unregulated (IUU) catches in the area for key stocks (e.g., giant red shrimp and blue and red shrimp) through operational targets

Again, the GFCM recommendation specifically aims to keep the fishing mortality of the exploited stock within the Fmsy level (Fishery mortality at MSY), but also to closely monitor landings and catches for management purposes, as mentioned above, effective assessment and intensive control of IUU.

Other regulations for both the Adriatic and Ionian Seas concern technical measures (Bellido et al., 2015), such as:

1) regulations on fleet and gear characteristics, especially related to fleet access to fishing grounds: In this case, there are controls on fishing times per day and week, as well as spatial and seasonal restrictions (see the information on species of concern in the Methodology: species distribution models and input data) in specific seasons or areas.
2) Regulations on which species may be caught: In this case, the composition of catches (allowed or prohibited species), minimum landing sizes and quotas, and catch limits are controlled

Despite the application of CFP, EAF, and DCF in the Mediterranean (and Adriatic), the main demersal and pelagic stocks exploited by European fleets have exploitation rates about three times higher than the estimated fishing mortality rate for MSY (FMSY), with a similar pattern for all GSAs and species (Cardinale et al., 2017). In Box 2, I have provided key information on the 'status' of the stock in the Adriatic and Ionian Seas (GSAs 17, 18, and 19).

The implementation of SDM in this context also aims to understand and incorporate a potential new fisheries management tool in the Adriatic and Ionian Seas that adds value to the fisheries management of the study area (see also Chapter 4).

Box 1: Synthesis of 'status' of demersal species in the Adriatic and Ionian Sea by GFCM-FAO stock assessment models

European hake in GSA 17 and 18: is the third most economically valuable species in the Mediterranean Sea (FAO, 2020b), caught primarily by bottom trawlers operating on the continental shelf (GFCM-FAO, 2021e). In addition, European hake is caught by longlines, mainly in Croatia and the Italian part of GSA 18, where the largest specimens are caught (GFCM-FAO, 2021e).
Catch increased from 2000 to 2006, then declined to the present. The 2019 management plans include some objectives such as ensuring fishing at MSY levels before 2026 or protecting nursery and spawning areas as essential fish habitat (EFH) and reducing discards by reducing unwanted catches and improving selectivity (GFCM-FAO, 2021e) The assessment of European hake will be conducted using the stock synthesis method (SS3 - (Methot & Wetzel, 2013) by the GFCM and the expert for each GSA, also taking intoaccount the age and length composition of the data, which come from the participating countries: Italy, Croatia, Albania and Montenegro.The biomass of European hake in GSAs 17 and 18 shows a fairly stable trend at the beginning of the time series, in 1994, but fluctuates over the time series and is considered in overexploitation (SAC, 2022).

European hake in GSA 19: Landings decline from 2006 to 2012, but the trend is stable through 2018 (GFCM-FAO, 2020a).
The MEDISEH project (Telesca et al., 2013) conducted a survey to identify key nursery areas, which identified nursery areas in Otranto and Santa Maria di Leuca, but did not identify spawning areas (GFCM-FAO, 2020a).
The trend in biomass and exploitation rate derived from stock assessment models is fairly stable for GSA 19 over the years, but is considered in overexploitation with relatively high biomass (SAC, 2022).

Red mullet in GSAs 17 and 18: The species is fished primarily in Italy and Croatia by beam trawl (OTB), where landings declined in both GSAs (data from 2006 to 2019 for Italy and from 2013 to 2019 for Croatia in GSA 17 and data from 2002 to 2019 for GSA 18 (GFCM-FAO, 2020b). Management plans for 2019 include technical measures such as a minimum size for conservation (11 cm) or a ban on fishing gear within three nautical miles. The stock assessment estimates an increase in spawning stock biomass (SSB) and recruitment in recent years. Only a short-term forecast was made for 2020-2022, showing a declining trend in SSB (GFCM-FAO, 2020b). The stock is considered in overexploitation (SAC, 2022).

Red mullet in GSA 19: the time series of landings has declined sharply from 2002 to 2020, and management prescriptions are based on technical measures. The MEDISEH project identified spawning areas near the Calabrian coast.
The assessment is done using XSA (Extended Survivor Analysis - (Shepherd, 1999) and the results show a declining trend in catch, spawning biomass and recruitment. The stock is considered in overexploitation with a relatively intermediate biomass (SAC, 2022).

Norway lobster in GSA 17 and 18: is a species of importance mainly in the Adriatic Sea due to its ecological characteristics, with a subpopulation living in the Jabuka/Pomo Pit area (Froglia & Gramitto, 1981); for this reason, the spatial assessment is considered complicated.

The catches derived in particular from the OTB and the time series of landings show fluctuating trends from 2013 to 2018 in Croatia, a decrease for Italy in GSA 17 and for Albania in GSA 18 (GFCM-FAO, 2019a).
Management regulations include technical measures such as a minimum conservation size, a fishing ban (30-45 days in summer), and a ban on fishing gear within three nautical miles. The Nephrops assessment is conducted using the Surplus Production model in Continuous Time (SPiCT - Pedersen & Berg, 2017), which combines information from GSA 17 and 18. Results indicate that biomass has been declining since the 1970s, particularly since 2010, and the stock is considered overfished.

Anglerfish in GSA 17 and 18: It's a species exploited by multispecies fisheries (GFCM-FAO, 2019b), but mainly by bottom trawls. It's a benthic species whose distribution depends especially on depth and sediment type (Vrgoč et al., 2004). Landings data are quite confusing, mainly because of the similarity between two species (*Lophius budegassa* and *L. piscatorius*), and the trend has been constant since the 1960s, with no significant declines.
Management regulations include technical measures such as no minimum landing size and a ban on trawling within three nautical miles and during 45 days in summer. Stock assessment is conducted using C-MSY (Froese et al., 2017) based on the Monte Carlo method. The results show a stable biomass trend into the 80s. Due to the high uncertainty of the CMSY model, the results should be considered qualitative (GFCM-FAO, 2019b), and the final trend considering the 2015-2018 time windows shows increasing fishing mortality and decreasing biomass. The stock is considered overexploited.

Deep water red shrimp in GSA 17 and 18: It's a target species in the central and southern Adriatic Sea, fished by multispecies trawls, especially by Italy and Croatia, with an increasing trend in landings from 1998 to 2016 (GFCM-FAO, 2017). Management rules are based on technical measures such as distance from the coast (> 3 nautical miles) and depth (> 50m) or rules on mesh size of nets. In addition, a biological protection zone (ZTB) was established in 2009 in the area off Bari.
The MEDISEH project discovered spawning and nursery areas, especially in the Eastern Adriatic and along the Croatian coasts.
The assessment is conducted by Assessment for all (a4a) and the results show an increase in spawning biomass from 2012 to 2016 and a decreasing trend in fishing mortality from 1998 to 2016, but the stock is still in overexploitation (SAC, 2022)

Common sole in GSA 17: It's one of the most important species in the northern Adriatic (Grati et al., 2013; Scarcella et al., 2011), fished mainly by beam trawls from Italy (56%) and set gillnets (~20%) from Italy, Slovenia and Croatia (GFCM-FAO et al., 2021c). Total landings show a fluctuating trend from the 1950s to the present, but on average are quite stable. Management regulations are based on technical measures such as minimum landing size (20 cm) or prohibition of fishing within three nautical miles.
Stock assessment is conducted by SS3 and the results show a decline in spawning stock biomass from the 1960s to 2020 with a concomitant increase in fishing mortality. The stock is considered overexploited with low fishing mortality (SAC, 2022).

Cuttlefish in GSA 17: total landings reconstructed from another data source (Fortibuoni et al., 2017; GFCM-FAO, 2021d) show a declining trend from the 1970s to 2018, it's a species used especially by OTB and TBB on the Italian and Slovenian sides.

Management regulations stipulate that fishing gear may not be deployed within three nautical miles, that there is no minimum landing size, and that temporal bans are mandatory in summer (GFCM-FAO, 2021d).
The assessment is conducted with C-MSY and the final result shows a decrease in biomass and an increase in fishing mortality until 2010, but with a decrease in the present. Nevertheless, the stock is considered overfished and in overexploitation (SAC, 2022).

Mantis shrimp in GSA 17: It's a species with significant landing values among crustaceans in the Adriatic ports of GSA17. It's not a target of specialized fisheries, but is exploited by multispecies trawl and gillnet fisheries, especially in Italy. Little information is available for Croatia (GFCM-FAO, 2021f). The trend in landings is upward from the 1950s to 2018 for the Italian side of GSA 17. The assessment is conducted using the SS3 method and the results show a decrease in spawning stock biomass from the 1950s to the present and an increase in fishing mortality (GFCM-FAO, 2021f). Nevertheless, the stock is considered overexploited with low fishing mortality (SAC, 2022).

No GFCM stock assessment is present for European horse mackerel and southern squid.

Possible role of spatial models in the management of fisheries

Fisheries management strategies in the Mediterranean and Adriatic Sea, which I reported in the 'Overview of fishing pressure and management regulation in the study area', are limited to control of fishing capacity, fishing effort, or technical and seasonal measures such as closing the fishery in summer or regulating mesh size. Spatio-temporal measures are also implemented, such as FRA, for the mentioned Jabuka/Pomo Pot area, but in this work I have considered some new important points that can emphasise the role of spatial management for the species in the study area, such as:

- All species involved are modelled including environmental variables that are fundamental in terms of climate change
- The area of overlap of more than one species, is especially important in the case of multi-targeting and activities of fishing vessels such as in the Adriatic and Ionian Seas
- Assessment of the main aggregation area in time and space for both life stages, adult and juvenile fish, which are usually not considered or not considered in a spatial context (except for the important role of FRA).

The distribution of marine species and their habitats is a complex and complicated "puzzle" that is interconnected at many levels (Nagelkerken et al., 2015). Knowledge and applications of the spatial approach are increasing to achieve sustainable use of resources and to assess the importance of marine habitat, especially when we talk about different life stages, such as adult or juvenile populations.
The Global Deal for Nature proposes the protection of 30% of the planet to address global impacts (Dinerstein et al., 2019), and in the Mediterranean, the coherent goal of protecting 30% of the sea by 2030 (O'Leary et al., 2016) includes the identification of new sites for the establishment of fisheries closed areas.

We know that the spatial structure of populations is influenced by the marine environment, including fish behaviour or fishing patterns. In this context, spatiotemporal models can help understand local distributions by linking them to habitat variables. Examining distributional shifts is critical to supporting ocean management, and spatially stratified models can account for the following factors population dynamics (Thorson, 2019; Thorson et al., 2021). Spatial population models have increasingly identified population changes to manage human impacts on marine resources. For exploited species, changes in spatial structure may be important to localize shifts across habitat gradients that could affect population resilience and vulnerability to harvests (Ciannelli et al., 2013). One of the greatest challenges in fisheries research is to stabilize broad-scale population models with fine-scale management strategies to avoid dramatic changes in population structure, although biotic and abiotic factors can control the dynamics of expanding species (Kerr & Goethel, 2014). In the 20th century, the spatial structure of marine populations was often ignored in fisheries assessments, particularly due to a lack of data (Jamieson & Campbell, 1998), but the following study has highlighted the importance of spatial structure and improved spatial modeling procedures. SDMs aim to predict the spatiotemporal distribution of resources, considering spatial complexity as an input to management recommendations. Many geostatistical techniques are included in the SDM branch, and since the last century, many of them use and consider not only environmental predictors, but also interactions between subpopulations and spatial fleet dynamics (Jamieson & Campbell, 1998). SDMs based on geostatistical methods (such as GAM or Kriging) can incorporate analysis of distributional shifts, taking into account the underlying correlation structure of spatial data, including centroid, density hotspot, or population density (Thorson et al., 2016). In addition, spatial planning and fisheries management assessments should consider climate change projections, and SDMs can help. Much research in recent decades has emphasized how changing oceanographic conditions lead to population redistribution through area expansion or contraction (Nye et al., 2009; Thorson et al., 2016).

All approaches that address spatial models include barriers to fisheries management recommendations based on three elements in particular: i) data, ii) models, and iii) management.

(i) Data: Much of the data included in SDM lacks spatial information and uncertain population structure, largely due to survey dynamics and inter- and intra-annual sampling variability that could be accounted for. In addition, data still need to be spatially explicit, which implies new improvements in genetic research structure and tagging information.

(ii) Models: require performance uncertainties, and the ability to evaluate operational management strategies (MSEs) is central to assessing the robustness of management frameworks for evaluation.

(iii) Management: in this case, there may be a mismatch between the scientific assessment of the spatiotemporal scale and the policy decision of the relevant committee, and communication between stakeholders and scientists and between stakeholders and managers is essential. It's important to ensure transparency in translating scientific recommendations and results into policy actions.

Assessing spatial dynamics requires knowledge of what type of spatial structure is present and, if present, how to determine conservation purpose (Kerr et al., 2017). In addition, using data at the same resolution at which they were collected in SDMs can provide direct information that can be linked to other spatial variables, as oceanographic satellite imagery and spatial techniques can use the same data as a spatially aggregated model that provides greater information content. (Thorson et al., 2017).

All of the approaches presented aim to incorporate spatial models into the management process to take action based on scientific advice, such as closed areas (e.g., FRA), establishing marine protected areas (MPAs), or setting regional quotas (La Valley & Feeney, 2013). In addition, spatial models are a powerful way to assess species co-occurrence or prevent bycatch of threatened species (Cosandey-Godin et al., 2014; Turner et al., 2016). Despite the importance of incorporating these models into fisheries management, communication among fishermen, stakeholders, policy makers, and scientists remains complicated and necessary to incorporate spatial considerations as a basis for management recommendations.

The main question is: How can SMDs be incorporated into management processes?
In order to develop a useful species distribution model and use it as a method to understand spatial dynamics, it could be essential to include guidelines to better understand the main process underlying inclusion in management recommendations. The following flowchart could be a good representation of the processes:

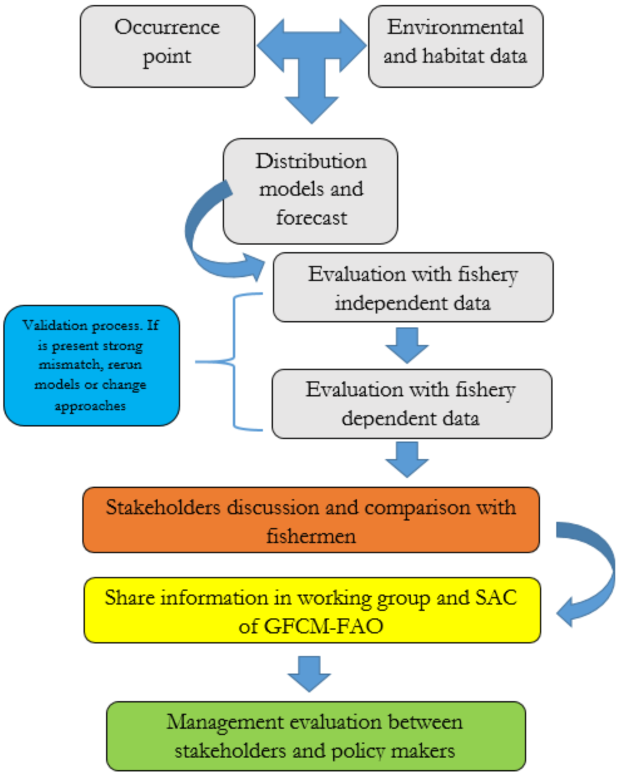

Figure 1.5: flow diagram illustrating steps for developing a good inclusion of SDMs into spatial management purposes. In the grey first step of SDMs processes, in blue is the validation process, in orange is stakeholder inclusion, and in green is the final management evaluation.

Following the initial processes of the diagram, starting with the use of survey data and the available environmental level, I have developed in this thesis different modeling approaches in the field of SDMs, for several species and life stages, a starting point in the process of evaluating spatial management, explained in particular in Chapter 4 and Chapter 5, also in relation to forecasts and climate change.
As I reported in the subsection Introduction: The Mediterranean Sea, the spatial measures taken by GFCM-FAO in the Mediterranean Sea mainly concern the establishment of FRA, the identification of vulnerable marine ecosystems or the mapping of the fishing footprint by VMS. All these actions are based on scientific advice provided by working groups and a pool of experts, but species distribution models are rarely included in the processes of spatial assessment of resources. SDMs have evolved over the years into a powerful tool for

understanding species occurrence, co-occurrence, and habitat assessment (Turner et al., 2016), but these methods and approaches are not used, for example, as a direct tool to inform spatiotemporal quotas, and management prescriptions are based on quantitative observations such as catch and effort. The GFCM requires data such as:

- Catch data per species
- Landing data per species
- Fishing activities and fishing effort
- Fishing fleet (e.g., number of fleet, gross tonnage, length overall, kW/hour, days at sea, fishing gear)
- Economic value (species value or operating costs)
- Biological information such as length, species, maturity, length, or sex data.

All of this information collected by Contracting Parties and cooperating non-Contracting Parties will be included in the Data Collection Reference Famework platform, and any information not covered by the GFCM recommendations, such as that collected by researchers, may be shared within the GFCM Working Groups and Scientific Advisory Committees (SAC) to contribute to the scientific advice. The reason why SDMs can be implemented in these processes is precisely because of this last point. Following the workflow shown in Figure 1.5, the main objective of this work is to provide a basis for the introduction of SDMs into the management process, where the steps include validation processes, stakeholder engagement, and information sharing in scientific advisory committees and the GFCM working group.

Methodology: species distribution models and input data

Understanding how life is distributed in the environment is a fascinating goal, but it becomes of overwhelming importance when the distribution of resources and their variability is key to managing resource use.
Several studies (Brodie et al., 2020; Guillaumot et al., 2020; Zurell et al., 2020) are devoted to explaining and predicting what factors determine species distributions. Biotic, abiotic, and distribution are the three basic factors (see Box.2) that determine the occupation of a given site by a species (Araújo et al., 2019; Barve et al., 2011; Hutchinson, 1957). It's not easy to understand the complex of processes, i.e., the importance of the three factors, in explaining the distribution of species, as well as how they respond to changes in the environment and the importance of combining the three main factors.

Species Distribution Models (SDMs, (Guisan & Zimmermann, 2000), are widely used in biology and ecology to map the potential distribution of species based on geoposition and environmental data (Brodie et al., 2020), including abiotic and biotic factors, to provide a probability of occurrence (in presence and absence) or an index of species density in space and over time. SDMs have been used in both terrestrial and marine contexts, with an increasing number of studies in the latter case since 2005 (Robinson et al., 2017). Examples of SDMs include various studies such as potential impacts of climate change on species (Chefaoui et al., 2018; Kearney et al., 2010), the distribution of invasive or unknown species (Barbet-Massin et al., 2018), scenarios for fisheries policy and management (Baudron et al., 2020), or habitat suitability of marine megafauna (Brodie et al., 2018). The central element of SDMs is the concept of niche, which has evolved in the ecological literature since 1917 (Grinnell, 1917) and has passed through milestones such as Hutchinson (Hutchinson, 1957). This concept is often confused with other terms such as habitat or environment, and in this introduction I'll clarify this definition following M. Kearney (Kearney, 2006):

"Habitat: a description of a physical place, at a particular scale of space and time, where an organism either actually or potentially lives"

A habitat, therefore, can be described without any reference to an organism, instead, a niche is:

"Niche: a subset of those environmental conditions which affect a particular organism, where the average absolute fitness of individuals in a population is greater than or equal to one."

This definition is the one used in this work. It is not the purpose of this paper to focus on the concept of niche or to discuss the differences between past and present definitions of this concept, but a brief explanation is necessary and due, especially in the context of models. The ecological niche is a concept (see Box 2) that does not distinguish between aquatic and terrestrial environments, but of course variables differ between the two, and in an aquatic ecosystem an important dimension includes, for example, temperature, dissolved oxygen, habitat structure, predators, and nutrients.

Box 2: factors that influence the species distribution

- The species requires important conditions to occupy a site and maintain stable populations
- The species must physically reach a site (Barve et al., 2011).
- The abiotic environmental conditions must be physiologically suitable for the species.
- The biotic environment must be suitable, i.e., there must be interactions with resources that allow the species to survive.

The first condition corresponds to the ability of the species to move from one place to another and is related to the biogeographic history of the species, i.e., the limitation of dispersal depends on its place of origin and other factors such as barriers to migration, biotic and abiotic vectors, or dispersal events. The second condition depends on abiotic conditions such as temperature or topography, i.e., the abiotic variables at the species' location are within the range of environmental conditions that the species needs to grow and maintain stable populations, also referred to as basic niches (Hutchinson, 1957). The third condition concerns biotic interactions (interactions with other organisms), which are influenced by the environment and its influence on all organisms at the local site. The abiotic conditions under which a species can survive, including interactions with other species, are called the realized niche and are what we observe when we study the distribution of a species.

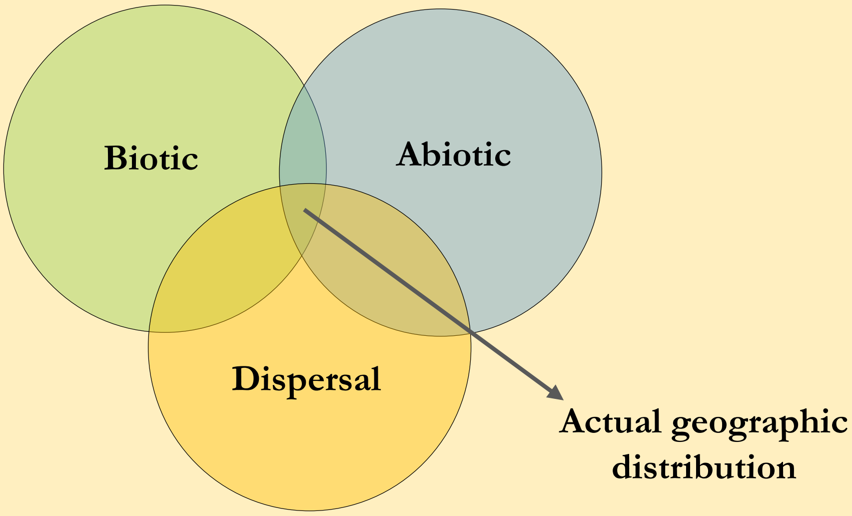

Figure 1.6: Three factors that influence the species distribution. The realized niche is the intersection of the green, blue and yellow circles

Moreover, there are two main directions in SDM: correlative and mechanistic methods. The first, used in this dissertation, correlates the presence/absence or density of a species in different areas based on environmental variables (e.g., temperature, topography, pH, etc.). A mechanistic approach, on the other hand, could incorporate physiological data, e.g., through an experiment conducted in the laboratory, and also consider the fitness of the species of concern, which could influence their distribution and abundance (Robinson et al., 2017). Finally, there is another method that integrates correlative and mechanistic approaches, called the hybrid model, which is based on environmental predictors, a niche population model, and physiological responses to climate factors (see Fordham et al., 2013).

In this work, I focused on a correlative approach to predicting the spatial distribution of demersal species in the study area, including under conditions of climate change, using statistical association between model-derived spatial environmental data (see Chapter 2, Chapter 3, Chapter 4) and occurrence records to implicitly assess the processes limiting species distributions. It is well known that in the correlative approaches, the parameter responses are not predefined and are modeled implicitly, which is simpler than mechanistic approaches that have a limitation due to the non- stable conditions (Plagányi et al., 2011, 2014).

Within the correlational approach of SDMs, many statistical techniques are commonly used, from regression methods (linear models, LMs, generalized linear models, GLMs, or generalized additive models, GAMs; (Hastie & Tibshirani, 1986), to machine learning methods (random forest, RF or neural network models, NNMs, (Breiman et al., 2018; Evans et al., 2011). Various techniques are therefore applied to hypothesize drivers of species distribution even at non-sampled sites, especially for climate change scenarios in ecological forecasts. Many of the aforementioned techniques can be implemented in open-source programs such as MaxEnt and BIOCLIM (see, e.g., (Elith et al., 2006; Phillips et al., 2006) or in R packages, and some implementations are user-friendly and it is very easy to obtain output results.

We must not be confused by the concept that a simple script model application means an understanding of the assumptions and limitations of that model, because there are many important considerations during model development, starting with the collinearity of our covariates (variables used to predict response variables, in this work, the covariates represent abiotic conditions), furthermore, the predictive performance of the model depends not only on the actual mathematical approach, but also on the characteristics of the species or the link between species and environment (Santika & Hutchinson, 2009), the sample size, the objective of the study, and the spatial scales (Wisz et al., 2008).

In this dissertation, I applied several SDMs techniques to evaluate the process behind each model and to interpret the results and limitations of the applied approaches. In the following section, I explain the main factor underlying SDMs and present some information about the species involved in the present work.

Abiotic factors: Environmental variable

The abiotic variables (e.g., temperature, nutrients, light) that affect a species' niche are all non-living factors. Understanding the underlying interaction between the environment and species is critical and has become even more important with the impacts of climate change (Parravicini et al., 2015). In the concept of ecological niche, it's the niche itself that allows species to live and exist in their environment, in which they play a unique role. We know that many factors can limit the occurrence of a species that aren't abiotic factors, such as competition, predator-prey relationships, parasitism, and others. Such factors weren't considered in this work, and the focus of the SDMs used here was also to understand and highlight the importance of environmental variables in terms of predicting and extrapolating outcomes.

The aquatic environment, particularly at the marine and ocean levels, is influenced by many external factors, ranging from natural factors such as wind, freshwater nutrient inputs, or oxygen to anthropogenic stressors such as pollutants or fisheries (Lewis, 2009). The most important abiotic factors are temperature, salinity, nutrients, oxygen, solar energy, turbidity, water level, waves, tides, and substrate. It's well known that temperature, the range of which is highly restricted in aquatic environments (the minimum is 0° in seawater), is fundamental to the ecology of phytoplankton, zooplankton, and associated predators at the trophic level (Lewis, 2009); in fact, temperature is a very important variable for most organisms, and living organisms require a certain range to grow, survive, and reproduce. In addition, temperature is critical for migration patterns and feeding, which are interrelated, and if temperature increases (e.g., due to climate change), many species may be affected and unable to adapt, possibly leading to a northward shift (Parravicini et al., 2015; Pereira et al., 2010)-see Chapter 5).

Regarding salinity, many species are adapted to live in a different area (euryhaline species), such as sea bass or gilthead sea bream, or species that live in the intertidal zone (intertidal species), while other species live in a specific salinity (stenohaline), such as some Gadidae species (e.g., haddock).

Since nutrients such as nitrate, phosphorus, and carbon are the most important, building macromolecules that organisms need to grow and live, such as DNA, RNA, proteins, amino acids, or carbohydrates, are crucial for an organism. Different aquatic habitats have low (e.g., coral reefs) or high (temperate waters) concentrations of these substances, which also depends on latitude, upwelling, or river discharge, making an area less or more productive accordingly. For example, in the study area of this work, especially in the northern Adriatic Sea, there are many river inputs and nutrient discharges that vary in the long term and interannually (Cozzi & Giani, 2011).

Oxygen is the element essential for respiration, photosynthesis, and chemical processes and is produced by algae, phytoplankton, and marine plants such as phanerogams (e.g., Poseidonia oceanica). Oxygen levels are affected by many factors, such as pollution and increased bacterial activity in the case of eutrophication (Glibert & Burford, 2017; Glibert, 2017), resulting in low oxygen levels, or in the case of a healthy ecosystem with high oxygen levels and a good balance between respiration, consumption, and production through photosynthesis.

The Mediterranean Sea (MS) is a semi-enclosed sea with a high variability in different characteristics, such as biogeochemical, physical or biological. Several studies have investigated the variability of the MS, ranging from biogeochemical data, for which long-term studies at the basin scale have been presented (Cossarini et al., 2021), to chlorophyll data retrieved from satellites (Colella et al., 2016), to interannual variability of oxygen trends (Li & Tanhua, 2020). This type of data can provide a robust spatiotemporal record of ocean features and describe the state and evolution of biogeochemical and physical features. Understanding the key processes underlying marine variables is essential because ecology, physiology, and economic activity are intimately linked to the balance of the marine ecosystem, which requires knowledge of resource status and trends.

If climate change projections are also taken into account, abiotic variables such as temperature or oxygen will change drastically, including stratification processes and water formation (Adloff et al., 2015; Soto-Navarro et al., 2020), and by the end of the 21st century the site MS could be warmer and drier according to global simulations (IPCC, 2022). In this context, all sub-basins of MS are affected by the future evolution of environmental conditions, including the Adriatic and Ionian Seas.

All these disturbances could have an impact on the distribution of species, especially on the basin with high biodiversity (Dulčić & Lipej, 2015), and economic activities, such as fishing and tourism, could also be strongly affected. The ecological niche defines the relationship between speciesand habitat, and this relationship can provide information about the ecology of a species at different scales (local or global), but is also useful for conservation and management purposes (Thorson et al., 2017).

In this work, physical and biogeochemical variables for the study area were extracted from two databases covering the Mediterranean Sea and available as part of the Copernicus Marine Environment Monitoring Service (CMEMS,https://marine.copernicus.eu/access-data; (Simoncelli et al., 2019; Teruzzi et al., 2019).

The CMEMS dataset for the analysis and prediction of the biogeochemistry of the Mediterranean Sea consists of daily/monthly 3D fields of different variables generated by the coupled transport-biogeochemistry model OGSTM-BFM (Lazzari et al., 2010, 2016) and the variable data assimilation scheme 3DVARBIO (Teruzzi et al., 2014, 2018) for surface chlorophyll.

The biogeochemical flux model (BFM) focuses on the biogeochemical cycling of carbon and nitrogen, phosphorus, and silicon and describes the interaction within and between the living organic and non-living organic compartments (Cossarini et al., 2021).

The datasets used here cover the period 1999-2018 with a spatial resolution of 1/16° and 72 uneven vertical levels.

The variables considered in this work were: water surface temperature (°C), water bottom temperature (°C), dissolved oxygen (mmol/m3) at the bottom, and water column averages for nitrate (mmol/m3), phosphate (mmol/m3), chlorophyll-a (mg/m3), particulate organic carbon (mg/m3), and pH, as well as surface salinity.

These variables were included because of their ecological importance to the selected demersal fish species and because of their importance in creating favourable conditions for productive habitat.

Abiotic factors: Effort

Fishing effort was estimated for 2008-2018 by integrating vessel monitoring system (VMS) and automatic identification system (AIS) data. The disaggregated VMS and AIS data include vessel-specific "pings" with information on vessel identity, position, speed over ground, and course. The VMS and AIS datasets were merged at the level of individual Italian and Croatian flag vessels using the VMS baseline platform (Russo et al., 2016; Russo et al., 2014), and no other VMS data are available from other countries (e.g., no VMS data from Montenegro or Albania are used in this work). Fishing trips were then interpolated and fishing positions (i.e., hauls) were separated from other non-fishing behaviors (steaming, resting, etc.). Fishing effort was estimated by vessel/cell for bottom otter trawls (OTB) and beam trawls (TBB) and expressed as total trawl time (in hours) per year with a spatial resolution of 1/16. Fishing effort was used as a variable across years, with the 'footprint' of this covariate assumed to be a proxy for the dynamics of the resource, based on the concept that fishermen follow the resource and know the best fishing grounds in the area.

Input survey data

MEDITS: Mediterranean International Bottom Trawl Survey

The Mediterranean Sea is a complex system with a variety of specific areas where, due to the small extent of the continental shelf along most coasts, benthic and demersal resources are exploited mainly near the shore.

Demersal fish are most affected by fisheries at the national level, and survey programs to assess the status of exploited stocks are essential. MEDITS (Mediterranean International Bottom Trawl Survey) provides basic information on benthic and demersal species, such as population structure (e.g., kg/km2) and demographic structure (length and size of major commercially exploited species), by surveying continental shelves and upper slopes of the Mediterranean Sea on a global scale.

A protocol developed in early 1994 was adopted for all EU countries in the Mediterranean Sea, covering the design of the survey, the sampling device (characteristics and handling), the information collected, the management of the data, up to the production of common standardized analyzes of the data, taking into account the characteristics of the areas covered by the survey (Bertrand & Relini, 2000).

The MEDITS survey program was updated in 2002 (Bertrand et al., 2002). The main objective of the survey is to cover the entire trawlable area in the Mediterranean Sea from 10 to 800 m depth off the coast of the country participating in the project. in 1996, the area was extended to cover almost the entire Adriatic Sea (including Slovenian, Croatian and Albanian waters), the study area of my work. In addition, MEDITS has been involved in the collection of fisheries data in the European communities since 2002 (DCF, Anon, 2000). Sampling is stratified and based on random stations (or hauls) within strata, with strata following the bathymetric range: 10, 50, 100, 500 and 800 m, also taking into account the geographical sub-area (GSA) defined by the General Fisheries Commission for the Mediterranean (GFCM, Fig. 1.7)

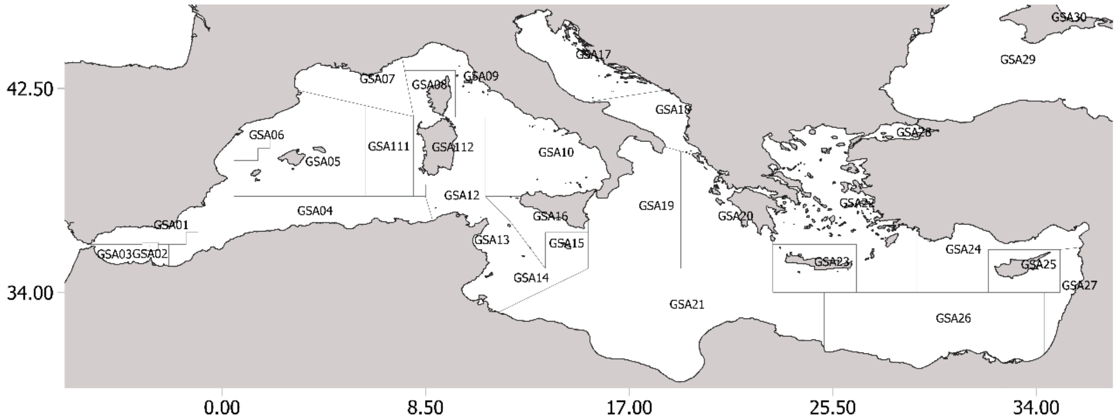

Figure 1.7: GSA (Geographic Sub Area) in the Mediterranean Sea. Longitude on x-axes, the latitude on y-axes.

More than 500 species are caught under MEDITS, but the most common are 38 (Table 1.2), ranging from fish to mollusks, which are identified in the MEDITS protocol as the most important from a commercial and biological perspective. For each of these species, there are indices of total number of individuals, length frequency distribution, sex (including sexual maturity stage), and total weight. For all other sampled fish, crustacean, and mollusk species, the total number and total weight for each haul are provided.

The net is a bottom trawl (Dremière et al., 1999) used for experimental fishing and its characteristics allow it to be used over the entire depth range and under the various conditions found in the study area. To increase the catch of demersal fish species, it has a vertical opening that is slightly larger than that of the professional gear most commonly used in the area. The mesh size on the codend is 20 mm (stretched mesh - Fig. 1.8). A device to track the geometry of the fishing gear has been systematically used only on board some of the sampling vessels since the beginning of the survey series. Finally, an algorithm that accounts for warp length and depth has been implemented to standardize the estimate of swept area during MEDITS surveys (MEDITS, 2007). Surveys are conducted each year during the spring and summer months, using the same vessel for each area as much as possible. The duration of the hauls is set at 30 minutes for depths less than 200 m and 60 minutes for depths greater than 200 m.

All collected data will be analyzed and an index on biomass (kg/km2) and number of individuals (n/km2) per square kilometer will be produced, using statistical methods approved by the MEDITS Steering Committee and included in a special software (Souplet, 1996). Table 1.1 lists the 38 target species from MEDITS and in bold the 7 species from MEDITS that were included in this work; images of these species are shown in Figure 1.8, downloaded from https://www.sibm.it/SITO%20MEDITS/principalemedits.htm. In conclusion, the MEDITS program is the best monitoring program over the years, able to provide very long data on bottom and demersal fish species, especially in our study area, the Adriatic and Ionian Seas, where more than 150 (on average) positions are surveyed every year thanks to the efforts of the biologists and technicians of this monitoring program.

Table 1.2: Most important species targeted by MEDITS. In bold, the species used in this work (fig. 1.8)

Scientific name	CODE	Common name
		English
Aspitrigla cuculus	ASPI CUC	Red gurnard
Boops boops	BOOPBOO	Bogue
Citharus linguatula	CITH MAC	Spotted flounder
Eutrigla gurnardus	EUTR GUR	Grey gurnard
Galeus melastomus	GALU MEL	Blackmouth catshark
Helicolenus dactylopterus	HELI DAC	Rockfish
Lepidorhombus boscii	LEPM BOS	Four-spotted megrim
Lophius budegassa	LOPH BUD	Black-bellied angler
Lophius piscatorius	LOPH PIS	Angler
Merluccius merluccius	MERL MER	European hake
Micromesistius poutassou	MICM POU	Blue whiting
Mullus barbatus	MULL BAR	Red mullet
Mullus surmuletus	MULL SUR	Striped red mullet
Pagellus acarne	PAGE ACA	Axillary seabream
Pagellus bogaraveo	PAGE BOG	Blackspot seabream
Pagellus erythrinus	PAGE ERY	Common pandora
Sparus pagrus	SPAR PAG	Common seabream
Phycis blennoides	PHYI BLE	Greater forkbeard
Raja clavata	RAJA CLA	Thornback ray
Scyliorhinus canicula	SCYO CAN	Smallspotted catshark
Solea vulgaris	SOLE VUL	Common sole
Spicara flexuosa	SPIC FLE	Picarel
Spicara smarts	SPIC SMA	Picarel
Trachurus mediterraneus	TRAC MED	Mediterranean horse mackerel
Trachurus trachurus	TRAC TRA	Atlantic horse mackerel
Trigla lucerna	TRIG LUC	Tub gurnard
Trigloporus lastoviza	TRIP LAS	Streaked gurnard
Trisopterus minutus capelanus	TRIS CAP	Poor-cod
Zeus faber	ZEUS FAB	John dory
Selacians[2]		
Aristaeomorpha foliacea	ARIS FOL	Giant red shrimp

Aristeus antennatus	ARIT ANT	Blue and red shrimp
Nephrops norvegicus	NEPR NOR	Norway lobster
Parapenaeus longirostris	PAPE LON	Deep-water pink shrimp
Eledone cirrhosa	ELED CIR	Horned octopus
Eledone moschata	ELED MOS	Musky octopus
Illex coindetti	ILLE COI	Broadtail squid
Loligo vulgaris	LOLI VUL	European squid
Octopus vulgaris	OCTO VUL	Common octopus
Sepia officinalis	SEPI OFF	Common cuttlefish

Figure 1.8: MEDITS species involved in this work. From left to right: Merluccius merluccius, Mullus barbatus, Nephrops norvegicus, Lophius budegassa, Illex coindetii, Parapenaeus longirostris and Trachurus trachurus.

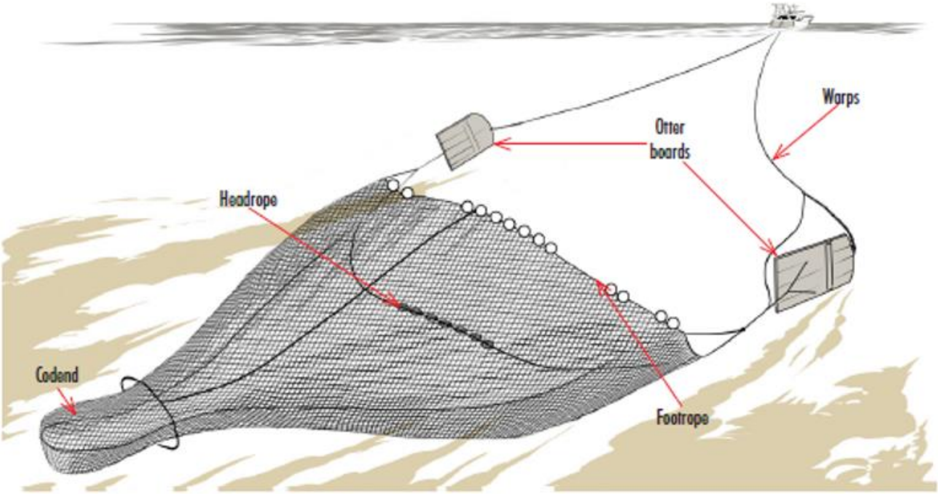

Figure 1.9: Type of gear used by MEDITS. Illustrator Alberto Gennari (source: FAO, 2020a),

SOLEMON: Sole Monitoring in the Adriatic Sea.

The SOLEMON (Sole Monitoring) survey is the only beam trawl survey (Fig. 1.10) conducted in the Adriatic Sea since 2005 and aims to collect data on the distribution and abundance index (kg/km2 or n/km2) of commercially exploited soil species specific to sole (*Solea solea*, Fig. 1.11). The program is coordinated by three countries, Italy, Croatia, and Slovenia. In addition to sole, other species of interest to the monitoring program include squid (*Sepia officinalis* - Fig. 1.11), mantis shrimp (*Squilla mantis* - Fig. 1.11), scallop *(Pectinidae*), queen conch (*Aequipecten opercularis*), turbot (*Scophthalmus maximus*), brill (*Scophthalmus rhombus*), and caramel shrimp (*Melicertus kerathurus*). The survey considers and reports information on latitude, longitude, depth, velocity, and duration, which are essential for developing the index of density or biomass.

In addition, beginning in 2007, SoleMon surveys adopted an integrated approach and added other tasks such as monitoring seafloor debris and megazoobenthos to the original objectives, which remain priorities (SoleMon, 2019).

Since 2009, SoleMon surveys have also been coordinated as part of ICES WGBEAM and included in the WGBEAM manual for offshore beam trawl surveys (SoleMon, 2019). In the Adriatic Sea, which is characterized by soft soils, a modified beam trawl called "Rapido" is used. It consists of a modified beam trawl (Hall-Spencer et al., 1999) with a rigid mouthpiece equipped with 46 iron teeth (6-7 cm long) in the lower part. Four runners are attached to the iron frame and a reinforced diamond mesh rubber net in the lower part to protect the polyamide net bag. The same gear is also used in the SOLEMON study The net has a length of about 2.7 m and can be used at depths from 5 to 100 m. The selectivity of the net is as low as possible to obtain good images of the sampled populations, including juveniles. Finally, the mesh size of the codend is 26 mm (stretch). The net is made of polyamide netting material (nylon).

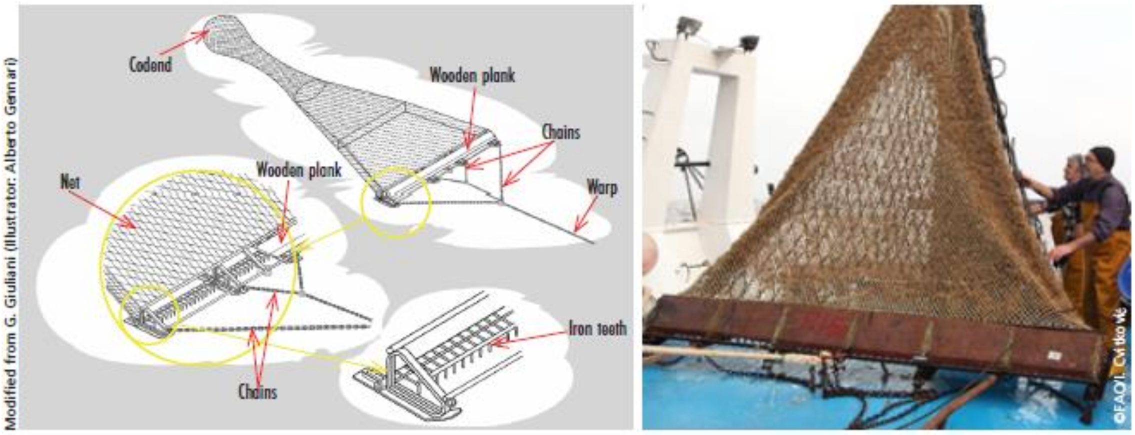

Figure 1.10: Fishing gear used by the SOLEMON survey. Source (FAO, 2020a)

Table 1.3: main target species from the SOLEMON survey. In bold species used in this work (Fig. 1.11)

Species	**Common name**
Solea solea	**Common sole**
Solea aegyptiaca	Egyptian sole
Platichthys flesus	European flounder
Scophthalmus maximus	Turbot
Scophthalmus rhombus	Brill
Merluccius merluccius	European hake
Mullus barbatus	Red mullet
Raja asterias	Mediterranean starry ray
Raja clavata	Thornback ray
Parapenaeus longirostris	Deep rose shrimp
Penaeus kerathurus	Caramote prawn
Nephrops norvegicus	Norway lobster
Squilla mantis	**Mantis shrimp**
Sepia officinalis	**Cuttlefish**
Pecten jacobaeus	Scallop
Aequipecten opercularis / Flexopecten glaber	Queen scallop

Figure 1.11. SOLEMON's main target species is used in this work. From left to right: common sole, cuttlefish, and mantis shrimp.

Species involved

Merluccius merluccius - European hake, bony fish: is one of the main targets of fisheries in the Adriatic Sea, accounting for 77% of landings in Croatia and 15% in Italy (Grati et al., 2018). It's one of the overfished species (Ulrich et al., 2019) affected by trawling in the area and is actually overfished and in the process of overfishing (SAC, 2022). It's considered a euritopic species, living at depths of 50 to 800 m, with juveniles living between 100 and 200 m and adults living between 100 and 150 m. It's also considered to be an euritopic species. In spring, adults migrate to shallow coastal waters to spawn, and juveniles show migratory patterns in search of food, while adults migrate to deeper waters in winter. It's important to highlight that the Jabuka/Pomo Pit area, thanks to its topography and oceanographic characteristics, is an environment with particular water exchange that influences nutrient cycling and local biodiversity (Marini et al., 2016). This area is the main nursery of the European hake (Druon et al., 2015, Arneri & Morales, 2000)

Females become sexually mature throughout the year, but especially in spring/summer, from May to July (Candelma et al., 2021). The species prefers muddy bottoms, but also occurs in muddy-sandy or sandy bottoms. The European hake can grow up to 135 cm in length, but the usual catch length is between 10 and 60 cm. The diet consists mainly of crustaceans and amphipods for hake up to 15 cm (juveniles); adults begin predation on sardines (*Sardina pilchardus*), red mullet (*Mullus barbatus*), horse mackerel (*Trachurus trachurus*), and cannibalism of juvenile hake (Froglia, 1973; Ungaro et al., 1993).

Mullus barbatus – red mullet, bony fish: it's the main target of the beam trawl fishery (OTB), about 96% of the total landings in tons in 2019 in GSA 17 and 18, for all countries in the area (Italy, Slovenia, Croatia, Albania, Montenegro) where overfishing occurs (SAC, 2022). The minimum size for conservation is 11 cm total length, the fishery is closed for 30-45 days in late summer, and trawling is prohibited within three nautical miles offshore or at depths of less than 50 m. The fishery is closed for 30-45 days in late summer.

It's found mainly in the eastern Adriatic during the spring spawning season on the muddy bottom between 5 and 200 m depth (Bertrand & Relini, 2000), where it prefers shallow water. Juveniles migrate from the coast to the open sea in autumn, where they can be found throughout the Adriatic shelf (Vrgoč, 2000). The size of this species can reach 30 cm, especially in females (Relini et al., 1999), but the usual length in catches is between 10 and 20 cm (GFCM-FAO, 2020b). Data obtained from the MEDITS survey may be critical for mullet because they have a short spawning season, usually in late spring, and recruitment occurs in the fall. Thus, in years when the survey ends in summer, there will be no or very few recruits (GFCM-FAO, 2020b). For this reason, this species was excluded from the results in some evaluations (e.g., Chapter 4, Fig. 4.4), especially for the juvenile life stage.

It's a carnivorous species, and the diet consists of endo- and mesoepi-biontic organisms, such as Polychaeta, Lamellibranchiata, and Crustacea (Froglia, 1988). The main predators of the mullet are the anglerfish (*Lophius budegassa*), the stingray (*Raja clavata*), the St. Peter's fish (*Zeus faber*), and European hake (*Merluccius merluccius*).

Nephrops norvegicus – Norway lobster, crustacean: it's mainly fished by bottom trawlers (OTB), Italy and Croatia. In addition, Norway lobster is caught in the northeastern channels of the Adriatic Sea and along the Croatian coast by small fishing vessels using traps. (GFCM-FAO, 2019a). The guard size is 20 mm carapace length, and the Norway lobster fishery is closed for 30-45 days in late summer. Trawling is prohibited within three nautical miles of shore or at depths less than 50 metres.

The species is distributed in depths from 30 to 400 m from the central to the southern part of the Adriatic Sea (Marano et al., 1998), in muddy bottoms where the species digs burrows to hide and lay its eggs. The oceanographic characteristics of the Jabuka/Pomo Pit area make it an ideal habitat for Norway lobster, especially with a high density of smaller individuals that grow slowly compared to other areas of the Adriatic (Froglia & Gramitto, 1981).

Data obtained from the MEDITS survey may be critical, especially in Jabuka/Pomo Pit area, The individuals in Jabuka/Pomo Pit are smaller than the other individuals in the basin, but not necessarily juveniles, and the MEDITS survey may not capture all of the information on the two life stages in the area where juveniles are not detectable because they live in the burrowed burrow during the early life stage (see discussion Chapter 4).

Maximum length is 26.5 cm (total length) (Crnković, 1965), and mature ovaries of females peak in spring and early summer (Froglia & Gramitto, 1981). Norway lobster feeds on other decapod crustaceans and small fishes that are part of the demersal communities in muddy bottoms.

Trachurus trachurus – European horse mackerel, bony fish: it's a species that occurs on sandy-muddy bottoms, especially near the continental shelf, and is fished with trawls. Few studies have provided information on horse mackerel in the Adriatic Sea, but it's known that it's usually found between 20 m and 200 m, spawns in spring (Jardas, 1996) and feeds mainly on fish, crustaceans, amphipods and decapods (Tortonese, 1975). Maximum length is about 70 cm, but the usual length is 22 cm, with a maximum weight of about 2 kg (Smith-Vaniz, 1986). Sexual maturity is about 24.3 cm (Tortonese, 1975).

Parapenaeus longirostris – deep rose shrimp, crustacean: of trawling in the Adriatic Sea, especially in the southern area along the coast of GSA 18, about 13% of the landings in this area (MiPAAF, 2011). Deepwater shrimp can grow up to 16 cm (males) and 19 cm (females)

(GFCM-FAO, 2017) and reach sexual maturity in the first year of life (Froglia, 1982). The main management rules are based on a limited number of fishing licenses and distance from shore or depth, i.e., more than three nautical miles from shore or more than 50 m depth. In 2008, the management plan specified a reduction in the number of fleets and time at sea. In 2009, two biological protection zones were established, off the coast of Bari and near the island of Tremiti (GFCM-FAO, 2017). In Montenegro, regulations are based on mesh size, limited number of fishing licenses or area restriction (no fishing zone up to 3 nautical miles (NM) off the coast or 8 NM for trawlers longer than 24 m LOA - Length Over All) (State Gazette of Montenegro, 8/2011).

Lophius budegassa – Angler fish, bony fish: exploited by trawling, it's common throughout the basin, particularly in the southern area along the coast of GSA 18 and the northeastern edge of the Pomo/Jabuka Pit transit area (GFCM-FAO, 2019b). The anglerfish is a benthic species distributed at depths from 500 m to 1000 m, where it prefers sandy-muddy bottoms (SIBM, 2017) and depth preference depends on size, with juveniles often found in shallow waters. L. budegassa feeds on bottom-dwelling fishes, and is a predator that attracts prey with the modified first ray of the dorsal fin (Stagioni et al., 2013). Juveniles feed primarily on small benthic fishes, and adults prefer blennies. The anglerfish has a high commercial value, but there is a significant lack of information on black anglerfish in the Adriatic Sea, especially on distribution and growth (Stagioni et al., 2013).

The spawning season lasts from February to June/July, with a maximum size of about 70 cm and a combined length at first sexual maturity of about 27-30, 26.5 cm for males and 30.5 for females (Ikica et al., 2015). Regarding management regulations, there is no minimum size, trawling is prohibited within three nautical miles or at depths less than 50 m, and the minimum mesh size is 16 mm (GFCM-FAO, 2019b). The ban is in effect for 45 days in summer, corresponding to the period with maritime compartments.

Illex coindetii – southern squid, mollusc: like all squid, I. coindetii has a fast metabolism, short life span, and rapid growth (Petrić et al., 2021). Catches are from both artisanal and bottom trawl fisheries and are also considered bycatch from large-scale fisheries (Arkhipkin et al., 2021). In the Adriatic Sea, especially in the Croatian part, squid accounts for a large proportion of the total cephalopods caught and is generally considered a valuable resource throughout the basin (Eurostat, 2020).

It's distributed from 100 m to 600 m and also reaches 1000 m depth (Petrić et al., 2021), females are larger than males, with average mantle length between 25 and 27 cm and 18 cm and 20 cm, respectively (Gonzalez & Guerra, 1996). It inhabits muddy, sandy, and detrital bottoms, migrating to shallow water in spring and returning to deep water in winter (Vecchione & Young, 2011). The species can spawn year-round, with peaks in summer and spring. Diet consists of fish, crustaceans (such as krill), and other cephalopods (Sánchez et al., 1998).

Solea solea – common sole, bony fish: fished mainly by shear beam trawl (TBB) in GSA 17 and along the southern Italian coast, is one of the most important fish species in the northern Adriatic, with a landing value of more than 20 million euros (GFCM-FAO, 2021c). In 2019, 56% of the catch in the Adriatic came from the Italian Rapido fishery, 20% from the Italian OTB fishery, 21% from the Italian and Slovenian set net fisheries, and 3% from the Croatian "Rampon" fishery.

It is a demersal species living on sandy and muddy bottoms (Tortonese, 1975), with evidence of genetic differentiation between stocks in GSA 17 and GSA 18 (FAO-ADRIAMED & Scarcella, 2014). Sole reproduction occurs from May to December (Tortonese, 1975), but in SOLEMON, reproduction in the central and northern Adriatic was found to occur from November to March, with a higher concentration of reproduction outside the western coast of Istria (Fabi et al., 2009). Length at first sexual maturity was estimated at 25.8 cm. Management regulations require a minimum size of 20 cm total length, fishing is prohibited within three nautical miles or at depths less than 50 m, fishing is closed for 30-45 days in late summer, and fishing is prohibited up to 6 nautical miles three months after the closure (GFCM-FAO, 2021c).

Squilla mantis – mantis shrimp, crustaceans: it is not a target of a specific fishery, but a component of multispecies trawls and gillnets, the associated species in GSA 17 being *Sepia officinalis* (squid), *Mullus barbatus* (red mullet) or *Eledone cirrosa* (octopus). In the Adriatic, 80% of the landings come from the Italian side, especially from trawling (83%), 11% from gillnet fishing and 6% from 'rapido' (GFCM-FAO., 2021f). The species lives on the continental shelf, up to 200 m, but the maximum was measured at 367 m (Vasconcelos et al., 2017). It usually digs a burrow with two circular openings on the sandy-muddy bottom where it hides during the day (Froglia, 1996), so most catches are made during the night.
In GSA17, females reach sexual maturity in their second year of life. Females with mature ovaries are observed in late winter in the central Adriatic (Froglia, 1996). Excreted females with still whitish glands are usually observed from April to September, when the sex ratio (M/F) is strongly in favor of males (Froglia, 1996). Management regulations do not specify a minimum length, fishing is prohibited within three nautical miles or at depths less than 50 m, fishing is closed for 30-45 days in late summer, and fishing is prohibited up to a distance of 6 nautical miles three months after summer fishing closes (GFCM-FAO, 2021f).

Sepia officinalis – cuttlefish, mollusc: it's caught mainly by otter trawl and beam trawl (OTB and TBB) in Italy, Croatia, and Slovenia, with 95% of landings in Italy, where the historical trend in catches is downward (GFCM-FAO, 2021d).
Squid is common in the Adriatic Sea on the continental shelf, where the depth limit is about 200 m (Guerra, 2006), and is considered a valuable resource. It's a species that prefers sandy and muddy bottoms, especially in areas covered with phanerogams (Relini et al., 1999). Its diet includes crustaceans, bony fish, mollusks, and bottom fauna such as polychaetes (Guerra, 2006). Squid show migration patterns: in winter they stay in the circalittoral zone where they become sexually mature, in spring the sexually mature animals migrate to shallow water to spawn, in summer the juveniles stay mainly in the infralittoral zone, and in autumn the recruits retreat to deeper water. The species can reach a maximum mantle length of 35 cm, but the average squid length is between 15 and 20 cm. Cephalopods can respond quickly and "actively" to environmental changes by migrating in search of more favorable conditions (Armelloni et al., 2020). For this reason, it'll be critical to consider the effects of the environment on species distribution and recruitment success to inform fisheries management of cephalopods (ICES, 2019), including squid. (Froglia, 1996). Management regulations don't specify minimum lengths, fishing isn't allowed within three nautical miles or at depths less than 50 m, fishing is closed for 30-45 days in late summer, and fishing is prohibited up to 6 nautical miles 30 days after closure (GFCM-FAO, 2021d).

Now follows the section on the outline of the work, with the summary for each chapter included in this work

Thesis' outline

Chapter 2

Chapter 2 includes work published in the Journal of Operational Oceanography, in Ocean State Report 5, 2021. In this section, I examine the role of environmental variables using the GAM approach with MEDITS and SOLEMON data and analyze biomass indices (kg/km2). The role of this chapter is to highlight the difference between models with and without abiotic covariates, which is visible in the results of the chapter.

Summary

Demersal species play a fundamental role in fisheries, and understanding their distribution through bottom trawl surveys is critical to fisheries management. However, data from bottom trawl surveys need to be supplemented with additional variables (biogeochemical, physical, and fisheries) to enable an integrated approach aimed at mitigating the effects of change on estimates of the spatial distribution of species biomass. Here, we analyze biomass indices for European hake, sole, mantis shrimp, mullet, and common cuttlefish from scientific trawl surveys conducted in the Adriatic and western Ionian Seas using a suite of generalized additive models (GAMs) with and without additional variables. The results show that the geostatistical model for estimating the distribution of different demersal species based on trawl data is improved when additional environmental variables are included. Such an integrated approach has relevant potential implications for stock assessment and identification of essential fish habitats on which to base fisheries management.

Chapter 3

Chapter 3 contains the work presented at the 2021 MeteoSea conference that is linked to Scopus. This chapter presents the methodology used, focusing on merging survey data and environmental layers, training and testing the spatial approach, and error assessment between models using the European hake as an example.

Summary:

Marine species distribution models are widely used in ecology and fisheries science to support management of exploited marine resources. This study focused on defining a procedure for developing an ensemble model that combines 5 different modeling approaches. For each approach, we implemented spatial training and testing datasets to evaluate the best performance of 9 models against a set of indicators. These models include different combinations of covariates, ranging from the simplest model (depth, year, and spatiotemporal variables) to the most complex model (which also includes oceanographic variables and fishing effort). We applied this procedure to develop a robust ensemble of models that accurately describes the spatial and temporal distribution of European hake (Merluccius merluccius) in the Adriatic and Ionian Seas.

Chapter 4

Chapter 4 contains the work discussed in Fish and Fisheries. In this section, I examine the role of environmental variables using three modeling approaches: GAM, RF and GBM using MEDITS and SOLEMON data, analyzing density indices (n/km2). The role of this chapter is to incorporate an ensemble model developed for ten demersal species for two life stages and to consider the spatial management approach using SDMs.

Summary:

Spatial fisheries management is widely used to reduce overfishing, rebuild stocks, and protect biodiversity. However, the effectiveness and optimization of spatial measures depends on correctly identifying ecologically meaningful areas, which can be difficult in the case of mixed fisheries. To apply a method generally to groups of target species, we developed an ensemble of species distribution models (e-SDM) that combines general additive models, random forest, and gradient-boosting machine methods, and integrates geopositional, oceanographic, and effort variables into a training and testing protocol. The determined best distributions for juveniles and adults are used to determine hot spots for fish aggregation and optimal fishing grounds for single or multiple target species. We applied e-SDM to juvenile and adult stages of 10 marine demersal species in the central areas of the Mediterranean Sea, where they account for 60% of total demersal landings. E-SDM combined density indices from two scientific bottom trawl surveys (MEDITS and SOLEMON) with geographic data (depth, latitude, longitude, and month), relevant 3D oceanographic variables (temperature, salinity, chlorophyll-a, dissolved nutrients and oxygen, particulate organic carbon, pH), and fishing effort (from vessel monitoring system). The e-SDM results were used to identify aggregation hotspots and optimal fishing grounds for each species and for the target species group of otter trawl and beam trawl fisheries. The results allowed us to review the effectiveness of existing fishery closure areas and identify optimal locations for new spatial management measures.

Chapter 5

Chapter 5 includes work on SDMs and climate change projection. In this section, I examine the role of future environmental variables through three modeling approaches, GAM, RF, and GBM, using MEDITS and SOLEMON data and analysis of density indices (n/km2). The role of this chapter is to include an assessment of range contraction/expansion of ten species in the lens of climate change.

Summary:
Predicting range shifts of marine species associated with climatic change is central to understanding biodiversity and spatial change, particularly in areas where resources are also critical to fisheries to ensure appropriate management. One of the most important tools for predicting future distribution is the Species Distribution Model (SDM), which uses environmental data to infer range limits and habitat suitability for a given species. In this work, we used correlative approaches to develop ensemble species distribution models (e-SDM) to assess the future distribution of ten demersal species in the Adriatic and western Ionian Seas and to identify aggregation areas for four different scenarios (2012, 2018, 2035 and 2050) for two life stages, adult and juvenile fish. The e-SDM was developed using three different approaches, i.e. generalized additive models (GAM), random forest (RF) and gradient boosting machine (GBM), combining data on the number of individuals per km2 and relevant oceanographic variables from Copernicus Marine Service. We highlighted the hot spot of aggregation, past and future density distribution, density difference between scenarios, and centroid of density for species in the study area by GSA (Geographic Sub Area, 17, 18, and 19). We also incorporated an assessment of future areas gained and lost as new potential range shifts for the ten species. The results show that densities of some important commercial species such as hake, mullet, and monkfish are shifting northward and their distributions are changing. This highlights the need for fisheries in the area to consider climatic changes when planning management measures to assess future economic impacts.

Chapter 6

Chapter 6 includes the final discussion and evaluation of the limitations, future perspective and implementation of this work. In the future, I would like to continue my work in the same field of SDMs and the possible implementation in a scientific advisory commission of the GFCM, hoping for a new spatial management approach, also based on my knowledge, as a community contribution in the important field of resource assessment in the Adriatic, Ionian or Mediterranean Sea.

Chapter 2

SDMs for demersal species

Developing spatial distribution models for demersal species by the integration of trawl surveys data and relevant ocean variables

INTRODUCTION

Marine fish and invertebrates that live and feed close to the marine seabed, i.e. the demersal species, play a fundamental role in fisheries. In the Mediterranean and Black Sea, these species constitute approximately 20% of the total landed weight (more than 220,000 tons/year for the period 2018-2020, FAO, 2022) and 50% of the total landed value FAO, 2022). In order to ensure the sustainability of exploitation, a set of fisheries management measures and restrictions are adopted also considering scientific information on the status of resources. Clearly, management actions are particularly relevant and impacting in large areas of the Mediterranean Sea where demersal resources play a central role in local fishing communities and economies, such as the Adriatic and Ionian seas. Therefore, it is of paramount importance to increase accuracy of scientific information used to inform management.

Scientific bottom trawl surveys provide quantification of abundance and biomass (hereafter termed indices) by species, i.e. fishery-independent data, that are used for manifold purposes related to management: stock assessment (Cotter et al., 2009) , evaluation of spatio-temporal distribution of demersal resources (Carlucci et al., 2018), estimates of population and community densities (Spedicato et al., 2019), and the development of ecosystem models (Grüss et al., 2018; Moullec et al., 2019b). Sampling protocols of multiannual surveys are usually standardised for sampling design, gear geometry, sampling season, sampling locations to allow comparability of the trawl survey data across space and time. However, unavoidable small deviances (e.g. sampling period or sampling location) or changes (e.g. vessel) during sampling may affect the abundance and biomass indices obtained from trawl surveys.

In order to test the potential benefits of using oceanographic and effort variables in addition to spatiotemporal covariates (latitude, longitude, depth, year and month) to improve species distribution models based on trawl survey data, Generalised Additive Models (GAMs) were chosen for their wide application and suitability with trawl survey data (Grüss et al., 2014; Lauria et al., 2017; Tserpes et al., 2019). GAMs allow to predict species abundance and biomass over the domain (Maunder & Punt, 2004; Potts et al., 2020; Rubec et al., 2016) and provide estimates useful for tuning stock assessment models (Cao et al., 2016; Orio et al., 2017). Furthermore, GAMs are deemed appropriate for mapping species distribution that is useful in ecosystem models (Fulton et al., 2011; Grüss et al., 2018), or for identifying Essential Fish Habitats (Colloca et al., 2015; Druon et al., 2015).

In addition to monitoring deviances, environmental changes and anthropogenic stressors may cause life-history responses, and their impacts on survey estimates are difficult to disentangle. Satellite data are successfully used to provide environmental variables (e.g. sea surface temperature; sea surface chlorophyll concentration) to be included in models to describe the spatial distribution of some pelagic species (Giannoulaki et al., 2008; Schismenou et al., 2017). However, these variables might be insufficient to model the distribution of demersal species, which may require additional oceanographic variables close to seabed such as those provided by the Copernicus Marine Environment Monitoring Service (CMEMS). The relative high number and the quality of the CMEMS products, as well as their high temporal coverage and spatial resolution, provide biogeochemical and physical oceanographic variables that can be useful to improve the analysis of abundance and biomass indices derived from trawl surveys (Sion et al., 2019; Tserpes et al., 2019).

In addition, the displacement of fishing fleets derived from satellite-based tracking devices, such as Vessel Monitoring System (VMS) and/or Automatic Identification System (AIS), is a valuable source of information on the distribution and spatial aggregation of marine resources (Bastardie et al., 2014; Russo, et al., 2014). The annual distribution of the fishery is indeed a good indicator of the distribution of the target resource, rather than a measure of the direct impact on it (which is a much longer-term impact). This also depends on the species. For two red shrimp species such as *Aristeus antennatus* and *Aritaeomorpha foliacea*, the distribution goes far beyond the fishing areas, an aspect that is very important for the management of these species. In this work I have not considered these two species, and further improvement may be interesting. I consider the species involved here as a good example of including fishing effort as a proxy in the area. Thus, the accuracy of the species distribution could be increased if fishing effort is included in the explanatory variables. In this work, therefore, I propose an integrated approach useful to fisheries management by combining trawl survey data, oceanographic variables and fishing effort estimates. Biomass indices of demersal fish from scientific trawl surveys carried out in the Adriatic Sea and in the Western Ionian Sea (Adriatic-Ionian macro-region, (EUSAIR, 2014) are analysed with a set of GAM approaches using as explanatory variables the relevant biogeochemical and physical variables from CMEMS products and the distribution of fishing effort from VMS/AIS data. The objective of the study is to contrast models with spatiotemporal variables only and with different sets of additional explanatory variables in order to explore the improvement on estimates of demersal species distribution when environmental variables and effort are included into species distribution models.

MATERIAL AND METHODS

I used data from the bottom trawl surveys conducted in the Adriatic Sea and North Western Ionian Sea, i.e. in the geographical sub-areas (GSAs) 17, 18 and 19 as defined by the FAO-GFCM (General Fisheries Commission for the Mediterranean Sea). I used MEDITS (Mediterranean International Trawl Survey; Spedicato et al., 2019) data from 1994 to 2018 that comprises on average 326 sampling sites (bathymetrical range 10–800 m) per year in the three GSAs and SOLEMON (Sole Monitoring; Grati et al., 2013; Scarcella et al., 2011) from 2005 to 2018, that comprises on average 70 sampling sites per year in GSA 17 (bathymetrical range 10–100 m). Indices of demersal species biomass (kg/km^2) were retrieved from the MEDITS dataset for European hake (*Merluccius merluccius*) and red mullet (*Mullus barbatus*) and from the SOLEMON dataset for common sole (*Solea solea*), mantis shrimp (*Squilla mantis*) and common cuttlefish (*Sepia officinalis*).

For each species, GAMs were applied to fit biomass indices by sampling site, set as a response variable, while spatiotemporal variables, oceanographic variables and fishing effort were tested as covariates. Among the spatiotemporal variables I used geographic coordinates (latitude, longitude expressed in UTM coordinates), depth (m), month and year of the observations. Among all the variables available from the 3D monthly CMEMS Mediterranean reanalysis fields relevant oceanographic variables were considered on the basis of known ecological importance for chosen demersal species (Bitetto et al., 2019; Carlucci et al., 2009b) as well as proxies for productivity and favourable environments. The relevant oceanographic variables considered were the water temperature (°C) and dissolved oxygen (mmol/m^3) at the sea bottom, water column averages of nitrate and phosphate concentration (mmol/m^3), chlorophyll-a (mg/m^3), particulate organic carbon (mg/m^3), pH and salinity. These variables were derived from the CMEMS dataset that covers the period 1999–2018, has a spatial horizontal resolution of 1/16° and 72 unevenly vertical levels (Simoncelli et al., 2019; Teruzzi et al., 2019). Furthermore, commercial trawling effort expressed as trawling time (in hours) per year at spatial resolution of 1/16° was estimated from VMS/AIS data for the period 2008–2018 (Russo, et al., 2014) and was tested as explanatory variable on the basis

of the evidence that fishing effort is a good track of species density. Although different time frames were initially adopted (depending on the available explanatory variables), here we report the analysis performed on the time frame 2008–2018 that allowed the complete overlap between trawl survey, CMEMS and effort datasets. The explanatory variables were preliminarily selected using the VIF approach (Variance Inflation Factor; Sheather, 2009) with a threshold of VIF<5 to avoid collinearity (Orio et al., 2017; Sion et al. 2019).
The results of the VIF analysis identified for all the species the spatiotemporal variables, i.e. year, month, depth, latitude, longitude, to be included as explanatory variables. Furthermore, the VIF analysis by species allowed to include additional explanatory variables without collinearity extracted from CMEMS reanalysis and fishing effort: the VIF results emerged as being species-specific. Thus the complete model for European hake included the spatiotemporal variables (X and Y) and the bottom temperature (TMP_bot), bottom dissolved oxygen (Dox_bot), nitrate concentration (nit), salinity (sal), bottom particulate organic carbon (poc), and fishing effort (eff). For the red mullet the following explanatory variables were retained after VIF analysis in the most complete model: month, latitude, longitude, year, depth, pH, chlorophyll-a (Chl), sea surface temperature (TMP_sst), bottom dissolved oxygen, nitrate, salinity and effort. For the common cuttlefish, the complete set of variables after VIF included month, latitude, longitude, year, depth, bottom temperature, bottom dissolved oxygen, nitrate, phosphate (pho) and effort. For common sole the complete set of variables included month, latitude, year, depth, average phosphate, bottom temperature, bottom dissolved oxygen, salinity, average phosphate, pH and effort. For mantis shrimp the set of variables are month, latitude, year, depth, bottom temperature, bottom dissolved oxygen, salinity, particulate organic carbon, pH and fishing effort (more details in Supplemetary Material Chapter 2 Supplementary material S2 and Table 2.1).

Table: 2.1. Best selected covariates for each species as final model. s indicates spline function.

Species	**Final Model**
European Hake	*R ~ s(X)+s(Y)+s(Year)+s(Depth)+s(Tmp_Bot)+s(Dox_Bot)+s(nit)+s(sal)+s(poc)+S(eff)*
Red Mullet	*R~factor (month)+s(X)+s(Y)+s(Year)+s(Depth)+s(Chl)+s(ph)+s(Tmp_sst) +s(nit)+s(Dox_bot) +s(sal)+s(eff)*
Common Sole	*R~factor (month)+s(Y)+s(Year)+s(Depth)+s(pho) +s(ph)+ s(sal)+ s(Dox_bot)+ s(Tmp_bot)+s(eff)*
Mantis Shrimp	*R~factor(month)+s(Y)+s(Year)+s(Depth)+s(Sal)+s(Tmp_bot) +s(poc)+s(ph)+s(Dox_bot)+s(eff)*
Cuttlefih	*R~factor(month)+s(X)+s(Y)+s(Year)+s(Depth)+s(Tmp_bot)+s(Dox_bot)+s(nit)+s(pho)+s(eff)*

Different GAM distribution families were applied in order to demonstrate the potential benefits of using additional variables disregarding the model structure. GAMs were developed using Gaussian probability distributions with identity link on trawl survey biomass data log-transformed for all species, except common cuttlefish, for which better results were obtained by using square root transformation. GAMs were also applied using Tweedie probability distributions with lognormal link on untransformed biomass indices. Furthermore, the Delta-GAM approach was implemented in two steps: (i) a binomial occurrence model was used to fit presence/absence data (binomial family error distribution logit link function), (ii) a Gaussian distribution model with identity link function on transformed biomass for presence-only data (Grüss et al., 2014; Lauria et al., 2017). A grid of regular points with the same resolution of the selected CMEMS product (1/16°) and covering the study area was created to predict species biomass distribution by the selected models (Spedicato et al., 2019; Tserpes et al., 2019). For Delta-GAM the final spatial distribution of species biomass as kg/km^2 is obtained by multiplication of Gaussian and Binomial models' predictions to the grid of the model's domain (Grüss et al., 2014; Lauria et al., 2017).

For each species and all GAMs distribution families (Delta, Gaussian and Tweedie), a back-stepwise approach was used. This started from the most complete integrated approach, given by the spatiotemporal variables (geographical coordinates, depth, year, month) combined with all the most meaningful additional biogeochemical, physical and fishing effort variables identified by VIF analysis (model 0). Then the back-stepwise approach consisted in decreasing the number of explanatory variables by successively removing those with lower F statistics until the model with spatiotemporal variables only was obtained. Thus, the back-stepwise approach resulted in a set of models having different explanatory variables to obtain the response variable ($R = \log$ kg/km^2 or presence/absence) (see SM, chpaterS2). Each model was subjected to a calibration-validation process, thus it was fitted on a training dataset made by randomly choosing 70% of the data (calibration) and testing it on the remaining 30% of records (validation). The training and testing were repeated using 50 runs on datasets randomly selected and without replacement. The best model was selected on the basis of measures of model performance evaluated through explained deviance (%ED) and prediction errors (AIC, Akaike Information Criterion) on the training datasets as well as correlation coefficient (R^2) of the model predictions on the test dataset.

For each model with decreasing number of explanatory variables (model 0, model 1, model 2, etc.), the mean of each measure of model performance (%ED, AIC, R2) was calculated from the 50 runs and compared using Tukey's test (Tukey, 1949). This comparison allows to assess the improvement of performances when different sets of additional variables were used in the models. The best model was chosen based on AIC, but other measures of performance were reported to show their general consistency.

The model chosen for each species was used to generate maps of biomass distribution (kg/km2) in the most important months (July and November for the MEDITS and SOLEMON species, respectively). These maps were used to identify areas of high biomass density (hotspots) in GSAs 17, 18, and 19. In addition, a set of spatial indicators (Woillez et al., 2009) allowed comparison of model performance in describing the spatial distribution of demersal species when additional explanatory variables were or were not included. The indicators are the dispersal area (SA), i.e., a measure of the area occupied by the population weighted by biomass; the latitude of the centroid of the data (CGY), which represents the mean geographic location of the population; the longitude of the centroid (CGX); the distance (D) between the centroid estimated from observations and the centroid estimated from predictions (Rufino et al., 2018; Woillez et al., 2009). Distributional statistics (first and third quartiles, median) and performance indicators (mean absolute error MAE and R2) were also estimated. Comparison of such indicators estimated from raw trawl survey data, from models based only on spatiotemporal variables, and from the selected best models using the full set of significant variables allows quantifying the improvement of the application of the integrated approach, i.e., embedding biogeochemical, physical, and fisheries factors in the species distribution models

RESULTS AND DISCUSSION

For European hake, mantis shrimp and common cuttlefish the Delta-GAM models were performing better while for the red mullet and common sole the best results were obtained using the Gaussian model and Tweedie, respectively (details are reported in Supplementary material). Figure 2.1 shows measures of performance (%ED, AIC, R2) resulting from the back-stepwise approach applied to the most appropriate family of GAM models for each species (only Delta-Gaussian is reported in the figure for European hake, mantis shrimp and common cuttlefish; the full Delta-GAM results for these species are reported in Supplementary material). Results for the 50 trials of training/testing demonstrate the model improvements when using CMEMS and effort variables in GAMs (Tukey's tests are reported in SM, Chapter 2 Supplementary material).

For European hake, the average AIC for Delta-Gaussian increased from 5600 for the model including the complete set of variables (model 0, panel I) to 5700 for the minimal model with spatiotemporal variables only (model 6, panel I). Coherently, the average %ED decreased from 0.32–0.29, and R^2 decreased from 0.24–0.23 from model with complete set of variables to model with spatiotemporal variables (Figure 2.1, panel I). For red mullet AIC increased from 6950 to 7340, %ED decreased from 0.57–0.47 and R2 decreased from 0.12–0.09 from the complete to the minimal model (Figure 2.1, panel II). For mantis shrimp AIC increased from 350 to 420, %ED decreased from 0.55–0.37, and R2 decreased from 0.44–0.38 from the complete to the minimal model (Figure 2.1, panel V). For common cuttlefish and common sole (panels III and IV) the differences in AIC and R2 are less marked when moving from the complete model (0) to the model with spatiotemporal variables (model 5 and 6) but yet the improvement is appreciable in terms of %ED. For all species analysed, the training/testing approach highlighted that best performances in terms of capabilities to represent trawl survey biomass data (ED% and R2) and performance indicators such as AIC were obtained when the integrated approach was used, i.e. when the spatial model for species distribution included biogeochemical, physical and fishing effort as additional explanatory variables (model 0).

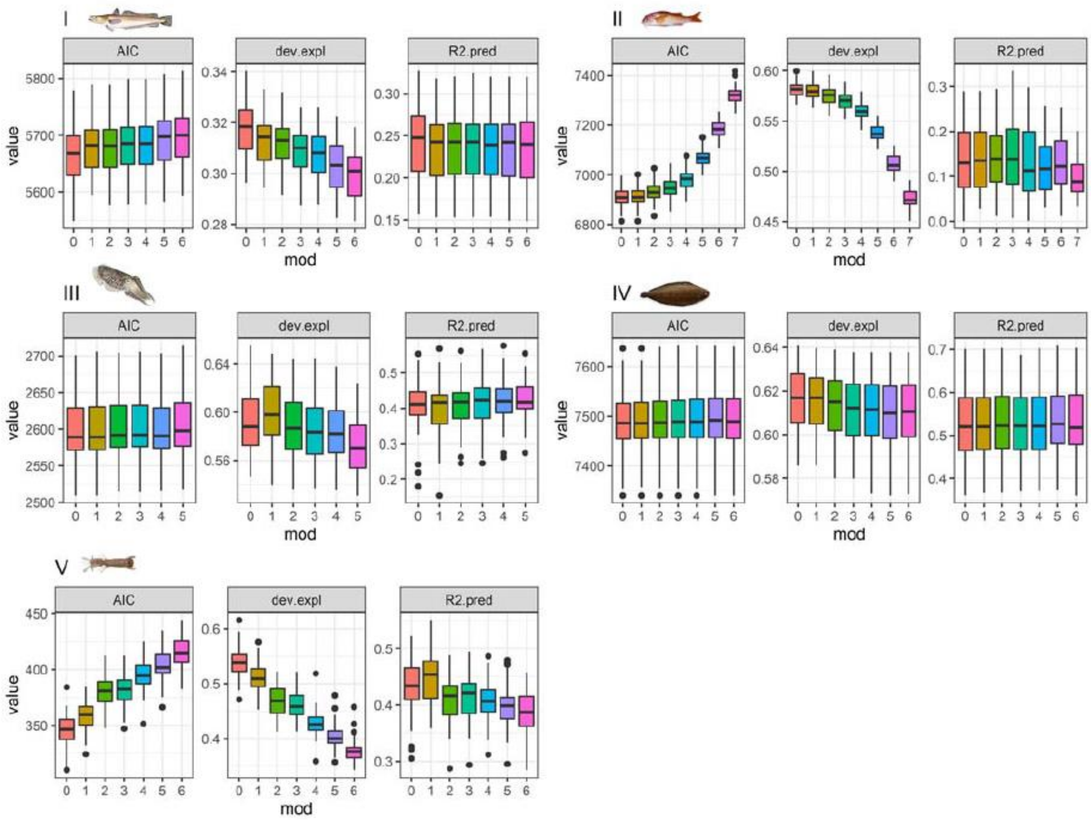

Figure 2.1: Performances of the best GAMs in describing the distribution of demersal species for models using a decreasing number of explanatory variables. The best model was Delta-GAM for European hake, common cuttlefish and mantis shrimp (shown the Delta-Gaussian in panels I, III and V, respectively), Gaussian for red mullet (panel II) and Tweedie for common sole (panel IV). For all species the starting model represents the one (model 0) including all the covariates resulting from VIF analysis and including spatiotemporal variables, environmental CMEMS variables and fishing effort. Successively one variable at each step is removed to reach the minimal model (model 6 for European hake, common sole and mantis shrimp; model 7 for red mullet; model 5 for common cuttlefish) with spatiotemporal variables only. Box-plots synthesise results of the 50 runs of the training/testing procedure in terms of Akaike Information Criterion (AIC), explained deviance (dev-expl) on the 70% training dataset and correlation coefficient (R2) for the remaining testing dataset.

For each demersal species the best model has specific significant covariates in addition to spatiotemporal variables. Bottom temperature, bottom dissolved oxygen, salinity, particulate organic carbon, and fishing effort resulted significant variables for European hake. The same variables and pH resulted significant for mantis shrimp. Chlorophyll-a, pH, sea surface temperature, bottom dissolved oxygen, nitrate and effort were significant for the red mullet. Bottom temperature, bottom dissolved oxygen, and phosphate for the common cuttlefish. Average phosphate and salinity were significant for common sole (more details in the SM – Chapter 2 Supplementary material).

Figure 2.2 shows distribution maps for the years 2008–2018 as obtained by the best complete model for European hake and red mullet based on MEDITS trawl survey data. For European hake (Figure 2.2 , left panel) the maps highlight higher biomass in 2008 and 2018, hot spots of biomass (as high as 100 kg/km^2) in the central-eastern part of the Adriatic Sea in recent years (particularly in 2018), low biomass of this species, especially in the northern part of the basin, and a prevalence of a north–south gradient. For the red mullet (Figure 2.2, right panel) results show that high biomass (up to 200 kg/km^2, particularly in years 2017/2018) is associated to coastal strip in the western part of the basin, while in the eastern part biomass is more widely distributed with a prevalence of south–north gradients. The application of the best complete GAM model for common cuttlefish, common sole and mantis shrimp based on SOLEMON trawl surveys result in distribution maps reported in figure 2.3. The hot spot for common cuttlefish is consistently identified in the North-East Adriatic, in front of the Istrian peninsula, with highest biomass (peaks of 2000 kg/km$^{2)}$ especially in 2008 and 2014 (figure 2.3, left panels). Common sole is showing higher densities along the North-western coast of the Adriatic, but high biomass is obtained also in the central part of the Northern Adriatic in recent years (2016–2018; central panels). The mantis shrimp resulted to be mainly distributed along the North-western coast in the area interested by the Po river plume with biomasses as high as 1500 kg/km^2 especially in the years 2011, 2012, 2018 (figure 2.3, right panels).

The spatial and temporal distributions shown are coherent with previous results (Sartor et al., 2017). For example, results from Sion et al. 2019 on European hake show for 2011 and 2013 higher biomass values in the eastern-central Adriatic sea, while in 2015 a general lower biomass of this species was estimated, with similar outcomes to the ones I found in this paper (Figure 2.2). Tserpes et al. 2019 also highlights a biomass increasing trend for red mullet after 2008, which is in line with the recent stock assessment outcomes (GFCM-FAO et al., 2020; Ulrich et al., 2019, SAC, 2022). Similarly, Figure 2.2 highlights that this biomass increase corresponds to a spreading of the population in the study area.

The set of indicators for evaluating performance of the complete (model 0) or spatiotemporal (model 6 or 7) models contrasted with observations show that the integrated approach embedding biogeochemical, physical and fishing effort variables has improved performance (Table 2.1). In particular, indicators in Table 2.1 suggest that models' distribution statistics (quartiles and median) are closer to observed data when the integrated approach is used (i.e. the model 0). Exceptions are the first quartile for common sole, the third quartile for common cuttlefish, and the median for mantis shrimp. It is worth to note the relevant improvement of median values for hake and cuttlefish (+55% and +53%, respectively) when the spatial model of species distribution includes additional biogeochemical, physical and fishing effort data (Table 2.1). MAE and R^2 showed that consistency of model to the data improves for all species (except R^2 for European hake) when additional variables are included (Table 2.1). The spatial indicators used to evaluate the modelling results in terms of variations of the area occupied by the populations and their mean geolocation (Woillez et al., 2009) show improvements for red mullet, common sole, and mantis shrimp when the models include additional biogeochemical, physical and effort variables. For all these species the centroids of spatial distribution and the spreading area of the best model (model 0) are closer to those estimated on the observed data than to models with no additional explanatory variables (model 6 or 7; Table 2.2). For European hake and common cuttlefish, the spreading area improved when additional explanatory variables are included, but not the centroid position. This result and some low improvements of model 0 with respect to the model with spatiotemporal variables only is possibly related to complex influences of other environmental factors such as seabed type and habitats on the spatial distribution of species (in particular for European hake and common cuttlefish). Overall, the approach quantified the relevance of biogeochemical and physical variables derived from CMEMS and fishing effort from VMS/AIS in improving the spatial distribution of demersal species based on trawl survey data. Results highlight species-specific improvements that should be considered also in relation to the use of spatial distribution model (Brodie et al., 2020)

Table 2.2. Comparison among indicators calculated on observations, i.e., the original trawl survey data, on the results of the best GAM model without additional explanatory variables (model 6 or 7) and results of the best GAM model including additional biogeochemical and physical variables and effort (model 0). Distribution indicators (first and third quartile, median), performance indicators (MAE, R2), and spatial indicators such as Spreading area (SA), latitudinal centroid (CGY) longitudinal centroid (CGX) and distance of the centroid of the model to that of data are reported for the five demersal species analyzed. The column "improvement" reports the improvement in the indicator value when using the model with environmental variables concerning indicator calculated on results of the model without additional variables (observations-model 0/observations-model 6 or 7).

	Red mullet				Cuttlefish			
	Observations	Model 7	Model 0	improvement	Observations	Model 6	Model 0	improvement
1st.Qu	0	3.11	2.38	23%	0	9.2	6.13	33%
Median	1.95	8.48	7.91	18%	133.48	116.22	125.45	53%
3rd.Qu	23.55	20.36	23.88	19%	558.44	474.37	465.51	-10%
R2	-	0.08	0.15		-	0.56	0.61	
MAE	-	39.97	36.89		-	240.96	227.83	5.44%
SA	701.6	1142.5	1094	11%	235.8	273.21	272.51	1.87%
CGX	15.52	15.98	15.73	55%	13.3	13.29	12.28	
CGY	42.59	42.52	42.8	-	44.66	44.74	44.75	-12.50%
distance	0	38.68	29.53	24%		9.43	10.2	-8.16%
	European hake				Mantis shrimp			
	Observations	Model 6	Model 0	improvement	Observations	Model 6	Model 0	improvement
1st.Qu	2.99	3.75	3.67	11%	0	2.65	1.22	54%
Median	15.75	13.68	14.82	55%	36.91	25.23	24.5	-6%
3rd.Qu	34.68	25.96	26.33	4%	326.95	90.19	115.48	10%
R2	-	0.32	0.32		-	0.3	0.46	
MAE	-	16.13	15.94		-	202.69	169.76	
SA	1552.02	2272.55	2263.34	1.30%	192.95	352.34	267.37	53%
CGX	16.18	16.18	16.16	-	13.01	13.15	13.01	100%
CGY	42.09	42.18	42.19	-11%	44.26	44.15	44.23	72%
distance	0	10.89	11.83	-8.63%		16.99	2.93	82%
	Common sole							
	Observations	Model 6	Model 0	improvement				
1st.Qu	127.07	103.43	92.21	-47%				
Median	439.64	296.35	302.75	4.46%				
3rd.Qu	1155.34	717.12	728.82	2.66%				
R2	-	0.35	0.44					
MAE	-	538.92	491.55					
SA	311.66	447.79	403.05	32%				
CGX	12.98	13.01	12.97	133%				
CGY	44.57	44.6	44.6	0				
distance		16.99	2.83	83%				

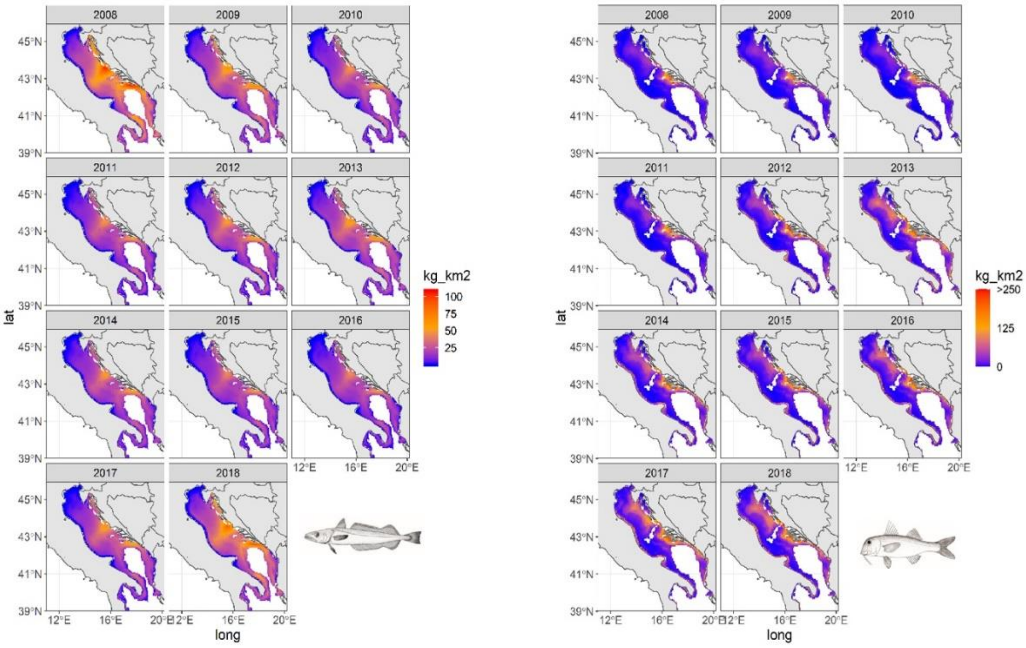

Figure 2.2: Yearly maps of estimated biomass (kg/km2) of European hake (left) and red mullet (right) in the Adriatic and Western Ionian Sea (GSA 17-18-19) obtained with the best GAM model applied on MEDITS trawl survey data for years 2008– and with all the additional environmental and effort variables (model 0).

Key objectives of the Common Fisheries Policy (EC, 2013) are the achievement of MSY in the short term and the implementation of an ecosystem approach to fisheries management which is often based on fishery independent data. Furthermore, for EU (Italy) and non-EU countries contracting parties (Croatia, Montenegro, and Albania) involved in the area of study, the GFCM recommendations, and particularly with the objectives set out in the GFCM 2030 strategy, regarding sustainable fisheries and aquaculture in the Mediterranean and the Black Sea, consolidating a regional regulatory framework based on the implementation of management plans for key fisheries, fisheries restricted areas (FRAs) and measures to minimize the incidental catch of vulnerable species and maximize the productivity of commercial marine living resources.

Thus I consider that the integrated approach proposed here represents an important step for incorporating anthropogenic (fishing effort) and other environmental stressors (biogeochemical and physical variables) into the advice for fisheries management.

The improved models including environmental and effort variables, in fact, can be used for year by year evaluations of species distribution, for explaining and understanding species displacement. This is of paramount importance for a spatially based management of the resources that relies upon the identification of best fishing grounds, spawning or nursery areas, and generally aiming at defining fisheries managed areas (Lauria et al. 2017). The improved accuracy of species distributions based on environmental and effort variables as obtained in this study can potentially support co-management initiatives involving fisheries organisations and other stakeholders (e.g. those carried out by the Mediterranean Advisory Council, MEDAC). In particular, sharing such outcomes with the bottom trawl industry could lead to an increase in the awareness of the sector and consequently to the reduction of the alarming footprint of the fisheries in the Adriatic and Western Ionian Seas (Amoroso et al., 2018).

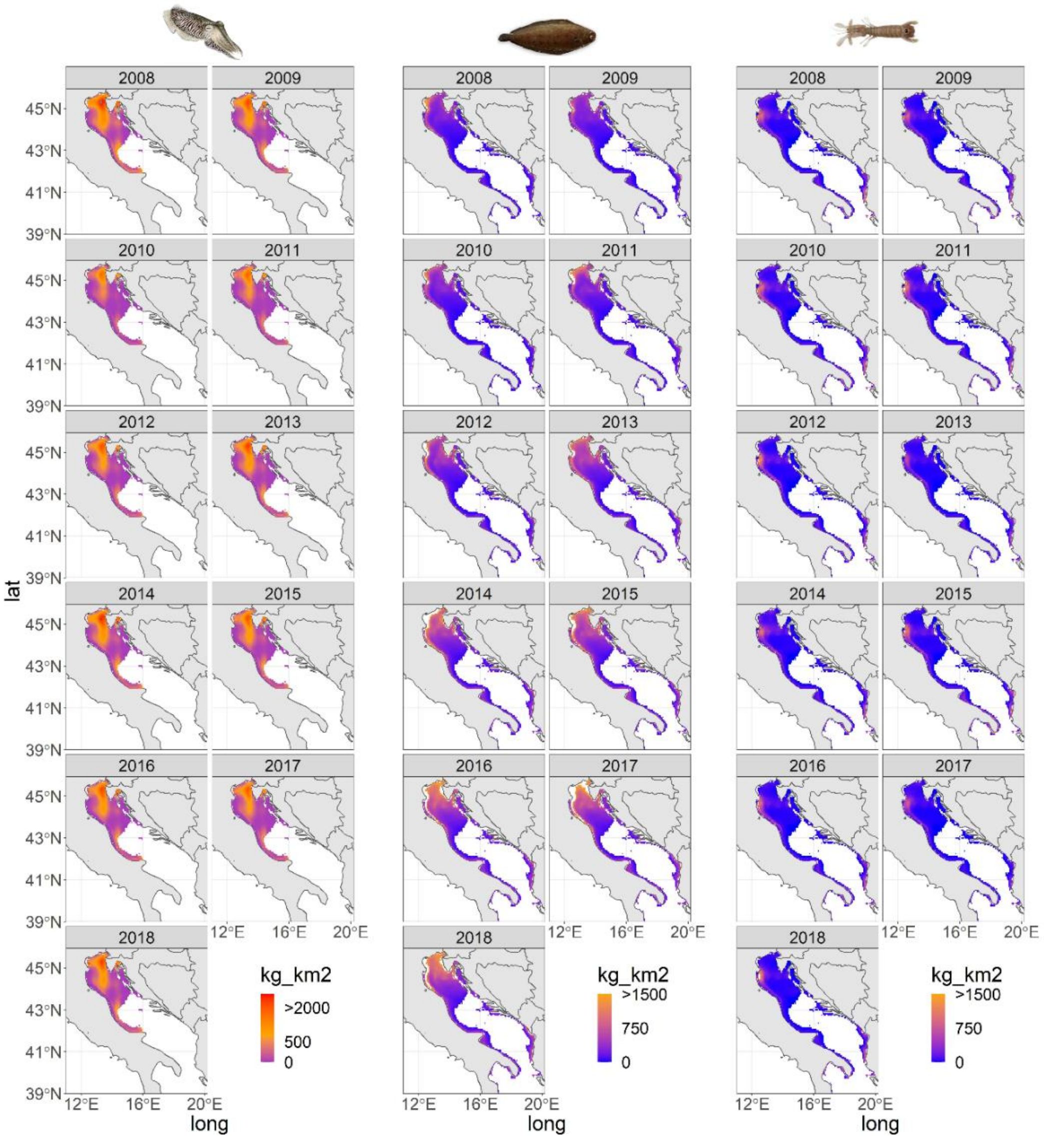

Figure 2.3. Yearly maps of estimated biomass (kg/km2) of common cuttlefish (left), common sole (centre) and mantis shrimp (right) in the Adriatic Sea (GSA 17-18) obtained with the best GAM model applied on SOLEMON trawl survey data for years 2008–2018 (Product Ref. 3.6.4) and with all the additional environmental and effort variables (model 0).

Furthermore, it is largely acknowledged that most of the presently used stock assessment models are too simplistic since they often consider species populations without integrating the role of key environmental drivers, which is a challenging but crucial frontier in the time of global changes. Taking into consideration environmental factors is also pivotal for the MSY objective, as climate change impacts on the fish community would require moving below fishing mortality at FMSY to ensure sustainable exploitation of marine stocks (Travers-Trolet et al., 2020). An optimised approach for the analysis of trawl survey data is relevant for the stock assessments and advice provided by Scientific Advisory Committee for fisheries of the General Fisheries Commission for the Mediterranean Sea (SAC-GFCM) and the Scientific, Technical and Economic Committee for Fisheries (STECF) of the European Commission, as fisheries-independent data are essential for fishery management. The prediction of biomass indices on the whole domain over time with the integrated models proposed here takes into account the influence of relevant oceanographic variables and could be appropriately used for tuning stock assessment models such as, for example, surplus production models that need the catch time series and the survey abundance aggregated indices.

Since most analytical stock assessment models use survey indices by age or length as tuning indices, a further step for future insights is represented by the modelling in similar way also demographic indices, as length and/or age. Moreover, modelling of demographic indices can be useful also for progressing on the geolocation of sensitive life stages of the species, thus addressing further key questions of spatial fishery management.

These spatial distribution models for demersal species were developed for the best extension of trawl survey data to the whole study area from 2008 to 2018. The approach developed here highlights the relevance of integrating oceanographic variables in the analysis of trawl survey data before their use as inputs in stock assessment (Cao et al., 2016) and ecosystem modelling (see for example, (Canu et al., 2010; Grüss et al., 2014, 2018). This approach sets the basis for providing projections of the potential effects on species distribution and biomass of future environmental changes.

Applying the identified best GAMs models for making future predictions of species distribution is facilitated by the availability of oceanographic variables under future scenarios of climatic changes and appears strongly conditioned to assumptions on the future distribution of fishing effort that are also dependent from policies and regulations. Therefore, using the models developed here for making future scenarios might be considered with caution, needing further specific investigations of model validity to changed conditions. Yet the models can still provide a first order approximation of potential large scale effects, such as displacements of biomass centre of gravity and spreading area due, for example, to climate change. Although the relative distribution pattern might be well predicted by the model, many factors, such as recruitment success and species interactions for example are not included, thus efforts should be addressed in the future for testing additional modelling approaches and for improving the accuracy of these species distribution models.

In conclusion, the present study aims at investigating the influence of environmental variables on the biomass distribution of the most important commercial fishery species in the Adriatic and Western Ionian basin by modelling the data obtained from trawl surveys using different GAM approaches. GAMs are commonly used because they have the advantage of accounting for spatial and temporal autocorrelation of the data. The approach used here robustly demonstrates in which cases oceanographic variables extracted from CMEMS products and effort from VMS/AIS, result in improving species distribution models. Although there is still room for improvements, the work presented here is a remarkable starting point for better understanding species-environment relationships and for understanding the benefits of integrating the CMEMS variables into the modelling of fishery independent data for predicting the species distribution in the Adriatic and Ionian basins.

Acknowledgements

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Chapter 3

Procedure in e-SDMs

Defining a procedure for integrating multiple oceanographic variables in ensemble models of marine species distribution.

INTRODUCTION

Species Distribution Models (SDMs, (Zimmerman & Guisan, 2000), are largely used in biology and ecology to map the potential distribution of species based on geopositional and environmental data (Brodie et al., 2020). SDMs are applied at different scales (local, regional, global), trying to represent species distribution, by implementing a range of methods on density (e.g. number of the individual), presence/absence, or biomass (Barcala et al., 2019). Many statistical techniques are commonly used in the SDMs, from regression method (linear models LMs, Generalised Linear Models, GLMs, or Generalized Additive Models, GAMs; (Maravelias et al., 2003; Olden & Jackson, 2002), to machine learning method (Random Forest, RF or neural networks models, NNMs, (Breiman et al., 2018). The model's predictive performance depends not only on the intrinsic mathematical approach but also on species characteristics or species and environment link (Santika & Hutchinson, 2009), sample size, the aim of the study, spatial scales (Wisz et al., 2008), and considering the availability of data. In marine systems, SDMs are increasingly applied for example, for explaining and predicting the expansion of invasive species (D'Amen & Azzurro, 2020), for showing the effects of climatic changes on ecologically key species (Franceschini et al., 2018), and for describing the distribution of exploited and vulnerable species using trawl survey data (Barcala et al., 2019; Lauria et al., 2017). Scientific bottom trawl surveys provide quantification of abundance and biomass (hereafter termed indices) by species, i.e., fishery-independent data, that are used for manifold purposes related to management: stock assessment, evaluation of the spatio-temporal distribution of demersal resources (Carlucci et al., 2018), estimates of population and community densities (e.g., (Mérigot et al., 2019; Spedicato et al., 2019) and the development of ecosystem models (e.g., (Grüss et al., 2018; Moullec et al., 2019). Despite the sampling protocols of multiannual surveys are usually standardized for sampling design, gear geometry, sampling season, and sampling locations to allow comparability of the trawl survey data across space and time, some changes may unavoidably occur. For most of the uses described above, there is, thus, the need to evaluate the impact of these deviations (e.g., sampling period or sampling location) or changes (e.g., vessel) on the abundance and biomass indices obtained from trawl surveys (Thorson et al., 2015).

Further, some approaches successfully include environmental changes and anthropogenic stressors as drivers to explain species distribution and infer future changes (Moullec et al., 2019b; Robinson et al., 2017). Satellite data are successfully used to provide environmental variables (e.g. sea surface temperature; sea surface chlorophyll concentration) to be included in SDM (Giannoulaki et al., 2008; Schismenou et al., 2017), taking advantage of the growing effort provided by the Copernicus Marine Environment Monitoring Service (CMEMS; e.g., (Sion et al., 2019; Tserpes et al., 2019) in producing 3-dimensional oceanographic variables. The growing number of SDM applications and approaches would benefit from a robust methodological approach aiming at i) testing different SDM approaches coherently also through the development of ensembles of models; ii) developing statistically sound and robust protocols for training and testing SDMs over data also evaluating progressive inclusion of meaningful explanatory variables. Furthermore, these models are deemed appropriate for mapping species distribution that is useful in ecosystem models (Grüss et al., 2014), or for identifying Essential Fish Habitats (Druon et al., 2015). This work aims at presenting a robust statistical protocol applied to the development of an ensemble of SDMs for marine demersal species, integrating relevant oceanographic variables and indices of anthropogenic pressure (e.g., fishing effort). We use the European hake (*Merluccius merluccius*), an important species in the Mediterranean Sea (FAO, 2022), particularly in the Adriatic and

Ionian Sea to show the suitability of the proposed approach, combining scientific trawl surveys data, relevant biogeochemical and physical variables from CMEMS products and the distribution of fishing effort from VMS/AIS data. The procedure utilizes spatial training and test data sets, metrics, and statistics, trying different models and approaches, contrasting models with spatiotemporal variables only, and with different sets of additional explanatory variables to explore the improvement on estimates of the distribution of marine species.

MATERIALS AND METHODS

A. *Study area*

The study area is the Adriatic Sea and the North-western (NW) Ionian Sea, situated in the northeast/east part of the Mediterranean Sea. The corresponding Geographic Sub Areas (GSA) are 17-18 and 19, as defined by the FAO GFCM (General Fisheries Commission for the Mediterranean Sea). Bathymetry data retrieved for our study ranged from 10 to 800 meters. The map of the distribution of the species ranged from 12'.00" E and 20'.00" E for longitude and 39.5'.00" N and 46'.00" N for latitude. The Northern Adriatic Sea is the shallower part of the Adriatic epi-continental shelf, with maximum depths of less than 70 m and a mean depth of 30 m, with seasonal variation of temperature and salinity conditions (Boldrin et al., 2005). The central part of the Adriatic basin is characterized by a meso-Adriatic depression, called Jabuka/Pomo Pit, reaching 260 m depth which is subjected to fishing activity restrictions coincident with a Fisheries Restricted Areas (FRAs) (FAO, 2022). The southern part of the basin (GSA 18) is characterized by a steep continental slope with the deepest bathymetry at 1250 m. The water mass circulation is characterized by a cyclonic gyre. (Civitarese et al., 2010). The NW Ionian Sea (GSA 19) is divided by the Taranto Valley into an eastern sector represented by a broad continental shelf and a south-western sector where the shelf is generally very limited and many submarine canyons are located along the coasts (Maiorano et al., 2010). GSA 19 covers a surface of about 16,500 km2 included between 10 and 800 meters in depth.

B. *Survey data*

The occurrence record for European hake was derived from the surveys conducted in the Adriatic Sea and NW Ionian Sea, in the geographical sub-areas (GSAs) 17, 18, and 19. I used MEDITS (Mediterranean International Trawl Survey) (Spedicato et al., 2019) data, which consists on average of 326 sampling sites per year in the three GSAs. I considered the period from 2008 to 2018 (a subset of the entire time series 1994-2018 MEDITS) due to the employment of the effort data (see C. effort data).

I used density indices (n/km2, n=number of individuals, km2=squares kilometers) to represent the distribution of European hake, one of the most important and commercially exploited species by otter trawl fishery in the Adriatic Sea (Soldo, 2015). Moreover, this species was selected for its biological and ecological role (FAO, 2020b; Maiorano et al., 2010; Soldo, 2015; Zorica et al., 2020).

C. Effort: see subsection of Chapter 1: Abiotic factors: Effort

D. *Oceanographic variables*

Among all the available variables from the 3D monthly CMEMS Mediterranean reanalysis fields (Teruzzi et al., 2019) relevant oceanographic variables were considered based on known ecological importance for the chosen demersal species (Bitetto et al., 2019; Carlucci et al., 2018) as well as proxies for productivity and favorable environments. The relevant oceanographic variables considered were (with respective model abbreviation): i) water surface temperature (°C, TMP_sst), ii) water bottom temperature (°C, TMP_bot), iii) dissolved oxygen at the sea bottom and surface ($mmol/m^3$, dox_bot), iv) water column averages of nitrate and phosphate concentration ($mmol/m^3$, nit & pho), v) chlorophyll-a (mg/m^3, chl), vi) bottom particulate organic carbon (mg/m^3, poc), vii) pH at the sea bottom (ph), viii) surface salinity (sal). These variables were derived from the CMEMS dataset that covers the period 1999-2018, has a spatial resolution of 1/16° and 72 unevenly vertical levels (Simoncelli et al., 2019; Teruzzi et al., 2019), and we used the data from 2008 to 2018.

E. *Models*

To test the potential benefits of using oceanographic and effort variables in addition to spatiotemporal covariates (UTM coordinates – east and north, - E.utm & N.utm respectively, depth, year, and month) for improving species distribution models based on trawl survey data, Generalized Additive Models (GAMs), Random forest (RF) (Breiman et al., 2018), and Gradient Boosting machine, (GBM) (Schapire, 2003), were chosen for their wide application and suitability with this type of data (Grüss et al., 2014; Lauria et al., 2017; Tserpes et al., 2019). I fitted indices of n/km2 by sampling site, set as a response variable, while explanatory variables tested were: i) geoposition variables (haul survey position expressed in UTM, easting (E.utm), and northing (N.utm) in km, ii) additional oceanographic variables; iii) fishing effort variables (eff_OTB). Among the minimal combination of variables, I used geographic coordinates (in UTM), depth (m), and the year of the observations.

To obtain an SDM I applied five different approaches that include: GAM, RF and GBM. In the case of GAM, I applied different distribution families to demonstrate the potential benefits of using additional variables disregarding the model structure. GAMs were developed using Gaussian probability distributions with identity links on log-transformed density data. GAMs were also applied using Tweedie probability distributions with a log-normal link on untransformed density indices. Furthermore, the Delta-GAM approach was implemented (See details in Chapter 2): RF is a Machine Learning technique that fits an ensemble of Classification Trees and combines their predictions into a single model (Breiman, 2001). For each tree in the forest, the algorithm starts selecting a subset from the training data, i.e., a bootstrap sample. The data not included in the current bootstrap sample are called Out-Of-Bag (OOB) records. For each bootstrap sample, a tree is grown by default to the maximum depth and left unpruned. This procedure is repeated *ntree* times, the latter is the total number of Classification Trees in the forest. Finally, the overall output of a RF is obtained based on the majority voting for classification tasks and by averaging the outcomes of all the trees for regression applications (Breiman et al., 2018). In this work I applied 5000 trees on data log-transformed, with a minimum number of variables for each split equal to 1/3 of the explained variable (R package randomForest), (Breiman et al., 2018).

Finally, Generalized Boosted Regression Models (GBMs) are a type of ensemble learning method for regression and classification problems. They work by combining the predictions of multiple "weak" models, such as decision trees, in a manner that reduces the overall error. The basic idea behind GBMs is to iteratively train weak models, with each model trying to correct the mistakes of the previous model. The process starts by training a simple model (such as a decision tree) on the data. The model's predictions are then used to compute the residuals (i.e., the difference between the true values and the predicted values). A new model is then trained on the residuals, and its predictions are added to those of the previous model. This process is repeated for several iterations, with the final model being the sum of the predictions of all the individual models.

The key to GBMs is the use of boosting, which is a technique that iteratively improves the performance of the model by giving more weight to observations that were misclassified in previous rounds. This allows the model to focus more on the difficult examples in the dataset, leading to improved performance overall.

For the GBM approach, I applied 10000 trees with a shrinkage of 0.01 (gbm package R, https://github.com/gbm-developers/gbm). The models used in this study have been already described and discussed in several publications (Breiman et al., 2018; Evans et al., 2011; Friedman, 2001; Ridgeway, 1999), I refer the reader to this literature for further information.

F. *Protocol for training and testing an ensemble of integrated SDMs*

A grid of regular points with the same resolution as the selected CMEMS product (1/16°) and covering the study area was created to predict species density distribution by the selected models (Spedicato et al., 2019; Tserpes et al., 2019). The explanatory variables were preliminarily selected using the VIF approach (Variance Inflation Factor) (Sheather, 2009) with a threshold of $VIF < 5$ to avoid collinearity (see also Orio et al., 2017; Sion et al., 2019). The results of the VIF analysis include year, depth, northing, and easting coordinates, as explanatory variables and constituted the minimal spatiotemporal model (ST). Furthermore, the VIF analysis allowed the inclusion of additional explanatory variables without collinearity extracted from CMEMS reanalysis and fishing effort. Thus the complete model is shown in table 3.1. For each approach (Delta, Gaussian, Tweedie, RF, and GBM), a forward stepwise approach was used. This started from the simplest model given by the minimal spatiotemporal explanatory variables (model A, with northing, easting, depth, and year) to combine it with all the most meaningful additional biogeochemical, physical, and fishing effort variables (from model C to L), identified by VIF analysis. Then the forward– stepwise approach consisted of increasing the number of explanatory variables by successively adding those with higher F statistics (derived from summary statistics of the fitting models, F-test ANOVA) until obtaining the model with full explanatory variables. Thus, the forward-stepwise approach resulted in a set of models having different explanatory variables of the response variable. Each model was subjected to a calibration-validation process, thus it was fitted on a spatial training dataset made by randomly choosing 70% of the data (calibration) and testing it on the remaining 30% of records (testing). The training and testing were repeated using 5 spatially data-set (fig. 3.1) on datasets randomly selected and without replacement, using the BlockCV package (Valavi et al., 2019). The best model was selected based on measures of model performance such as explained deviance (%ED) and prediction errors (AIC, Akaike Information Criterion) of the training datasets; correlation coefficient (R^2) and mean absolute error (MAE) of the model predictions on the testing dataset (fig. 3.2). Furthermore, the validation process includes an application of the best model for each approach on the observed data (fitting and prediction on the same data) and an evaluation of MAE and R2. Finally, I obtained an ensemble model where each best model for each approach is weighted on the respective R2 derived from the validation process. The ensemble model is used to obtain maps of the density distribution (n/km2) for each year that allow identifying areas of high biomass density (hot-spots) in the GSAs 17, 18, and 19.

I represent in this work the ensemble model with spatial temporal variables, with and without effort, and environmental variables, to highlight the relative differences between the two approaches.

G. *Errors*

The predicted values on a grid of regular points (with the same resolution of the selected CMEMS product 1/16°) covering the study area are compared with the data surveys. The model error from the ensemble model is defined as the percentage value of the absolute difference, eq.1:

$$\frac{\sum_{j=1}^{n}\left(\left(\frac{\left|y_{i,j}-x_{i,j}\right|}{x_{i,j}}\right)*100\right)}{n_j} \qquad (1)$$

Where j is the j-th year of the predicted values, n the number of data for j-th year, yi is the predicted value on the grid and xi is the survey data, i is the i-th value of the haul survey or predicted value.

RESULTS

I identified the best model for each approach (table 3.1). Our results showed that the best model includes different environmental variables based on the respective approach, identified by the spatially training and test data set, in which each fold is running by 9 different models. Furthermore, the metrics for the best model for each approach, for the entire data set of European Hake, are shown in table 3.2.

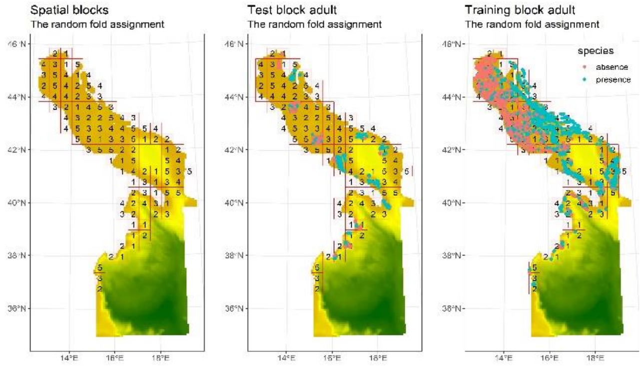

Figure 3.1. Spatially training and testing example for European hake of spatial blocks (from package BlockCV R). Left panel: subdivision of the study area in blocks for 5 fold. Central panel: test blocks for fold 1, Right panel: training plot for the remaining fold: 2,3,4,5.

Table 3.1. The best model for each approach. acronymous: R= response variables: presence/absence for delta-binomial, n/km2 for tweedie, log-n/ km2 for others models. spline function for GAM models is indicated as s(…). for the other acronyms see cap. models and effort.

Approach	Best model
Delta-binomial	R ~ s(E.utm, N.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Delta-gaussian	R ~ s(E.utm, N.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Gaussian	R ~ s(E.utm, N.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot)+ s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho).
Tweedie	R ~ s(E.utm, N.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
RF	R ~ (E.utm) + (N.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)
GBM	R ~ (E.utm) + (N.utm) + (year) + (TMP_bot) + (depth) + (dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)

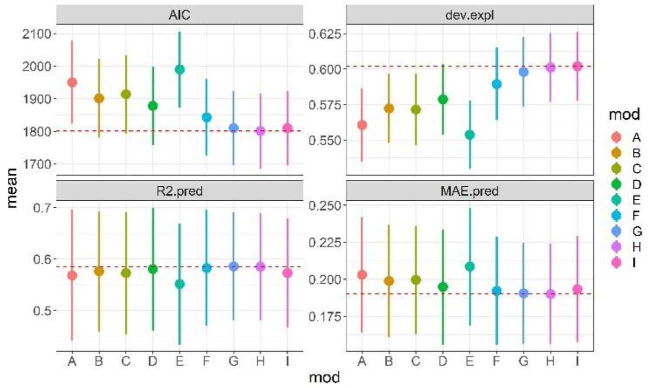

Figure 3.2. Example of result from delta-binomial approach for the 9 models running for the 5 spatially training and testing fold. AIC=Akaike information criterion on testing data set. Dev.expl= Explained deviance on testing data set. MAE.pred= Mean absolute error for predicting test fold. The red dotted line coincides with the best model for each metric (For AIC and MAE, small is better, and vice versa doe dev.expl) On x-axes the models the model used, see bottom table).

Table 3.2: all formulas used for training and test routine. All the abbreviation is explained in the previous sub-chapter of chapter 3 (D. Oceanographic variables). Between formula tested is included a model with depth and temperature interaction (model H)

Model	Formula
A	PA ~ s(E.utm,N.utm)+s(year)+ s(depth)
B	PA ~ s(E.utm,N.utm)+s(year)+ (depth)+s(TMP_bot)
C	PA ~ s(E.utm,N.utm)+s(year)+ s(depth)+s(dox.bot)
D	PA ~ s(E.utm,N.utm)+s(year)+ s(depth)+s(TMP_bot)+s(eff_OTB)
E	PA ~ s(E.utm,N.utm)+s(year)+ s(depth)+s(dox.bot)+s(eff_OTB)
F	PA ~ s(E.utm,N.utm)+s(year)+ s(depth)+s(TMP_bot')+s(dox.bot) + s(eff_OTB)+s(sal)
G	PA ~ s(E.utm,N.utm)+s(year)+ s(depth)+s(TMP_bot)+s(dox.bot) + s(eff_OTB)+s(sal)+s(poc)
H	PA ~ s(E.utm,N.utm)+s(year)+ s(depth')+s(TMP_bot)+s(dox.bot) + s(eff_OTB)+s(sal)+s(poc)+s(nit)+s(pho)
I	PA ~ s(E.utm,N.utm)+s(year)+ te(TMP_bot,depth)+s(dox.bot) + s(eff_OTB)+s(sal)+s(poc)+s(nit)+s(pho)

Table 3.3. Metrics for each approach for spatiotemporal model (ST) and spatiotemporal model plus effort and environmental variables (ST + ENV). In the first column: AIC= Akaike Information Criterion, Dev.expl.: Explained deviance. MAE= Mean absolute error. The red text highlight the best performance between the two approaches.

METRICS & MODEL	ST	ST + ENV	METRICS & MODEL	ST	ST + ENV
AIC			**Dev.expl.**		
DELTA	2470/5783.98	**2279.57/5700.50**	Delta	55%	**58.25%**
GAUS	15217.27	**14808.36**	Gaus	60.5%	**64.8%**
TW	32841.32	**32448.76**	TW	50.2%	**55.8%**
RF	X	X	RF	82.12%	**83.19%**
GBM	X	X	GBM	74%	**77%**
MAE VALIDATION					
DELTA	117.43	**112.67**			
GAUS	167.27	**160.84**			
TW	144.70	**135.42**			
RF	86.44	**59.51**			
GBM	153.61	**142.86**			

Fig.3.2 shows the results of the delta-binomial approach. In this case, it is visible how model H could be selected as the best model (for dev.expl also model I) for this approach. Following this procedure, the best model identified by the spatially training and test procedure is running on the entire dataset, and the metrics results are shown in Table 3.3. It's evident how the model with environmental variables and effort performed better with respect to the spatiotemporal one. Between the model tested I included also an interaction between depth and temperature, with tensor smoothing (*te* in the formula of the model I) considering the two variables strongly correlated from the oceanographic point of view, but not in collinearity analysis running before to fit the models. Nonetheless, the best model, in terms of the diagnostic used (AIC, dev.expl, R^2 and MAE) is model H, which include also depth and bottom temperature but not in terms of interaction between them.

Furthermore, the final prediction map (fig. 3.3), shows the density distribution in terms of the number of individuals per square kilometer for the two ensemble models with or without additional environmental variables. It is evident how for some years (2016-2017-2018) the density increase, especially for the central basin. The index reaches ~800/900 number of individuals per square kilometer, especially along the Croatian coast and Jabuka-Pomo Pit area in the center of the Adriatic Sea.

DISCUSSION

I have presented here a procedure for developing ensemble models of species distribution, including a protocol for training and test data set. The procedure adopts models with an increasing number of explanatory variables from spatiotemporal only to spatiotemporal plus environmental and fishing effort variables to describe the spatial structure. Results highlight the differences when abiotic factors and effort are introduced in the models.

Using a statistical approach implementing a series of performance indicators I have shown through the 9 models for each approach that using additional explanatory variables improves the capacity of the model to explain data. This procedure results in a decrease (on average, fig. 3.4) of the errors between observed survey data and predicted data. I know that species are not homogeneously distributed across space and time, thus this kind of approach can be used to better understand the process of respective pattern distribution. Including spatiotemporal and environmental covariates in SDMs can produce improved results that facilitate extrapolation of this procedure to areas not included or to future simulations under climatic changes (see also Panzeri et al., 2021). For these reasons, this robust methodology can be easily exported in a different context to improve the knowledge about the process driving species' distribution and highlight hot spot areas useful for fisheries management purposes.

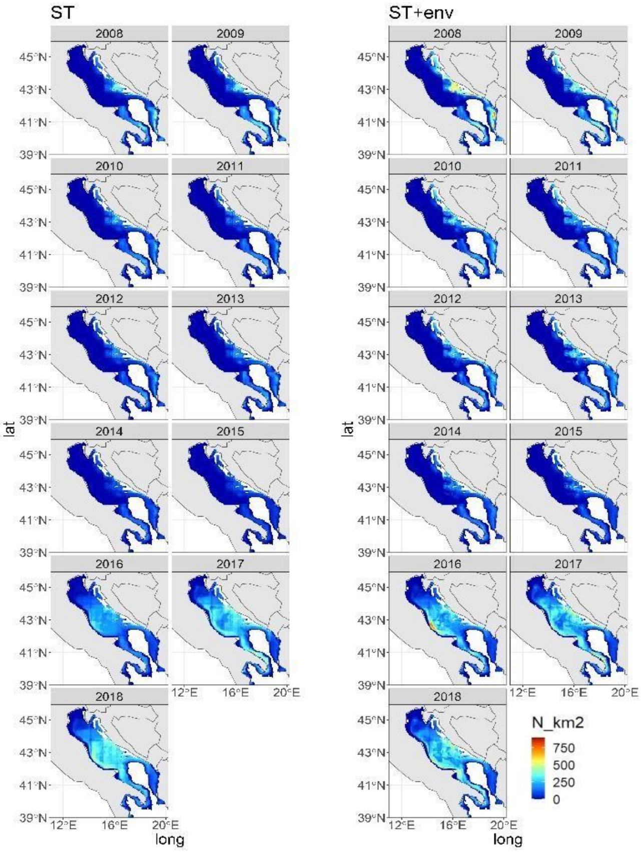

Figure 3.3. Distribution map of European hake in the Adriatic Sea for Ensemble model spatiotemporal (ST, left panel) and spatiotemporal plus environmental and effort variable (ST+Env, right panel).

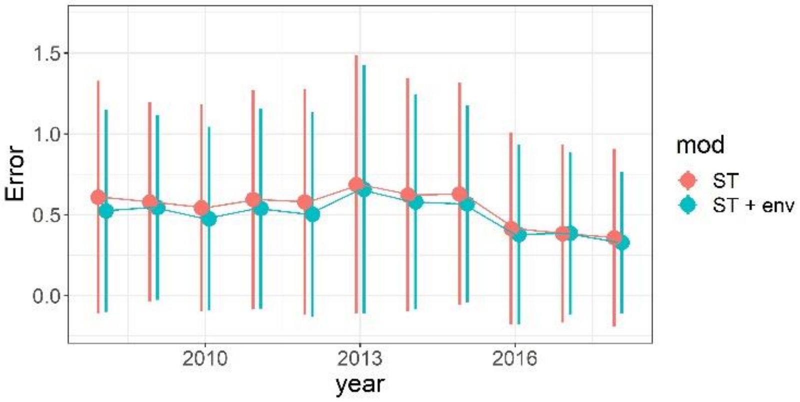

Figure 3.4. Result from evaluated mean error process (y-axes) over years (x-axes) for ensemble spatio-temporal model (ST) and spatio-temporal model plus environmental covariates and effort (ST +Env).

Furthermore, a final evaluation of all models applied and the ensemble model approach, all with the environmental variable included (after the evaluation of best performance between the model with or without the env variable, plot 3.4), is visible in figure 3.5 with value on table 3.4, where x-axes show the approaches used (delta, gaus, TW, RF, GBM, and ENS – for acronyms see plot legend) and y-axes the absolute mean percentage error (mean(pred-obs/obs*100), see eq.1 of this chapter) overs years and overs space (longitude and latitude values of the prediction grid) between predicted values and observed survey values. Each model includes the point range bar as 25° (under the point) and 75° (over the point) percentile of the difference distribution between predicted and observed values. The ensemble model used it's a compromise between all models applied, considering the smoothing approach of GAM and the 'tree' approach of machine learning. The idea behind choosing the ensemble of the model is to minimize the final error but is evident how, being weighted on the R^2 over the different models, the best solution could be random forest or Delta GAM, but I conder that nowadays no one model could be applied for all data and a good compromise between different approach is the best solution to grasp information from each type of model, trough smoothing and machine-learning approaches.

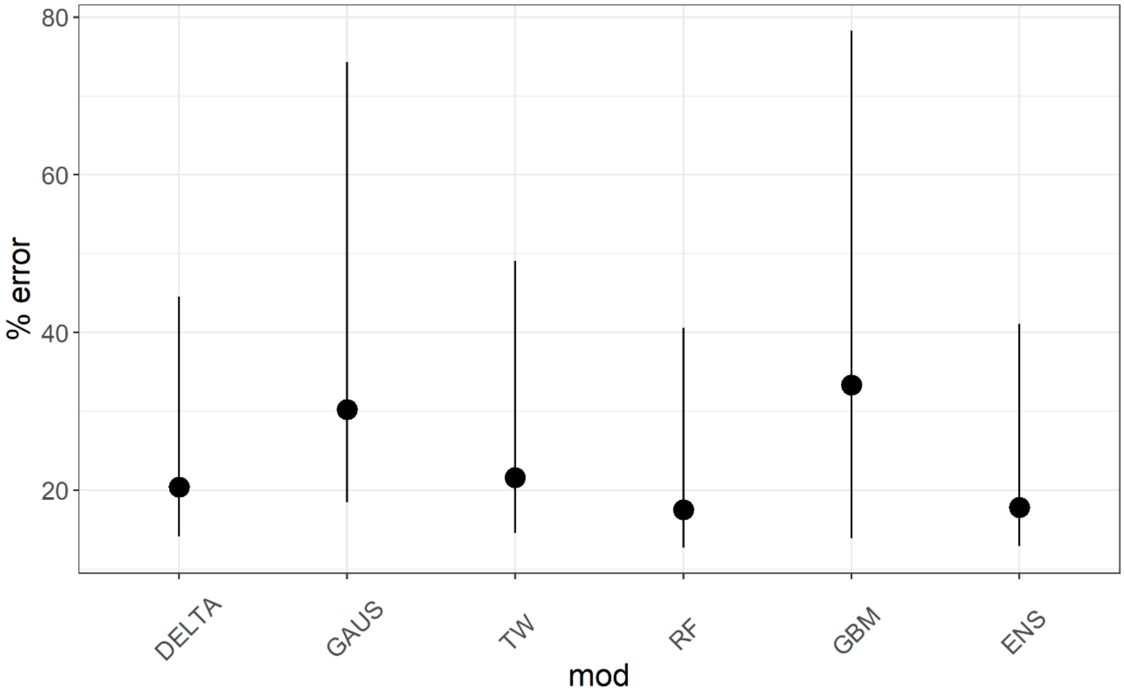

Figure 3.5: the absolute mean percentage error between predicted values on grid and observation data (y-axes) over time (years) and space (latitude and longitude), for each model (mod x-axes: delta=delta, gaus=gaussian, TW=tweedie, RF= random forest, GBM, generalized boosted method, ENS= ensemble). The error bar range indicates the 25° and 75° percentile under and over the point respectively.

Table 3.4: values of the mean percentage error and quartile range for each approach between prediction and observation, shown in Figure 3.5. In the column: % error, Quart25= 25° percentile of % error distribution, Quart75=75° percentile of % error distribution.

	% error	Quart25	Quart75
Delta	20.42	6.30	24.13
Gaus	30.27	19.40	44.94
Tw	21.62	7.05	27.45
Rf	17.54	4.81	23.06
Gbm	33.35	19.40	44.94
Ens	17.81	4.88	23.25

$$\frac{\sum_{i=1}^{n}\left(\frac{|pred_i - obs_i|}{obs_i}\right)*100}{n} \quad \text{eq.1}$$

Where *pred* are predicted values and *obs* observed values, for each *i* point of the grid.

Chapter 4

Spatial management

Identifying priority areas for spatial management of mixed fisheries using an ensemble of multi-species distribution models

(under review)

INTRODUCTION

Spatial management of fisheries is considered one of the pillars to achieve sustainable exploitation of marine renewable resources (Grorud-Colvert et al., 2021). In the Mediterranean Sea, for example, fisheries are largely managed through effort control, and, for rebuilding overexploited stocks, current management is mostly based on technical measures on selectivity and temporal bans (Bellido et al., 2020) as well as on spatial closures (Claudet et al., 2008; Pérez-Ruzafa et al., 2017; Scarcella et al., 2014) and other spatial-based measures (OECM, (Gurney et al., 2021). The global deal for nature suggests the protection of 30% of the Earth for contrasting global impacts (Dinerstein et al., 2019), and the coherent objective of protecting 30% of the sea by 2030 (O'Leary et al., 2016), in the Mediterranean also entails defining new locations for the establishment of Fisheries Restricted Areas (FRA). There is a wide consensus that such restricted areas, to provide the best trade-off between benefit on stock status and effects on fisheries, must be highly relevant for target species by protecting sensitive ontogenetic phases of the population, i.e., spawning and nursery grounds (Colloca et al., 2015; Dambrine et al., 2021; Laman et al., 2018). Thus Essential Fish Habitat (EFH) for adults in spawning seasons can be considered relevant for spatialized temporary fishing bans aiming at reducing fishing mortality (Russo et al., 2020; Russo et al., 2016), whilst EFH for juveniles can be useful to strengthen recruitment (Matić-Skoko et al., 2020). Mapping areas where aggregation of juveniles and adults are associated or dissociated, moreover, provides valuable information for fishers as an effective tool to avoid catching undersize specimens and as a strategy for indirectly increasing fishing selectivity and smoothing socio-economic impacts of the landing obligation (Dolder et al., 2018; Milisenda et al., 2021).

Abundance and biomass data over space, as obtained from scientific bottom trawl surveys, are of paramount importance for setting appropriate EFH for demersal resources (Colloca et al., 2015). However, even if standard sampling protocols are used in scientific surveys, spatial and temporal mismatches among hauls might occur and different modeling approaches have been developed for interpolation-extrapolation of trawl survey data (Thorson et al., 2015). Species Distribution Models (hereafter SDMs) are widely used to infer the potential species distribution (either as presence/absence or abundance) based on geopositional and environmental data (Brodie et al., 2020). SDMs are applied to describe single species distribution at different scales (local, regional or global), by implementing a range of methods on density (e.g. number of individuals), presence/absence, or biomass (Barcala et al., 2019). In the demersal fishery context, SDMs are increasingly applied to describe the distribution of exploited and vulnerable species (Lauria et al., 2017) or to develop conservation measures (Colloca et al., 2015). These models are deemed appropriate for mapping species distribution that is essential for identifying EFH (Druon et al., 2015; Luan et al., 2018; Sion et al., 2019a), as well as for protecting marine ecosystems (Fanelli et al., 2021; Fulton et al., 2011; Grüss et al., 2014).

Several approaches are used to develop SDMs including linear models (LMs), Generalized Linear Models (GLMs), Generalized Additive Models (GAMs) (Maravelias et al., 2003; Olden & Jackson, 2002), machine learning methods such as Random Forest (RF) or artificial neural networks (ANN) (Breiman, 2001). Although some approaches to model species distribution and infer future trajectories are better suited for including environmental changes and anthropogenic stressors as drivers (Moullec et al., 2019; Robinson et al., 2017), a general model is seldom applicable to different species (Colloca et al., 2015) since predictive performance depends not only on the intrinsic mathematical approach but also on sample size (Wisz et al., 2008) and the links between species distribution and environment (Santika & Hutchinson, 2009). Therefore, an ensemble of approaches might be a solution to account for different species-specific conditions (see previous discussion in Chapter 3) represented by the quality of data, explanatory variables, and specific trawl survey coverage and help in moving beyond previous approaches (Colloca et al., 2015). The ensemble approach can provide the basis for generalizing the integration of trawl survey data with other variables (geoposition, oceanographic and biogeochemical drivers, fisheries drivers) to obtain the best extrapolation of the hauls information to the whole domain under study, the position of hot spots of aggregation and, ultimately, to determine both optimal fishing grounds (OFG) and EFH (e.g., Thorson et al., 2015) for multiple species, the target of mixed fisheries.

In this work, I followed a protocol developed in Chapter 3 for training and testing an ensemble of species distribution models (e-SDM of meaningful explanatory variables. The e-SDM is used for describing EFH for 10 demersal species in the central part of the Mediterranean Sea (Adriatic and North Western Ionian Seas) that constitute approximately 60% of the demersal landings in the area. The objective is to provide a robust determination of areas that are ecologically meaningful to increase the efficacy of spatial fisheries management by identifying EFH for juveniles and adults of marine species. Areas where species-specific EFH are overlapping, enable to identify priority areas for spatial management of the two main and typically mixed fisheries of the area, i.e., the bottom otter trawl and the bottom beam trawl, for the sake of rebuilding multiple exploited demersal stocks. Results also provide a basis for evaluating FRAs established or under evaluation.

MATERIALS AND METHODS

The ensemble of SDM (e-SDM) & Protocol for model training and testing

For the ensemble of model and for the training and test routine I followed the same protocol developed in chapter 3 (Procedure in e-SDMs - Chapter 3)

The evaluation of the error is quite difference respect the equation 1 in chapter 3 (see Chapter 3). The values predicted on each grid point of the domain with the e-SDM were compared with the surveys data to calculate the average relative residual as:

$$ARRi = \left(\frac{|y_i - x_i|}{x_i}\right) * 100 \qquad \text{(Eq. 1)}$$

Where x_i is the survey data and y_i is the model prediction on the grid and, *i* is the i-th value of the haul survey. The spatial distribution of the residual is mapped by interpolation using the Inverse Distance Weighting (IDW) for each year to extend the residuals to the whole domain assuming that the measured values closest to the prediction location have more influence than the farther points (Lauria et al., 2017). Yearly maps of relative residuals were averaged into a single average map of relative residuals by juveniles and adults of each species.

Hot spot detection

EFH for each species and stage were identified using the Getis-Ord Gi* index (Gi hereafter) (Getis and Ord, 1992) applied on the e-SDM prediction over the years, i.e.,

$$Gi_{s,i,j,l} = \frac{\sum_{j=1}^{n} w_{i,j}x_j - \underline{X}\sum_{j=1}^{n} w_{i,j}}{S\sqrt{\left[\frac{n\sum_{j=1}^{n} w_{i,j}^2 - \left(\sum_{j=1}^{n} w_{i,j}\right)^2}{n-1}\right]}} \qquad \text{(Eq. 2)}$$

Where $Gi_{s,i,j,l}$ is Gi for species (s) at the grid point of coordinates (i,j) and life stage (l, adults or juvenile), x_j is the attribute value for feature j, $w_{i,j}$ is the spatial weight between features i and j, n is equal to the total number of features, S is the standard deviation of previous parameters. The spatial weight $w_{i,j}$ was set equal to 8 (number of cells around our cell in analysis to calculate distance weight) after evaluation of several alternatives (w=4,6,8,16). The hot spots were defined as those grid points with Gi values above the third quartile, and hot spots for mixed fisheries (separately for OTB and TBB) were identified as grid points defined as hot spots for multiple species. Furthermore, the difference of Gi values for adults and juveniles by each species were used to identify the optimal fishing grounds (OFG), i.e., the areas with potentially high selectivity for adults (Gi adult - Gi juvenile >> 0) and the worst fishing ground where juveniles concentrate more than adults (Gi adult - Gi juvenile << 0). Gi differences between adults and juveniles cumulated among species allowed obtaining general maps of gradients of potential selectivity by gear as a tool for defining best and least opportune fishing grounds.

Study area

The e-SDM approach was tested in the central Mediterranean Sea, namely the Geographic Sub Areas (GSA) 17-18 and 19 as defined by the FAO-GFCM (General Fisheries Commission for the Mediterranean Sea) corresponding to the Adriatic Sea and the North Western Ionian Sea (Figure 4.1). This spatial domain is rich in spatial heterogeneity connected with large gradients in oceanographic drivers and climatic factors (Artegiani et al., 1997; Carlucci et al., 2018; Cushman-Roisin et al., 2001; D'Onghia et al., 2012, 2016; Davolio et al., 2017; Grilli et al., 2020). The northern Adriatic Sea is the shallow part of the Adriatic epi-continental shelf, with a maximum depth of around 70 m and a mean depth of 30 m. Its physical and biogeochemical features are strongly influenced by the runoff of important rivers including the Po. In the central part of the Adriatic Sea, a depression with a maximum depth of 260 m (Jabuka/Pomo pit) is characterized by the local discontinuity in the oceanographic conditions and is defined as a large FRA since 2017 (FAO, 2020). The southern part of the Adriatic (GSA 18) is characterized by a steep continental slope reaching depths of approximately 1250 m. The north-western Ionian Sea (GSA 19) acts as a cross-road basin connecting the Levantine basin, the Strait of Sicily, and the southern Adriatic Sea, where the so-called Adriatic Deep Water (ADW) spreads into the Ionian bottom layers (Budillon et al., 2010). The Adriatic and Ionian oceanographic features are notably interlinked and are subjected to relevant decadal variability associated with the reversal of the Northern Ionian Gyre (Reale et al., 2017).

The species focus of the work are the most important species exploited by the bottom trawl fishery (otter or beam trawl) in the Adriatic and western Ionian Sea (Farrugio et al., 2015; GFCM-FAO, 2020) and are monitored in scientific surveys. Key commercial demersal species are European hake (*Merluccius merluccius,* Merlucciidae), Norway lobster (*Nephrops norvegicus,* Nephropidae), red mullet (*Mullus barbatus,* Mullidae), Blackbellied angler fish (*Lophius budegassa,* Lophiidae), European horse mackerel (*Trachurus trachurus,* Carangidae) and shortfin squid (*Illex coindetii,* Ommastrephidae). In deeper areas (depth>200 m) of the

Southern Adriatic and North Western Ionian the deep-water rose shrimp (*Parapenaeus longirostris,* Penaidae) is also among the main commercial targets of otter trawlers. Common sole (*Solea solea,* Soleidae), mantis shrimp (*Squilla mantis,* Squillidae), and common cuttlefish (*Sepia officinalis,* Sepiidae) are extremely important for the fisheries economy of the northern Adriatic Sea where the vast shallow trawlable area is exploited by different towed gears including the beam trawl (Pranovi et al., 2000). These species constitute ~60% of the total demersal fish landings in the GSAs 17, 18, and 19. Although the exploitation status of these 10 demersal species is evolving positively, many of them are still overexploited (FAO, 2022, SAC, 2021) and the Regional Fisheries Management Organization (i.e., the GFCM) is envisaging the determination of new actions to include in the next multiannual plans, including spatial management areas (Carlucci et al., 2018; Colloca et al., 2017; Maiorano et al., 2010).

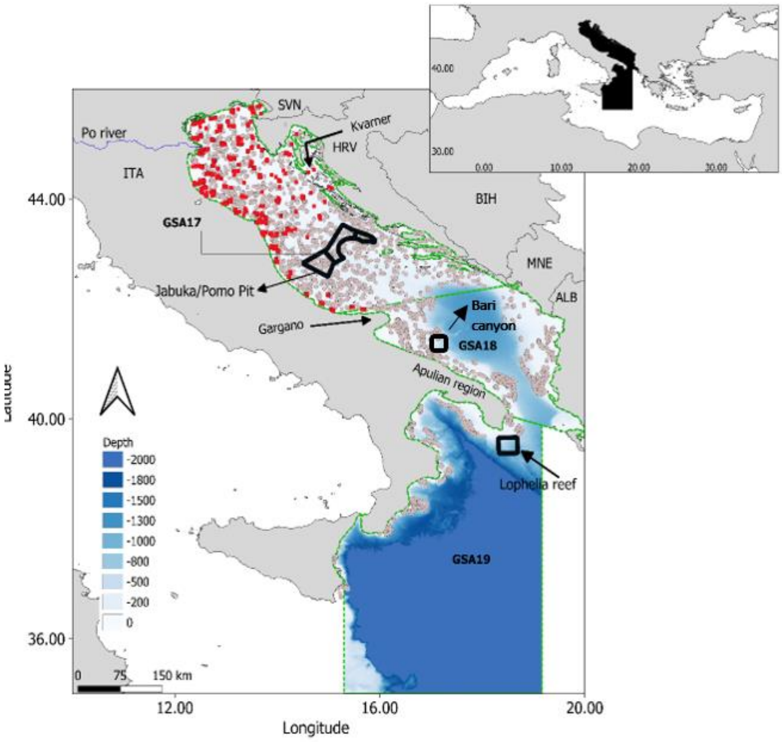

Figure 4.1: The study area of the Adriatic and north-western Ionian Sea covering the GSAs 17-18-19 (delimited by green dotted lines) with bathymetric layers up to 2000 m. Position of hauls for MEDITS (grey dots, years 1999 - 2018) and SOLEMON (red squares, years 2005-2018) trawl surveys are shown. Main geographical features and countries surrounding the domain are indicated, i.e., Italy (ITA), Slovenia (SVN), Croatia (HRV), Bosnia-Herzegovina (BIH), Montenegro (MNE), Albania (ALB). The map also reports established FRAs according to FAO (2020).

Input data

Trawl Survey data

Indices of demersal species density (number of individuals for a unit of area or N km^{-2}) by haul for the years 2008-2018 were retrieved from the MEDITS bottom otter trawl (Mediterranean International Trawl Survey; (Spedicato et al., 2019) and from SOLEMON beam trawl (Sole Monitoring; (Grati et al., 2013; Scarcella et al., 2011). The dataset consisted of an average 326 MEDITS hauls per year in the GSA 17-19 and an average of 70 SOLEMON hauls per year in GSA 17. By considering the efficiency of gear in catching each species, MEDITS trawl survey data were used for European hake, red mullet, angler fish, European horse mackerel, Norway lobster, deep-water rose shrimp, and shortfin squid, while SOLEMON data were used for common sole, mantis shrimp and common cuttlefish. Adult and juvenile abundances were considered separately using a species-specific cut-off size based on the biological information reported in Table 4.1.

Table 4.1: Demersal species considered in the analysis and the size threshold between the adult and juvenile stage defined based on cited literature. CL= carapace length, ML= mantle length, TL=total length.

Species	**Common name**	**Size class limit (cm)**	**Source**
Merluccius merluccius	European hake	14 TL	(Flamigni, 1983)
Mullus barbatus	Red mullet	9-10 TL	(Jukić & Piccinetti, 1981)
Nephrops norvegicus	Norway lobster	2.5 CL	(Froglia & Gramitto, 1988)
Parapenaeus longirostris	Deep-water rose shrimp	1.5 CL	https://www.faoadriamed.org/html/Species
Lophius budegassa	Blackbellied angler fish	33 TL	(Carlucci et al., 2009; Jardas, 1985)
Illex coindetii	Shortfin squid	15 ML	https://www.faoadriamed.org/html/Species
Trachurus trachurus	European horse mackerel	14 TL	https://www.faoadriamed.org/html/Species
Solea solea	Common sole	19 TL	(Colloca et al., 2015)
Squilla mantis	Mantis shrimp	2.5 CL	(Colella et al., 2016)
Sepia officinalis	Cuttlefish	10 ML	https://www.faoadriamed.org/html/Species/SepiaOfficinalis.html

Oceanographic variables

Physical and biogeochemical variables for the Adriatic Sea and North Western Ionian were extracted from two databases covering the Mediterranean Sea and available within the Copernicus Marine Environment Monitoring Service (CMEMS, https://marine.copernicus.eu/access-data; (Simoncelli et al., 2019; Teruzzi et al., 2019) The datasets are the results of the combination of modeled and satellite data through advanced assimilation techniques (reanalysis) and cover the period 1999-2021 with a spatial resolution of 1/16° and 72 unevenly vertical levels. The variables considered in this work were water surface temperature (°C, TMP_sst), water bottom temperature (TMP_bot, °C), dissolved oxygen (mmol/m^3) at the bottom and surface (dox_bot and dox_sur respectively), water column averages of nitrate (nit, mmol/m^3), phosphate (pho, in mmol/m^3), chlorophyll-a (chl, mg/m^3), particulate organic carbon (poc, mg/m^3) and pH, as well as surface salinity. These variables were considered because of their ecological importance for the chosen demersal species (Bitetto et al., 2019; Carlucci et al., 2018; von Schuckmann et al., 2021) and for their importance in offering favourable conditions for a productive habitat.

Effort data

The effort was estimated for the period 2008-2018 by integrating Vessel Monitoring System (VMS) and Automatic Identification System (AIS) data. VMS and AIS disaggregated data include vessel-specific sets of “pings” containing information on vessel identity, position, speed over ground, and heading. VMS and AIS datasets were merged at the scale of individual Italian and Croatian flagship vessels (no other countries’ VMS data was available in the area of study) using the VMS base platform (Russo et al., 2016; Russo et al., 2014). Fishing trips were then interpolated and the fishing set positions (i.e. hauls) were separated from other non-fishing behaviors (steaming, resting, etc.). The fishing effort was estimated by vessel/cell for bottom otter trawls (OTB) and beam trawls (TBB) and expressed as total trawling time (in hours) per year with a spatial resolution of 1/16°.

Results

The Variance Inflation Factor analysis resulted in non-collinearity (VIF < 5) for latitude (UTM), longitude (UTM), depth, year, bottom temperature, bottom oxygen, nitrate, phosphate, salinity, particulate organic carbon, and both OTB and TBB effort covariates for all species. For red mullet, non-collinearity was also found for surface temperature and chlorophyll-a. Table 4.2 shows all models and covariates chosen for each life stage and species after training and test steps (see also the Supplementary material). The set of diagnostic indicators, i.e., %ED, AIC, MAE, showed that models using spatio-temporal, oceanographic and effort variables (complete model) performed better than models including only spatio-temporal variables (see Supplementary Material, Table S4.2). Results of the validation of the complete models are shown in Table 4.2 through the R^2, whose values are used for weighting the elements of the model ensemble

Table 4.2: Performances of the best SDM identified for each approach (Delta, Gaussian, Tweedie, Random Forest, and gradient boosting machine method). Performances are evaluated using the R^2 statistics for adults and juveniles of each species.

European hake	Adult	Juvenile	Angler fish	Adult	Juvenile
Delta	0.41	0.38		0.23	0.26
Tweedie	0.33	0.33		0.24	0.27
Gaus	0.1	0.13		0.22	0.19
RF	0.82	0.77		0.79	0.71
GBM	0.18	0.16		0.29	0.22
Red mullet			European horse mackerel		
Delta	0.18	0.09		0.14	0.05
Tweedie	0.16	0.07		0.21	0.05
Gaus	0.07	0.019		0.06	0.004
RF	0.53	0.55		0.79	0.47
GBM	0.06	0.06		0.2	0.01
Norway lobster			Mantis shrimp		
Delta	0.28	0.19		0.54	0.57
Tweedie	0.3	0.31		0.52	0.63
Gaus	0.22	0.14		0.32	0.44
RF	0.78	0.72		0.81	0.8
GBM	0.28	0.29		0.56	0.53
Shortfin squid			Common sole		
Delta	0.31	0.28		0.55	0.41
Tweedie	0.33	0.24		0.56	0.46
Gaus	0.18	0.12		0.5	0.39
RF	0.78	0.67		0.89	0.82

GBM	0.24	0.12		0.58	0.68
Deep-water rose shrimp			Common cuttlefish		
Delta	0.25	0.26		0.62	0.60
Tweedie	0.32	0.21		0.6	0.61
Gaus	0.1	0.14		0.44	0.47
RF	0.79	0.77		0.86	0.85
GBM	0.11	0.22		0.58	0.56

Hot spots of aggregation

The Gi calculated on the e-SDM results and averaged over years for adults and juveniles is shown in Figure 4.2 and 4.3 for otter trawl and beam trawl target species, respectively. These maps show hot spots of aggregation across stages and species, highlighting the EFH for each. The Gi for the OTB species (those better sampled by MEDITS otter trawl survey, Fig.4.2) show that adults of the European hake are mainly concentrated in the eastern part of the Adriatic Sea, along the Croatian, Albanian and Montenegrin coasts (Fig. 4.2A). Similarly, the juveniles are located in the east-central part and along the South Adriatic Pit (Fig 4.2B). Adults of Red mullet showed hot spots distributed in the southern Croatian and Montenegrin coast (Fig. 4.2C) and juveniles also have hot spots in shallow areas in the North-Apulian region, close to the Gargano promontory, and along the Montenegrin coast (Fig. 4.2D). Adults and juveniles of the Norway lobster show high abundance areas located in the Jabuka/Pomo Pit area, in the Kvarner (Croatia) and along the South Adriatic Pit (Fig. 4.2E and 4.2F). Both adults and juveniles of blackbellied angler fish are mainly concentrated in the eastern part of the South Adriatic Pit, along the Montenegrin coast and in the western part along the south Apulian coast (Fig. 4.2G and 4.2H). The hot spots for the deep-water rose shrimp are located in the south part of the basin and in the western Ionian region, along the Calabrian coast (Fig. 4.2I and 4.2L). Shortfin squid adults showed hot spots located in the Croatian coast and Kvarner island, in the east part of the basin (Fig. 4.2M) while hot spots for juveniles are concentrated in the south part of the basin, along the Apulian region and Montenegrin coast (Fig. 4.2N). The European horse mackerel hot spots resulted in the south-east part of the Adriatic Sea, close to the southern Croatian coast and Montenegro area, also in the western part around the South Adriatic Pit for both adults (Fig. 4.2O) and juveniles (Fig. 4.2P).

Figure 4.3 shows the areas of aggregation for adult and juvenile of the target species of beam trawlers, i.e., Common sole, Common cuttlefish and Mantis shrimp. Adults of the Common sole are mainly concentrated in front of the Istria peninsula and northward of the Po River Delta (Fig. 4.3A), while juveniles are especially concentrated in the southern part of the Po River Delta (Fig. 4.3B). Both adults and juveniles of the cuttlefish have hot spots of aggregation located in front of the Istrian peninsula, with the highest values for juveniles (Fig. 4.3C and 4.3D). The Mantis shrimp life stages are both mainly located in the southern zone of the Po River Delta (Fig. 4.3E and 4.3F).

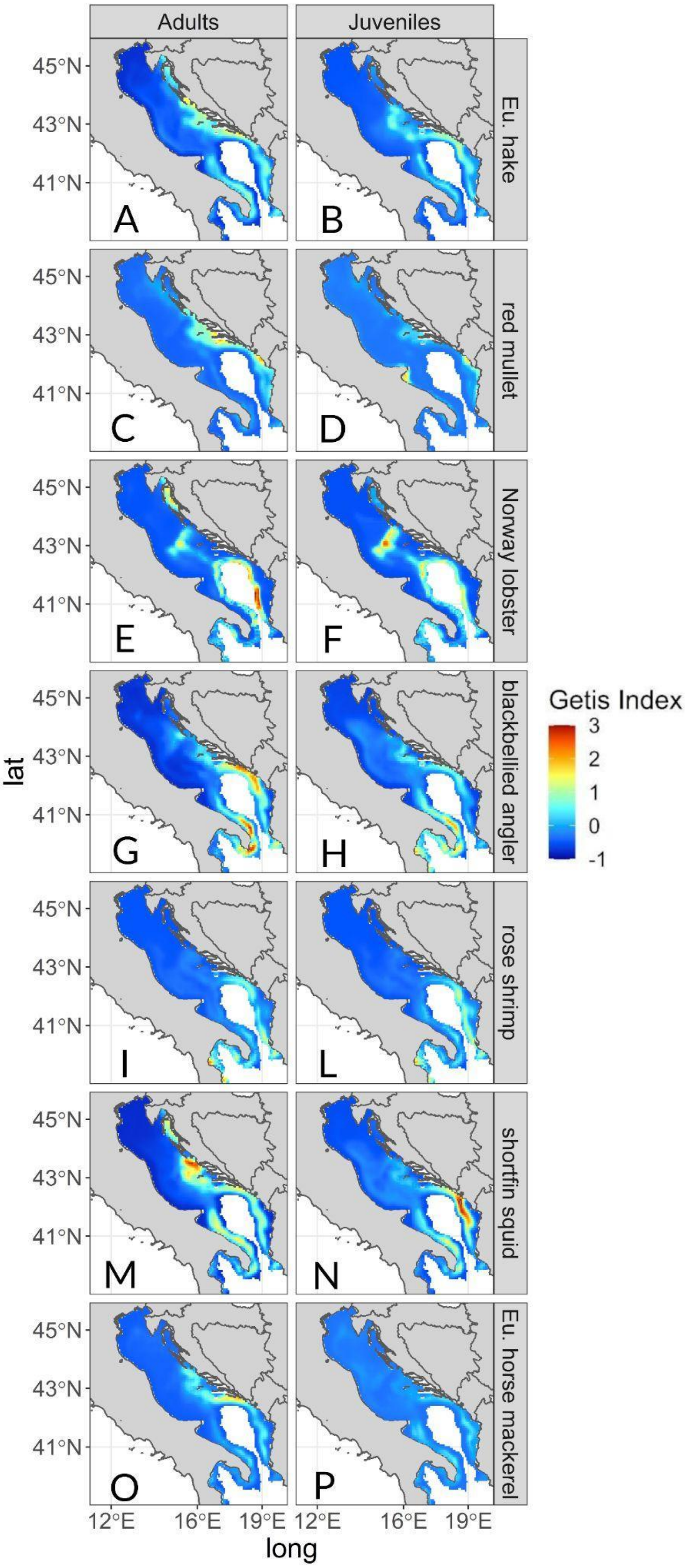

Figure 4.2. Maps of the hot spots indicating the Essential Fish Habitat for each stage and each demersal species sampled with otter bottom trawl and investigated using MEDITS trawl survey data. EFH is identified by the high values of the Getis index value for adult (left panel) and juvenile (right panel).

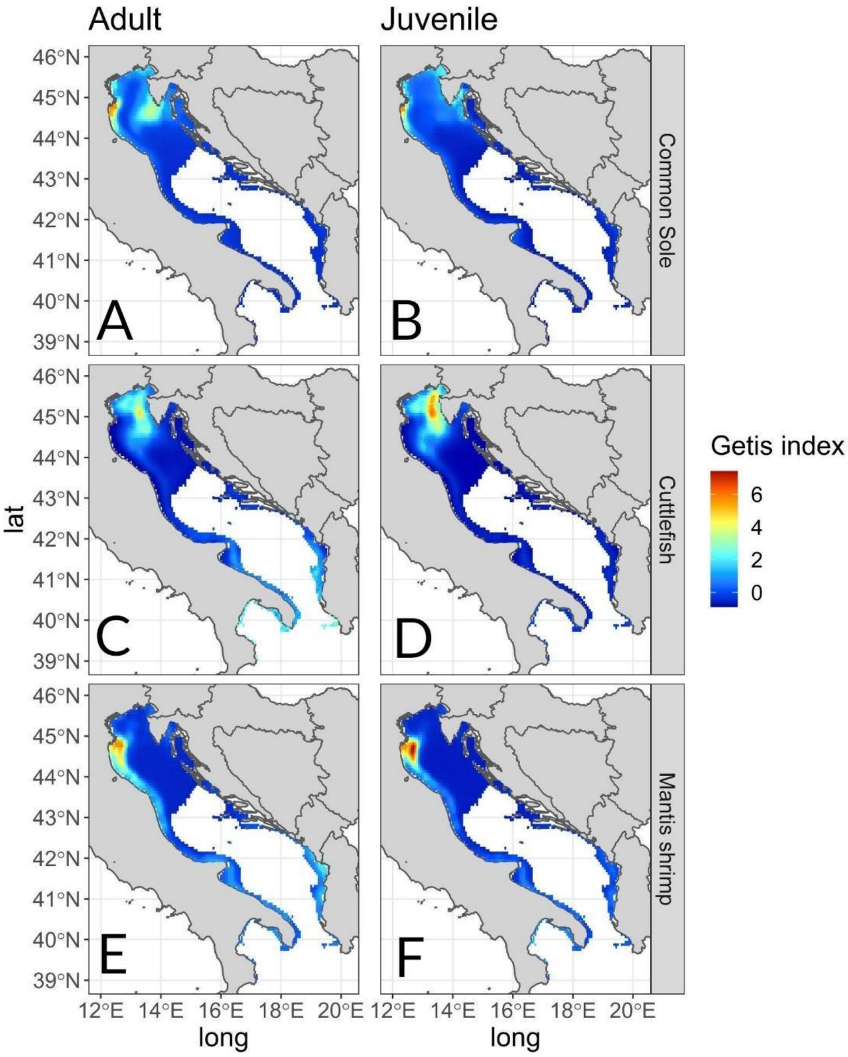

Figure 4.3. Maps of the hot spots indicating the Essential Fish Habitat for each stage and each demersal species investigated using SOLEMON beam trawl survey data. EFH is identified by high Getis index value, for adults (left panel) and juveniles (right panel).

Figure 4.4 summarizes the hot spots of aggregation for juveniles and adults of multiple species by main target gear, excluding red mullet. Adults of species targeted mainly by otter trawl (European hake, Norway lobster, European horse mackerel, Blackbellied angler) have common hot spots in the east part of the basin, along the Croatian and Montenegrin waters with large areas where up to 5 species share the EFH (Fig. 4.4A). Similar areas are also common hot spots for a subset of juveniles of these species (Fig. 4.4B). Cumulative hot spots for the groups of demersal species targeted mainly by beam trawl (Common sole, Cuttlefish and Mantis shrimp) are located in the northern Adriatic Sea: a narrow central strip in the Northern Adriatic represents an area where hot spots cumulate for the adults of these species (Fig. 4.4C), while for juveniles (Fig. 4.4D) the most relevant hot spots are located in front of the Po river and along the western coast, just south of it. The eastern Adriatic shores, especially in the southern Adriatic, have great potential to be EFH for adults of several OTB species (left). For juveniles, the gradients are less pronounced and highlight the importance of the Jabuka/Pomo Pit, the northeast Adriatic area influenced by the Po river as well as the

Puglia region and Albanian coasts. For TBB, the areas with cumulative hot spots are those in front of the Po river for juveniles and closer to the Istria peninsula for adults.

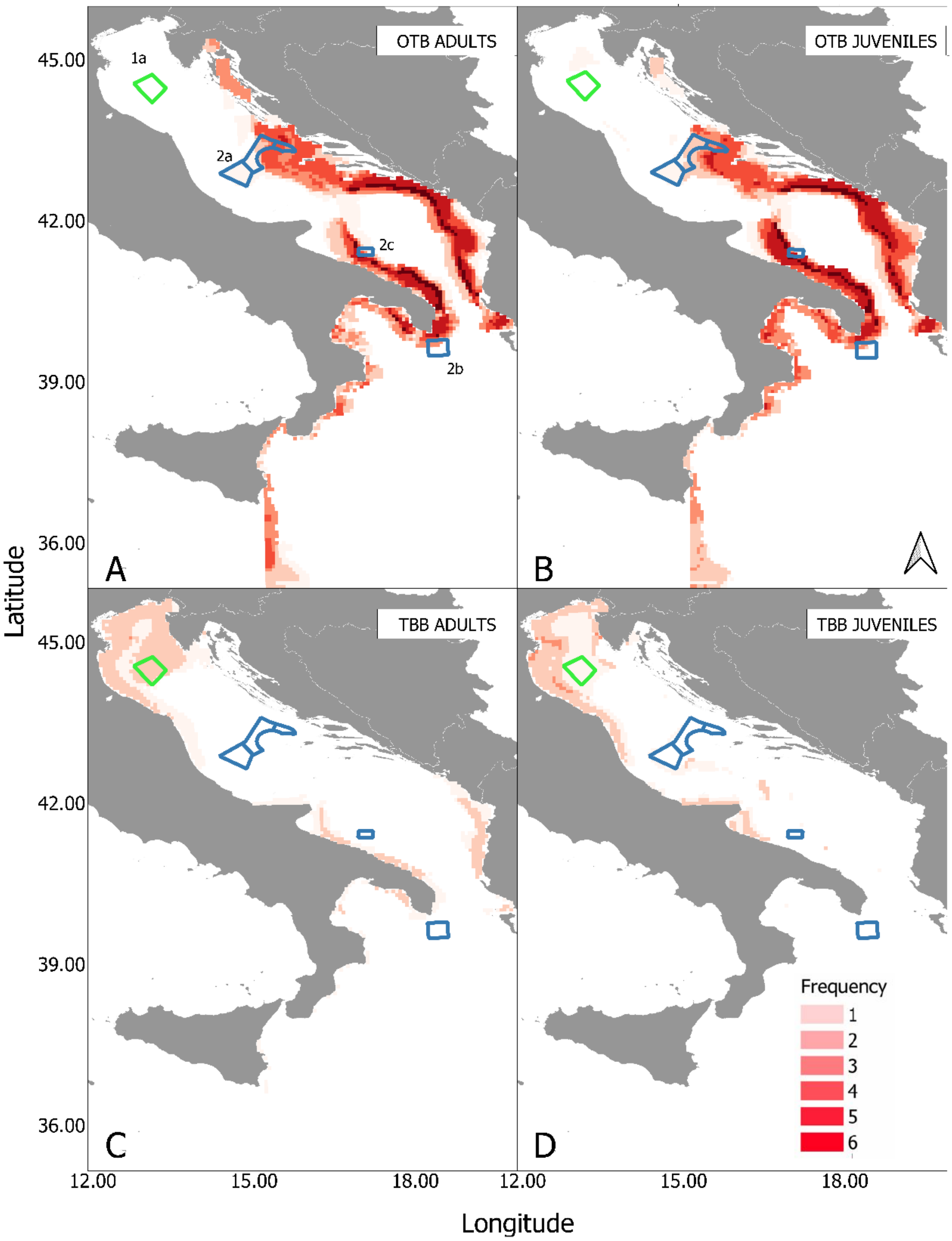

Figure 4.4: Results of overlapping EFH for adults (left panels, A and C) and juveniles (right panel, B and D) for the species main targets of otter trawls (OTB, panels A and B) and beam trawlers (TBB, panels C and D). Values refer to the number of species having Gi greater than the third quartile in each grid cell. Delineated new FRAs under discussion in green (1a: Northern Adriatic Sanctuary;) and already established FRA in blue (2a: Jabuka/Pomo Pit; 2b: Lophelia reef, 2c Bari canyon)

Potential selectivity in the fishing grounds

Gi index differences between adults and juveniles for demersal species are presented in Figure 4.5. Red areas are those with positive differences and preferred fishing grounds are indicated where the selectivity for adults of the species should be high. For example, the Kvarner Gulf is the OFG for Norway lobster and the central eastern Adriatic for Shortfin squid, Red mullet, European horse mackerel and European hake. The southern Adriatic coastal strip is the OFG for the Cuttlefish, and the area in front of Istria, in the Northern Adriatic Sea, is the OFG for Sole. Conversely, the areas with negative differences indicate places that should be avoided by fisheries, because the aggregation of juveniles overwhelms the aggregation of adults and thus are considered poorly selective fishing grounds. These areas include the Jabuka/Pomo Pit for Norway lobster, the northern-eastern Adriatic for Cuttlefish, the north-western Adriatic for Mantis shrimp, and the north strip coast of Istria for Sole. (Figure 4.5). The Jabuka/Pomo Pit area is quite sensitive (see limitations and transferability of approach in this chapter) to data on Norway lobster and future improvements are needed, or to evaluate whether or not the inclusion of this species could be an advantage for this type of approach in the SDMs.

Cumulated Gi for the species target of the two mixed fisheries (Figure 4.6) indicate large areas in the eastern part of the Adriatic Sea that should be OFG for otter trawl because they are areas where Gi for adults prevail over those for juveniles, while the Gulf of Manfredonia and the Jabuka/Pomo Pit area are areas to avoid (Fig. 4.6A). For beam trawl, an area in the northern Adriatic Sea, south of Istria, is identified as the OFG, while the Gulf of Trieste and an area off the Po river mouth should be the least selective areas (Fig. 4.6B).

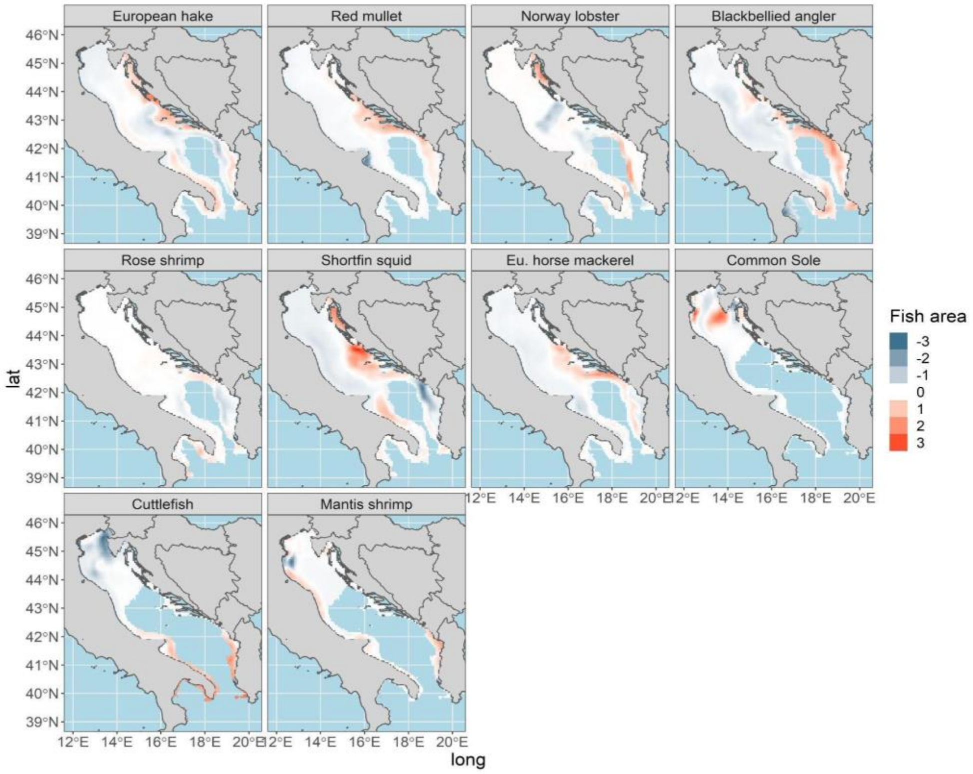

Figure 4.5: Gi difference between adult and juvenile values: reddish areas indicate prevalence of adults and bluish prevalence of juveniles. It can be seen how the most important area of adult (red colour) is located in the eastern area of the basin, especially for the MEDITS survey species, particularly for European hake, Red mullet, Shortfin squid and European horse mackerel. Some specific areas are optimal fishing grounds, such as the Kvarner zone for Norway lobster

and south Croatian and Montenegrin coasts for Blackbellied anglerfish. In the north-east part are highlighted important and better fishery areas for Sole, Cuttlefish and Mantis shrimp (SOLEMON species), especially in the Istria region (adults of Common sole), Gulf of Trieste (juveniles of Cuttlefish) and south Po River Delta (juveniles of Mantis shrimp).

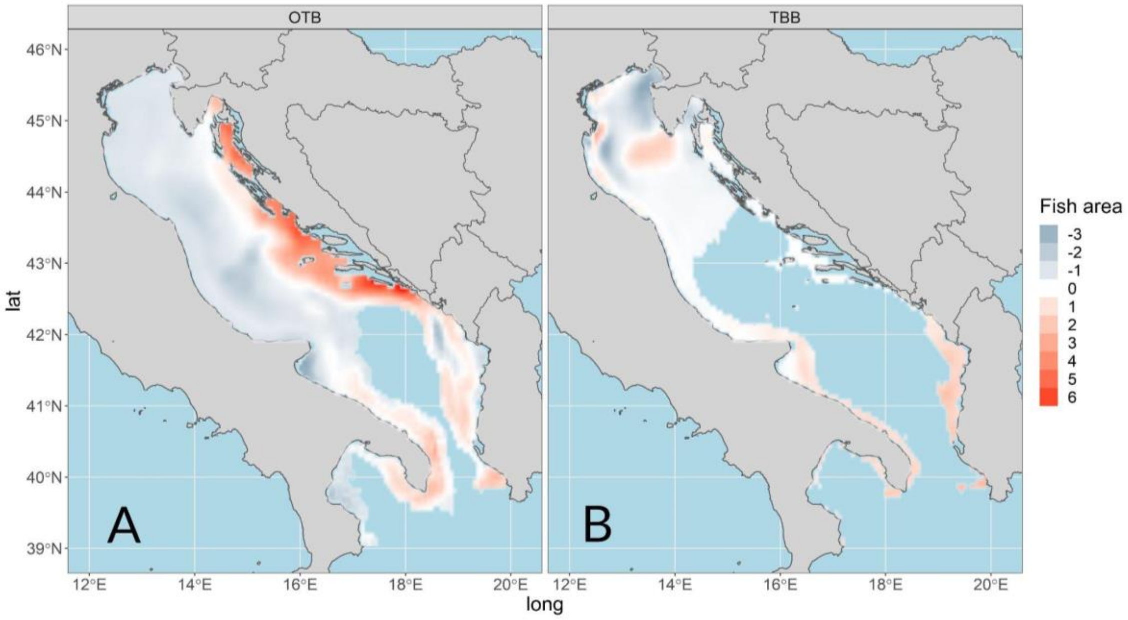

Figure 4.6: Gi differences between adults and juveniles for the species target of the two bottom trawl gears (A: OTB for MEDITS, B: TBB for SOLEMON). The darker the red indicates areas with a greater prevalence of adults and the darker the blue areas with a greater prevalence of juveniles.

Discussion

Although the new EU Common Fisheries Policy (https://ec.europa.eu/info/research-and-innovation/research-area/environment/oceans-and-seas/eu-common-fisheries-policy_en) is largely based on the adoption of spatial measures (such as FRAs) and has among its main objectives the protection of increasingly larger portions of marine environments, there is a surprising shortage of metadata and analyses related to the distribution of exploited species. This lack of large-scale processing and modeling is even more striking when compared to the availability of considerable environmental data in open-access Copernicus and Emodnet platforms. One of the reasons for this problem is surely the great effort required to collect and analyze biological data in combination with other spatial information. In this context, the application of an ensemble of models to fit spatially explicit abundance data of marine demersal species, integrating also oceanographic and effort data, highlighted the potential of this approach for spatial fisheries management.

The first result of this study is that the capability of models to explain the survey data had a minimal but significant improvement by including oceanographic variables and effort data: such a result was consistent across models and species (Supplementary material, Chapter 4 Supplementary material). Similarly, to other attempts (Thorson et al., 2015), the improvement is not outstanding, also because of the inherent high variability of species distribution, yet this improvement has the potential to facilitate extrapolation to unsampled areas and allow for better future projections based on climate simulations. Results highlight the different capabilities of different SDM approaches in explaining the species and stages distribution, and looking at individual model performance, the random forest is generally better in terms of explained deviance and R^2 compared to the other models. However, the ensemble of models weighted with R^2 assures robustness, good performances, and avoids distortions (Melo-Merino et al., 2020) and especially the e-SDM has the notable benefit of being a methodology that can be generalized for all species, ensuring accurate distributions.

Average distributions from e-SDM by species represent an update of previous findings ((Colloca et al., 2015), and hot spots identified with e-SDM by species are coherent with EFH obtained in previous works (such as (MEDISEH, 2013), in particular for the adult phase of European hake, red mullet, deepwater rose shrimp, Norway lobster, and shortfin squid. However, as an effect of the introduction of oceanographic parameters as explanatory variables, hot spot areas identified based on e-SDM results showed greater continuity than hot spots identified in MEDISEH project, which were more accurate punctual and directly connected with trawl survey hauls.

The identification of the hot spot areas for each species, based on the combination of the best models for each approach combined into an ensemble, is a replicable, robust, and valuable protocol to define both the essential fish habitats of a single species and the overlapping areas of species aggregation (Fig. 4.4), also useful to identify where to place MPAs or FRAs in the future (Angeletti et al., 2021; ISMAR-CNR et al., 2018).

The results of this study confirm the importance of the Pomo/Jabuka pit area, fully supporting the maintenance of the fishery restricted area (GFCM-FAO, 2018), especially for some life stages of the commercially important species such as European hake (adults) and Norway lobster (juveniles/adults), but also for shortfin squid (adults). Furthermore, the results from e-SDM enable identifying overlapping hot spots for adults of target species of TBB in the north-east part of the Adriatic basin, close to the tip of the Istrian peninsula (Fig. 4.4), which coincides roughly with the area previously proposed and named as the ”Northern Adriatic Sanctuary” (Grati et al., 2013; Scarcella et al., 2011). Nevertheless, the area in front of the Istria peninsula represents a more selective spot for the presence of adults, i.e., it is also an OFG for TBB (Fig. 4.6), thus suggesting the need for additional cost-benefit analyses to confirm the effectiveness of this proposed FRA. Furthermore, the deep areas in front of the Puglia region are also identified as hot spots, that support the established FRA in the Bari Canyon.

The hot spot results suggest new potentially important areas be protected, such as the area in front of the Po River Delta which is important for juvenile stages of mantis shrimp and common sole (Fig. 4.3). It is worth noting that off the south-eastern coasts of the basin (Fig. 4.2 and Fig. 4.4) there is a wide and highly important area for several demersal adult species targeted by OTB vessels, while the northern part of the GSA17, in front of the Po river mouth, is highly important for juvenile stages of species caught with TBB. These seem to be ecologically significant areas: these grounds might be considered in the future as they appear biologically optimal areas for establishing new areas of management.

Furthermore, contrasting adults and juveniles hot spots allow for identifying the optimal fishing grounds by species (Fig. 4.5) and fisheries (OTB and TBB) (Fig. 4.6). Maps obtained from e-SDM enable identifying areas (in red) with high potential for catching adults while avoiding juveniles (thus increasing selectivity of the fisheries operations). Conversely, areas, where juveniles are predominant (dark blue), are thus areas where fisheries should be avoided both for the low presence of adults and high presence of juveniles, with a potentially large proportion of catches subjected to landing obligation (Celić et al., 2018). Figure 6 shows that red-colored areas, i.e., areas where there is a high aggregation of adults, are mainly in the eastern part of the Adriatic Sea for OTB and basically in a strict regime of landing obligation while the western part of the Adriatic basin has lower selectivity. For TBB, a central area in front of the Po river proved more selective, i.e., where more adults are aggregating (Fig. 4.6).

Thus, although the main large areas of aggregation confirm previous results (Colloca et al., 2015), our results in terms of EFH (Fig. 4.6) highlight the relevant role of the southern and eastern Adriatic Sea as relevant fisheries management areas both for overlapping hot spots (Fig. 4.4A, 4.4B) and for the prevalence of adults (Fig. 4.6A).

It is worth noting that the spatial definition of FRA should consider additional aspects that go beyond the biologically significant areas as identified in this work. In fact, for a full evaluation of best management areas also social and economic impacts should be considered, as well as indirect ecological impacts induced by setting spatial fisheries restrictions. Identified EFH and OFG might be areas where to focus analyses of other social, economic and political aspects (e.g. impacts from other sources; costs for enforcement; the presence of hampering activities, etc.) to establish optimal spatial management measures as foreseen by the Multiannual Management Plans (GFCM Compendium, 2021b). Therefore, the identification of areas of overlapping EFH is just the first step for the identification of potential EFH and OFG of ecological significance. Additional information on fisheries activities, costs for the implementation, control, and effectiveness, all need to be evaluated before fully establishing new management rules. For instance, trophic cascade effects of fisheries management in identified EFH and OFG might be evaluated with complex multispecies models (e.g., EwE, Ecospace: (Agnetta et al., 2019), while socio-economic effects of areas identified for management using e-SDM might be evaluated with opportune bioeconomic tools (e.g., Bemtool, (Bitetto et al., 2019; D'Andrea et al., 2020). Such ecosystem approaches might also help in assessing if spatial fisheries management should be considered together with other measures for reducing the effort to reach the ecological and economic sustainability of fisheries.

Nevertheless, the combined overlapping EFH provides a general indication on where management actions are potentially having the best ecological efficacy on marine populations, considering the prevalence of mixed fisheries in the area, which is already an innovative and useful result for management.

Limitations and transferability of the approach

Species have relevant movements according to the season and inter-annual spatial dynamics cannot be fully grasped by the annual trawl sampling, which is an inherent limitation of the data used that cannot be overcome with the e-SDM approach. Therefore, the EFH are more relevant for the species whose important aggregation phases (reproduction for adults, nursery for juveniles) coincide with the sampling period (summer for MEDITS (Tsikliras et al., 2010) and fall for SOLEMON species) (Scarcella et al., 2014). Overall, ontogenetic shifts and movements are fairly well-represented for all species except *Mullus barbatus,* whose results may appear inconsistent with biological available knowledge, due to the mismatch between the survey and the maximum recruitment period in the area (Tsikliras et al., 2010). This is why the overlapping hot spots in Fig. 4.4 are calculated excluding the red mullet.

The data on Norway lobster may also be critical due to differences at the subpopulation level of this species in the Jabuka/Pomo Pit area. The individuals in Jabuka/Pomo Pit are smaller than the other individuals in the basin, but not necessarily juveniles, and the MEDITS survey may not capture all of the information on the two life stages in the area where juveniles are not detectable because they live in the burrowed burrow during the early life stage.

Furthermore, the selectivity of the net used in the trawl survey is also a limitation for the representativeness of catches of smaller individuals or species with more or less benthic habitus. I used the two distinctive trawl surveys to partly overcome this issue, but clearly, the selectivity of the gear used in scientific trawl surveys can influence both the juveniles'/adults' data. Overall, the generally higher relative bias of e-SDM for juvenile species should be considered a result of the lower selectivity for juveniles in the trawl survey which derives from their generally lower predictability in e-SDM.

The e-SDM approach allows for training and testing models with different numbers of explanatory variables that could be readily applied to identify the distribution of species and possibly pinpoint the most opportune areas for fisheries management in other systems. This should be done with caution where the coverage of scientific trawl surveys is limited: although the availability of explanatory variables allows for inferring hot spots even in areas where trawl surveys are not carried out, such extrapolation could be highly inaccurate.

Application of the approach to pelagic species also seems promising, although it is expected that the high intra- and inter-annual variability, connected to recruitment, would increase the uncertainty of the e-SDM estimates. Furthermore, although the considerable movements of these species might decrease the reliability of annual or average maps of hot spots, the use of the e-SDM approach and hot spot detection focusing on key months might contribute to informing management also for the small pelagic spatial planning.

The spatial resolution of 1/16 of degree used is quite good for a basin-wide analysis but further analyses might be done at a higher resolution to better identify local EFH, also considering recent advancements in the CMEMS products (Cossarini et al., 2021; Escudier et al., 2021) and the larger spatio-temporal coverage of effort data. Furthermore, the approach might be improved by including variables representing benthic habitats (or other bottom features, e.g., rugosity), which can help increase the accuracy of the e-SDM and improve the definition of effective areas for fisheries management. Although the inclusion of oceanographic variables in the e-SDM approach helps trace abundances and distributions to a specific month, future approaches should target high frequency and all-year-round data coming, for example, from the combined use of logbooks and VMS/AIS data. It is however not a given that such fishery-*dependent* data, although having high-frequency temporal coverage, would give more robust results than scientific-based fishery-*independent* information provided by trawl surveys.

Furthermore, the inclusion of oceanographic parameters in the e-SDM allows for future considerations of management areas in the context of climate change (Thorson et al., 2015). For instance, an e-SDM implementation based on projections of oceanographic data regarding different emission scenarios (Representative Concentration Pathway or RCP4.5 o RCP8.5, (Taylor et al., 2012), could be an opportunity to understand the potential changes in the area of aggregation of species, or the center of gravity along the basin, considering the environmental variables the most important driver for these kinds of models and approach, avoiding the distortion due to the geoposition of the survey, that are impossible to prevent or extrapolate. Therefore, the importance of the physical and biogeochemical variables is strongly addressed also for these future purposes. Thus, although this work has improved the spatial resolution of SDM and is based on a longer time series than previous works (Colloca et al., 2015), it also has the potential to set the basis taking into account climate changes in future EFH and thus in fisheries spatial management.

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Data availability statement

Raw trawl survey data and Vessel Monitoring system can be requested from the Ministry of Agriculture of Italy and Croatia. Oceanographic variables used in this work are available at Copernicus Marine Service (https://marine.copernicus.eu/it). All treated data are available at the project FAIRSEA platform (https://fairsea.inkode.it/#/login) and access can be requested from the corresponding author. Hot spots and optimal fishing ground maps will be available directly upon request.


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Chapter 5

Future distribution

Future Distribution of demersal species in a warming Mediterranean sub-basin

Introduction

Assessing and predicting the spatial and temporal distribution of marine species is one of the current challenges in times of climate change, as the increasing spread of invasive species and the pole shift of organisms are among the causes of current changes in biodiversity (Parravicini et al., 2015; Pereira et al., 2010). Because the range and distribution of species could change in response to climate change (Baudron et al., 2020; Pinsky et al., 2020; Román-Palacios & Wiens, 2020), understanding such changes could help define less affected management areas in the future or optimize existing ones, especially with respect to species that are commercially important to fisheries (Melo-Merino et al., 2020; Pinsky et al., 2020).

Ocean warming is accelerating, and recent observations confirm that it has accelerated rapidly in recent decades (Cheng et al., 2018, 2019; IPCC, 2022). This is particularly true for the Mediterranean Sea, a semi-enclosed basin widely recognized as an important hotspot for marine biodiversity (Cuttelod et al., 2009) as well as for climate change (Darmaraki et al., 2019; Giorgi, 2006). Climate projections for the basin show an overall warming of seawater associated with general acidification, deoxygenation, and a decrease in biomasses and nutrients in the water column (Reale et al., 2022; Solidoro et al., 2022; Soto-Navarro et al., 2020). In addition, the increase in frequency and intensity of marine heat waves (Darmaraki et al., 2019; Frölicher & Laufkötter, 2018) will impact the marine ecosystem and biodiversity (Lejeusne et al., 2010; Marbà et al., 2015; Smale et al., 2019), with potential consequences for fisheries and aquaculture. In particular, the Adriatic and Ionian sub-basins of the Mediterranean Sea, which are closely connected, show changes such as an increasing northward shift of thermophilic species (Dulcic & Grbec, 2000; Dulčić et al., 2011) together with rarity or disappearance of cold-water species (Boero & Bonsdorff, 2007; Templado, 2014), especially in the Adriatic Sea, whose further northward migration is prevented due to its nature as a dead end (Ben Rais Lasram et al., 2010). Moreover, possible future changes in climatic conditions in these two sub-basins would favor an increase in invasive species such as Siganus luridus or Lagocephalus sceleratus (D'Amen & Azzurro, 2020), which could affect the dynamics of the local food web (Occhipinti-Ambrogi, 2007).

A great diversity of fisheries characterizes the sub-basin, where resource exploitation began a thousand years ago (Farrugio et al., 2015). In addition, the great biodiversity, high productivity and collection of long-term data series (Fortibuoni et al., 2017) represent important added values of the study area. In the northern and central Adriatic Sea, intensive fishing leads to overfishing of many species such as hake, Norway lobster, and red mullet (Fortibuoni et al., 2017; Russo et al., 2019).

Therefore, temporal and spatial monitoring of demersal (and commercial) species is essential to understand the status and health of the ecosystem, especially in this area where overfishing has increased (Colloca et al., 2013; EU Commission, 2018; FAO, 2020b), particularly in the context of climate change. In the Adriatic and Ionian Seas, current management policies are mainly based on technical measures with temporal or spatial prohibitions (Bellido et al., 2020; Claudet et al., 2008; Scarcella et al., 2014), such as control of fishing capacity, reduction of fishing effort, or temporary or permanent closure (Cardinale et al., 2017), as in the Pomo/Jabuka Pit area.

From this point of view, despite the lack of data at specific times of the year, modeling the spatial distribution of marine species is important to develop appropriate management and conservation measures.

To address the challenge of climate change and species distribution shifts, the number of ecological niche models and so-called species distribution models (SMDs) has increased in recent decades (Robinson et al., 2017). These models, also known as correlative or empirical approaches, typically correlate occurrence (presence/absence) or biomass/density data with environmental variables (as explicit/covariant variables) to predict species distributions, including in response to climate change (Kearney & Porter, 2009).

The implementation of SDMs aims to understand and incorporate a potential new tool for fisheries management in the Adriatic and Ionian Seas, where spatial planning and management should be considered, especially in a context where many fisheries activities, species and countries are involved. The distribution of marine species and their habitat is a complex and complicated "puzzle" that is interconnected at many levels (Nagelkerken et al., 2015). Knowledge and applications of spatial approaches are increasing to achieve sustainable use of resources, assess the importance of marine habitat, especially when we talk about different life stages such as adult or juvenile populations, and incorporate future predictions.

Some approaches are better suited to incorporate environmental changes in the present and in the future. An ensemble of approaches may be one solution to address the different species-specific scenarios, following current approaches (Moullec et al., 2019; Robinson et al., 2017), and going beyond others (Colloca et al., 2015). In this work, I develop an ensemble species distribution model (e-SDM) that follows the protocol developed in previous work (Chapter 2 and Chapter 3) and incorporates a main approach such as Generalized Additive Models (GAM - (Hastie & Tibshirani, 1986) and two main machine learning approaches, Random Forest (Breiman, 2001) and Gradient Boosted Machine (Friedman, 2001). I evaluate changes in the distribution of ten groundfish species over four 5-year time windows: the recent past (2008:2012, hereafter 2012), the present (2014:2018, hereafter 2018), and two future time windows (2031:2035, hereafter 2035 and 2046:2050, hereafter 2050), the latter under Representative Concentration Pathway (RCP) 8.5 (Taylor et al., 2012). I analyzed hotspot areas for species and time windows, focal areas in different time windows, and gained/lost/preserved areas of target species.

Material and method

Study area

FAO-GFCM (General Fisheries Commission for the Mediterranean) designates the Northern Adriatic Sea, the Southern Adriatic Sea, and the Ionian Sea as Geographic Subarea (GSA) 17, 18, and 19, respectively. The Northern Adriatic Sea is a relatively shallow basin (mean depth 30 m, maximum depth about 70 m). The Southern Adriatic Sea (SAS, GSA 18; Fig. 2.1) is characterized by complex topography with a steep continental slope reaching up to 1250 m, muddy bottoms, relict sands, and rocky bottoms (Alfirević, 1981), as well as canyons and cold-water coral megahabitats (D'Onghia et al., 2012). Between the northern and southern Adriatic Sea is a deep depression called the Jabuka/Pomo Pit area (maximum depth 260 m), which is subject to restrictions and recommendations for fishing (FAO, 2020b).

The Adriatic Sea is the main source of dense water for the eastern Mediterranean (Cardin et al., 2011) and is connected by the Strait of Otranto to the Ionian Sea (IS), which is located in the central part of the Mediterranean and connects the western and eastern Mediterranean basins. In particular, the western part of the IS (hereafter WIS - GSA 19) is a kind of crossing point for the different water masses that are part of the Mediterranean thermohaline circulation (MHTC): Modified Atlantic Water (MAW) moving eastward, Levantine Intermediate Water (LIW) moving westward, and Adriatic Deep Water (ADW) propagating to the deepest layers of the Ionian Sea (Budillon et al., 2010; Reale et al., 2017).

The study area is very rich in spatial heterogeneity with a large gradient of climatic factors (D'Onghia et al., 2012; Grilli et al., 2020) and a complex system of water circulation that influences the inversion of the Northern Ionian Gyre (NIG) from anticyclonic to cyclonic (and vice versa), influenced by the bimodal oscillation system (Civitarese et al., 2010). The latter is very important in the area for the transport of organic matter (Boldrin et al., 2009), affecting biotic communities and biodiversity (Civitarese et al., 2010) and primary productivity (Lavigne et al., 2018).

In addition, the study area is characterized by important and specific biocenoses and facies, such as the facies of Atrina pectinata in the Adriatic Sea and white coral in IS (Cerrano et al., 2015).

There are numerous fishing activities, fish farming and anthropogenic pressures in the area (Pranovi et al., 2016; Punzo et al., 2017): In particular, the Adriatic Sea is heavily exploited by trawl and beam trawl fisheries (Colloca et al., 2013, 2017; Pranovi et al., 2000). In the Jabuka-Pomo Pit area, the situation is developing positively after 2017, although several demersal species such as European hake (*Merluccius merluccius*) and Norway lobster (*Nephrops norvegicus*) are still overfished (Colloca et al., 2017; FAO, 2020b; GFCM-FAO, 2018) (Colloca et al., 2017; GFCM-FAO, 2018; FAO, 2020).

The SDM ensemble

See in Procedure in e-SDMs Chapter 3

Input data

Trawl Survey data

See Chapter 4 input data.

Temporal evolution of thermohaline and biogeochemical properties in the Adriatic and Ionian Sea

The mean values of thermohaline and biogeochemical properties in the Adriatic and Ionian Seas in the four time windows selected for analysis were derived from reanalysis and climate simulation data.

Thermohaline and biogeochemical properties in the Adriatic and Ionian Seas were taken from operational models for the Mediterranean Sea (Simoncelli et al., 2019; Teruzzi et al., 2019), which have a spatial resolution of 1/16° and 72 non-uniform vertical levels. Data for the period 1999-2019 were extracted from two reanalysis datasets available for the Mediterranean Sea under the Copernicus Marine Environment Monitoring Service (CMEMS, https://marine.copernicus.eu/access-data). Future climate projections for the period 2005-2100 were produced using the same modeling system MFS16- OGSTM-BFM under a specific emission scenario (RCP8.5; see (Reale et al., 2022). The anomalies of future simulations, calculated as the difference between the value of each variable in each of the two future time windows (2035 or 2050) and the current climate simulation period (2005-2020), were added to the current time value (2018) to avoid trends and false seasonal signals. The variables considered in this work were: Sea surface temperature (°C, TMP_sst), bottom temperature (TMP_bot, °C), dissolved oxygen (mmol m-3) at the bottom and surface (dox_bot and dox_sur, respectively), average nitrate (nit) and phosphate (pho) concentrations in the water column (in mmol/m3), chlorophyll-a (chl, mg m-3), particulate organic carbon (poc, mg m-3), average water column pH, and surface salinity (sss). These variables were included because of their known importance to the selected groundfish species (Bitetto et al., 2019; R. Carlucci et al., 2018) and their general ecological significance.

Effort data

See Chapter 3 - C. *Effort data*

Future projections, Hot spot, and Centre of Gravity

After running the best model derived from the training and testing routine for the period (2008-2018), I used the fitted model to simulate the density of groundfish species on a regular longitudeand latitude grid. I calculated an average of the density index over the years for each scenario (2012, 2018, 2035, and 2050) and developed the final ensemble model by weighting the density obtained using the three approaches (Eq. 1) by the corresponding R2 (Table 5.1). The final results include a density map (see Section S5 in the Supplementary Material, Figure S5.2).

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$$d_{x,y,ens} = \frac{\sum(d_{x,y} * \ R_{GAM}^2 + d_{x,y} * \ R_{RF}^2 + d_{x,y} * \ R_{GBM}^2)}{(R_{GAM}^2 + \ R_{RF}^2 + R_{GBM}^2)} \qquad eq.1$$

Here, $d_{x,y}$ are the density values at each point in the range (x,y) as the mean over the years for each scenario, and R^2 is the value derived from Table 5.1 for each model (GAM, RF, GBM). I also calculated the relative density anomaly between 2018 and 2035 or 2050 as:

$$\mathrm{Ay} = \frac{d_{2035/50\,,x,y} - d_{20180,x,y}}{\frac{d_{2018\,,x,y} + d_{2035/50,x,y}}{2}} \qquad eq.2$$

.

In addition, I used the density distribution of the Getis ord-Gi* (Getis & Ord, 1992) to highlight the hotspot between the past and future periods. For the best graphical representation, I chose a third quartile threshold for the 4 hotspot scenarios.

For each time window, species, age, and GSA, I also performed a centroid analysis (COG). The dimension of each COG (Figure 5.4) depends on the median of the 2012 positive Getis ord-Gi* values, which were used as a reference point for filtering the other time windows, dividing the number of filtered cells for each time period and GSA by the total number of cells in the area (Eq. 3), highlighting potential changes in COG and density over space and time.

$$threshold = Median(Getis_{2012,gsa} > 0)$$

$$eq.3$$

$$S_{y,gsa} = log\ log\ \left(\frac{nCells_{y,gsa > threshold}}{nCells_{20xx,gsa}}\right)$$

Where $nCells$ is the dimension of the grid (3681 cells) of the four time periods (where y = 2012 or 2018 or 2035 or 2050) after application of the threshold (median of the positive Getis ord-Gi* values of 2012) for each GSA ($gsa\ in\ eq3$).

I represented also the values over a third quartile (>= 75 %) derived from Getis ord-Gi* statistic, to highlight the most important aggregation area for all four scenarios. From these values we calculated the potential 'gained-loss-preserved' area considering the difference of occupancy point between 2018 (the most recent year of our period) and the future scenario 2050, that is, the grid's cell that, after Getis ord-Gi* >= 75%, are present (gained), not present (lost) or conserved for both between the last year of available survey data (2018) and 2050-time window (fig. 5.5).

Results

The summary of the AIC and the deviation explained by the three approaches are summarized in Table S5.1 (Supplementary Material). The machine learning approaches (RF and GBM) are on average better than the approach of delta- GAM, and the explained deviation and R2 are higher. In the validation results (Table 5.1), the R2 is higher for the RF and GBM approaches, especially for RF, with values above 0.60 for all species except adult and juvenile mullets. One of the best fits is observed for squid with RF and GBM for both life stages (R2= 0.90), followed by juvenile squid (GBM - 0.95) and Norway lobster with 0.80 and 0.72 for adults of RF and GBM, respectively, and 0.77 and 0.89 for juveniles of RF and GBM, respectively.

Density values estimated by e-SDM in the four time windows for the 10 groundfish species are shown in the Supplementary Material, while Figure 5.1 illustrates the adult European hake distribution results. The density of adult hake increases in both time windows, especially in the Kvarner area, and for juveniles in the Jabuka/Pomo Pit area in the center of the Adriatic Basin. This is also confirmed by the hot spot (> 75%) (Figure 5.2 Chapter 5 Supplementary material). Figure 5.3 also confirms the decrease of biomass along the central Croatian coast (blue values) and a strong increase towards the north, off the Istrian peninsula (red values), indicating that there is a potential movement of resources in terms of biomass in the future basin suitability area, with a loss of habitat from the central-eastern part of the Adriatic.

In addition, data from COG (Figure 5.4) show that there is a northward shift along the Croatian coast, particularly for adult fish in GSA 17, and a southward shift in GSA 19. Adult red mullet (Figure S5.2) accumulated off the Istrian Peninsula in both time periods, although outliers indicate high potential variability in this species. The difference map (Figure S5.3) shows very high values (> 0, red area) for the entire basin, but a negative difference for the western coast of the Adriatic (< 0, blue area). Norway lobster shows no particular changes in density in both juvenile and adult stages (S5.2), with a small change in the map COG (Figure 5.4), showing a northward (eastward) shift in GSA 17A with decreasing density (< 0, blue area, Figure S5.3) was found in the Jabuka/Pomo Pit area and increasing density at the edges of the Otranto Depression in GSA 18 (> 0, red area, Figure S5.3), but data on Norway lobster need to be carefully examined because the MEDITS trawl survey can provide only limited information on juveniles of this species. The small animals in the Jabuka/Pomo pit are not necessarily juveniles (see discussion in Chapter 6). There is a dramatic decline in adult southern squid in 2035 and 2050 along the southern Croatian coast in GSA 18 (< 0, blue area in Figure S5.3) and on the eastern Croatian coast in the juvenile stage (Figure S5.3). The hotspots for adult and juvenile fish in GSA 17 and 19 do not show significant changes, but a shift to the east is observed for adult fish in GSA 18.

For both adult and juvenile anglerfish, the map shows a decline in density (Figure S5.3) along the shorelines of GSA 18 (Kvarner area), with COG moving northward in GSA 17 (Figure 5.4). For adult deepwater shrimp, the positive values (red values, > 0 - Figure S5.3) for both life stages are observed along the east coast of the Adriatic Sea and the negative values (blue values, < 0) along the west coast. For juvenile deepwater shrimp, a sharp decrease in density is observed in the coming years (blue values, Figure S5.3), especially on the west coast of the basin, and an increase in the Kvarner area and the northeastern part of the basin. The COG of deep-water shrimp shows a southward change only for the adults of GSA 19.

As for SOLEMON species, sole shows an increase in density in the Kvarner area mainly along the western coast of the basin and off the Istrian peninsula, although the COG does not show any particular changes in hot spots for either life stage (Figure S5.4). The mantis shrimp show a dramatic decrease around the Istrian peninsula, both for adults and juveniles, and an increase only for juveniles (red values, Figure S5.3) in the Kvarner area, although also in this case COG (Figure 5.4) shows no particular changes.

Finally, the density difference between adult and juvenile squid (Figure S5.3) will decrease along the northwest coast of the basin, with significant changes at hot spots for both life stages.

Fig. 5.5 shows the gained-lost-sustained area for all species between 2018 and 2050. The red areas are the gained area, say the hot-spot area (shape Getis ord-Gi* values) above the third quartile, which is only available for the year 2050. It is clear that for some species, such as anglerfish, European horse mackerel, European hake, red mullet, and common sole for adults, and the same species plus shortfin squid for juveniles, a new potential area is "colonised" with species shifting northward. In addition, species such as anglerfish and red mullet for adults and juveniles show a westward shift. A green area shows the lost area, particularly visible for anglerfish, European horse mackerel, European hake, and Norway lobster for adults, and anglerfish, red mullet, shortfin squid, and Norway lobster for juveniles, with potential habitat loss primarily in the southern Adriatic (see anglerfish and European hake adults, Figure 5.5) or on the west coast for species such as red mullet. The protected area (blue area, Figure 5.5) is the "protected hot spot' for both years, 2018 and 2050, where habitat fragmentation is observed for some species (such as anglerfish, European hake, European horse mackerel, Norway lobster for both life stages) due to the area lost or gained as a result of shifting the listed species to the west or north.

Finally, when considering both the MEDITS and SOLEMON surveys, I highlighted overlapping areas where Figure 5.6 summarises juvenile and adult aggregation hotspots for multiple species by major target gear for each scenario. Adult species caught mainly by otter trawls (left panel, MEDITS survey species such as European hake, Norway lobster, European horse mackerel, Blackbellied angler, and red mullet) have common hot spots in the eastern part of the basin, along the Croatian and Montenegrin waters with large areas where up to 5-6 species share habitats. Increasing abundance of these MEDITS species is observed between the different scenarios, especially in juveniles near the Istrian peninsula and Po delta in 2035 and 2050, but also along the Montenegrin coast. The abundance of SOLEMON (right panel, Figure 5.6), adults and juveniles, increases northward in the future scenarios along the northern Italian coast, but also along the Montenegrin and Albanian coasts (3 species = brown-red area).

Table 5.1: Results of R^2 from the validation process, for adults and juveniles of the studied species (common name, alphabetic order). These values are used for the weighted e-SDM. (see the cap. 'The SDM ensemble' in material and method)

Adult	GAM	RF	GBM	Juvenile	GAM	RF	GBM
Anglerfish	0.21	0.81	0.68	Anglerfish	0.18	0.72	0.47
Common sole	0.21	0.67	0.89	Common sole	0.16	0.60	0.70
Cuttlefish	0.65	0.90	0.90	Cuttlefish	0.42	0.72	0.95
Deep rose shrimp	0.27	0.73	0.41	Rose shrimp	0.24	0.75	0.53
Eu. Horse mackerel	0.11	0.73	0.81	Eu.Horse mackerel	0.40	0.59	0.21
European hake	0.30	0.80	0.50	European hake	0.41	0.75	0.53
Mantis shrimp	0.43	0.76	0.85	Mantis shrimp	0.40	0.77	0.87
Norway lobster	0.27	0.80	0.72	Norway lobster	0.17	0.77	0.89
Red mullet	0.13	0.57	0.30	Red mullet	0.12	0.40	0.50
Shortfin squid	0.20	0.70	0.56	Shortfin squid	0.27	0.74	0.44

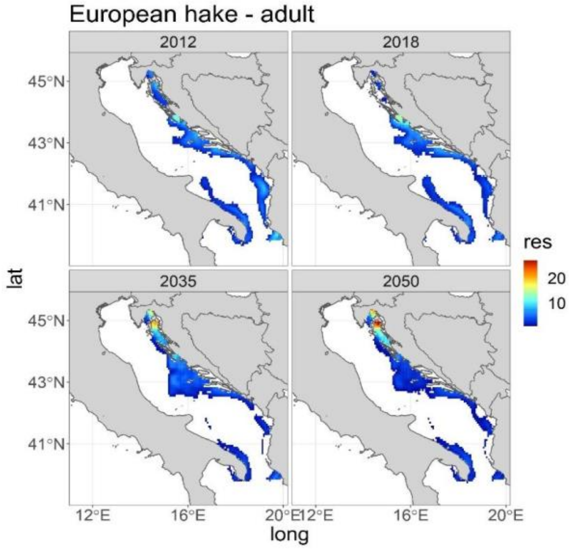


Figure 5.1: distribution density in n/km² for European hake adults in the study area for the four scenarios. The results of the others species are in the supplementary material.

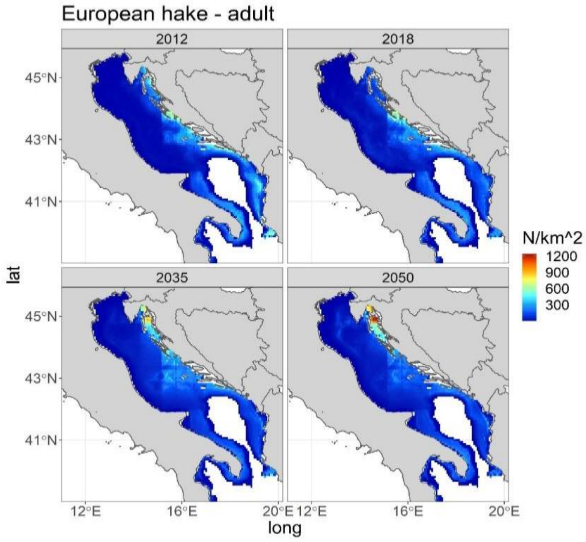


Figure 5.2: hot spot area (>75%) from Getis ord-Gi values (res=result in the legend) for the adult of European hake in the study area for the four scenarios in analysis.*

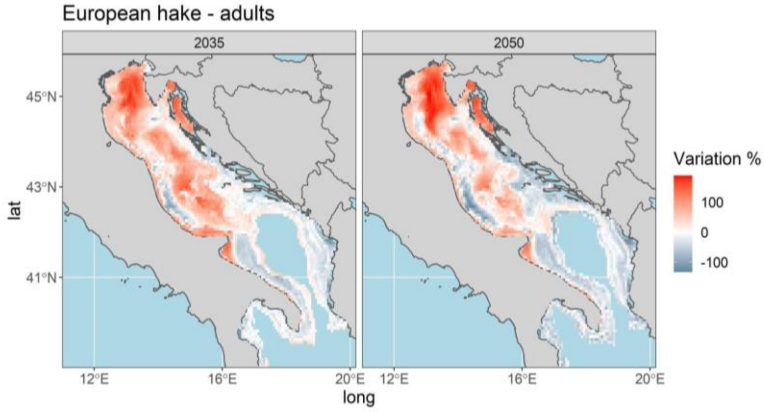
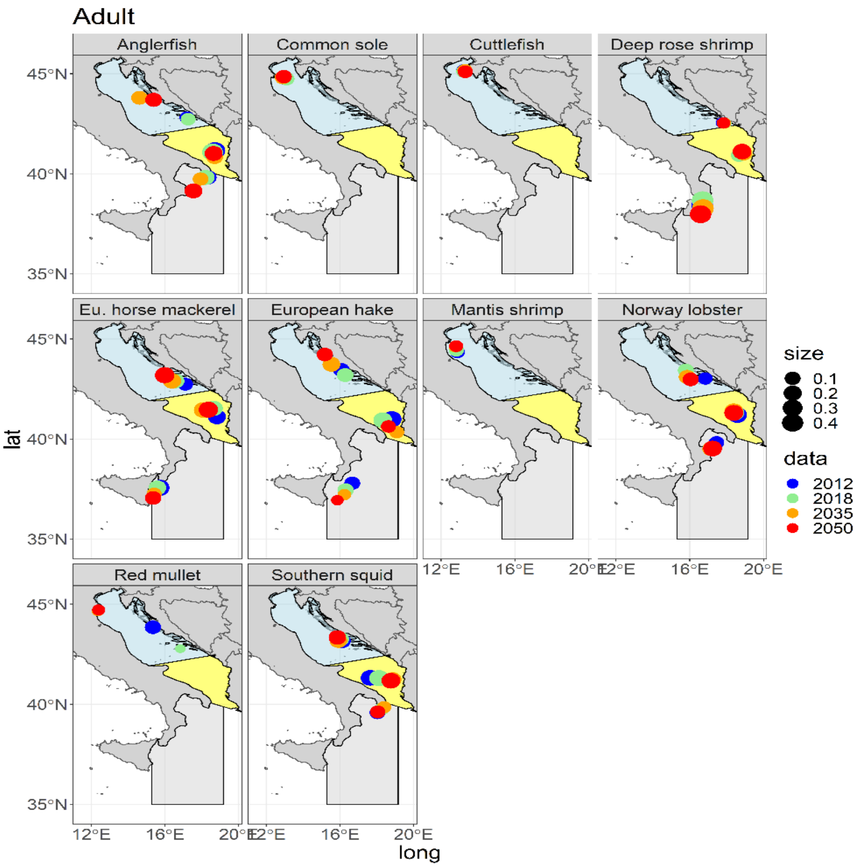


Figure 5.3: example of difference (eq.1) between 2018 density of adult European hake and the two future scenarios, 2035 left panel and 2050 right panel. Negative values (blue) indicate a decrement in density, and red values an increase.



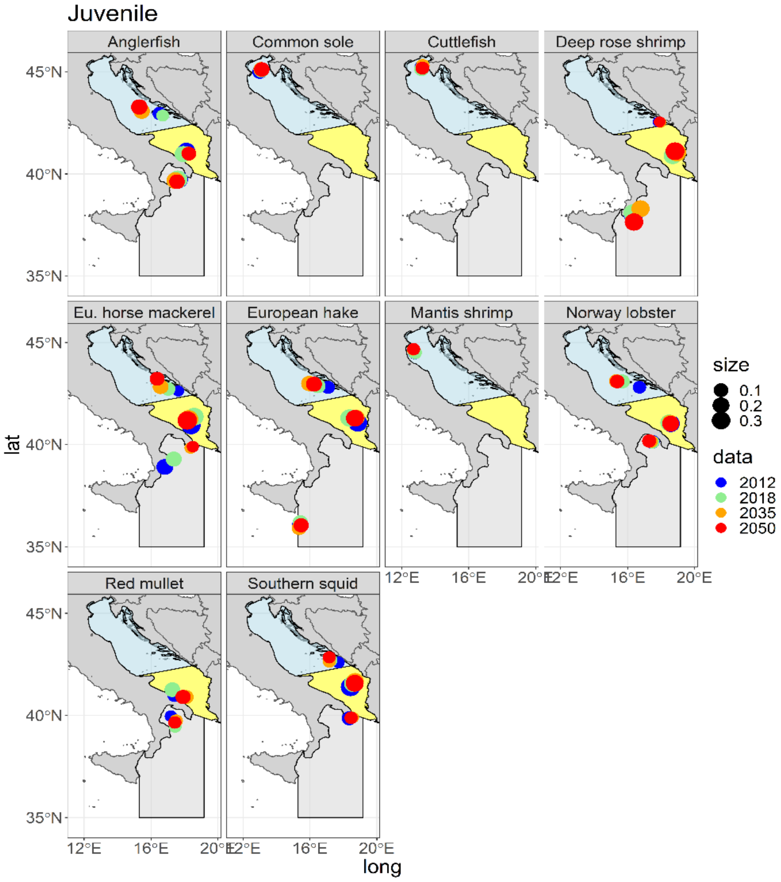


Figure 5.4: COG analysis for the adult (left) and juvenile (right) for each GSA (light blue= GSA17, yellow= GSA18, grey=GSA19) and species for the 4 scenarios (blue=2012, green=2018, orange=2035, red=2050) based on Getis ord-Gi values, with value 'size' depending on eq. 3.*

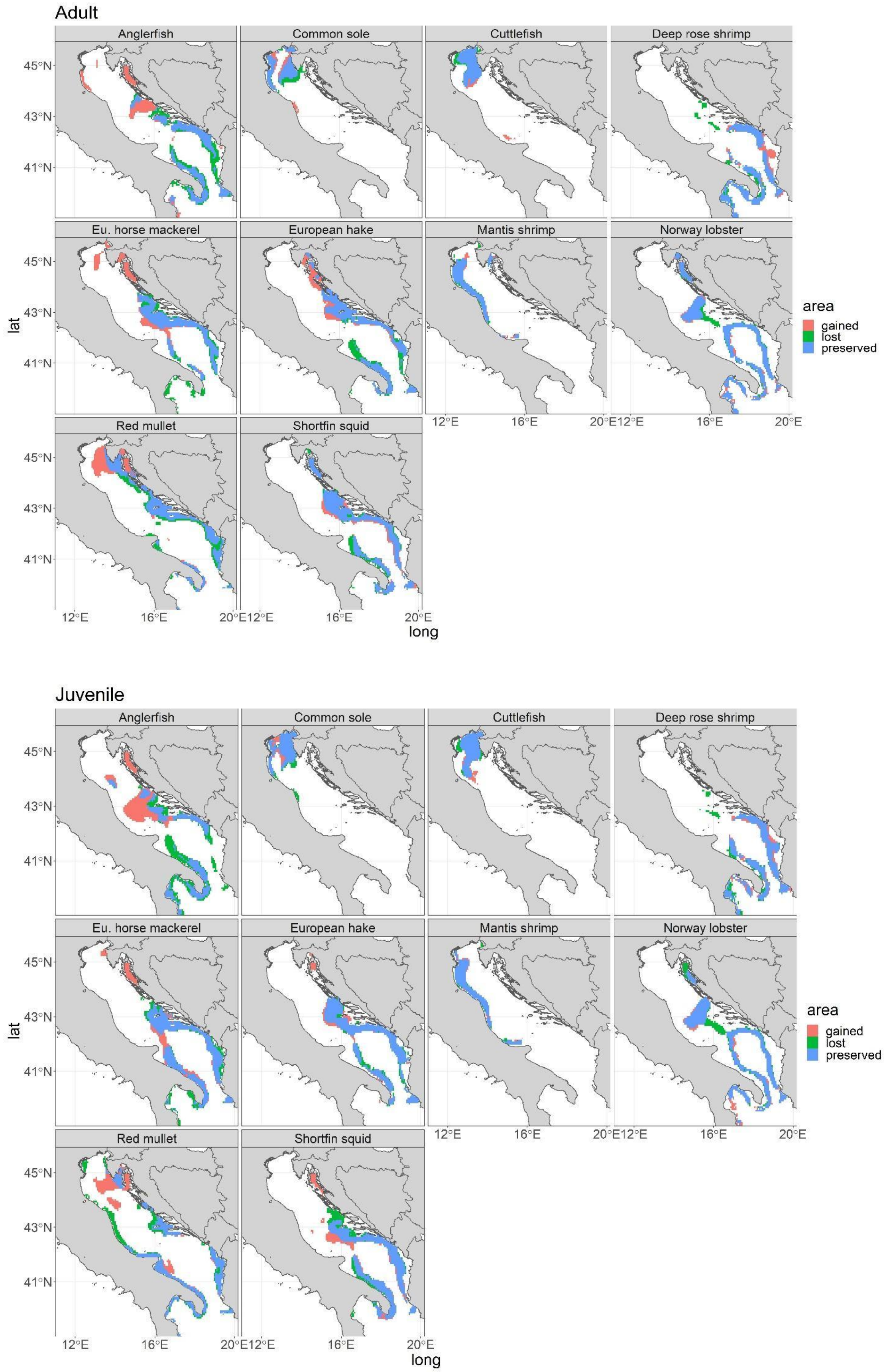


Figure 5.5: gained, lost and preserved area for each species for the year 2050 for adult (above panel) and juvenile (below panel). Each area is composed of grid cells not overlapping (gained), overlapping (preserved) and absent (lost) from the Getis ord-Gi values >75° percentile, between the most recent scenario 2018 and the future scenario 2050.*

Discussion

Warming of the Mediterranean Sea could lead to significant changes in population dynamics, genetic loss (Chefaoui et al., 2018), invasion of alien species (Azzurro et al., 2019), or reduction and expansion of the range of species, as we show in this work. MS and the Adriatic Sea have been extensively studied under climate change, with food web structure (Albouy et al., 2014), the local trophic status (Sfriso et al., 2019), the overall effect of climate on future biodiversity, the comparison of SDMs and multispecies trophic models (OSMOSE - (Moullec et al., 2022) or the biotic response to long-term climatic changes (Scarponi et al., 2022) have been considered. No study in the Adriatic and Ionian Seas has examined the distribution of species under climate change conditions with this resolution of environmental levels (CMESM products) and with an ensemble approach of different models, including fishery-dependent data as covariates and fishery-independent data as response variables from two types of surveys (MEDITS and SOLEMON). The survey data used in this work represent a very long time series of the dynamics of commercial species in the Adriatic and Ionian Seas and provide a good and satisfactory estimate of the distribution of the population in terms of abundance and density, representing a good 'picture' of the realized niche. To emphasize this concept, in this study I developed a quantitative (distribution in terms of n/km2 or density differences, Fig. S5.2 and Fig. S5.3, respectively) and qualitative (CoG and area gained/lost, Fig. 5.4 and 5.5, respectively) representation of the future potential distribution of the main commercial species in the Adriatic Sea, using for the first time in this area the RCP projection from CMEMS data developed by Reale M. et al. 2022. The species of interest in this work live in a temperate zone, specifically in a dead-end basin where displacement and migration are limited. Different patterns between northern and southern species were observed in our results. Southern/central species such as anglerfish, European horse mackerel, southern squid, Red mullet, and European hake are expected to disperse northward in both life stages in the future (Figure 5.5), especially along the eastern coast of the Adriatic Sea. Species that are more established in the northern area, such as sole, mantis shrimp, and squid, do not show any particular changes in area or CoG increase. This suggests that the northward shift in density and CoG distribution is more pronounced in the central and southern portions of the study area. For the central/southern species, the density (Figs. S5.2 and S5.3) increases towards the north, especially along the Croatian coast, e.g., for European hake for both life stages, anglerfish, and also European horse mackerel, which is concentrated in the area of Quarnero and the Istrian peninsula. The northward expansion of the area occupied by the above species indicates polarity between species with temperature affinity, i.e. shifts expected from warming sea temperature (Poloczanska et al., 2016).

In this study, I highlight that the main commercial species, representing 15% of the total landings in the area, may change their location and density in the near future, likely affecting fishing activities and seasonal patterns. Considering the 4 species that are experiencing significant changes in density and hotspots (Figure S5.4), I assume that hake, red mullet, monkfish, and horse mackerel for adults and red mullet, monkfish, and horse mackerel for juveniles (including red mullet, but as I pointed out in Chapter 4, it is not well covered in the MEDITS survey) are the stocks that will be most affected by climate change in the next few years and that will 'conquer' new areas in the north, with unpredictable commercial and economic impacts. Northern species, on the other hand, are unlikely to be impacted by fisheries, but will be stressed by the 'invasion' of central/southern species. Summarizing the hotspots (above the third quartile, Figure S5.4) for juvenile and adult accumulation of multiple species may help us understand future prospects for fisheries grounds and management measures, particularly in the FRA area or in the potential new FRA zone. Figure 5.6. shows the number of species surveyed for the MEDITS and SOLEMON surveys in total (abundance) for each grid cell, showing a loss of diversity, especially for juveniles in the southern part of the basin, and increasing abundance of species in the northern part of the study area.

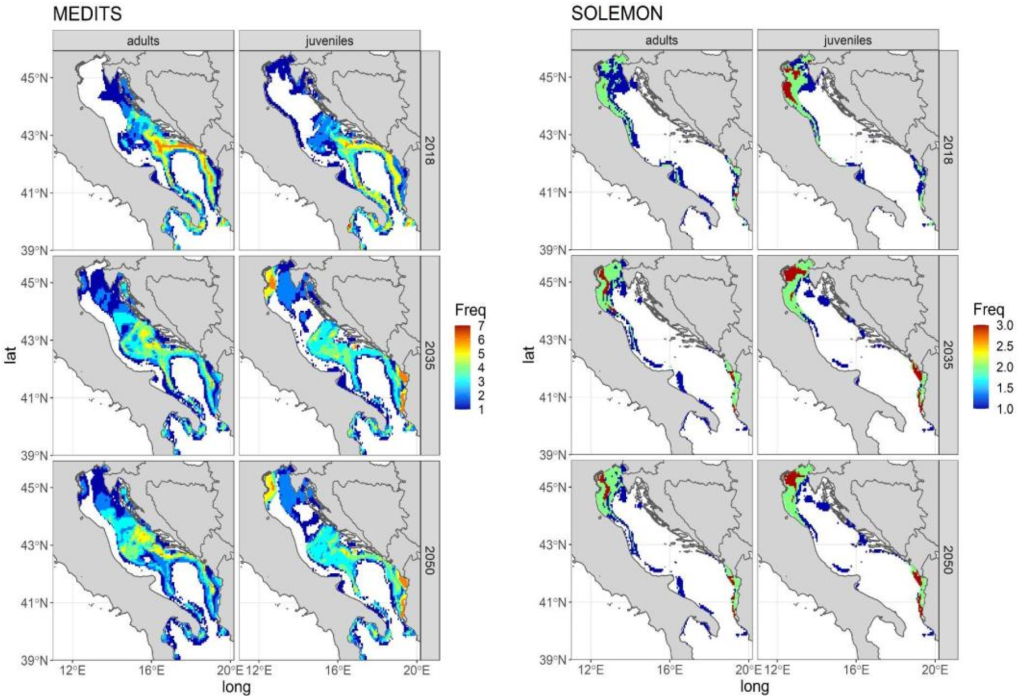


Figure 5.6: Results of overlapping hot-spot for MEDITS species (left panels, adults and juveniles) and SOLEMON species (right panel, adults and juveniles). Values (legend title: Freq = frequency) refer to the number of species having Gi greater than the third quartile in each grid cell for the three main scenarios, 2018 (first-panel row), 2035 (middle panel row), and 2050 (bottom panel row).

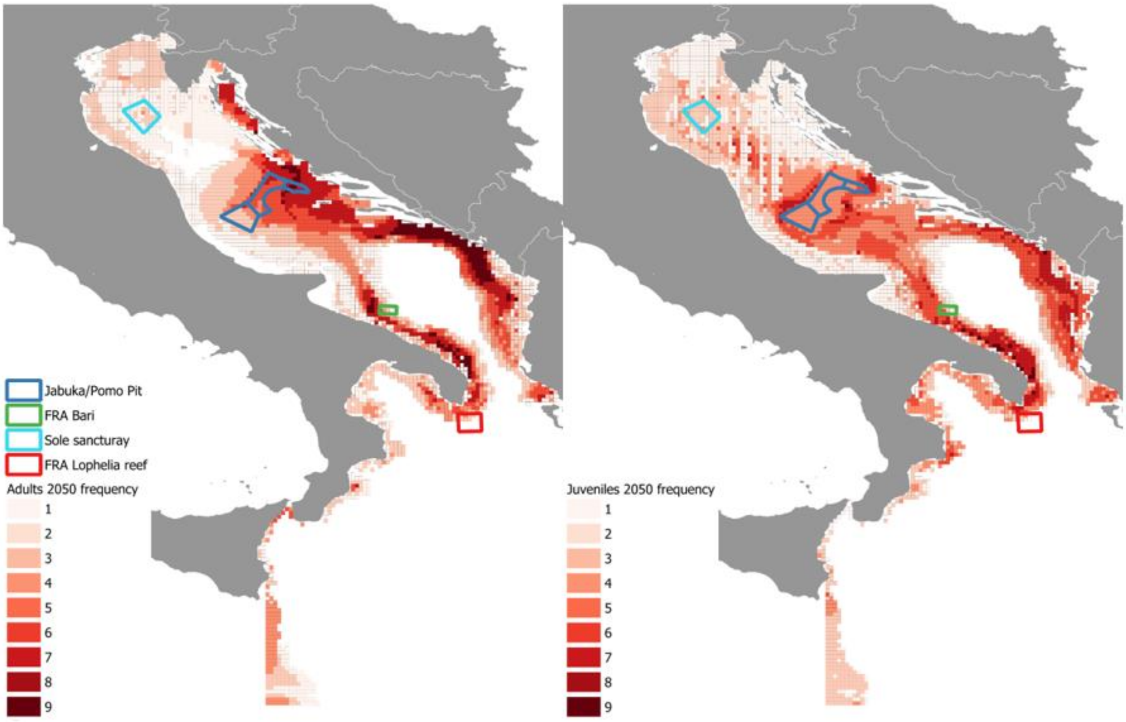


Figure 5.7: Results of overlapping hot-spot for adults species (left panels) and juveniles species (right panel). Values (legend frequency adults or juveniles) refer to the number of species having Gi greater than the third quartile in each grid cell for the 2050 scenarios. Overlapping FRA and important managing area are visibile, as Jabuka/Pomo Pit area (dark blue), Bari and Lophelia FRA (green and red respectively) and Sole sanctuary (light blue).

Figure 5.7 shows the future range of all species (except mullet-see Chapter 4) for adults and juveniles of both surveys and illustrates the overlap FRA in the study area.

A possible representation of the future range of the species could be beneficial to improve the spatial management of the area. In this context, we know that fisheries management in the studied area is based on different approaches, including the adoption of spatial measures such as FRA. Possible future changes in the suitable area, as I have evaluated in this work, could lead to a change in the fishery area for the species concerned and directly affect the port and fishing activity in the Adriatic and Ionian Seas.

Considering mainly the MEDITS species for which a change in range is expected, the increase in abundance of species near the Istrian Peninsula and the Po Delta (Figs. 5.6) could affect fishing grounds in this area, or conversely, the decline of some species in the central part of the Adriatic, especially juveniles (Fig. 5.6 - Juveniles), could change the effort and number of vessels operating in this area, leading to a change in port operations and fisheries management.

Successful establishment of a particular species in a new area depends not only on biotic and abiotic characteristics, but also on dispersal ability, sex ratio, demographic structure, and adaptability to new environmental conditions. In addition, we do not know whether species arriving at a new site with similar conditions, due to expansion of suitable range in the future and reduction of current range, are likely to succeed in establishing species that have not yet "settled."

The limitations of this study are primarily the data used, which are from a spring-summer trawl survey, and the interannual dynamics, which cannot be fully represented. The use of the same models includes the limitations and advantages mentioned in Chapter 4 regarding the inclusion of oceanographic variables related to climate change to evaluate the management area under future climatic conditions. Fishing effort could also be a limitation of the models, as this covariate is unpredictable in future years. The decision to use the fishing effort covariates in this work as well is due to their importance as a proxy for resource dynamics and distribution. The area is heavily impacted by fisheries and it is important that it continues to be exploited in the future.

Chapter 6

General discussion

Disentangling the role of Environmental data

Although the integration of environmental covariates into marine species distribution models is increasingly used (Essington et al., 2022; Goodman et al., 2022; Thorson et al., 2015), application to pelagic resources is often considered in the Mediterranean (Giannoulaki et al., 2008), mainly because of easier accessibility and broader coverage of surface and submarine oceanographic variables. In this work, the implementation of environmental covariates estimated from 3D Copernicus fields improved the accuracy of the models (expressed in terms of diagnostic values such as AIC, explained error, and prediction error) and was used in all applications (see Training and Testing Routine, Chapter 2, Chapter 3, Chapter 4). As expected, the covariates are specific to the individual species and life stages, with some of these covariates being significant (see bottom temperature or oxygen for species such as European hake or red mullet, see, e.g., Table S2.3 and S2.18, respectively) and other variables having no significant effect on modelled biomass (see results for sole in Table S2.7 in the Supplementary Material). Variables used in SDMs should be biologically significant and meaningful for each demersal species and are selected based on the physiological fitness of the species (Zimmerman & Guisan, 2000). Notably, different environmental variables can lead to different model predictions and performance (Johnson & Gillingham, 2005). However, collinearity among environmental variables is problematic because the statistical model cannot disaggregate the role of correlated variables, which could lead to overemphasis of their effects. For this reason, combining many environmental variables or factors during the training and testing routine is essential, and the first step is to remove a highly correlated variable, for example, by analysing an indicator such as the variance inflation factor (Sheather, 2009) or by Pearson and Spearman tests (Dormann et al., 2007).

In this work, I used a number of different environmental predictors ranging from temperature, oxygen, and chlorophyll to particulate organic carbon and basic nutrients such as nitrate and phosphate, and combined survey datasets with these measurements over the period from 1999 to 2018 (MEDITS and SOLEMON survey datasets). Before using these variables in the training and testing routine (see Chapter 3 and Chapter 4), collinearity analysis was performed (VIF and Pearson).

All of the feedback analyses applied in Chapter 2, Chapter 3, and Chapter 4 were critical to understanding the role of environmental factors in explaining past data, but the application of this type of model was also extended to future scenarios (Chapter 5), which are so important in the current issue of climate change because changes in oceanographic variables can cause fish dispersal or concentration (Hilborn & Walters, 1992).

In addition, environmental factors are fundamental to fish colonisation, and drastic climatic changes could lead to a change in biomass and distribution trends, and a possible predator-prey relationship should also be considered, such as a climatic influence on forage fish dynamics (see, e.g., Suca et al., 2021), which is important for some predators (such as hake), or a shift northward, e.g., to polar regions (see Baudron et al., 2020).

In this context, the development of SDM based on survey data with long time series is crucial to show the possible changes in a sub-Mediterranean basin such as the Adriatic and Ionian Seas, which is so important from a fisheries perspective (FAO, 2020b).

Estimating the potential future distribution of species

In Chapter 5, I estimated the potential range changes that could affect the major commercial species in the Adriatic and Ionian Seas, as shown in Figures 5.4, 5.5, and 5.6. Climatic changes in the Mediterranean have been well and extensively studied for decades, and a recent study highlighted that acidification, oxygen depletion, nutrients, and biomass could change under a warming scenario (Reale et al., 2022), with significant changes expected in the coming years. Understanding how the species could change the aggregation area in this context (see Figure 5.4 - 5.5 - 5.6), and assessing the impacts on adults and juveniles, is central to the study area, where fishing activities, port, landings, and economic activities associated with fishing are critical.

The analysis (Chapter 5) indicated that not all species will be affected under future environmental conditions altered by climate change. Particular emphasis was placed on differences in species such as red mullet and anglerfish or European horse mackerel that will result in relevant habitat change, with large areas currently considered hotspots becoming much less relevant for these species and instead more likely to be distributed in northeastern areas near the Istrian Peninsula and Quarnero Islands (Figure 5.5). Other species such as adult southern squid and Norway lobster were unaffected by predicted environmental changes (Figure 5.5), a result that may reflect the high adaptive capacity of these species. Overall, it appears that northern species (e.g., common sole, cuttlefish) are not greatly affected by climate change-induced impacts, as the centre of gravity shows no relevant changes (Figure 5.4). For species such as European hake, or red mullet and anglerfish, the prediction showed that a northward shift is likely, leading to an equalisation of the future area between northern and central-southern species in the Adriatic. These results are the first in the studied area using an ensemble approach following a protocol developed in this thesis (Chapter 3 and Chapter 4).

The spatio-temporal information resulting from this type of model could be integrated into the spatial fisheries management of the area, as I indicated in the introduction and in Chapter 2 and Chapter 4. Managing this information, such as species occurrence, area where multiple species congregate, efforts to maintain hot spots with juvenile fish, highlighting biodiversity, and possible future changes in the distribution or spread of invasive species, is critical in an ever-changing world, and fisheries stakeholders and policy makers should consider this aspect as well. In the next subsection, "Discussion," I will explore this possibility.

Contribution to the management processes

Stock assessment in the Adriatic and Ionian Seas is conducted by two major international committees, SAC of the GFCM (Scientific Advisory Committee to the General Fisheries Commission for the Mediterranean) and STECF (Scientific, Technical and Economic Committee for Fisheries), which evaluate stock assessment models in a single species context (Ulrich et al., 2019). These committees use information on catch, survey data, landings, discards, and fishing activities for stock assessment tools for selected key commercial species. Stock assessments typically produce estimates of at-sea biomass, spawning stock biomass and recruitment, and fishing mortality over time. These estimates form the basis for establishing reference points such as biomass at MSY (for MSY, see the introductory chapter Overview of fishing pressure and management regulation in the study area) and fishing mortality at MSY: comparison of these reference points with the current situation of individual stocks allows determination of exploitation status, which forms the basis for management recommendations. All of this information is important for understanding stock status, but it depends not only on good fishery-dependent data (catch and effort), but also on fishery-independent information such as trawl survey indices used to tune stock assessment tools. Trawl survey data are already used to reconcile stock assessment tools whenever possible, but often using simple weighted averages of densities or geostatistical interpolation.

The potential inclusion of oceanographic variables in SDM and comparison between indices (e.g., biomass trend or centroid) could provide a great opportunity to better understand the ecological dynamics of key commercial resources (and discarded or threatened species) and provide more accurate biomass trends to support stock assessment models.

SDM approaches are considered a good starting point to provide the most accurate map of distribution, hotspots, density index, and correlation with environmental variables with stock assessment results to evaluate macro or regional areas of interest for management. For example, SDM results have been useful in demonstrating the ecological importance of several demersal species in the Croatian coast or central Adriatic. With respect to the Pomo/Jabuka Pit, the model developed in this work confirms the importance of this part of the Adriatic (FAO, 2022) as an important hotspot for adult hake, juveniles and adult Nephrops, highlighting the overlap of areas with multiple species (hake - lobster - squid - anglerfish, Figs. 4.4 and 5.6) and demonstrating how SDMs can continue to support decision-makers who need to assess the relevance of new regulated areas.

SDMs use location (georeferenced data) and information about environmental conditions to predict distribution and estimate the relationship between the variables used using a variety of different mathematical and statistical approaches. The predictive map produced as the main output of SDMs can provide reproducible and detailed information that expert opinion cannot. For these and other reasons, the integration of SDMs into stock assessment, fisheries management, spatial fisheries management, and policy evaluation is becoming increasingly important.

The literature identifies 2 main limitations to the use of SDMs in management decisions:

1. SDMs are complicated to interpret, e.g., variation in the quality of the data input and the model used can lead to different predictions of the distribution. In this case, a cautious interpretation of the results is required, evaluating the representation of the potential (basic niche) or actual (realized niche) distribution (Guisan et al., 2013; Morisette et al., 2017).
2. The second criticism concerns model development and evaluation, which require the involvement of experts and ecological modelers, including questioning and interpretation of results (Addison et al., 2013; Morisette et al., 2017).

Establishing guidelines is fundamental to incorporating SDMs into management processes, especially in a context with economically important values such as in the fisheries sector. It is not my intention to propose new guidelines in this context, and following the examples of Araújo et al. (2019), Guisan et al. (2013), and Morisette et al. (2017), I can argue that some of the results highlighted in this work could be useful for resource assessment in an important fishery area such as the Adriatic and Ionian Sea, considering these approaches as a starting point for policy management assessment.

Following Figure 1.5 in Chapter 1, sharing this information with the GFCM working group and SAC could be a way to evaluate spatial management from three important perspectives:

1. SDM experts could improve the knowledge of "stock assessors' and vice versa
2. Information sharing between SDM experts, stock assessors, and stakeholders could improve the assessment of key commercial species in the study area, e.g., following this work as a case study (Adriatic and Ionian Seas)
3. Management assessment could consider different aspects, approaches and expertise, especially in relation to climate change.

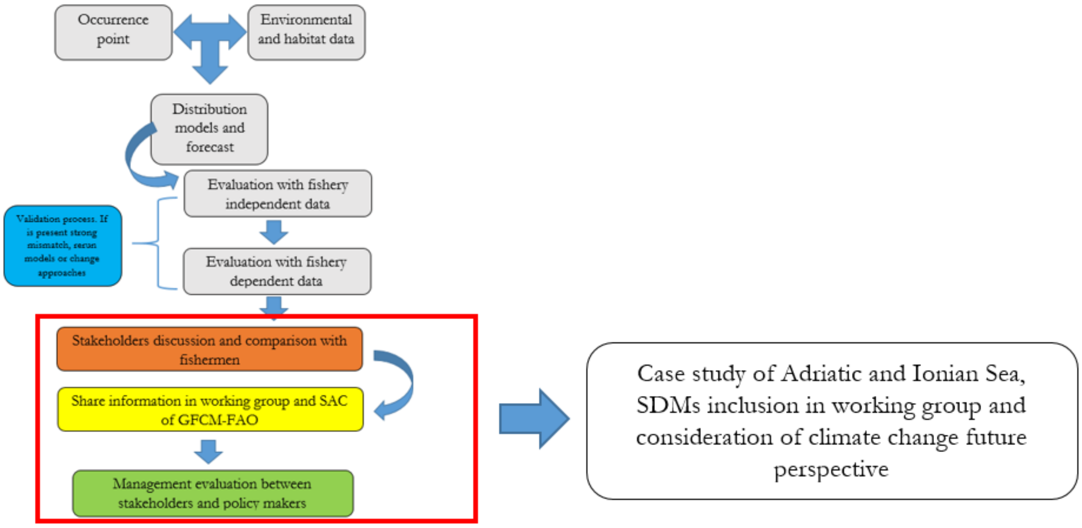


Figure 6.1: example of inclusion of this work as a case study in the working group, SAC and stakeholder evaluation of GFCM-FAO.

The idea of managing spatial assessment using an SDM approach that takes into account the assemblage of many species at the same time or the co-occurrence of key species (see future multispecies perspective) could be fundamental in such an important study area as the Adriatic and Ionian Seas.

One of the objectives was to identify and propose the use of SDMs for the assessment and management of multispecies fisheries, taking into account environmental and effort variables in an area so strongly influenced by fisheries. In addition, SDMs can be considered as long-term strategies for EAF that also have visible economic and marine conservation benefits. In addition, local knowledge of the area can be useful in minimizing mismatches between conservation and fisheries objectives. Identifying hotspots, defined as geographic areas with consistent biological composition that are subject to known fishing pressure, is a first step toward incorporating the SDM approach into practical fisheries management, including consideration of different life stages such as adult and juvenile fish.

This study shows that in the Adriatic and Ionian Seas there are many target species of demersal fisheries and high biodiversity throughout the area, highlighting the need to adopt management plans that consider the spatial distribution of resources. The selectivity of the bottom trawl fishery is low, bycatch is significant in the area, and the co-occurrence and exploitation of multiple target species is evident, and SDM can help identify important target species and key aggregation areas for fishing in time and space. The example FRA of

Jabuka/Pomo Pit for hake and Nephrops shows that pressure on these species is decreasing and catches are increasing (FAO, 2021).

The results of this work also highlight the need for spatial fisheries management that takes into account both fisheries and the protection of specific species and biodiversity areas (example of the west coast of the Adriatic Sea in Croatia and Montenegro, see Fig. 4.4).

One way to achieve this protection could be, for example, not to fish some areas for a certain period of time in order to restore the stock, which could allow spatial management of fishing activities such as trawling, alternating areas designated for fishing with areas designated for conservation.

Following Russo et al. (2019b) or Dimarchopoulou (2018), we know that the application of spatial management and spatial/temporal fishery closures has led to recovery of fish stocks. The management approach proposed here is a starting point for a new assessment of spatial management in the GFCM and SAC assessment processes, aiming to optimize knowledge of the area as a case study where fisheries resources are 'under pressure' and strong recovery is needed.

All these processes in the world of SDM have some limitations, especially in terms of modeling steps, evaluation of performance, uncertainty and sensitivity of models, and differences between implemented approaches.

Some studies argue that SDMs rarely predict the 'true' biology of real populations (Lee-yaw et al., 2022), especially depending on the focus of the study, distinguishing different categories such as occurrence and abundance studies, population fitness/performance studies, and genetic diversity studies.

Lee-yaw et al. (2022) consider that especially for the first two branches of studies, i.e., SDM occurrence and abundance studies, the prediction and extrapolation of results are quite good, and several studies also evaluated the performance of the implemented models. In this work, I have used several approaches that address calibration and prediction of occurrence and density data, evaluation of environmental variables, and a final representation of the demersal fish species in the study area. These are the reasons why I think this is useful for various aspects of fisheries science, from resource assessment to qualitative and quantitative outcomes to a management perspective, as I said earlier. Of course, as with all studies and modeling approaches, there are limitations to the method presented, which I will explain in the next subsection.

Limitations

The current literature is replete with examples of correlative species distribution models, and in the last 20 years, mostly on marine species (Melo-Merino et al., 2020). As I have previously reported, these models have been used in a variety of study areas, from climate change (Kearney, 2006) to recovery actions and conservation decisions (Guisan et al., 2013) to extrapolation of data (Guillaumot et al., 2020) to define a standard protocol for SDMs (Zurell et al., 2020). The techniques vary and examine habitat suitability (with presence or presence/absence data) or abundance of animals or plants (e.g., count or density data), but we need to remember some limitations of these types of approaches. As I discussed in Chapter 4, the species sampled in this study are sampled during the summer (MEDITS) or winter (SOLEMON) seasons, and infra- and inter-annual dynamics are not fully explained because of sampling design limitations. One of the main problems associated with SDMs is that all sample data are incomplete and biased. The survey or sampling campaign is limited to a specific time period (season or time of day) and a specific area of space, and therefore represents a subset of all potential distributions of a given species or ensemble of species (in my case). In this context, it is important to keep in mind that sampling bias may result in not capturing all information about a species and the environmental gradient in which it occurs. For example, an occurrence site could be exceptional because of the unusual habitat of that species, confusing the user about the actual conditions under which a population or species is viable. For this reason, good resolution of the model and grid of predictions is useful to match the spatial occurrence of the species and environmental variables used. The data used in this work from the survey carried out in the Adriatic and Ionian Seas represent good information on the spatial and temporal dynamics of the resources, clearly limited to a specific season, taking into account the two main seasons of reproduction and spawning of the resources concerned (see Chapter 4), and using the best available resolution of the environmental covariates coming from CMEMS products, this product having been recently improved (Cossarini et al., 2021), which is useful for the future perspective of my work (see next chapter Future perspective). I also believe that for species such as mullet and Nephrops, the MEDITS survey is not so representative and that some bias in the data could occur, especially when we consider the survey season due to the discrepancy between the survey and the maximum recruitment period in the area, as in the case of mullet, where shifts and movements are not quite well represented. In the case of Norway lobster, the data may be uncertain due to differences at the subpopulation level for this species in the Jabuka/Pomo Pit area, as I pointed out in the discussion in Chapter 4

Another issue affecting SDMs is the correct 'taxonomy' used to identify this species, building a large and useful database of georeferenced sightings, and avoiding putative information or incorrect taxonomy (Lozier et al., 2009). Again, I consider the data used to be a good representation of the species in question in terms of taxonomy and maturity stage determination. A long and qualified time series of survey data fully represents the aspect of the resources involved used in another study (Colloca et al., 2015; Lauria et al., 2017), data that I analyzed with confidence knowing the work of the experts involved in the surveys, as well as the standardized procedures used and the relative ease of identifying the species covered in this species.

The prevalence of the data, i.e., the percentage of presence/absence of a given species at the sampling site, could also be a limitation in the modeling process. The percentage of prevalence between 20% and 75% can provide good results (McPherson et al., 2004), but prevalence is not a factor, and if there are good covariates in the development of the models and if accurate training is performed, the modeling processes can be considered accurate (Jiménez-Valverde & Lobo, 2006).

For adults of European hake, red mullet, common sole, cuttlefish mantis shrimp, and for juveniles of European hake, red mullet, southern squid, European horse mackerel, common sole, cuttlefish, and mantis shrimp, the prevalence of the data reaches and exceeds the 40% mark, and for the other species it ranges from 25% to 40%, with the exception of Norway lobster and anglerfish, all limitations already presented in the discussion in Chapter 4. I therefore consider that the data used for almost 8 out of 10 species are a good representation of the occurrence of these resources in the Adriatic and Ionian Seas. For two species, adult anglerfish and juvenile and adult Norway lobster, the survey, in this case MEDITS, is not as representative, and all results need further improvement, but, as discussed earlier, this type of approach is useful to understand the basic dynamics of this species, also taking into account the assessment of the error resulting from the modeling processes (Supplementary Material S4).

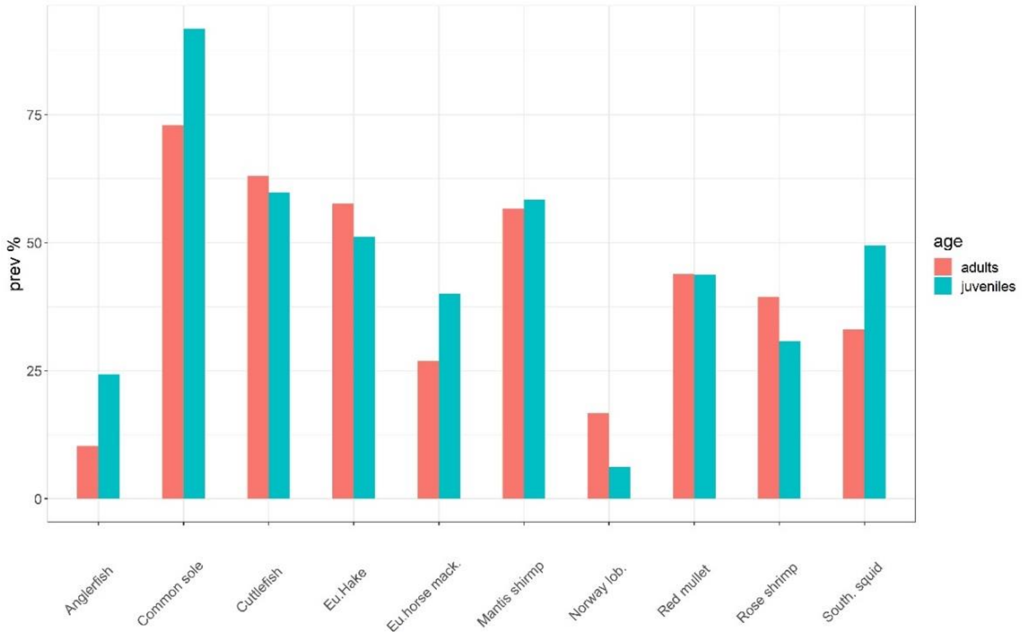


Figure 6.2. percentage of prevalence data (presence) respect the total dimension of the sample, for each species (x lab) and age

In addition, a minimum sample size of more than 30 is recommended (Wisz et al., 2008), and in our case the size always exceeds 1000 data points for each species and life stage. Therefore, the available information considered over the years is a very complete data set well suited for this type of approach.

Regarding the projection of the model output, the final prediction or extrapolation results in the form of a distribution map, habitat suitability map, and probability of presence/absence in the expansion area, we need to keep in mind and understand that the projection grid should cover the area accessible to our species of interest in the available time period, and that the background data (prediction/extrapolation grid) should be limited to the same area (Barve et al., 2011), because if the background data are outside the sampling of the staging area, the results could be biased and the assessment metrics inflated (VanDerWal et al., 2009). All data used in this study are in a fully sampled area, over time and space, with the final representation being a good snapshot in time of year of the resource, in terms of predicting outcomes and not an extrapolation, say a final and exhaustive 'interpolation' between the grid and the most determined environmental variable (CMEMS) with a full survey dataset of demersal resources.

We don't know all of the factors behind a species' ability to disperse, at least not in this context and area, as variables other than climate can also influence and control dispersal, but I consider the multivariate and multimodal approach used here to be a fully explanatory study of the location, distribution, and potential approach to evaluating the management of the resource in question.

Based on the idea that there is no single approach that works best for all species at every spatial and temporal scale, I considered using multiple modeling approaches by combining them into an ensemble. Based on the idea that each model (when fitted) can capture some features of the species distribution, I combined all models and weighted them based on the correlation coefficient.

The statistical models applied generated a functional relationship between data and covariates that is assumed to be correct, but it's not easy to meet these assumptions, especially in some cases such as climate change conditions (Elith & Leathwick, 2009) (Elith et al., 2006). Other assumptions in SDMs are those of the presence-only model, where the generation of pseudo-absence is necessary (see, e.g., the MAXENT model), but the interpretation of the results isn't straightforward. In this work, using survey data, there is a lot of absence data, meaning that the species is absent or very rare at this site over the several years of the survey. In my case, the Tweedie family or delta approach are the two types of models that specifically account for the presence of many zeros and work well with this type of data. Of course, these models aren't the best for all types, and the machine learning approach such as the Random Forest ended up being better at representing the data than other approaches (see Chapter 4- Discussion).

We must remember that no two models give identical results, and this is the main reason why I chose to use weighted ensemble models. An ensemble model can help identify the differences between models (Araújo & New, 2007; Roura-Pascual et al., 2009) and identify the uncertainties that arise from the different choices made during the modeling process and highlight where one model performs better and other models don't. All models used are subject to uncertainties, e.g., due to sampling design, precision, and predictor resolution (Stohlgren et al., 2010), but the ensemble of models is a good application, especially when weighted based on the diagnostics of each model implemented in the modeling processes.

The novelty of the approach consists in the systematic application of the SDM models in the form of an ensemble of different models on trawl survey data of the Adriatic and Ionian Seas containing a large set of environmental variables, and in the evaluation of the different performances in terms of diagnostic parameters such as AIC, MAE, R2, for different models in a spatial training and testing routine, for two life stages (adult and juvenile fish), with a prediction and evaluation of past, present and future projection that it's something new in the field of study, taking into account all the assumptions and limitations that I've previously reported.

Future perspective

In this last chapter I will present all the aspects concerning the possible improvement of the models and approaches I have applied in this thesis. First, I would like to highlight some important points that I can further develop in the future, namely:

1. Improving the resolution of covariates, considering the final distribution of species and the correlative results between environmental variable and response variable (presence/absence or density).
2. Introducing the concept of dispersion in SDMs.
3. Applying the Bayesian approach or a statistical method such as Gaussian Markov Random Field, used in some approaches and packages in R, with a 'background' script based on Template Model Builder (TMB) to investigate the possible improvement of my models in a multispecies context.
4. Application of the same model I used here, but to new species, including pelagic species and not just demersal species.
5. Application of SDMs with 'new' data, such as genetic information.

I will briefly review the previous points to illustrate the possibility of extending my models, which I was unable to introduce during the three years of work on this dissertation due to time constraints.

1. Use of new resolution of the covariates of the model applied

As mentioned earlier, the predictor variables used here were derived from CMEMS products, and the resolution used in this work is 1/16° (see Chapter 3 and Chapter 4). With this resolution, the final grid used to predict the results (see the final distribution map in the previous chapter) consists of "cells" or "pixels" of about 6 km per side, which was the best resolution when I started this work. Continued improvement in modeling processes (Cossarini et al., 2021) has led to a new resolution of CMEMS variables, which is now 1/24°, with a grid cell of about 4 km. The possible new pooling of data between my response variables (presence/absence or density) and these new high-resolution covariates could lead to an improvement in the models, perhaps an increase in the significance of certain variables or an increase in the explained variance of the fitted model. We must also keep in mind that the computational time required for prediction on a high-resolution grid is longer, but can be managed with remote approaches and code refinement.
The results presented here are robust and complete to what I have presented, but improvement could be a satisfying exercise from a modeling standpoint and for improving understanding of the relationship between species and environmental variables in the field.

2. Dispersal: species movement

Understanding how the species are distributed and especially the dynamics of the range of expansion, also considering the climate change scenario, is of paramount importance. Implementing dispersal into SDMs remains an exception rather than the rule, and recent SDMs and research have begun to include transitory habitats (Huang et al., 2020) or species and taxa present simultaneously (Lehtomäki et al., 2019).
When we talk about species movement, we usually refer to the dispersal ability of the organism (animals and non-sessile) and use the term 'dispersal' instead of movement because it is the accessibility of habitats by species or a population that is considered, not the movement itself (Datry et al., 2016; Elith et al., 2006). Dispersal ability depends not only on the characteristics of an organism but also, and more importantly, on the nature of the habitat type. Habitats, except in rare cases, are not clearly delineated areas that do not have a constant boundary over time and where communities always remain stable. This characteristic also depends on the scale at which the habitat is observed and where our points of occurrence are located. For SDMs, a well-defined area in space is better than complex areas, which clearly depends on the characteristics of the ecosystem studied and the species involved. For example, in species such as Norway lobster in the Adriatic Sea, larval dispersal and recruitment to the benthic stage depend on environmental variables, and it is especially important to assess dispersal characteristics in an SDM.
Furthermore, in SDMs, movement is described as post-hoc inference of movement with a dichotomous response: a habitat is accessible or not (Guisan et al., 2006). In this case, prior knowledge of an organism's characteristics may be required to provide a good description of movement and to distinguish between movement due to migration or habitat displacement, rather than movement related to biological traits. Quantifying dispersal is not

straightforward, but is necessary to improve predictions and quantify uncertainty (Holloway et al., 2016). Not many software tools have been developed in the literature to understand dispersion dynamics, and they do not implement the latest methods for accurate modeling. Some R packages that have been developed include components of dispersal rate in terms of species-specific or occurrence and background subsamples, for example, 'MIGCLIM' and 'ecospat" (Di Cola et al., 2017; Engler et al., 2012). However, there is no SDM software that can efficiently implement environmental subsampling and integrate dispersal capability to assess changes in habitat suitability for many species and climate models.

It is well known that fish are generally mobile species and that movement can be very important to their dispersal, including from a fisheries management perspective.

In this work, I did not use dispersal properties, which could be a new aspect for further improvements of the presented model. The data used in my work include many aspects derived from abiotic variables and fishing effort, but without the dispersal aspect. Considering the definition of "niche" (see General Introduction - Introduction), I can consider the models presented as a fine snapshot of the state of the species involved over space and time, in correlative and diversified approaches. Given the limitations of these processes, I contend that the implementation of the capacity for movement may present a new challenge for subsequent work.

3. Application of new modeling approaches in a single and multi-species context

SDMs continue to evolve, and new modeling approaches and packages in R have been introduced to the community, such as VAST (Thorson, 2019; Thorson & Barnett, 2017), HMSC (Ovaskainen et al., 2017; Tikhonov et al., 2020), and sdmTMB (Anderson et al., 2022).

- VAST - Vector Autoregressive Spatio-Temporal model - is a model developed with TMB (Template Model Builder - package TMB - (Kristensen et al., 2016) using Laplace approximation and stochastic partial differential equation (SPDE - (Lindgren et al., 2011) was developed. VAST also works in a multispecies context used in fisheries or for land ecology studies (Thorson et al., 2016; Thorson & Barnett, 2017). There is a growing literature on joint-species distribution models (JSDM), and VAST includes a geostatistical method to account for spatial similarity and density-dependent processes. The VAST package is also used for management purposes (Thorson 2019) or to improve the estimated abundance index (Thorson et al., 2015). In summary, VAST is largely used in the context of single or multiple species analysis, but contains a very advanced mathematical approach and an R package that is not user-friendly, so collaboration with the developer is required.

- HMSC - Hierarchical Model of Species Communities - is a flexible framework for customizing JSDMs that allows the integration of species information in the form of presence/absence or density data and environmental covariates, as well as features such as phylogenetic relationships in a spatiotemporal context. As far as I know, HMSC is not widely used in marine contexts, and in fact only two main studies have used this model in marine species (Kenchington et al., 2019; Zhang et al., 2020) in Finnish and Chinese waters, respectively. No JSDMs have been applied in the Adriatic and Ionian Seas, with the exception of ecosystem models such as Ecopath with Ecosim, which have been applied in the Adriatic (Celić et al., 2018; Libralato et al., 2010) or in other parts of the Mediterranean (Agnetta et al., 2019; Coll & Libralato, 2012), but where the approach, results and 'philosophy' of the model are quite different. The HMSC is a model with fixed, random, or spatial autocorrelation effect and Bayesian approaches with a very high predictive performance tested between more than 30 JSDMs (Norberg et al., 2019). Implementing these models in my study area could be a significant improvement, as this is the first study of JSDMs in this area and with this new approach.

- sdmTMB - Species Distribution Model with Template Model Builder -, sdmTMB is an open-source R package that allows rapid implementation of complex nonlinear random effects (latent variable) models like the established AD Model Builder (ADMB) package and also provides easy access to parallel computation. Estimation with TMB is done using maximum marginal likelihood. SdmTMB does not include assessment of multiple species co-occurrence or density dependence, but it is a very easy model to run and very fast. In addition, the user can include as a covariate, for example, prey abundance, to simulate whether the response variable (our analyzed species) might change with respect to this density-prey covariate. Despite a very fast coding and user interface, the diagnostic and performance results take time to study and understand all the processes based on the Bayesian and Gaussian Markov random field with SPDE, which is the mathematical-statistical core of this model.

Exploring the possible improvement of the models I use here using these kinds of 'new' approaches could be an opportunity for me and the field of study. Not many cross-species models using SDMs have been developed in this field. For this reason, in these years of work, after a thorough investigation of different approaches in the field of SDMs, a new approach using these models in a multi-species context could be a challenge that I would like to take on.

4. Application of presented models on new species

The models presented in this thesis concern only demersal fish species, in particular some of the most important species from a commercial point of view (see Chapter 4). The MEDITS and SOLEMON surveys collect information on hundreds of species, although groundfish species and bottom species clearly predominate due to the nature of the gear used and the objective of the surveys. Other species could be important to analyze and compare with the results presented here, e.g., from the MEDITS survey: species such as whiting (*Merlangus merlangus*), common pandora (*Pagellus erythrinus*), Atlantic mackerel (*Scomber scomber*), or European squid (*Loligo vulgaris*) could be very interesting species that are not frequently studied despite their commercial importance. For the SOLEMON survey, we must consider that trawling is an interesting type of fishery because, thanks to the nature of the gear, it can catch some species that are difficult to reach with other gears, although it is one of the fisheries with the greatest impact in the entire Mediterranean Sea (Colloca et al., 2017). The SOLEMON survey catches interesting species such as scallops (Pettinidi), brill (*Scophthalmus rhombus*), purple moray (*Bolinus brandaris*) or queen scallop (*Aequipecten opercularis*), which are ecologically interesting and also commercially important (Fortibuoni et al., 2017; Ulrich et al., 2019). Some of the mentioned species are not very mobile, such as pectinidi or dyer moray, and it could be very interesting to analyze the relationship between environmental variables and the location of these resources over time and space, especially considering their low ability to move and also the fact that these species are not assessed mainly due to lack of data and biological information (Armelloni et al., 2021).

Moreover, pelagic species and not only demersal species such as anchovies (*Engraulis encrasicolus*) or sardines (*Sardina pilchardus*) have been studied, but there are still no studies on SDMs. One of the main problems is data collection, and the eco-survey program (Leonori et al., 2011; MEDIAS Handbook, 2019) is one of the most important fishery-independent activities to obtain information on this migratory species, especially on the Italian side, and sharing information for Italy and Croatia could be an opportunity. Indeed, due to the migratory nature of anchovies and sardines in the Adriatic Sea, it is not easy to obtain information on these pelagic species, and the application of SDM could be an interesting challenge to assess the status of the resource, which has been widely studied and evaluated (FAO, 2020b). For this reason, a comparison between the current assessment, eco-survey, and SDMs is a great opportunity to understand the dynamics, status, and biomass of the two stocks. CMEMS products and satellite products (e.g., chlorophyll data) can provide useful information that can be used as predictors in the SDMs, taking into account the first layer and the sea surface or up to 200-250 m where species are more abundant.

5. Application of SDMs with ’new’ information about species

What types of data can be included in the SDMs?

We have seen that the SDMs model works with presence/absence data or only presence and pseudo-absence data (MAXENT - (Elith et al., 2011), density data in the form of biomass (e.g., Chapter 2) or count data (number of individuals, e.g., Chapter 3, Chapter 4, Chapter 5), and index (e.g., kg/km2).

What about genetic data?

The use of genetic markers is not widespread, and the representation of spatial genetic structure is not straightforward (Hampe et al., 2010). When we talk about SDMs, especially those that use presence/absence data and lead to prediction of habitat suitability-which is not the same as probability of occurrence-these models assume that a species has a single niche and all individuals respond equally to changes in abiotic conditions. However, there is evidence that many species are organized in a different genetic lineage that may be adapted to a local condition (Hereford, 2009; Leimu & Fischer, 2008), with potential adaptation to respond to environmental change (Shaw & Etterson, 2012). Many of the studies conducted are on plant genetic structure, and the use of genetic information in SDMs with marine species is not widespread. Some of the future applications and challenges in SDMs are the applications of the models discussed in this paper using survey-derived information, such as the survey of a genetic sample, environmental DNA, say, in situ information about the DNA of a particular species present (or not) at a particular survey site. If one has information about the DNA in a particular area and knows whether or not the species is present there, one could model that presence/absence information, not from the fish caught directly during the survey, but from the "genetic' presence of that species at "that point." Collecting the data, analyzing the genetic code and assuming that the species is 'really" present are difficult, but represent a new challenge in the development of SDMs 'world'. In the Adriatic and Ionian Sea area, no model with this kind of information is currently used, but the main problem is obviously the collection and sequencing of the genetic data that are collected.

Conclusion

> *'The main purpose of all fishing models is to understand and inform decision-makers about the possible consequences of fishing activities themselves.'*
>
> (Hollowed et al., 2000).

The PhD project focused on the spatio-temporal dynamics of some demersal fish species in the Adriatic and Ionian Seas in order to develop SDMs incorporating abiotic (environmental variables) and human activity dynamics (proxy for fishing effort) in the mentioned area. The spatial models considered are statistical models such as GAM, Random Forest and GBM. The objective was to use statistical models to study the dynamics of some demersal fish species such as hake, mullet and sole, in order to evaluate their distribution in relation to environmental variables and sampling activities. The available data come from experimental fishing campaigns conducted in the Adriatic and Ionian Seas, such as MEDITS (Mediterranean International Trawl Survey) and SOLEMON (Sole Monitoring), including data from 1999 to 2018. In particular, the more statistical approaches used served to highlight the most sensitive areas for certain species, mainly based on size (juveniles and adults), in order to subsequently use several SDM approaches. The results suggest that the applicability of these models could be implemented in the fisheries management of the area, considering the importance of the species of concern from an ecological and commercial perspective. In light of climate change, understanding the potential "shift" of species in the area is central to good spatial assessment and management of resources, improving knowledge in the sector.

The main idea behind the project was to understand the capabilities of SDMs in the area and in this fisheries context, to explore different options and approaches, and to model the main dynamics of the affected species.

Many results have come out of this work, and I wanted to pick out the ones that are most important to me, with the understanding that any new potential improvements and studies that come out of this work could be useful to fisheries science. I know that new approaches will be possible in the future as research continues in this area that examines the ecology, biology, distribution, and resulting fisheries management of the area under consideration.

If I get the chance, I would like to go in that direction.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ICEBERG
CASTLETOWNBERE FISHERMENS
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HALSTER FISH SALES LTD
MIDDLETON SEAFOODS
FOYLE FISHERMENS CO-OP
UNAUTHORISED USERS
ANTCAR FISH EXPORTS LTD

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Supplementary

Material and info

Summary sup. material

Chapter 2 Supplementary material

Description

This supplementary material is providing all details for the choices of the most appropriate approach, identification of the set of variables that result in the best model through training and testing, and a descriptive summary of the best model and its properties. The above is reported for each species (European hake, common sole, mantis shrimp, common cuttlefish ad red mullet). Therefore, the document is organized by species and for each, a set of sections are reported as in the following:

Identification of the most appropriate approach: these sections have briefly presented the results of different GAM families (Delta-GAM, Tweedie, and Gaussian) applied to the trawl survey data for the species and compared using mean absolute error (MAE) and correlation coefficient (R^2). These comparisons are done for the model with the full set of variables identified by the VIF (see Materials and Methods in the paper) and for the minimal model with geopositional variables only.

Best models identification: in these sections are identified the most appropriate approach adopted on models with different explanatory variables. 50 runs with training (70% of the data) and testing (the remaining 30% of the data) selected randomly are used implementing a back-stepwise, i.e., from the complete model with all explanatory variables identified by VIF (model 0) to the minimal geopositional model (model 5,6 or 7 depending on the species). The variables used in each model are described and the measures of the model's performance (explained deviance (%ED); Akaike Information Criterion (AIC) of the training datasets; correlation coefficient (R2)) derived from 50 runs of the training and test analysis are reported in the box plots. The results of Tukey's test are also reported.

Spline and residual best model: in this section, we show the spline curve derived from the best model chosen, delta (binomial and Gaussian) for European hake, common cuttlefish and mantis shrimp, Gaussian for red mullet, and Tweedie for common sole.

Summary of the model: in this section are reported the summary table of the best model (mod 0) for the respective best approach for each species. The summary is derived from software R, where the models are run and the final results are mapped.

1. European hake

1.1. Identification of the most appropriate approach

Table S2.1: performance statistics for the different approaches tested in both the model with the complete set of relevant oceanographic variables selected by VIF and the model with minimal geopositional variables.

	With all additional variables (model 0)		Minimal geopositional variables (model 6)	
	MAE	R2	MAE	R2
DELTA-GAM	**16.13853**	**0.306771**	16.28943	0.297505
Tweedie	16.74836	0.342713	16.92313	0.331782
Gaussian	16.24252	0.308074	16.38106	0.298852

The most appropriate approach among those GAMS tested was thus identified in the Delta-GAM approach.

1.2. Best models identification

Several Delta-GAM models with different explanatory variables were analysed in the training and testing procedure.

Model_0 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)+s(TMP_bot)+s(dox_bot)+s(nit)+s(sal)+s(poc)+s(eff)
Model_1 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)+s(TMP_bot)+s(dox_bot)+s(nit)+s(sal)+s(poc)
Model_2 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)+s(TMP_bot)+s(dox_bot)+s(nit)+s(sal)
Model_3 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)+s(TMP_bot)+s(dox_bot)+s(nit)
Model_4 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)+s(TMP_bot)+s(dox_bot)
Model_5 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)+s(TMP_bot)
Model_6 <- R~β+ factor(month)+s(Y)+s(X)+s(year)+s(depth)

Where the response variable R = log kg/km^2 (delta-gaussian) or presence/absence (delta-binomial) in the DELTA model. Delta-GAM box plots are reported in the main text.

Table S2.2: Tuckey test delta binomial and delta Gaussian for European hake

delta-binomial	mod 0	mod 1	mod 2	mod 3	mod 4	mod 5	MOD 6
aic	c	b	b	b	b	ab	a
dev.expl.	a	b	bc	b	b	c	d
r2	a	a	a	a	a	ab	a
delta gaussian							
aic	b	ab	ab	ab	ab	ab	d
dev.expl.	a	ab	ab	b	bc	cd	d
r2	a	a	a	a	a	a	a

1.3. Splines, summary and residuals of the best model (model 0)

In the following, the results of the Delta-GAM applied to European hake (splines, residuals and summary): results for Delta-binomial.

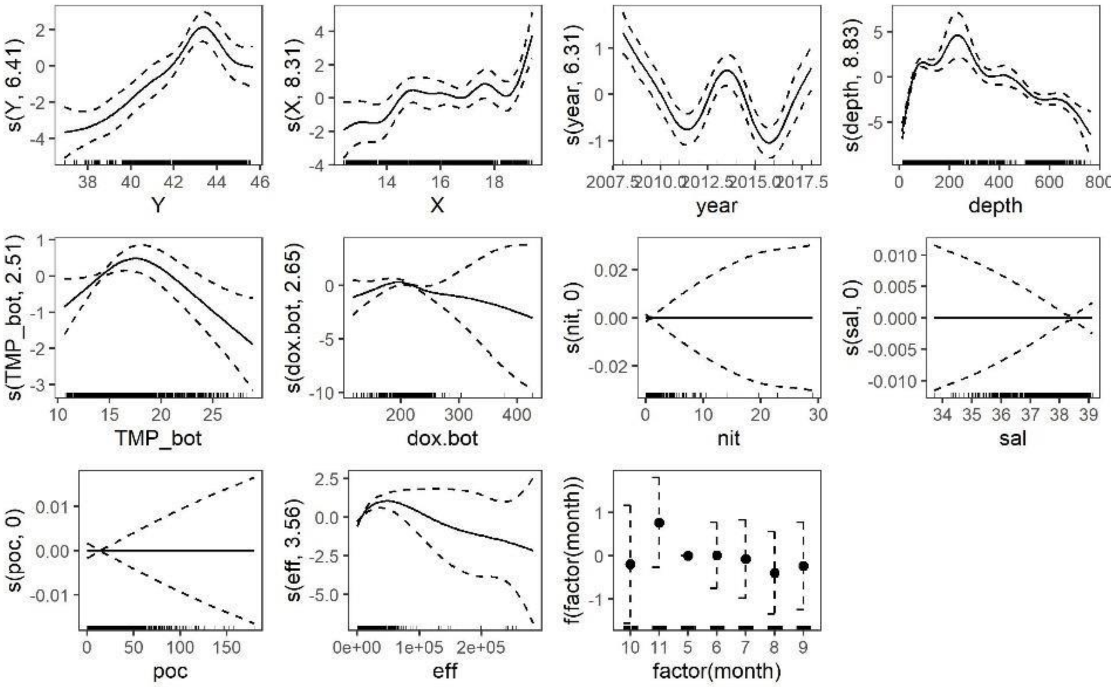


Figure S2.1: spline for the best model (model 0) of delta binomial for European hake

Table S2.3: Summary tables delta-binomial mod 0 European Hake

	Estimate	Std.Error	z.value	p.value
Intercept	3.69	0.45	8.13	3.97*e-16***
Factor(month) 6	0.009	0.39	0.02	0.98
Factor(month) 7	-0.07	0.46	-0.16	0.86
Factor(month) 8	-0.39	0.48	-0.81	0.41
Factor(month) 9	-0.23	0.51	-0.46	0.64
Factor(month) 10	-0.19	0.69	-0.28	0.77
Factor(month) 11	0.76	0.53	1.44	0.14

Covariates	Edf	Ref.df	Chi.sq	p.value
X	6.64	9	119.89	< 2e-16***
Y	8.30	9	42.05	2.65e-07***
Year	6.30	9	100.02	<2e-16***
Depth	8.83	9	363.35	<2e-16***
TMP_bot	2.50	9	20.65	8.53e-06***
Dox_bot	2.64	9	10.31	0.004**
Nit	0.00	9	0.00	0.89
sal	0.00	9	0.00	0.79
poc	0.00	9	0.00	0.23

eff	3.55	9	37.62	5.11e-09***
Diagnostic				
R2	0.55			
Dev.expl	55.9%			
UBRE	-0.54			

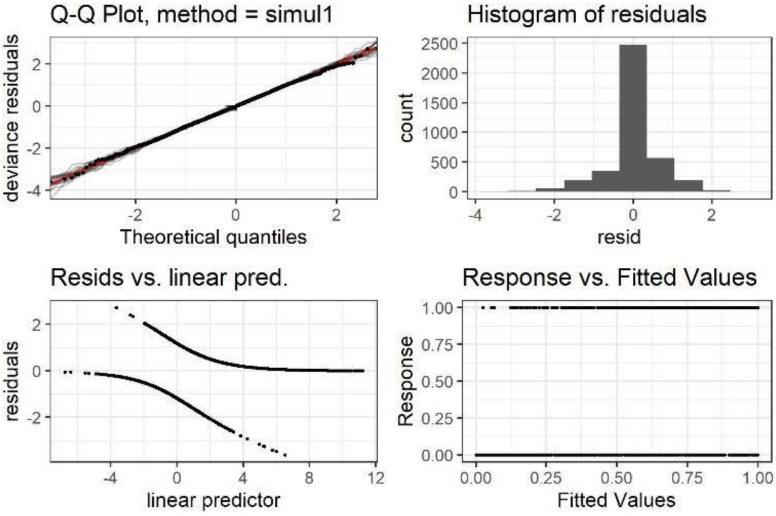


Figure S2.2: residual derived from model 0, delta binomial, for European hake

In the following, the results of the Delta-GAM applied to European hake (splines, residuals and summary): results for Delta-gaussian.

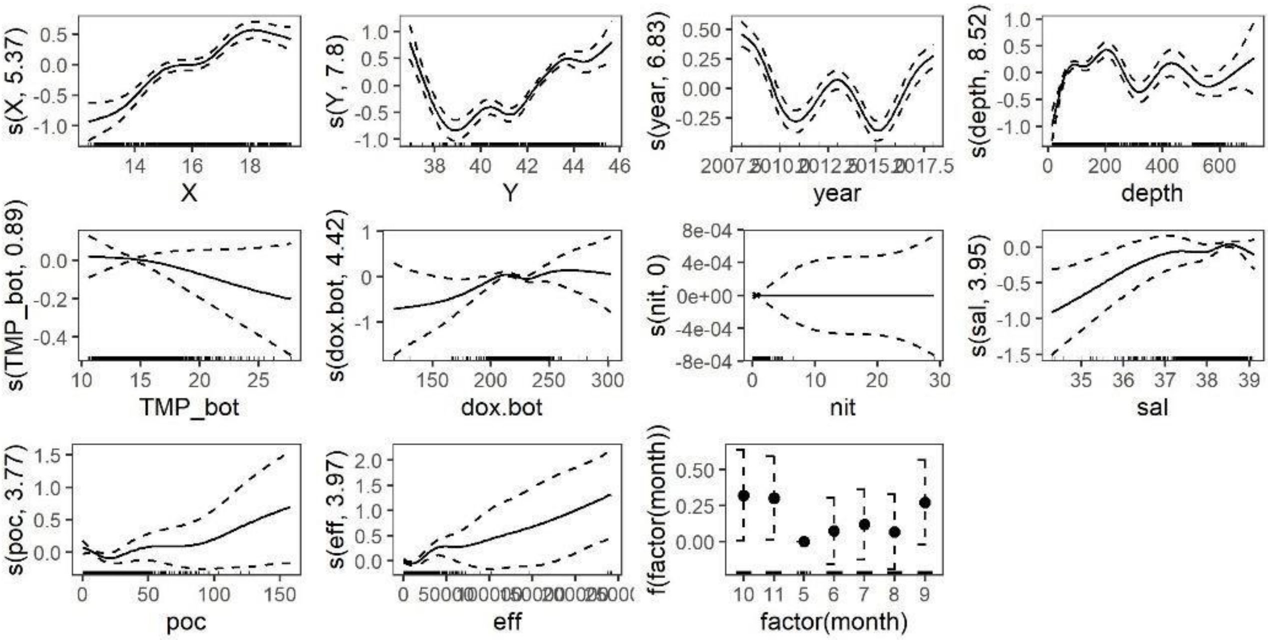


Figure S2.3: spline for the best model (model 0) of delta gaussian for European hake

Table S2.4: Summary tables delta-gaussian mod 0 for European hake

	Estimate	Std.Error	t.value	p.value
Intercept	2.90	0.11	24.64	<2e-16
Factor(month) 6	0.07	0.11	0.64	0.52
Factor(month) 7	0.11	0.12	0.95	0.34
Factor(month) 8	0.06	0.13	0.51	0.60
Factor(month) 9	0.27	0.14	1.81	0.06
Factor(month) 10	0.32	0.16	2.00	0.04*
Factor(month) 11	0.30	0.14	2.032	0.04*

Covariates	Edf	Ref.df	F	p.value
X	5.37	9	9.29	<2e-16***
Y	7.80	9	18.97	<2e-16***
Year	6.83	9	26.27	<2e-16***
Depth	6.51	9	12.24	<2e-16***
TMP_bot	8.87	9	0.23	0.08
Dox_bot	4.42	9	1.42	0.007**
Nit	4.53	9	0.00	0.74
Sal	3.94	9	1.37	0.005**
Poc	3.77	9	1.11	0.01*
Eff	3.97	9	2.76	1.03e-05***

Diagnostic	
R2	0.30
Dev.expl	31.6%
GCV	0.76

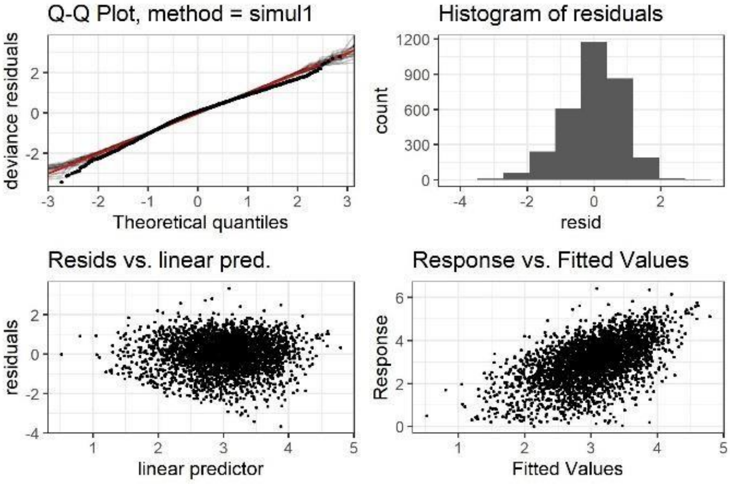


Figure S2.4: residual derived from model 0, delta GAUSSIAN, for European hake

2. Common Sole

2.1. Identification of the most appropriate approach

Table S2.5: performance statistics for the different approaches tested in both the model with the complete set of relevant oceanographic variables selected by VIF and the model with minimal geopositional variables.

	With all additional variables (model 0)		Minimal geopositional variables (model 6)	
	MAE	R2	MAE	R2
DELTA-GAM	483.2629	0.510396	491.4670	0.511032
Tweedie	**437.3220**	**0.577585**	444.4685	0.550458
Gaussian	482.0236	0.510482	489.6441	0.511277

The most appropriate approach among those GAMS tested was thus identified in the Tweedie GAM approach.

2.2. Best models identification

Several Tweedie models with different explanatory variables were analysed in the training and testing procedure.

Model_0 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+s(pho) +s(ph)+ s(sal)+ s(dox.bot)+ s(TMP_bot)+s(eff)

Model_1 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+s(pho) +s(ph)+ s(sal)+ s(dox.bot)+ s(TMP_bot)
Model_2 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+s(pho) +s(ph)+ s(sal)+ s(dox.bot)
Model_3 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+s(pho) +s(ph)+ s(sal)
Model_4 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+s(pho) +s(ph)
Model_5 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+s(pho)
Model_6 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)

Where the response variable is $R = kg/km^2$. The box-plot of Tweedie model is reported in the main text.

Table S2.6: Tuckey test Tweedie for common sole

Tweedie	Mod 0	Mod 1	Mod 2	Mod 3	Mod 4	Mod 5	Mod 6
AIC	a	a	a	a	a	a	a
Dev.Expl.	a	a	a	a	a	a	a
R2	a	a	a	a	a	a	a

2.3. Splines, summary and residuals of the best model (model 0)

In the following, the results of the Tweedie-GAM applied to common sole (splines, residuals and summary)

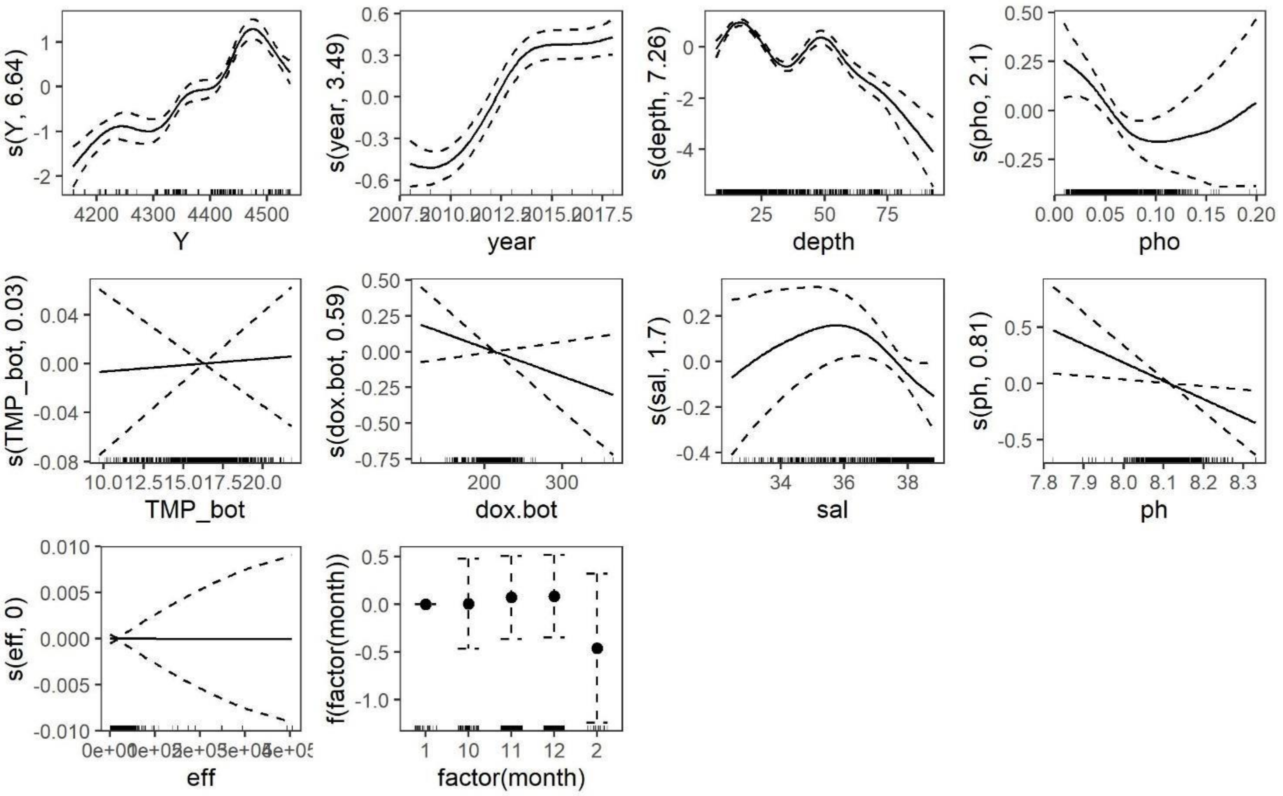


Figure S2.6: spline for the best model (model 0) of tweedie for common sole

Table S2.7: Summary tables Tweedie, mod 0, for common sole

	Estimate	Std.Error	t.value	p.value
Intercept	6.09	0.21	28.61	<2e-16***
Factor(month) 2	-0.46	0.39	-1.15	0.24
Factor(month) 10	0.006	0.24	0.02	0.97
Factor(month) 11	0.07	0.22	0.32	0.74
Factor(month) 12	0.08	0.22	0.38	0.70

Covariates	Edf	Ref.df	F	p.value
Y	6.64	9	25.55	<2e-16***
Year	3.48	9	13.74	<2e-16***
Depth	7.25	9	34.92	<2e-16***
Pho	2.09	9	1.24	0.001**
Ph	0.80	9	0.64	0.005
Sal	1.70	9	0.64	0.01**
Dox_bot	0.59	9	0.21	0.06
Tmp_bot	0.02	9	0.004	0.19
Eff	0.0002	9	0.00	0.70

Diagnostic	
R^2	0.56
Dev.expl	62.6%
-REML	3783.4

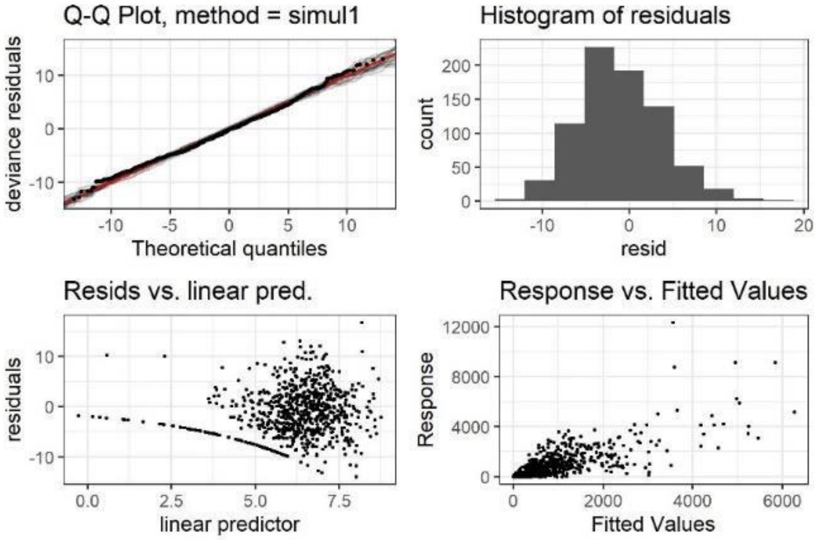


Figure S2.7: residual derived from model 0, tweedie, for common sole

3. Mantis Shrimp

3.1. Identification of the most appropriate approach

TableS2.8: performance statistics for the different approaches tested in both the model with the complete set of relevant oceanographic variables selected by VIF and the model with minimal geopositional variables.

	With all additional variables (model 0)		Minimal geopositional variables (model 6)	
	MAE	R2	MAE	R2
DELTA-GAM	**185.1325**	**0.328499**	208.8765	0.209921
Tweedie	192.2052	0.436241	215.6992	0.355822
Gaussian	186.4174	0.319229	206.8905	0.229974

The most appropriate approach among those GAMS tested was thus identified in the Delta-GAM approach.

3.2. Best models identification and Tukey test

Several delta-GAM models with different explanatory variables were analysed in the training and testing procedure.

Model_0 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+ s(sal)+s(TMP_bot) +s(poc)+s(ph)+s(dox.bot)+s(eff)
Model_1 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+ s(sal)+s(TMP_bot) +s(poc)+s(ph)+s(dox.bot)
Model_2 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+ s(sal)+s(TMP_bot) +s(poc) +s(ph)
Model_3 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+ s(sal)+s(TMP_bot) +s(poc)
Model_4 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)+ s(sal) +s(TMP_bot)

Model_5 <- - R~β+ factor(month)+s(Y)+s(year)+s(depth)+ s(sal)
Model_6 <- R~β+ factor(month)+s(Y)+s(year)+s(depth)

Where the response variable R = log kg/km^2 (delta-gaussian) or presence/absence (delta-binomial) in the DELTA model. Since the Gaussian part of the Delta-GAM is reported in the main text, here we reported only results for Delta-binomial on presence/absence data.

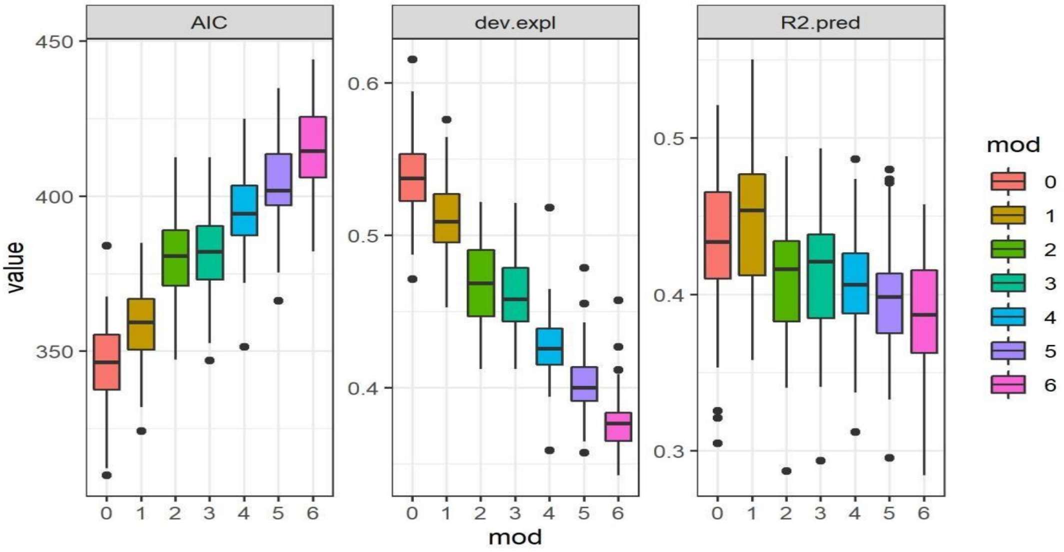


Figure S2.8: box plot from training and test analysis of delta-binomial model for mantis shrimp.

Table S2.9: Tuckey test delta binomial and delta gaussian for mantis shrimp

delta-binomial	mod 0	mod 1	mod 2	mod 3	mod 4	mod 5
aic	a	B	c	d	d	f
dev.expl.	a	B	c	c	d	f
r2	a	ab	bc	cd	cd	d
delta gaussian						
aic	a	B	c	d	d	f
dev.expl.	a	B	c	c	d	f
r2	a	ab	bc	cd	cd	d

3.3. Splines, summary and residuals of the best model (model 0)

In the following, the results of the Delta-GAM applied to mantis shrimp (splines, residuals and summary): results for Delta-binomial.

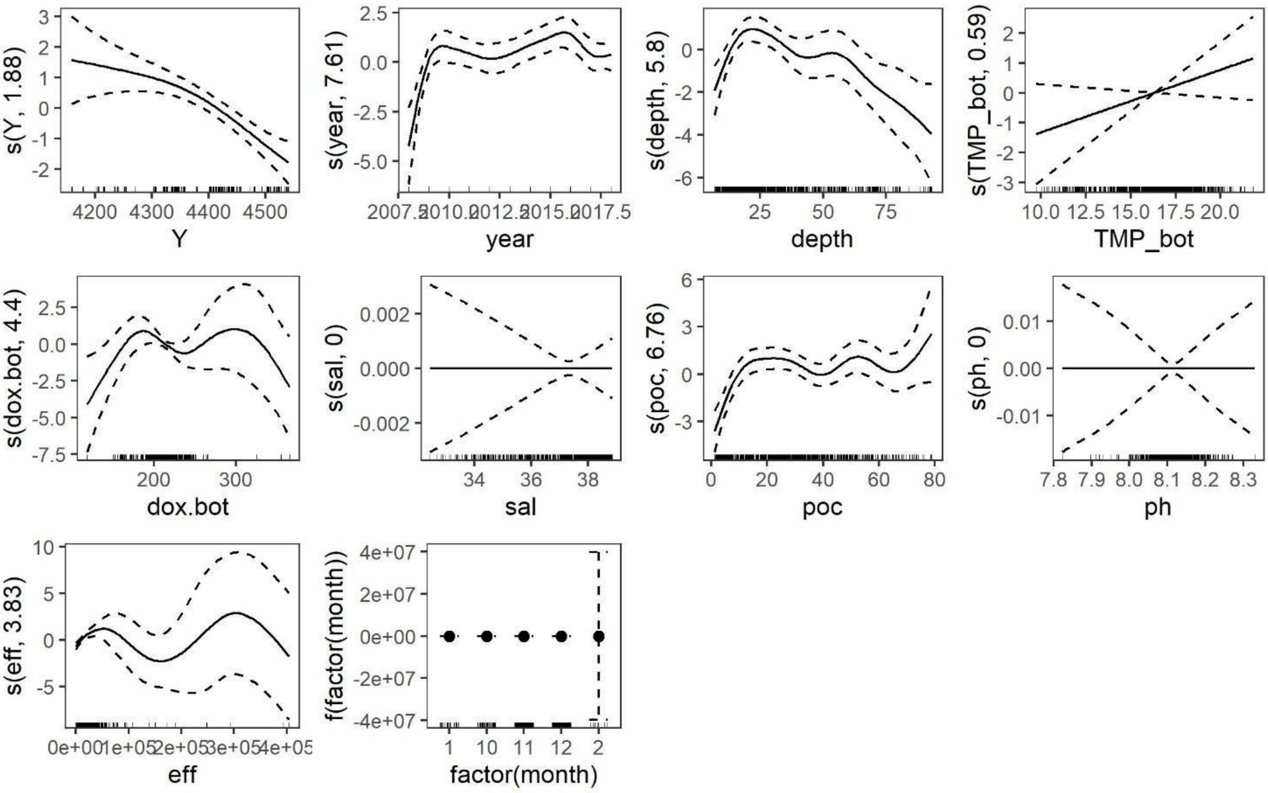


Figure S2.9: spline for the best model (model 0) of delta-binomial approach for mantis shrimp.

Table S2.10: Summary tables delta binomial, mod 0, for mantis shrimp

	Estimate	Std.Error	z.value	p.value
Intercept	1.39	1.55	0.89	0.37
Factor(month) 2	-0.99	2.023e+07	0.00	1.00
Factor(month) 10	-3.34	1.75	-1.90	0.05
Factor(month) 11	-0.60	1.68	-0.35	0.72
Factor(month) 12	0.52	1.60	0.32	0.74
Covariates	Edf	Ref.df	Chi.sq	p.value
Y	1.88	9	29.46	6.38e-09***
Year	7.60	9	25.72	0.0003***
Depth	5.80	9	33.52	5.75e-07***
Sal	3.63e-06	9	0.00	0.55
TMP_bot	0.58	9	2.61	0.02*
Poc	6.76	9	49.91	3.90e-08***
pH	7.79e-05	9	0.00	0.26
Dox_bot	4.39	9	13.26	0.004**
Eff	3.82	9	18.23	0.0003***

Diagnostic	
R^2	0.62
Dev.expl	58.8%
UBRE	-0.32

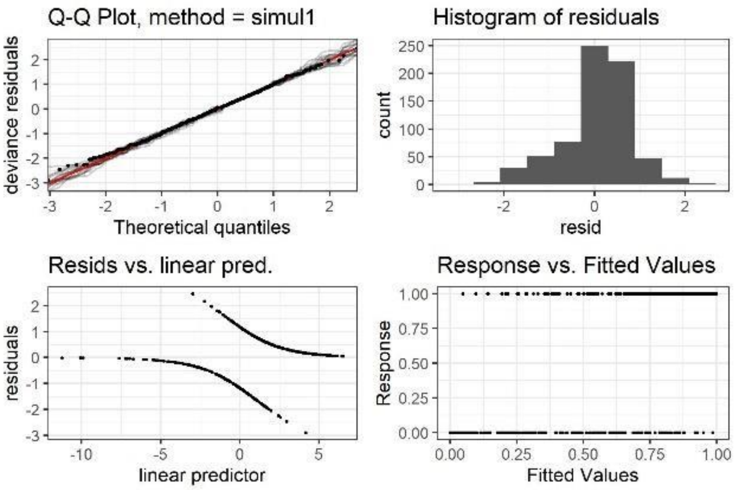


Figure S2.10: residual derived from model 0, delta binomial, for mantis shrimp

In the following, the results of the Delta-GAM applied to mantis shrimp (splines, residuals and summary): results for Delta-gaussian.

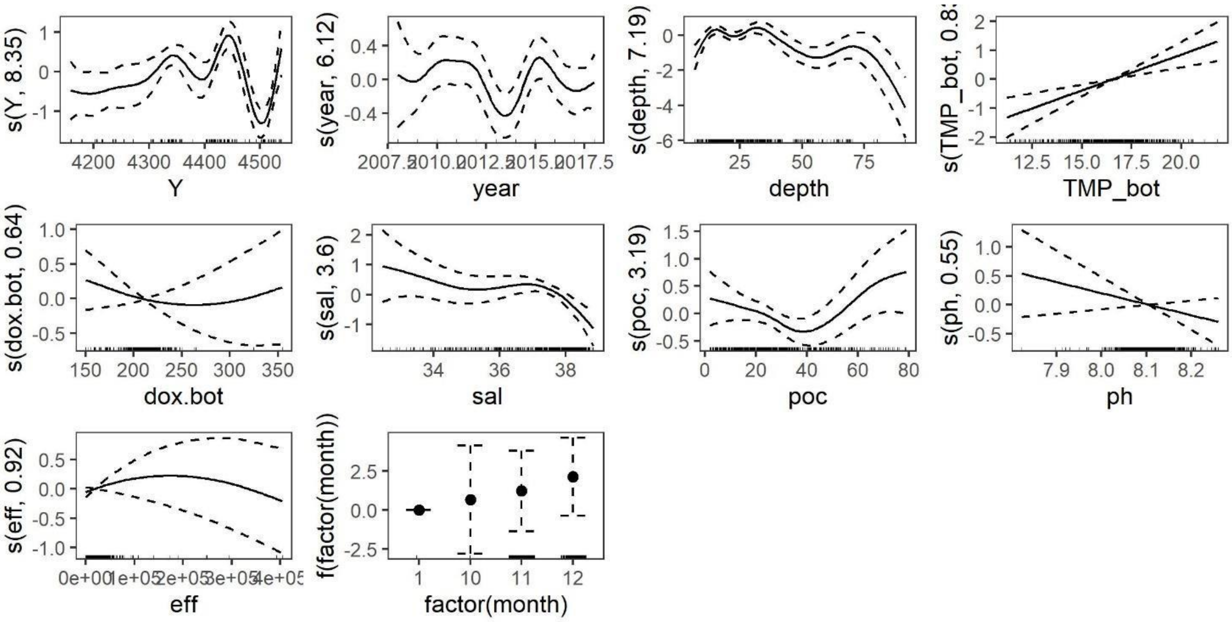


Figure S2.11: spline for the best model (model 0) of delta-gaussian approach for mantis shrimp

Table S2.11: Summary tables Delta-gaussian, mod 0 for mantis shrimp

	Estimate	Std.Error	t.value	p.value
Intercept	3.62	1.30	2.78	0.005**
Factor(month) 10	0.66	1.76	0.37	0.70
Factor(month) 11	1.20	1.32	0.91	0.36
Factor(month) 12	2.11	1.26	1.66	0.09

Covariates	Edf	Ref.df	F	p.value
Y	8.34	9	11.65	<2e-16***
Year	6.11	9	1.75	0.009**
Depth	7.18	9	5.73	2.95e-09***
Sal	3.60	9	2.21	6.46e-05***
TMP_bot	0.82	9	1.58	7.98e-06***
Poc	3.19	9	1.61	0.0008***
pH	0.54	9	0.22	0.04*
Dox_bot	0.64	9	0.16	0.07
Eff	0.91	9	0.20	0.12

Diagnostic

R^2	0.44
Dev.expl	48.5%
GCV	1.58

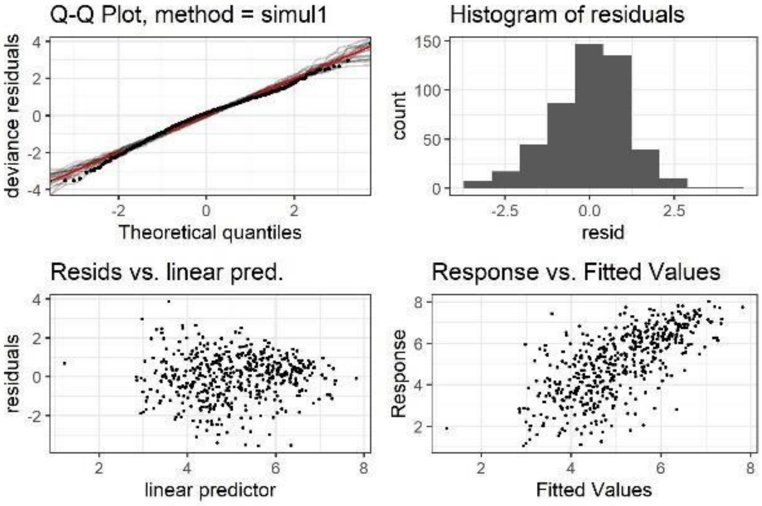


Figure S2.12: residual derived from model 0, delta gaussian, for mantis shrimp

4. Common Cuttlefish

4.1. Identification of the most appropriate approach

Table S2.12: performance statistics for the different approaches tested in both the model with the complete set of relevant oceanographic variables selected by VIF and the model with minimal geopositional variables.

	With all additional variables (model 0)		Minimal geopositional variables (model 6)	
	MAE	R2	MAE	R2
DELTA-GAM	**232.8418**	0.55711464	234.9617	0.550559
Tweedie	283.4962	0.4186344	289.2299	0.384666
Gaussian	236.7232	0.56298136	238.3843	0.556386

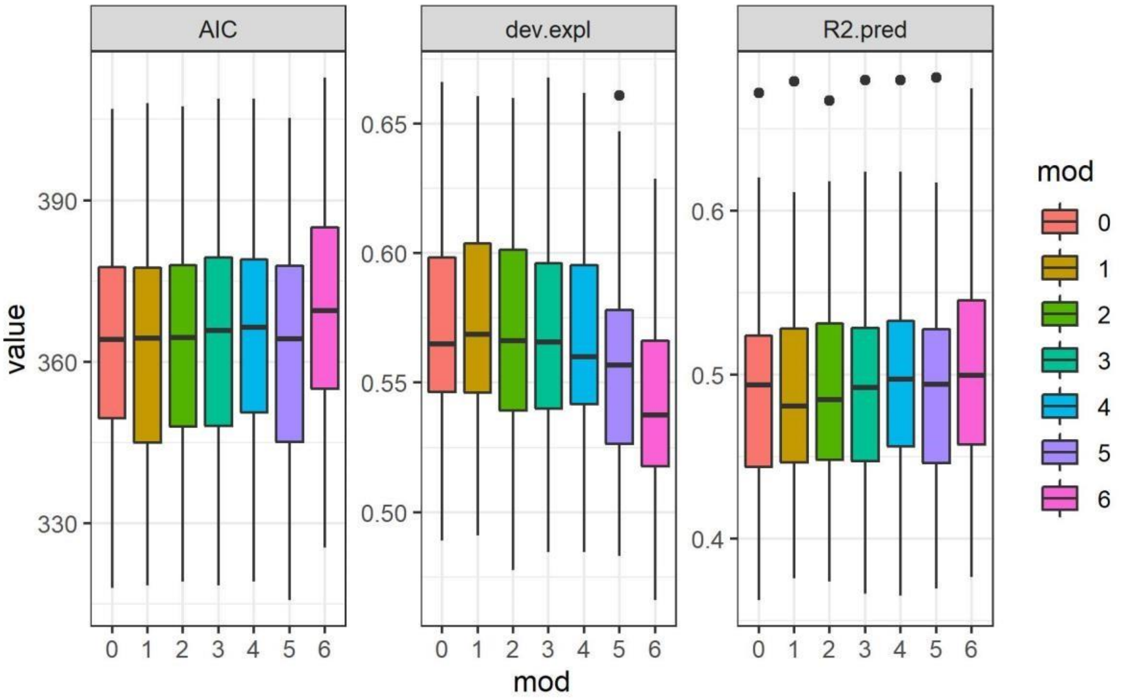
The most appropriate approach among those GAMS tested was thus identified in the Delta-GAM approach.

4.2. Best models identification and Tukey test

Several delta-GAM models with different explanatory variables were analysed in the training and testing procedure.

Model_0 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(TMP_bot)+s(dox.bot)+s(nit)+s(pho)+s(eff)"
Model_1 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(TMP_bot)+s(dox.bot)+s(nit)+s(pho)"
Model_2 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(TMP_bot)+s(dox.bot)+s(nit)"
Model_3 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(TMP_bot)+ s(dox.bot)+"
Model_4 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(TMP_bot)" Model_5 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)"

Where the response variable R = log kg/km^2 (delta-gaussian) or presence/absence (delta-binomial) in the DELTA model. Since the Gaussian part of the Delta-GAM is reported in the main text, here we reported only results for Delta-binomial on presence/absence data (Figure S4.1)



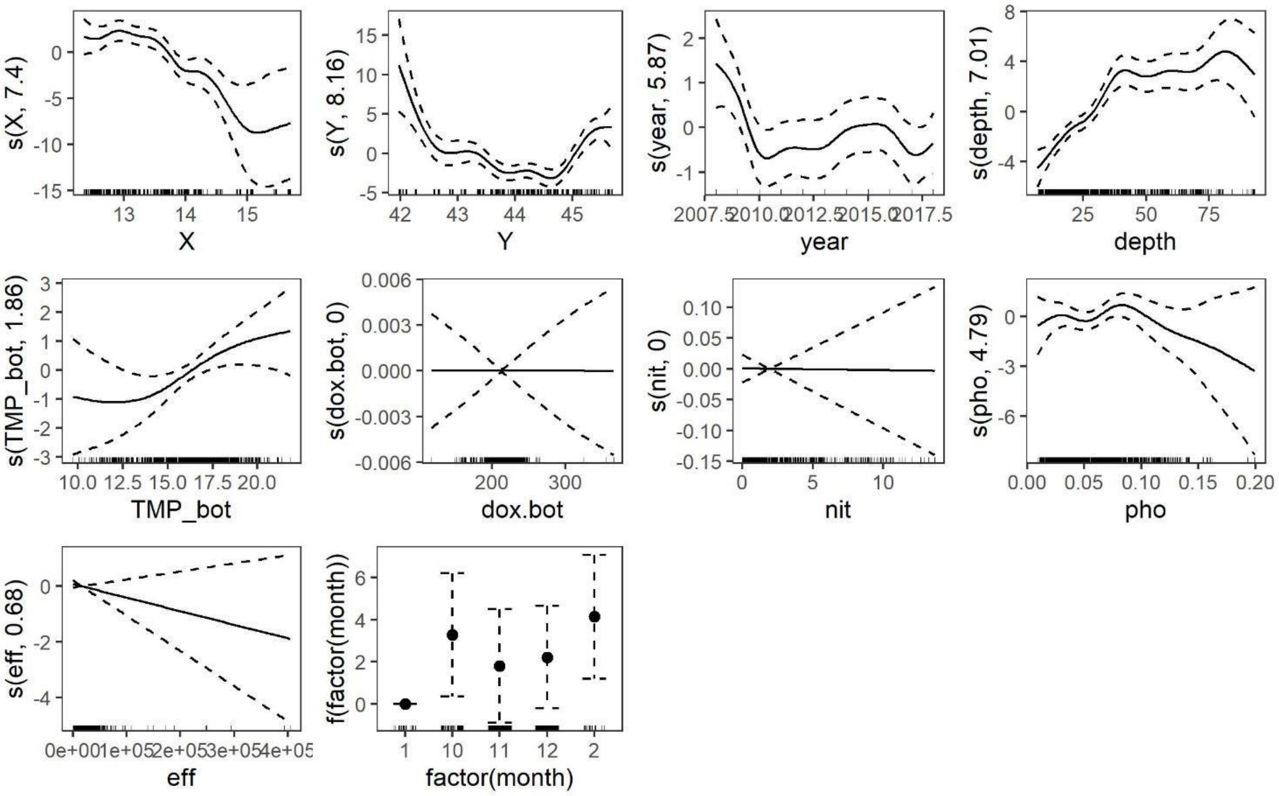
FigureS2.13: box plot from training and test analysis of delta-binomial model for common cuttlefish.

Table S2.13: Tuckey test delta-binomial and delta-gaussian for common cuttlefish

delta-binomial	mod 0	mod 1	mod 2	mod 3	mod 4	mod 5
aic	a	a	a	a	ab	b
dev.expl.	ab	a	ab	abc	c	c
r2	a	a	a	a	a	a
delta gaussian						
aic	a	a	a	a	a	a
dev.expl.	ab	a	ab	abc	bc	c
r2	a	a	a	a	a	a

4.3. Splines, summary, and residuals of the best model (model 0)

In the following, the results of the Delta-GAM applied to common cuttlefish (splines, residuals, and summary): results for Delta-binomial.



FigureS2.14: spline for the best model (model 0) of delta-binomial approach for common cuttlefish.

Table S2.14: Summary tables Delta-binomial mod 0 common cuttlefish

	Estimate	Std.Error	z.value	p.value
Intercept	-0.45	1.26	-0.36	0.71
Factor (month) 2	4.13	1.50	2.75	0.005**
Factor(month) 10	3.27	1.49	2.19	0.02*
Factor(month) 11	1.81	1.38	1.31	0.18
Factor(month) 12	2.22	1.24	1.78	0.07

Covariates	Edf	Ref.df	Chi.sq	p.value
X	7.4	9	32.44	1.09e-05***
Y	8.16	9	81.48	3.87e-16
Year	5.86	9	13.84	0.019*
Depth	7.00	9	84.90	<2e-16***
TMP_bot	1.85	9	7.49	0.007**
Dox_bot	1.20e-05	9	0.00	0.57
Nit	5.96e-03	9	0.006	0.28
Pho	4.78	9	9.51	0.05*
Eff	6.75e-01	9	1.51	0.12

Diagnostic	
R^2	0.59
Dev.expl	55.8%
-UBRE	-0.33

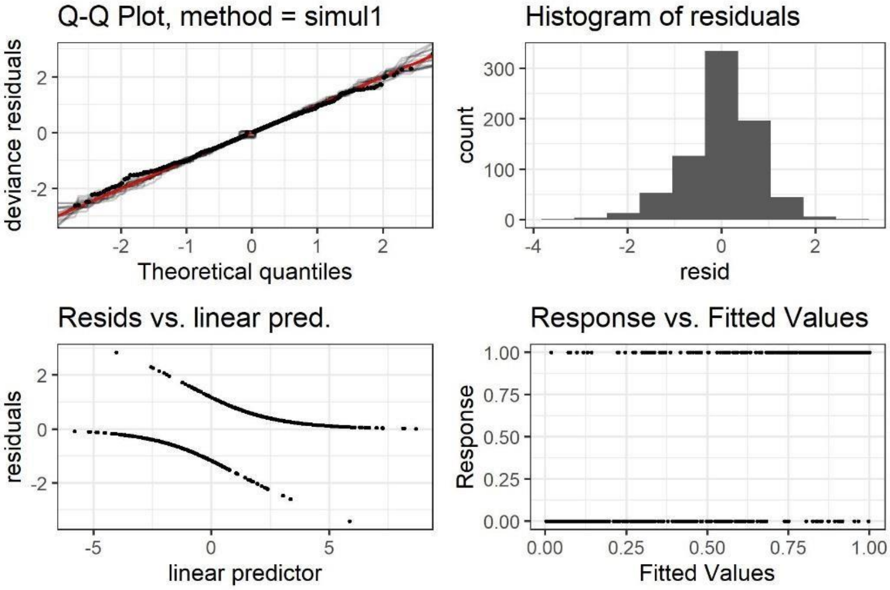


Figure S2.15: residual derived from model 0, delta binomial, for common cuttlefish.

In the following, the results of the Delta-GAM applied to common cuttlefish (splines, residuals and summary): results for Delta-gaussian.

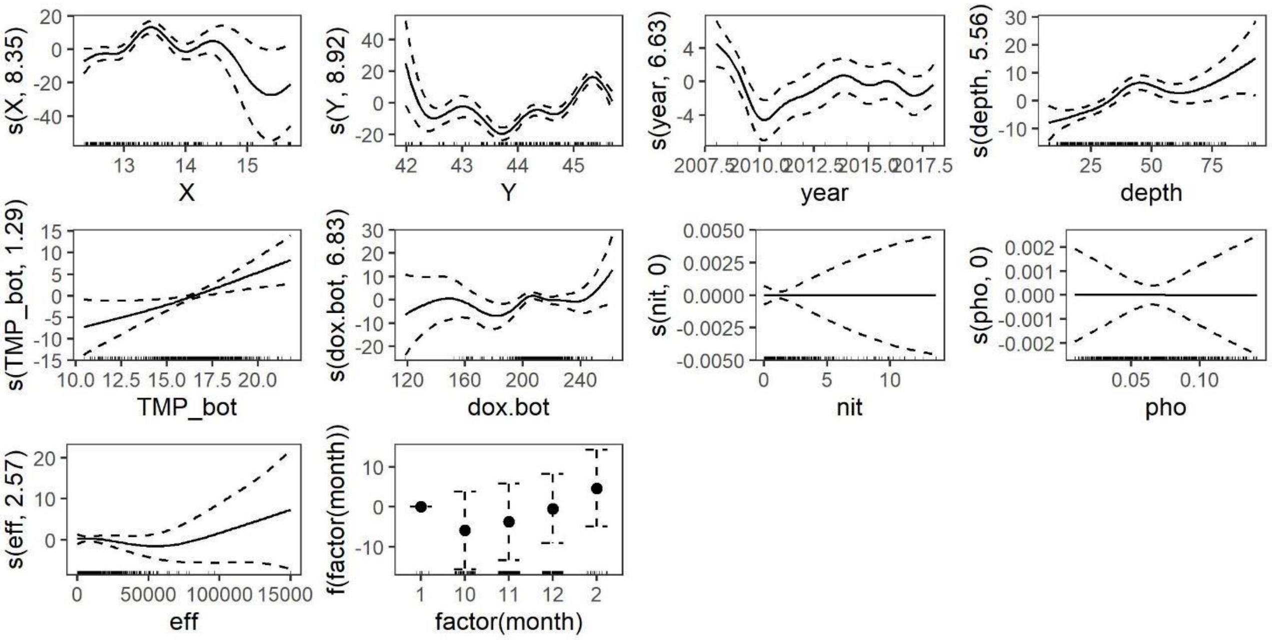


Figure S2.16: spline for the best model (model 0) of delta-gaussian approach for common cuttlefish.

Table S2.15: Summary tables Delta-gaussian, mod 0, for common cuttlefish.

	Estimate	Std.Error	z.value	p.value
Intercept	23.20	4.63	5.01	7.7e-07***
Factor (month) 2	5.00	4.94	1.01	0.31

Factor(month) 10	-5.28	4.96	-1.06	0.28
Factor(month) 11	-2.51	4.89	-0.51	0.60
Factor(month) 12	0.09	4.48	0.02	0.98

Covariates	Edf	Ref.df	F	p.value
X	7.26	9	8.28	2.09e-14***
Y	8.27	9	23.14	<2e-16***
Year	7.05	9	2.61	0.0009***
Depth	4.86	9	2.63	2.41e-05***
TMP_bot	9.80e-01	9	0.71	0.004**
Dox_bot	7.12	9	1.87	0.01*
Nit	3.61e-01	9	0.005	0.70
Pho	3.20e-05	9	0.00	0.39
Eff	3.65	9	0.61	0.17

Diagnostic	
R^2	0.52
Dev.expl	56.6%
GCV	82.9

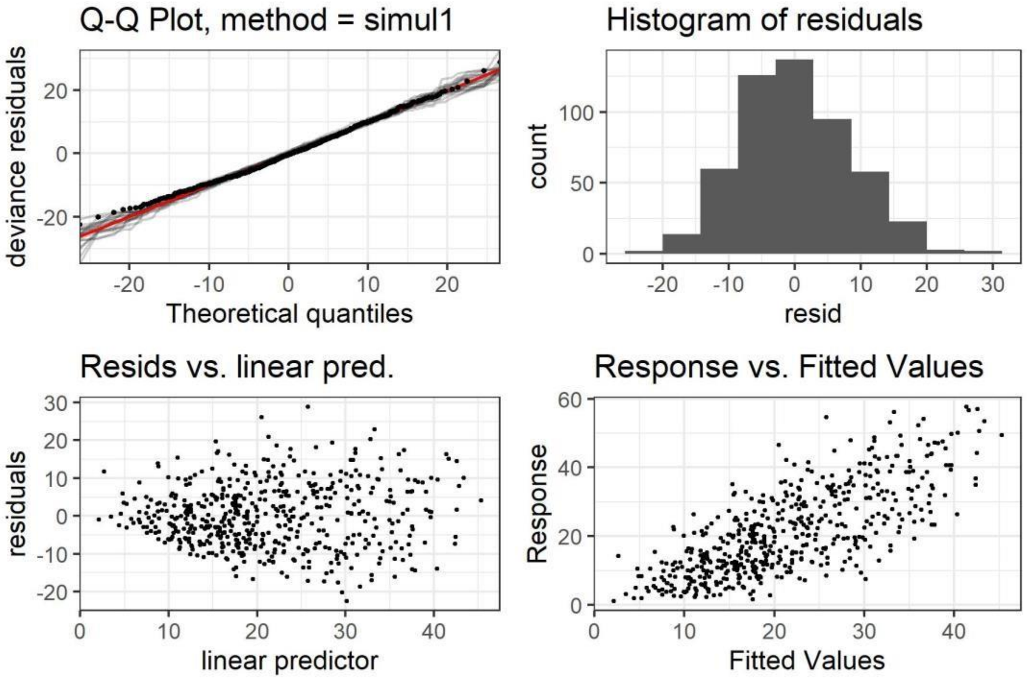


Figure S2.17: residual derived from model 0, delta gaussian, for common cuttlefish.

5. Red mullet

5.1. Identification of the most appropriate approach

Table S2.16: performance statistics for the different approaches tested in both the model with the complete set of relevant oceanographic variables selected by VIF and the model with minimal geopositional variables.

	With all additional variables (model 0)		Minimal geopositional variables (model 6)	
	MAE	R2	MAE	R2
DELTA-GAM	36.774	0.118	39.016	0.108
Tweedie	40.373	0.242	45.546	0.155
Gaussian	**36.987**	**0.119**	39.275	0.109

The most appropriate approach among those GAMS tested was thus identified in the Gaussian approach.

5.2. Best models identification and Tukey test

Several Gaussian models with different explanatory variables were analysed in the training and testing procedure

Model_0 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)+s(ph)+s(TMP_sst) +s(nit)+s(dox.bot) +s(sal)+s(eff)"
Model_1 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)+s(ph)+s(TMP_ sst) +s(nit)+s(dox.bot) +s(sal)”
Model_2 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)+s(ph)+s(TMP_ sst) +s(nit)+s(dox.bot)"
Model_3 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)+s(ph)+s(TMP_ sst) +s(nit)"
Model_4 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)+s(ph)+s(TMP_ sst)”
Model_5 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)+s(ph)”
Model_6 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth)+s(CHL)
Model_7 <- " R~β factor(month)+s(X)+s(Y)+s(year)+s(depth) "

Where the response variable is $R = \log kg/km^2$ in the Gaussian model. The Gaussian box-plot is reported in the main text.

Table S2.17: Tuckey test Gaussian for red mullet

Tweedie	Mod 0	Mod 1	Mod 2	Mod 3	Mod 4	Mod 5
AIC	ef	e	d	c	b	a
Dev.Expl.	b	c	d	e	f	a
R2	a	a	ab	ab	ab	b

5.3. Splines, summary and residuals of the best model (model 0)

In the following, the results of the Delta-GAM applied to red mullet (splines, residuals and summary) for gaussian model.

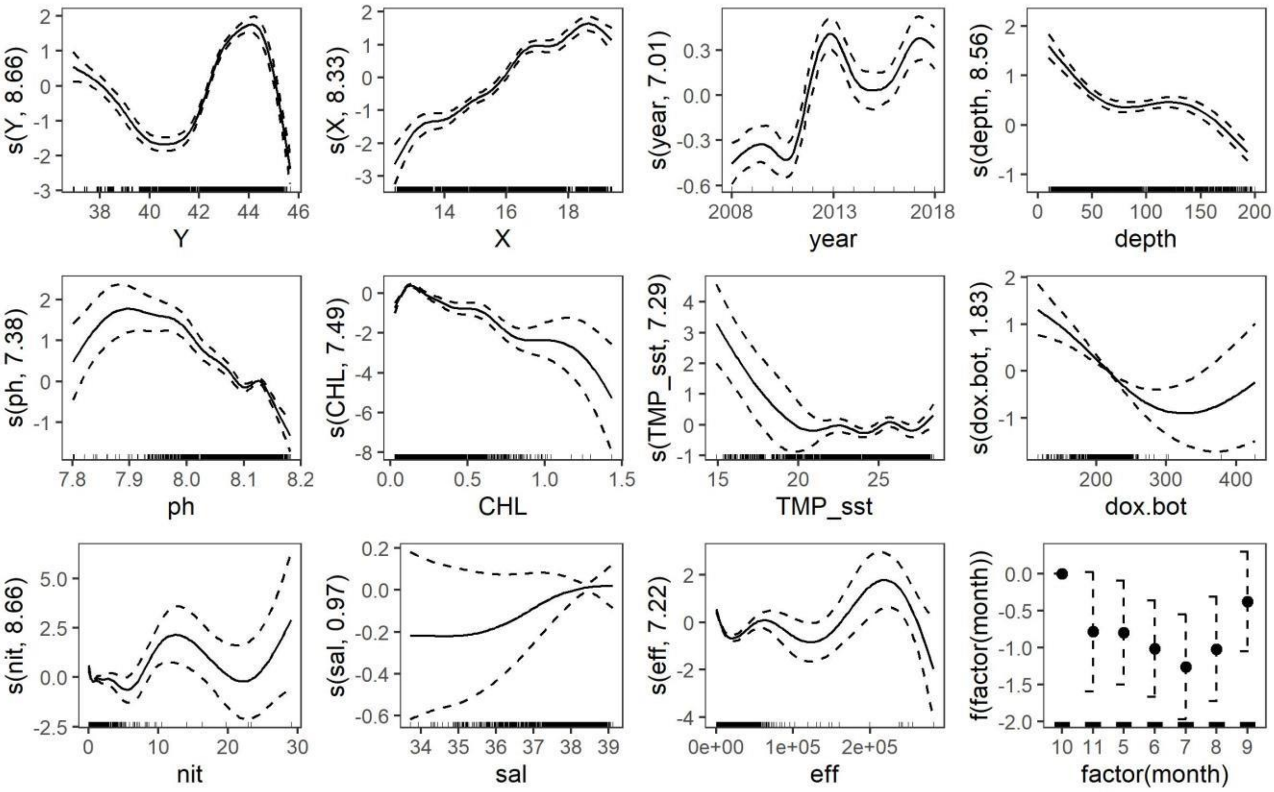
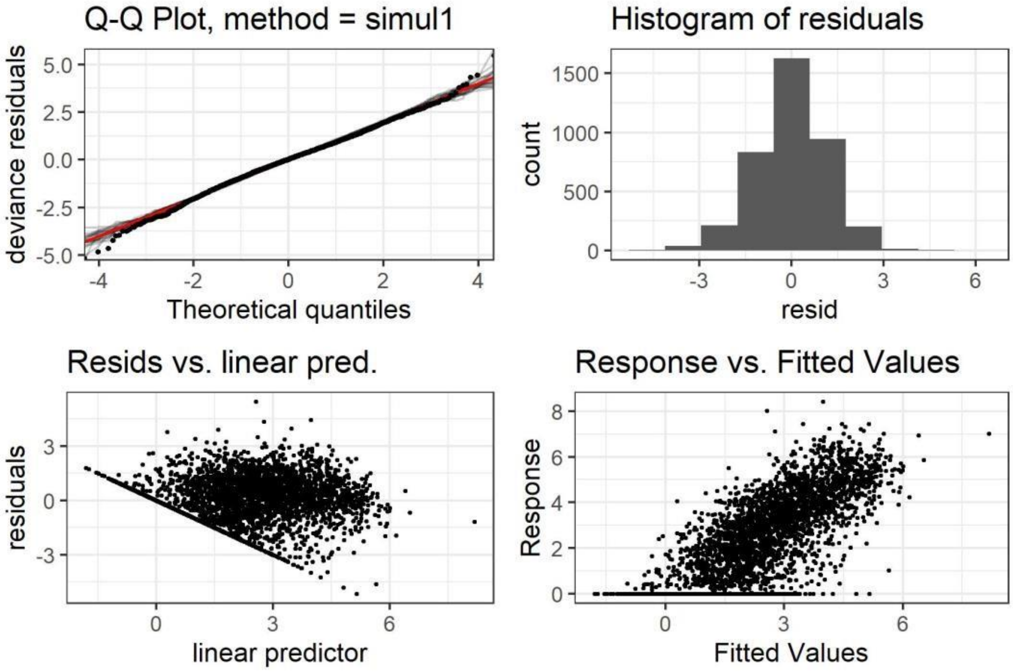


Figure S2.18: spline for the best model (model 0) of gaussian approach for red mullet.



FigureS2.19: residual derived from model 0, gaussian, for red mullet.

Table S2.18: Summary tables Gaussian mod 0, for red mullet.

	Estimate	Std.Error	t.value	p.value
Intercept	3.11	0.30	10.32	<2e-16***
Factor (month) 11	-0.78	0.41	-1.91	0.055 .

Factor(month) 5	-0.79	0.35	-2.22	0.02*
Factor(month) 6	-1.01	0.33	-3.05	0.002**
Factor(month) 7	-1.26	0.36	-3.50	0.0004***
Factor(month) 8	-1.02	0.35	-2.28	0.0045**
Factor(month) 9	-0.37	0.34	-1.10	0.27

Covariates	Edf	Ref.df	F	p.value
Y	8.66	9	109.55	<2e-16***
X	8.33	9	35.73	<2e-16***
Year	7.01	9	16.48	<2e-16***
Depth	8.55	9	77.92	<2e-16***
CHl	7.49	9	19.38	<2e-16***
pH	7.38	9	17.46	<2e-16***
TMP_sst	7.29	9	11.63	<2e-16***
Nit	8.66	9	7.53	2.75e-12***
Dox_bot	1.83	9	4.85	1.39e-13***
sal	0.96	9	0.24	0.08
Eff	7.22	9	27.17	<2e-16***

Diagnostic

R^2	0.64
Dev.expl	65.4%
GCV	1.41

Chapter 4 Supplementary material

Table S4.1: Best model and choosing covariates for each approach and species, for adult and juvenile

Merluccius merluccius	Best model adult	Best model juvenile
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + te(TMP_sst, depth) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) +s(TMP_bot) + s(TMP_sst) + s(dox.bot) + s(eff_OTB) + s(sal)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot)+ s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho).	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(TMP_sst) +s(dox.bot) + s(eff_OTB) + s(sal)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) +s(TMP_bot) + s(TMP_sst) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (TMP_sst) + (eff_OTB)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (TMP_bot) + (depth) + (dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (TMP_bot) + (TMP_sst) + (depth) + (dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)
Mullus barbatus		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_sst, depth) + te(CHL, TMP_sst) + s(eff_OTB) + s(sal) + s(nit)+s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_sst, depth) + te(CHL, TMP_sst) + s(eff_OTB) + s(sal) + s(nit) + s(pho)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_sst)+ s(CHL) + s(eff_OTB) + s(sal) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_sst) + s(CHL) + s(eff_OTB) + s(sal) + s(nit) + s(pho)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_sst, depth) + te(CHL, TMP_sst) + s(eff_OTB) + s(sal) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_sst, depth) + te(CHL, TMP_sst) + s(eff_OTB) + s(sal) + s(nit) + s(pho)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_sst, depth) + te(CHL,TMP_sst) + s(eff_OTB) + s(sal) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_sst, depth) + te(CHL, TMP_sst) + s(eff_OTB) + s(sal) + s(nit) + s(pho)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (CHL) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_sst) + (eff_OTB)

Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_sst) + (CHL) + (eff_OTB) + (sal) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_sst) + (CHL) + (eff_OTB) + (sal) + (nit) + (pho)
Nephrops norvegicus		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year)+te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) +s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (TMP_bot) + (depth) +(dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (TMP_bot) + (depth) + (dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)
Lophius budegassa		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) +(dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_OTB) + (sal)

Parapenaeus longirostris		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) +(dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (TMP_bot) + (depth) + (dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)
Illex coindetii		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot,depth)+ s(dox.bot)+ s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_OTB) + (sal) + (poc) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_OTB) + (sal)
Trachurus trachurus		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)

Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot)+ s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_OTB) + s(sal) + s(poc) + s(nit) + s(pho)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)	N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_OTB) +s(sal) + s(poc) + s(nit) + s(pho)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (eff_OTB)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth)+(TMP_bot)+(dox.bot)+ (eff_OTB) + (sal) + (poc) + (nit) + (pho)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_OTB) + (sal)
Solea solea		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (grain)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (nit) + (pho) + (ph) + (grain)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) +(dox.bot) + (eff_TBB) + (sal) + (poc) + (nit) + (pho) + (ph) + (grain)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (TMP_bot) + (depth) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (nit) + (pho) + (ph) + (grain)
Squilla mantis		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(dox.bot) + s(eff_TBB) + s(grain)	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(ph) + s(grain)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)

Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year)s(depth) + s(TMP_bot) + s(eff_TBB) + s(grain)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(ph) + s(grain)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) +s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year)+(depth) + (TMP_bot) + (eff_TBB) + (grain)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (grain)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (ph) + (grain)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (ph) + (grain)
Sepia oficinalis		
Best model Delta-binomial	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph)+ s(grain)	PA ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(ph) + s(grain)
Best model Delta-gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc)+ s(ph) + s(grain)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + te(TMP_bot, depth) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)
Best model Gaussian	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) s(pho) + s(ph) + s(grain)	log.N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(ph) + s(grain)
Best model Tweedie	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(poc) + s(nit) + s(pho) + s(ph) + s(grain)	N_km2 ~ s(X.utm, Y.utm) + s(year) + s(depth) + s(TMP_bot) + s(dox.bot) + s(eff_TBB) + s(sal) + s(grain)
Best model RF	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (nit) + (pho) + (ph) + (grain)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (ph) + (grain)
Best model GBM	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (grain)	log.N_km2 ~ (X.utm) + (Y.utm) + (year) + (depth) + (TMP_bot) + (dox.bot) + (eff_TBB) + (sal) + (poc) + (nit) + (pho) + (ph) + (grain)

Table S4.2: resume table for each species, approach and source data (A= MEDITS, B=SOLEMON) for adult and juvenile of the best model spatio-temporal + environmental and spatio-temporal only.

A,

ADULTS

Species	Metrics & Model	ST	ST + ENV	Species	Metrics & Model	ST	ST + ENV
Merluccius merluccius	*AIC*			*Mullus barbatus*	*AIC*		
	Delta	2470/5783.98	**2279.57/5700.50**		*Delta*	2144.16/4747.96	**1996.27/4711.30**
	Gaus	15217.27	**14808.36**		*Gaus*	14960.85	**14674.75**
	TW	32841.32	**32448.76**		*TW*	26051.88	**25786.97**
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.expl.				*Dev.expl.*		
	Delta	55%	**58.25%**		*Delta*	51.75%	**54.7%**
	Gaus	60.5%	**64.8%**		*Gaus*	61.4%	**64.6%**
	TW	50.2%	**55.8%**		*TW*	60.8%	**65.6%**
	RF	82.12%	**83.19%**		*RF*	79.7%	**81.05%**
	GBM	74%	**77%**		*GBM*	62.00%	**68.00%**
	MAE validation				*MAE validation*		
	Delta	117.43	**112.67**		*Delta*	159.76	**156.37**
	Gaus	167.27	**160.84**		*Gaus*	208.24	**193.97**
	TW	144.70	**135.42**		*TW*	202.17	**188.48**
	RF	86.44	**59.51**		*RF*	132.41	**96.28**
	GBM	153.61	**142.86**		*GBM*	208.18	**187.68**
Norway lobster	*AIC*			*Lophius budegassa*	*AIC*		
	Delta	2196.14/1854.38	**2084.90/1827.71**		*Delta*	1603.81/231.77	**1568.71/225.65**
	Gaus	12743.48	**12566.76**		*Gaus*	8089.52	**8022.34**
	TW	10692.52	**10604.12**		*TW*	**5602.34**	5609.86
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.expl.				*Dev.expl.*		
	Delta	33.18%	**37.1%**		*Delta*	38.8%	**40.5%**
	Gaus	37.2	**40.7%**		*Gaus*	19%	**21.2%**
	TW	56.2%	**60.8%**		*TW*	37.1%	**40.8%**
	RF	56.9%	**58.29%**		*RF*	25.02%	**25.02%**
	GBM	49.7%	**55.2%**		*GBM*	28.1%	**34.5%**
	MAE validation				*MAE validation*		
	Delta	17.62	**17.14**		*Delta*	3.39	**3.31**
	Gaus	17.47	**17.21**		*Gaus*	3.39	**3.37**
	TW	20.06	**19.15**		*TW*	3.35	**3.26**
	RF	13.45	**11.00**		*RF*	2.72	**2.46**
	GBM	16.85	**16.64**		*GBM*	3.33	**3.30**
Parapenaeus longirostris	*AIC*			*Illex coindetii*	*AIC*		
	Delta	2544.85/5247.91	**2447.89/5116.53**		*Delta*	1832.513/2282.064	**1725.173/2231.267**
	Gaus	17167.51	**16951.65**		*Gaus*	9620.091	**9497.957**
	TW	28141.39	**27825.22**		*TW*	12289.34	**12209.77**
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.expl.				*Dev.expl.*		
	Delta	47.3%	**51.35%**		*Delta*	39.1%	**43.75%**
	Gaus	56.1%	**58.9%**		*Gaus*	55.5%	**57.8%**
	TW	60.7%	**66.1%**		*TW*	55.9%	**59.4%**

	RF	76.09%	**77.58%**		*RF*	72.26	**72.89%**
	GBM	51.2%	**56.3%**		*GBM*	49.2%	**54.3%**
	MAE validation				*MAE validation*		
	Delta	506.86	**500.45**		*Delta*	18.67	**17.99**
	Gaus	599.02	**590.74**		*Gaus*	19.23	**18.98**
	TW	660.79	**589.25**		*TW*	20.82	**20.04**
	RF	440.04	**305.51**		*RF*	13.42	**10.53**
	GBM	604.94	**554.59**		*GBM*	19.38	**18.85**
Trachurus trachurus	*AIC*						
	Delta	1941.624/2638.973	**1817.748/2630.21**				
	Gaus	11384.1	**11218.45**				
	TW	13224.76	**13086.21**				
	RF	X	X				
	GBM	X	X				
	Dev.expl.						
	Delta	36.55%	**41.15%**				
	Gaus	49%	**52.2%**				
	TW	63.1%	**67.6%**				
	RF	61.91%	**63.4%**				
	GBM	50.1%	**55.6%**				
	MAE validation						
	Delta	85.11	**83.35**				
	Gaus	85.45	**84.60**				
	TW	112.87	**100.64**				
	RF	70.75	**60.90**				
	GBM	84.44	**82.84**				

JUVENILE

Species	Metrics & Model	ST	ST+Env	Species	Metrics & Model	ST	ST+Env
Merluccius merluccius	*AIC*			*Mullus barbatus*	*AIC*		
	Delta	1327.50/5307.11	**1167.79/5247.99**		*Delta*	1970.25/5572.02	**1854.43/5463.01**
	Gaus	13195.64	**12948.99**		*Gaus*	16274.07	**15756.64**
	TW	27137.82	**26970.76**		*TW*	29644.05	**29242.2**
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.expl.				*Dev.expl.*		
	Delta	57.7%	**61.5%**		*Delta*	56.05%	**59.55%**
	Gaus	65.8%	**68.5%**		*Gaus*	59.1%	**64.9%**
	TW	63.2%	**65.8%**		*TW*	67.2%	**72.5%**
	RF	84.71%	**86.14%**		*RF*	82.36%	**84.51%**
	GBM	67.00%	**72.00%**		*GBM*	60.00%	**70.00%**
	MAE validation				*MAE validation*		
	Delta	254.77	**251.86**		*Delta*	1047.28	**1024.26**
	Gaus	304.73	**292.14**		*Gaus*	**1216.51**	1241.63
	TW	297.08	**290.26**		*TW*	1619.55	**1444.20**
	RF	205.05	**153.31**		*RF*	882.22	**695.06**
	GBM	284.33	**275.07**		*GBM*	1198.61	**1108.46**
Norway lobster	*AIC*			*Lophius budegassa*	*AIC*		
	Delta	888.56/582.12	**859.00/569.92**		*Delta*	3048.83/1760.04	**2983.02/1734.36**
	Gaus	8004.63	**7821.69**		*Gaus*	12747.46	**12681.88**
	TW	5343.63	**5292.23**		*TW*	12153.9	**12033.97**

	RF	*X*	X		*RF*	X	X
	GBM	*X*	X		*GBM*	X	X
	Dev.ex pl.				*Dev.ex pl.*		
	Delta	34.7%	**39.45%**		*Delta*	31.45%	**34.15%**
	Gaus	26.2%	**30.5%**		*Gaus*	29.8%	**31.4%**
	TW	62.1%	**69.5%**		*TW*	40.3%	**45.2%**
	RF	54.3%	**54.6%**		*RF*	42.94%	**42.86%**
	GBM	40.87%	**44.62%**		*GBM*	41.7%	**45.82%**
	MAE validation				*MAE validation*		
	Delta	4.34	**4.23**		*Delta*	11.41	**11.23**
	Gaus	4.83	**4.79**		*Gaus*	11.05	**10.98**
	TW	5.02	**4.72**		*TW*	12.19	**11.62**
	RF	3.88	**3.49**		*RF*	8.36	**6.76**
	GBM	4.61	**4.61**		*GBM*	10.83	**10.74**
Parapenaeus longirostris	*AIC*			*Illex coindetii*	*AIC*		
	Delta	1839.91/3506.65	**1737.17/3459.44**		*Delta*	2886.635/5889.34	**2709.038/5841.301**
	Gaus	13414.98	**13278.76**		*Gaus*	16502.91	**16256.42**
	TW	17677.51	**17587.34**		*TW*	32093.92	**31881.61**
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.ex pl.				*Dev.ex pl.*		
	Delta	48.35%	**51.9%**		*Delta*	50.65	**53.75%**
	Gaus	57.3%	**59.2%**		*Gaus*	56.8	**59.9%**
	TW	66.4%	**69%**		*TW*	53.7	**57.3%**
	RF	76.37%	**77.83%**		*RF*	78.83%	**79.66%**
	GBM	51.2%	**56.3%**		*GBM*	53.2%	**58.3%**
	MAE validation				*MAE validation*		
	Delta	170.69	**168.15**		*Delta*	320.19	**304.60**
	Gaus	179.32	**179.05**		*Gaus*	399.08	**384.48**
	TW	221.87	**212.41**		*TW*	403.53	**378.57**
	RF	144.27	**109.75**		*RF*	252.47	**169.49**
	GBM	176.71	**170.11**		*GBM*	379.81	**378.43**
Trachurus trachurus	*AIC*						
	Delta	2542.39/5660.29	**2364.47/5633.43**				
	Gaus	16588.01	**16274.05**				
	TW	27392.71	**27202.61**				
	RF	X	X				
	GBM	X	X				
	Dev.ex pl.						
	Delta	34.7%	**37.7%**				
	Gaus	49.4%	**54%**				
	TW	52.3%	**56.6%**				
	RF	67.95%	**68.6%**				
	GBM	53.1%	**59.1%**				
	MAE validation						
	Delta	715	**710**				
	Gaus	728.27	**723.06**				
	TW	1081.99	**1029.33**				
	RF	626.51	**555.58**				
	GBM	723.80	**718.33**				

B

ADULT

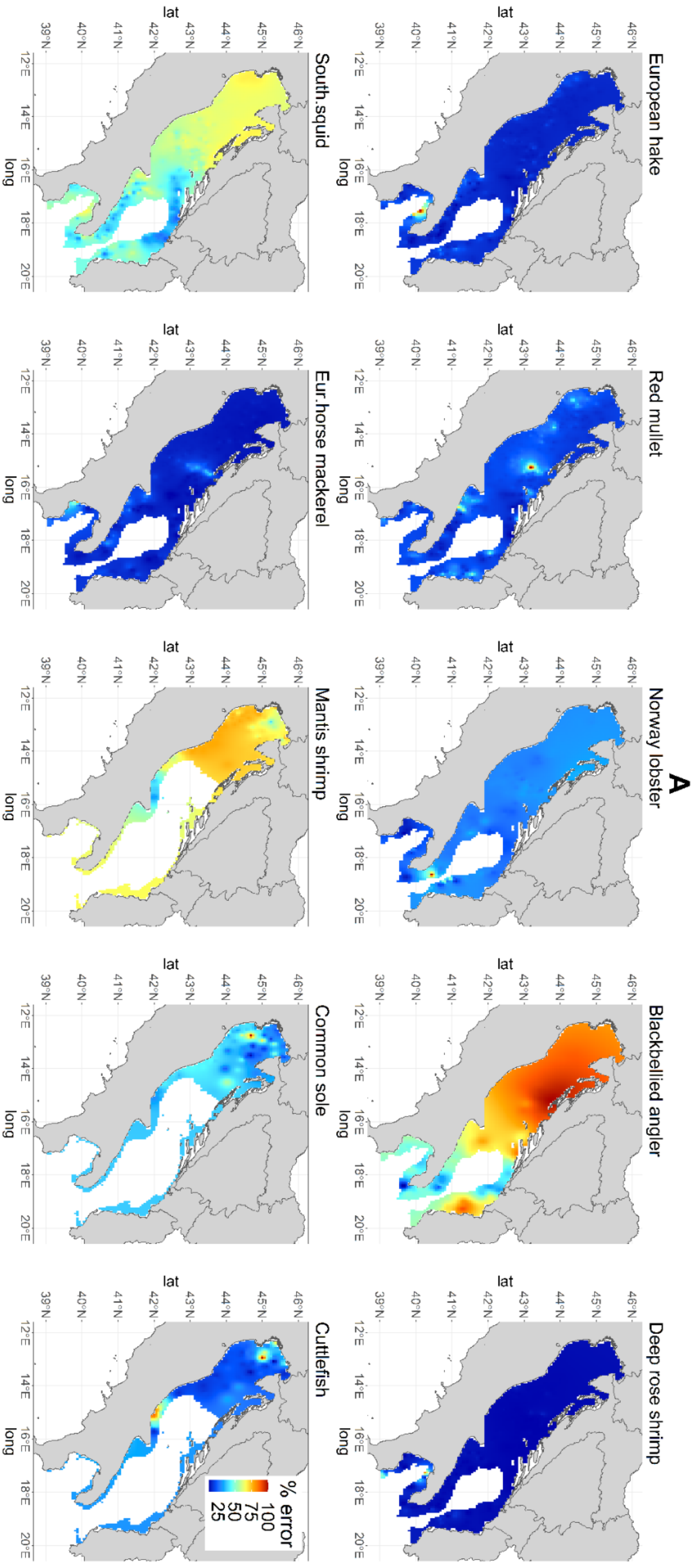
Species	Metrics & Model	ST	ST + Env	Species	Metrics & Model	ST	ST + Env
Solea solea	*AIC*			*Squilla mantis*	*AIC*		
	Delta	274.14/1690.81	**260.73/1667.53**		*Delta*	335.08/1099.28	**307.82/1061.75**
	Gaus	2592.94	**2555.25**		*Gaus*	2685.18	**2626.36**
	TW	9741.83	**9720.53**		*TW*	**5929.22**	**5882.07**
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.expl.				*Dev.expl.*		
	Delta	60.3	**64.35**		*Delta*	57.95%	**61.4%**
	Gaus	67.2%	**69.4%**		*Gaus*	65.8%	**68.6%**
	TW	62.2%	**65%**		*TW*	63.8%	**65.5%**
	RF	71.12%	**69.21%**		*RF*	72.96%	**74.28%**
	GBM	74.00%	**77%%**		*GBM*	64.00%	**70.00%**
	MAE validation				*MAE validation*		
	Delta	297.85	**284.54**		*Delta*	258.29	**247.93**
	Gaus	315.86	**304.07**		*Gaus*	302.17	**292.70**
	TW	303.24	**291.74**		*TW*	277.02	**271.73**
	RF	201.08	**167.61**		*RF*	198.41	**159.63**
	GBM	279.46	**272.50**		*GBM*	277.74	**251.39**
Sepia officinalis	*AIC*						
	Delta	449.31/1078.49	**421.68/1036.87**				
	Gaus	2584.59	**2526.42**				
	TW	6041.61	**5980.47**				
	RF	X	X				
	GBM	X	X				
	Dev.expl.						
	Delta	51.95%	**56.3%**				
	Gaus	68.8%	**72.3%**				
	TW	62.1%	**66%**				
	RF	66.8%	**69.4%**				
	GBM	60%	**64%**				
	MAE validation						
	Delta	86.88	**79.40**				
	Gaus	**91.53**	96.10				
	TW	99.18	**86.51**				
	RF	61.09	**53.76**				
	GBM	85.34	**79.69**				

JUVENILE

Species	Metrics & Model	ST	ST +Env	Species	Metrics & Model	ST	ST +Env
Solea solea	*AIC*			*Squilla mantis*	*AIC*		
	Delta	100.57/913.26	**56.66/881.74**		*Delta*	369.30/1251.27	**322.50/1211.34**
	Gaus	1294.22	**1258.64**		*Gaus*	2763.17	**2673.62**
	TW	4396.64	**4363.85**		*TW*	6348.66	**6241.78**
	RF	X	X		*RF*	X	X
	GBM	X	X		*GBM*	X	X
	Dev.expl.				*Dev.expl.*		
	Delta	73.5%	**81%**		*Delta*	57.57%	**63.5%**

		Gaus	81%	**83%**			*Gaus*	67.1%	**71.4%**
		TW	72%	**75.3%**			*TW*	64.3%	**71.4%**
		RF	78.37%	**76.41%**			*RF*	**73.3%**	72.78%
		GBM	87.00%	**90.00%**			*GBM*		
	MAE validation					*MAE validation*			
		Delta	568.67	**569.21**			*Delta*	313.63	**284.34**
		Gaus	566.61	**564.08**			*Gaus*	337.93	**327.19**
		TW	571.25	**554.36**			*TW*	327.21	**283.21**
		RF	458.83	**390.47**			*RF*	230.55	**196.22**
		GBM	465.59	**415.47**			*GBM*	322.26	**300.59**
Sepia officinalis	*AIC*								
		Delta	465.55/970.64	**422.80/927.41**					
		Gaus	2487.49	**2401.32**					
		TW	5557.61	5452.47					
		RF	X	X					
		GBM	X	X					
	Dev.expl.								
		Delta	56.3%	**61.8%**					
		Gaus	67.4%	**72.1%**					
		TW	66%	**72.9%**					
		RF	65.7%	**69.45%**					
		GBM	73.00%	**78.00%**					
	MAE validation								
		Delta	111.49	**99.70**					
		Gaus	118.33	**113.50**					
		TW	115.40	**102.75**					
		RF	84.86	**68.67**					
		GBM	109.04	**97.55**					

The distribution of Average relative residuals between data observed and predicted data is shown in Figure S4.1. Considering all species on average, the relative residual is around 40%. More in detail, for adults of European hake the relative error is on average, 25-30% in the entire area, and higher error is shown in the southern area of the basin, especially close to the Calabrian region, while for Juvenile the relative error map is generally high (on average 90%). For Red mullet for both Adults and Juveniles results show on average 20-25% error and as high as 35% error for some spots in the Pomo Pit area. The e-SDM applied to the Norway lobster showed approximately 37 % relative error on average for the adults' entire area, and some spots with higher values in the south part of the basin, while the model showed much higher error for the Juveniles. The relative error for both adults and juveniles of Black-bellied angler was high, i.e., on average approximately 90% and 75%, respectively. High error for this species was found in the north and central part of the Adriatic Sea while juveniles showed the highest relative error in the north and smallest values in the southern part of the basin. The e-SDM was predicting European horse mackerel with low error values both for adults and juveniles (approximately 20%) and Deep-water rose shrimp with an average relative error of 20% and 50% for adults and juveniles respectively. For Shortfin squid the relative error of the e-SDM was approximately 50% on average both for adults and juveniles. e-SDM showed good performances for Mantis shrimp for which an average error of approximately 20% was calculated for areas shallower than 100 m from SOLEMON survey for both adults and juveniles; for common sole an average relative error of 50% for adults and 15% for juveniles was obtained while for Cuttlefish relative estimated error was 30% and 20% for adults and juveniles, respectively.


A
European hake
Red mullet
Norway lobster
Blackbellied angler
Deep rose shrimp
South.squid
Eur.horse mackerel
Mantis shrimp
Common sole
Cuttlefish
% error
100
75
50
25
lat
long
39°N
40°N
41°N
42°N
43°N
44°N
45°N
46°N
12°E
14°E
16°E
18°E
20°E

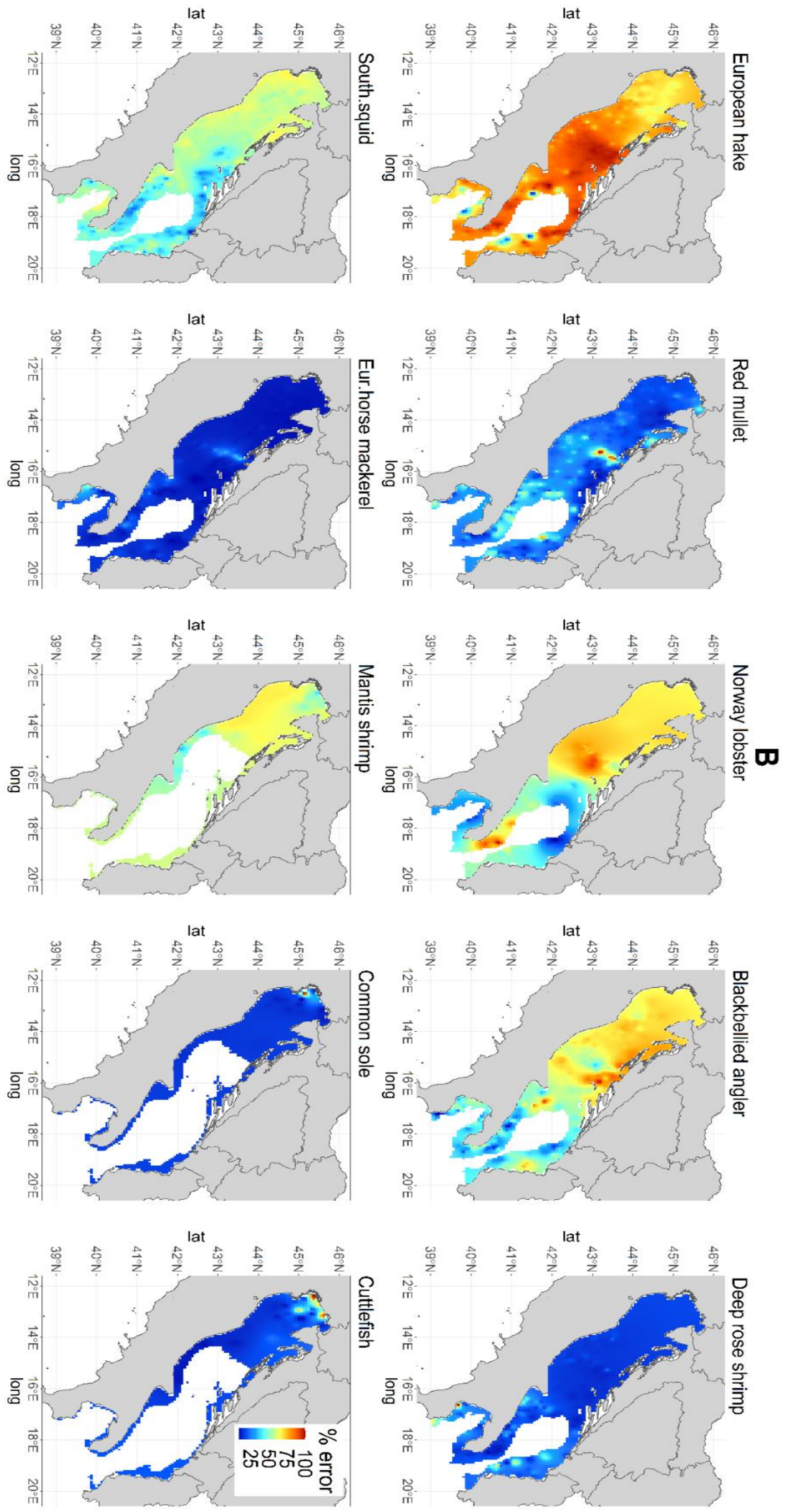


Fig.S4.1: Relative average residual map for adult (panel A) and juvenile (panel B) for each species from IDW interpolation and equation 1.

Chapter 5 Supplementary material

In the following plot I represented the relative importance of each covariate for each model and life stage:

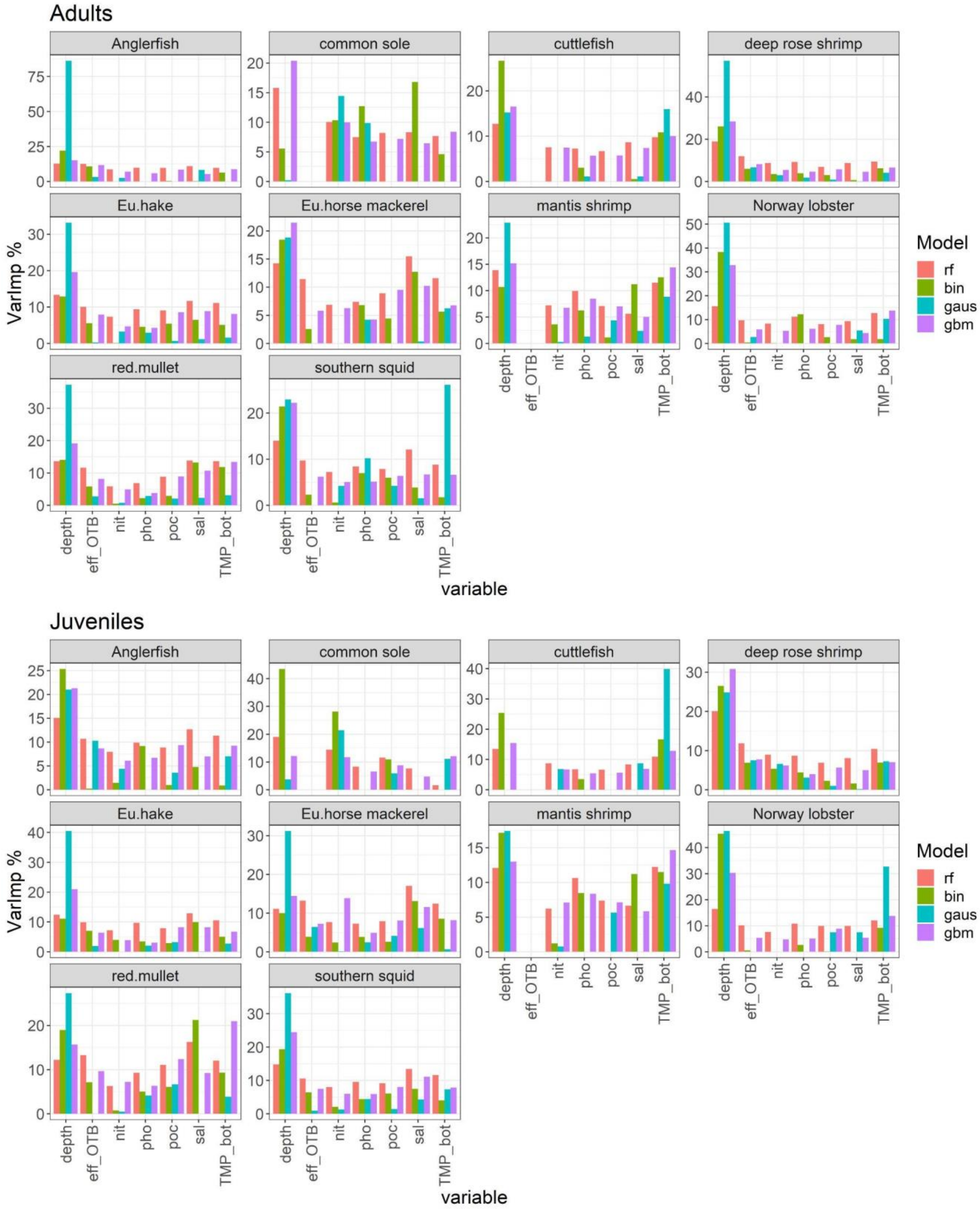


Figure S5.1: variance importance (y-axes) in percentage for each covariate (x-axes), models (different colors), and species.

Table S5.1: Metrics for each species, life stage, and approaches used in chapter 5.

A: ADULTS

MEDITS

Species	*Metrics & Model*	*Results*	*Species*	*Metrics & Model*	*Results*
Merluccius merluccius	***AIC***		*Mullus barbatus*	***AIC***	
	Binomial	*2833.27*		*Binomial*	*4953.05*
	Delta-gaus	*5985.59*		*Delta-gaus*	*9133.83*
	RF	*X*		*RF*	*X*
	GBM	*X*		*GBM*	*X*
	Dev.expl.			***Dev.expl.***	
	Binomial	*48.5%*		*Binomial*	*47.2%*
	Delta-gaus	*50.7%*		*Delta-gaus*	*42.6%*
	RF	*74.7%*		*RF*	*71.19%*
	GBM	*77%*		*GBM*	*65%*
Norway lobster	***AIC***		*Lophius budegassa*	***AIC***	*Result*
	Binomial	*4054.30*		*Binomial*	*3010.99*
	Delta-gaus	*3708.30*		*Delta-gaus*	*2077.13*
	RF	*X*		*RF*	*X*
	GBM	*X*		*GBM*	*X*
	Dev.expl.			***Dev.expl.***	
	Binomial	*39.3%*		*Binomial*	*17.7%*
	Delta-gaus	*22%*		*Delta-gaus*	*39.1%*
	RF	*56.16%*		*RF*	*23.62*
	GBM	*56%*		*GBM*	*35.3%*
Parapenaeus longirostris	***AIC***		*Ilex coindetii*	***AIC***	
	Binomial	*4745.51*		*Binomial*	*4100.44*
	Delta-gaus	*8857.28*		*Delta-gaus*	*4806.87*
	RF	*X*		*RF*	*X*
	GBM	*X*		*GBM*	*X*
	Dev.expl.			***Dev.expl.***	
	Binomial	*48.3%*		*Binomial*	*43.4%*
	Delta-gaus	*36.4%*		*Delta-gaus*	*18.6%*
	RF	*72.9%*		*RF*	*65.28%*
	GBM	*52%*		*GBM*	*55%*
Trachurus trachurus	***AIC***				
	Binomial	*3199.43*			
	Delta-gaus	*4056.98*			
	RF	*X*			
	GBM	*X*			
	Dev.expl.				
	Binomial	*45.5%*			
	Delta-gaus	*26.1%*			
	RF	*59.2%*			
	GBM	*62.3%*			
SOLEMON					
Solea solea	***AIC***		*Squilla mantis*	***AIC***	
	Binomial	*276.24*		*Binomial*	*573.96*
	Delta-gaus	*1366.43*		*Delta-gaus*	*1090.62*
	RF	*X*		*RF*	*X*
	GBM	*X*		*GBM*	*X*
	Dev.expl.			***Dev.expl.***	
	Binomial	*74.6%*		*Binomial*	*55.4%*
	Delta-gaus	*34.1%*		*Delta-gaus*	*43.1%*
	RF	*69.86%*		*RF*	*61.9%*
	GBM	*75%*		*GBM*	*80.2%*
Sepia officinalis	***AIC***				
	Binomial	*690.75*			
	Delta-gaus	*1479.99*			
	RF	*X*			
	GBM	*X*			
	Dev.expl.				
	Binomial	*45.2%*			
	Delta-gaus	*59.5%*			
	RF	*64.7%*			
	GBM	*64%*			

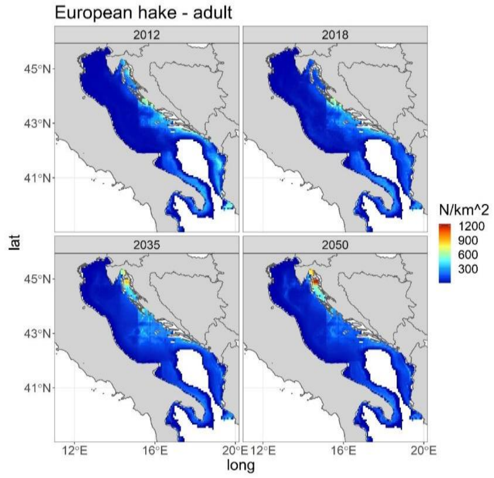
B: JUVENILE

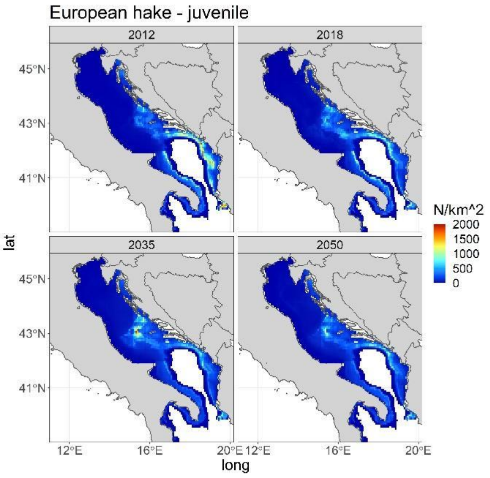
MEDITS

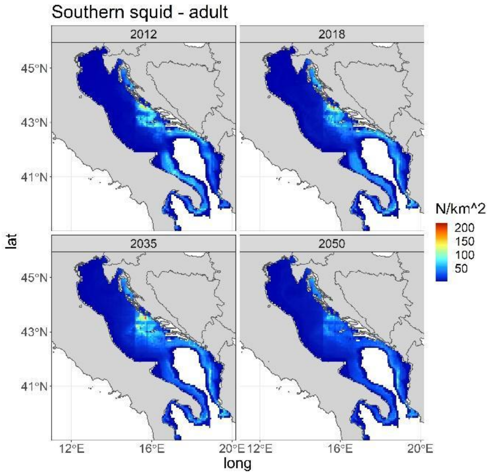
Species	Metrics & Model	Results	Species	Metrics & Model	Results
Merluccius merluccius	**AIC**		*Mullus barbatus*	**AIC**	
	Binomial	1861.17		Binomial	1980.88
	Delta-gaus	5325.47		Delta-gaus	2460.68
	RF	X		RF	X
	GBM	X		GBM	X
	Dev.expl.			**Dev.expl.**	
	Binomial	62.4%		Binomial	50.3%
	Delta-gaus	41.6%		Delta-gaus	46.9%
	RF	79.16%		RF	65.35%
	GBM	72.2%		GBM	60.2%
Norway lobster	**AIC**		*Lophius budegassa*	**AIC**	Result
	Binomial	1704.46		Binomial	6141.94
	Delta-gaus	1316.84		Delta-gaus	9495.56
	RF	X		RF	X
	GBM	X		GBM	X
	Dev.expl.			**Dev.expl.**	
	Binomial	49.9%		Binomial	21.6%
	Delta-gaus	27.3%		Delta-gaus	18.4%
	RF	53.5%		RF	37.14%
	GBM	45%		GBM	44%
Parapenaeus longirostris	**AIC**		*Ilex coindetii*	**AIC**	
	Binomial	4109.97		Binomial	5360.32
	Delta-gaus	13109.67		Delta-gaus	9719.76
	RF	X		RF	X
	GBM	X		GBM	X
	Dev.expl.			**Dev.expl.**	
	Binomial	40.8%		Binomial	42.1%
	Delta-gaus	20.6%		Delta-gaus	44.2%
	RF	47.63%		RF	70.43%
	GBM	53.2%		GBM	55%
Trachurus trachurus	**AIC**				
	Binomial	4914.66			
	Delta-gaus	10254.2			
	RF	X			
	GBM	X			
	Dev.expl.				
	Binomial	45%			
	Delta-gaus	21.7%			
	RF	64.2%			
	GBM	59%			

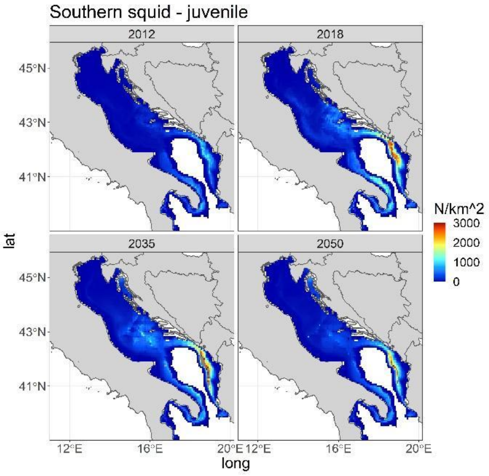
SOLEMON

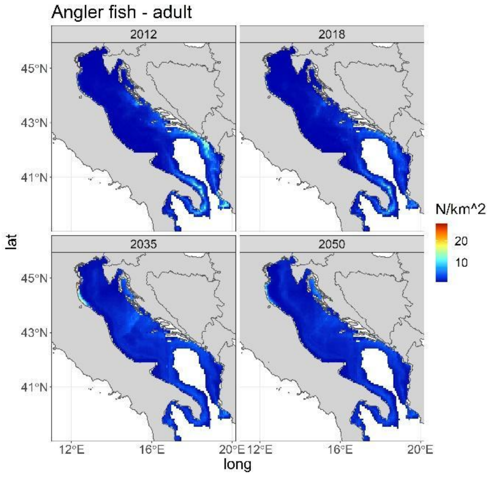
Solea solea	**AIC**		*Squilla mantis*	**AIC**	
	Binomial	69.77		Binomial	560.51
	Delta-gaus	850.21		Delta-gaus	1243.8
	RF	X		RF	X
	GBM	X		GBM	X
	Dev.expl.			**Dev.expl.**	
	Binomial	67.7%		Binomial	56%
	Delta-gaus	25.8%		Delta-gaus	49%
	RF	32.31%		RF	63.04
	GBM	86.8%		GBM	80%
Sepia officinalis	**AIC**				
	Binomial	462.13			
	Delta-gaus	790.92			
	RF	X			
	GBM	X			
	Dev.expl.				
	Binomial	55.6%			
	Delta-gaus	43.2%			
	RF	63.48%			
	GBM	77.3%			

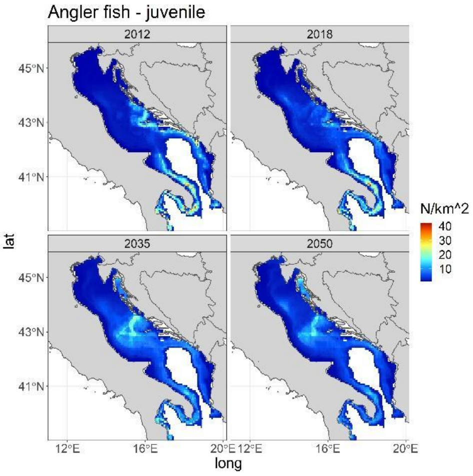

European hake - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
N/km^2
1200
900
600
300
12°E
16°E
20°E
long

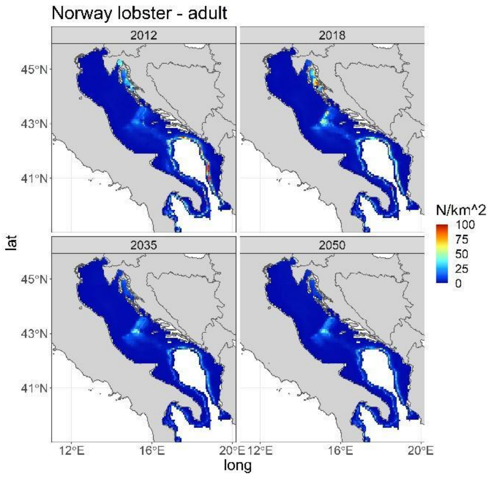

European hake - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
N/km^2
2000
1500
1000
500
0
12°E
16°E
20°E
long

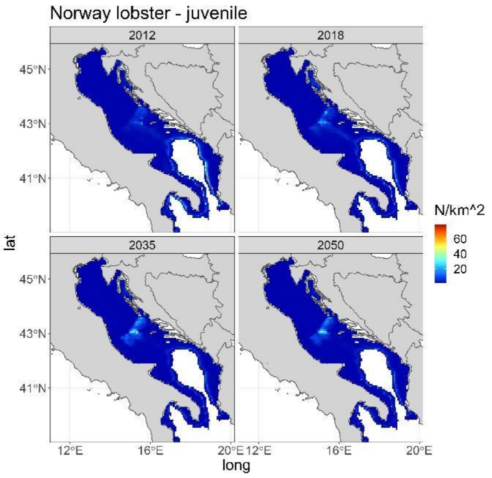

Southern squid - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
N/km^2
200
150
100
50
12°E
16°E
20°E
long

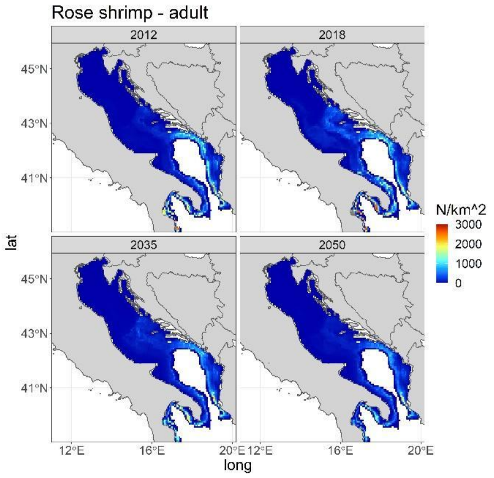

Southern squid - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
N/km^2
3000
2000
1000
0
12°E
16°E
20°E
long

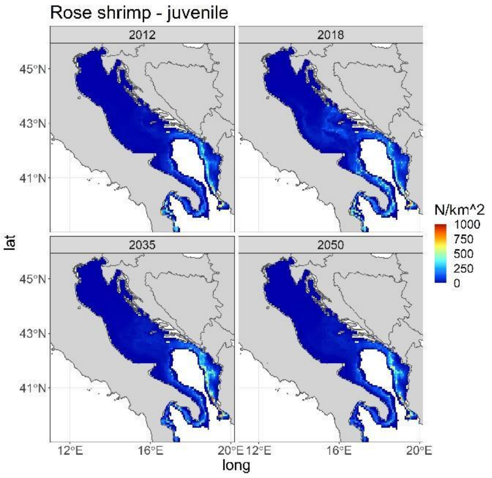

Angler fish - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
N/km^2
20
10
12°E
16°E
20°E
long

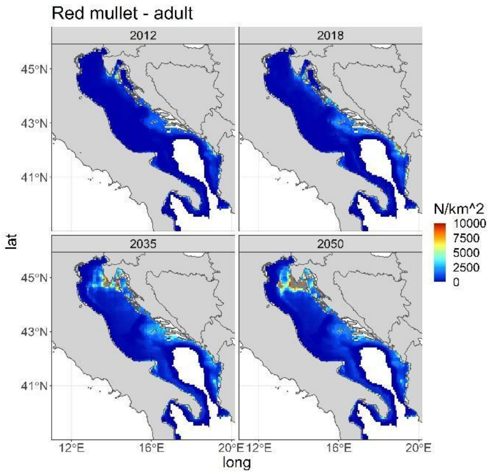

Angler fish - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
N/km^2
40
30
20
10
12°E
16°E
20°E
long

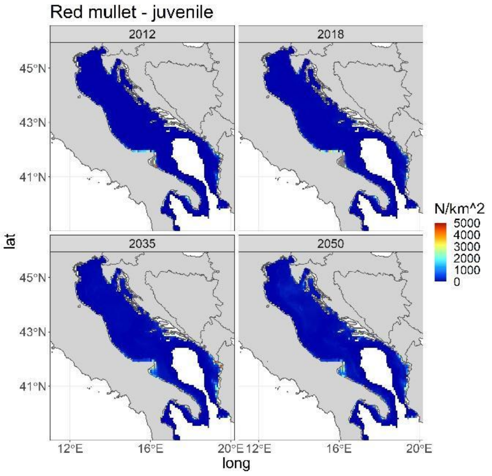

Norway lobster - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
100
75
50
25
0

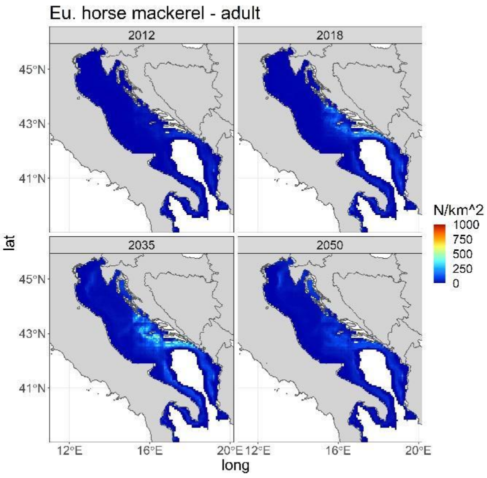

Norway lobster - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
60
40
20

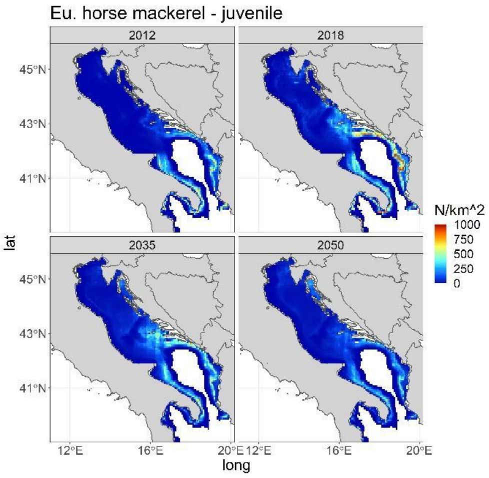

Rose shrimp - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
3000
2000
1000
0

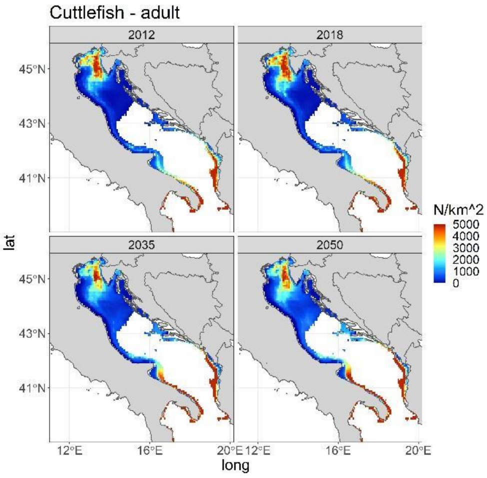

Rose shrimp - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
1000
750
500
250
0

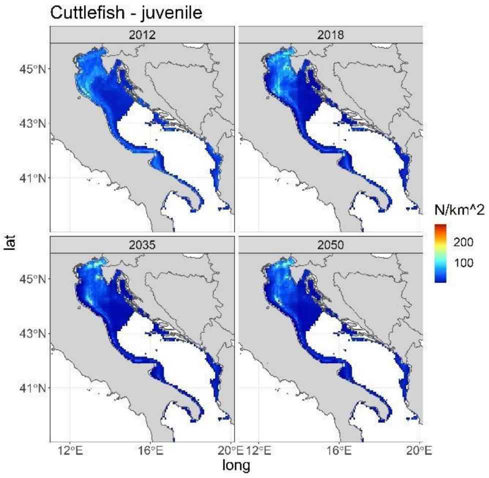

Red mullet - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
10000
7500
5000
2500
0


Red mullet - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
5000
4000
3000
2000
1000
0


Eu. horse mackerel - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
1000
750
500
250
0


Eu. horse mackerel - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
1000
750
500
250
0


Cuttlefish - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
5000
4000
3000
2000
1000
0


Cuttlefish - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
N/km^2
200
100

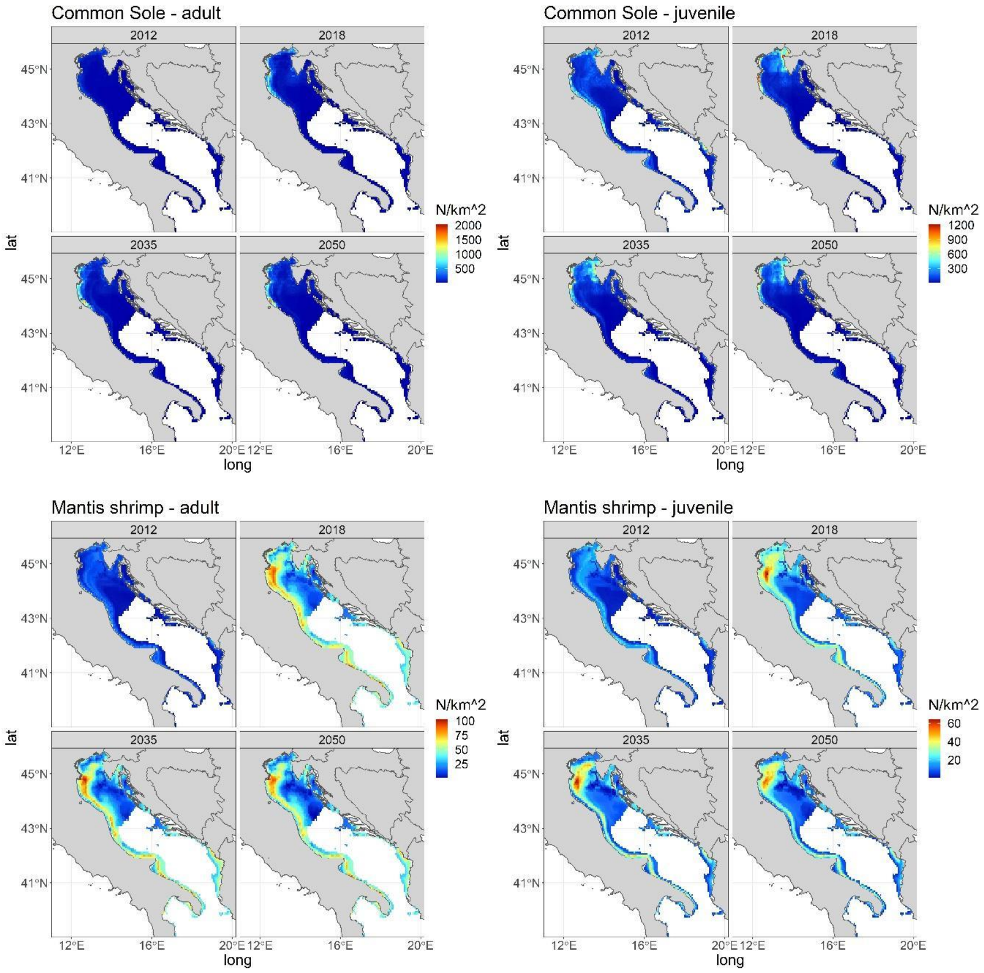
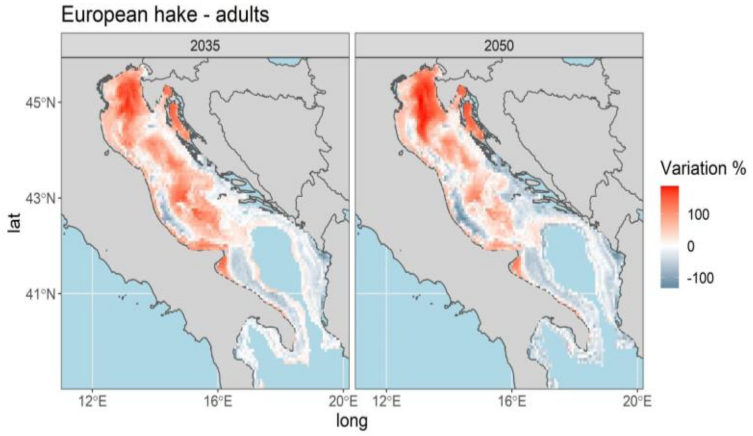
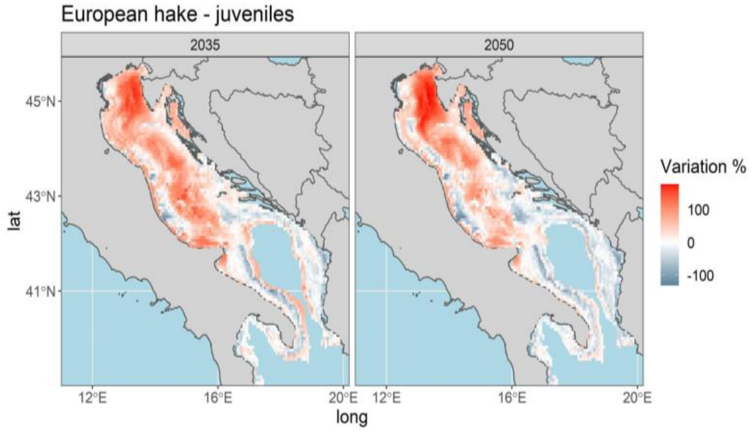
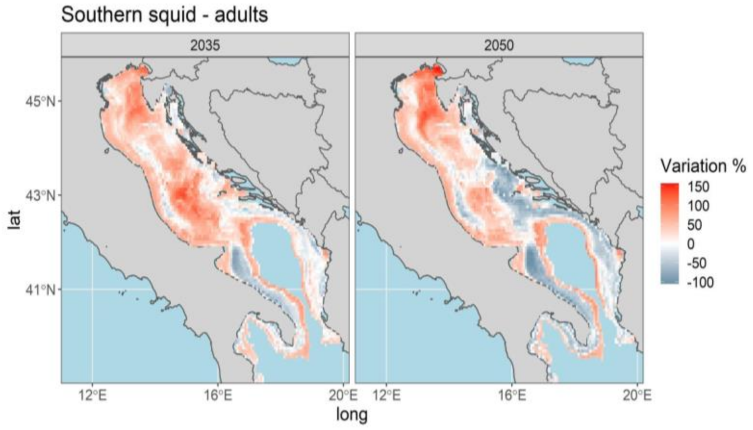
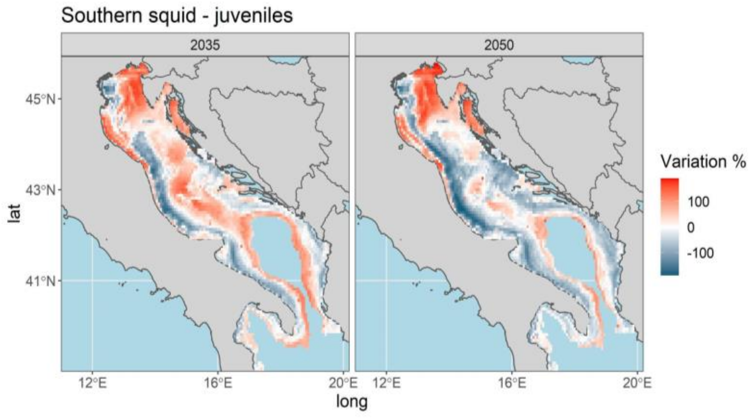


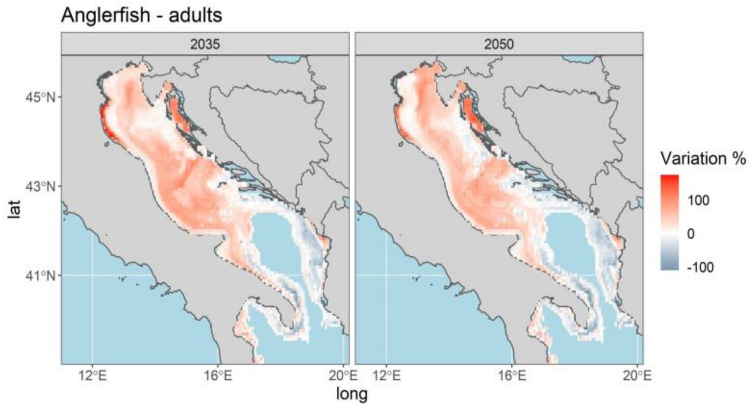
Figure S5.2: density distribution (n/km2) for each species (title of the plot), scenario (title of the panel), and age (plot's title: adult or juvenile)

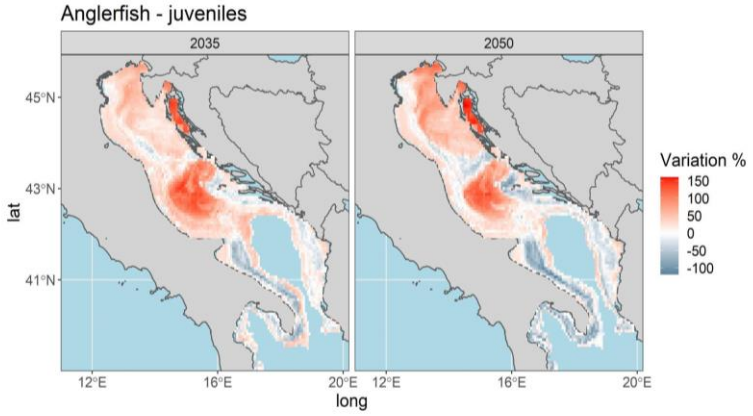

European hake - adults
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100

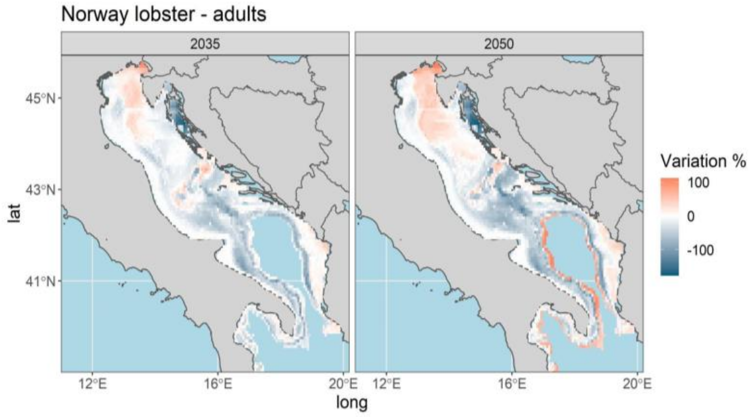

European hake - juveniles
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100

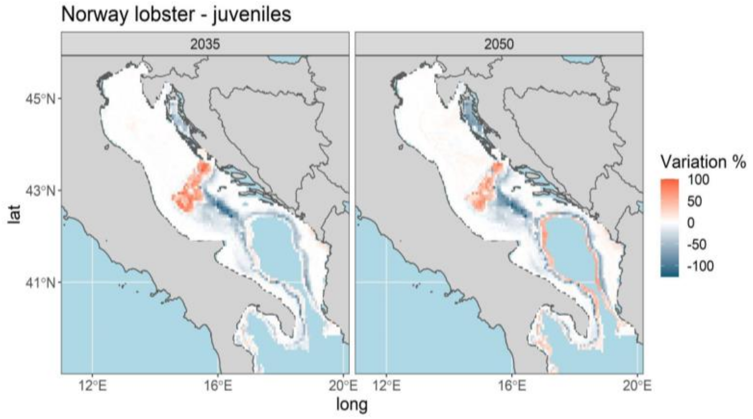

Southern squid - adults
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
150
100
50
0
-50
-100

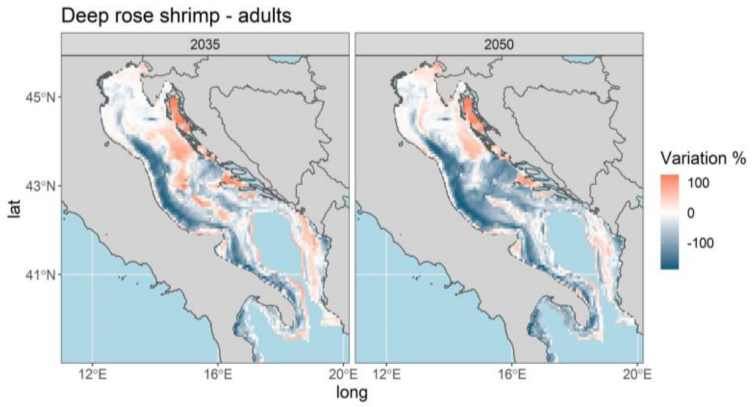

Southern squid - juveniles
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100

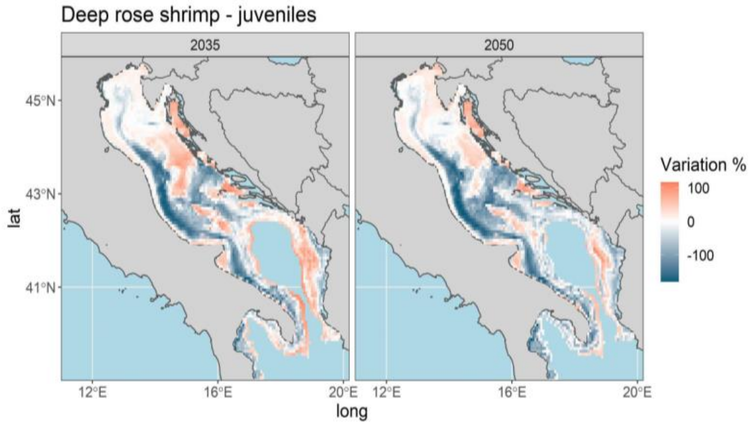

Anglerfish - adults
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100

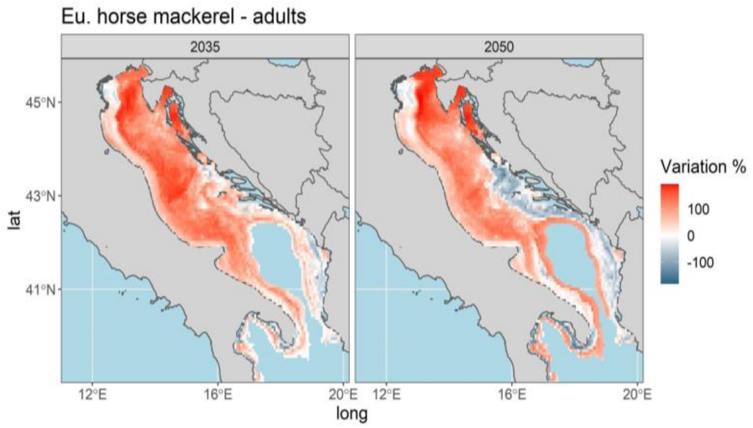

Anglerfish - juveniles
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
150
100
50
0
-50
-100

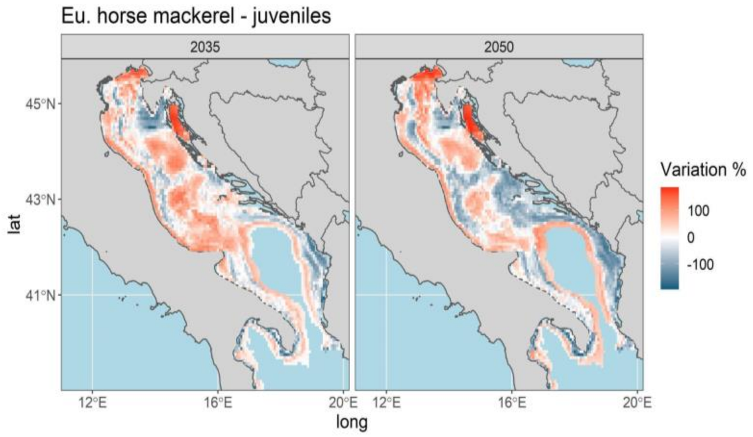

Norway lobster - adults
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100

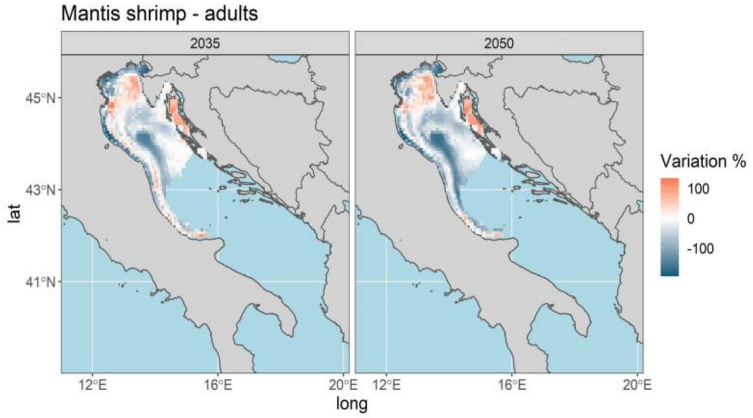

Norway lobster - juveniles
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
50
0
-50
-100

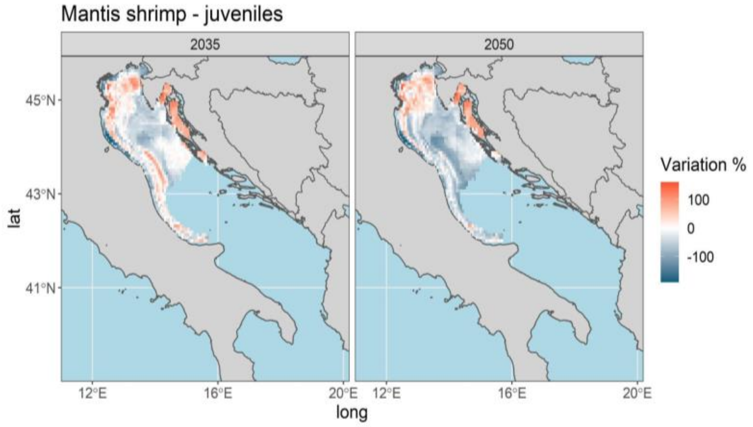

Deep rose shrimp - adults

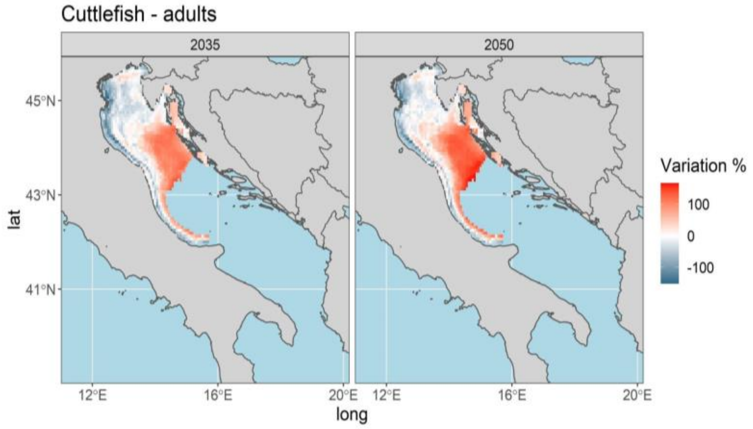

Deep rose shrimp - juveniles

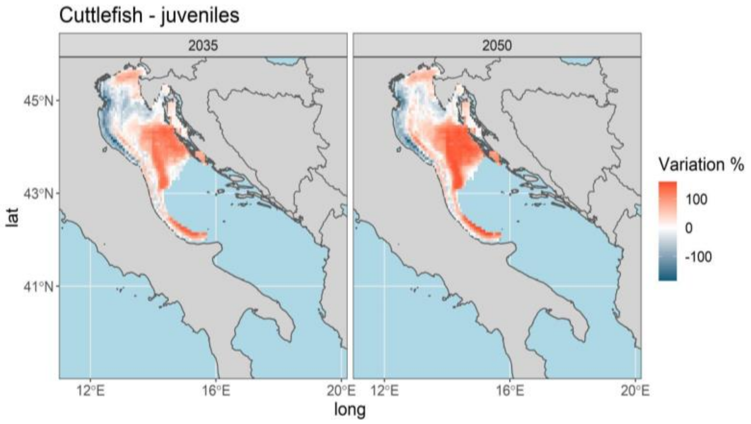

Eu. horse mackerel - adults

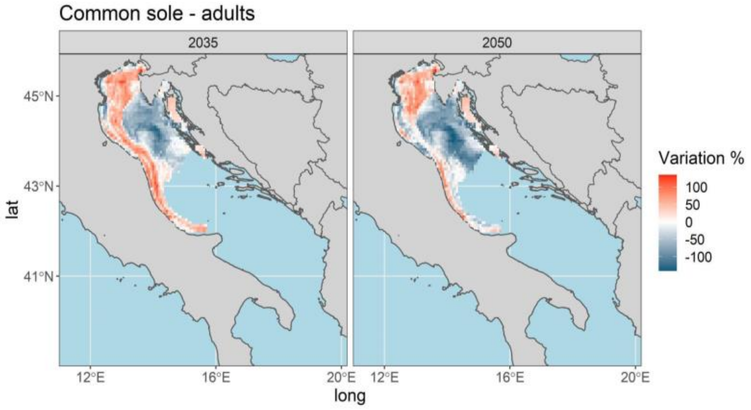

Eu. horse mackerel - juveniles


Mantis shrimp - adults
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100


Mantis shrimp - juveniles
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100


Cuttlefish - adults
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
Variation %
100
0
-100





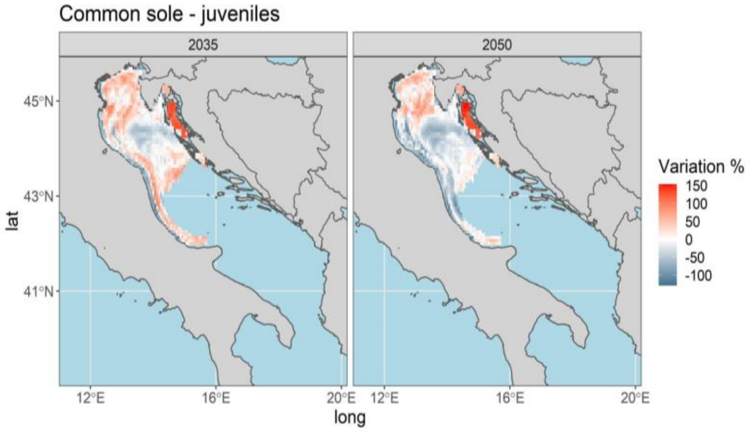
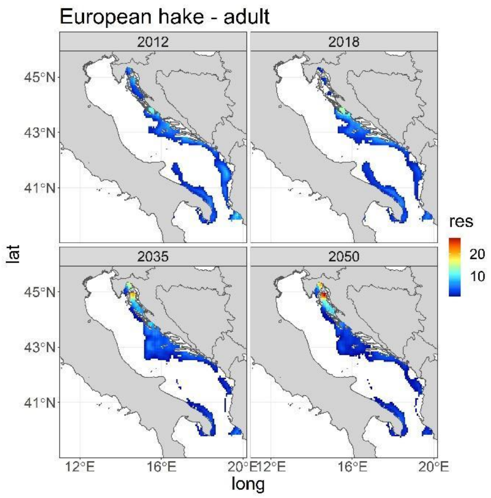
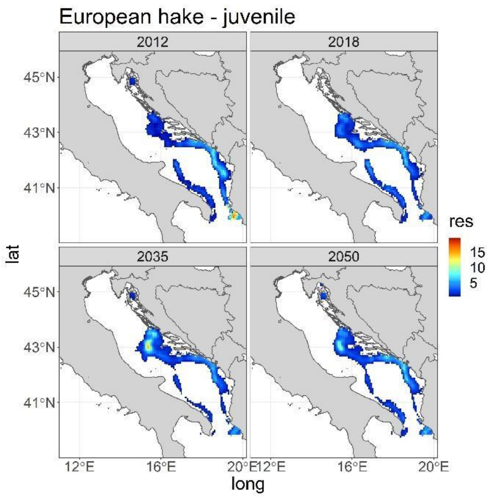
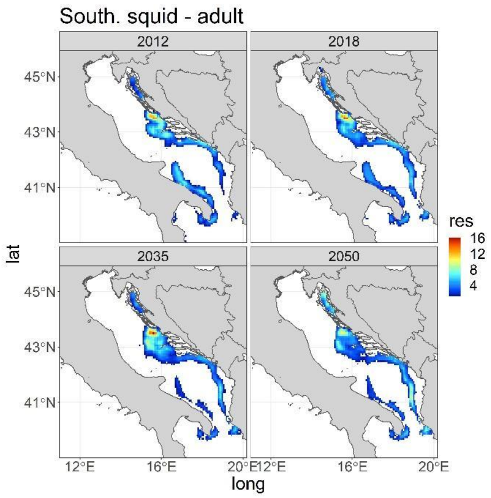
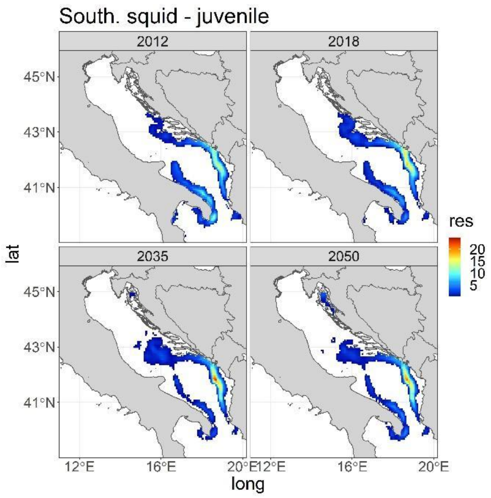


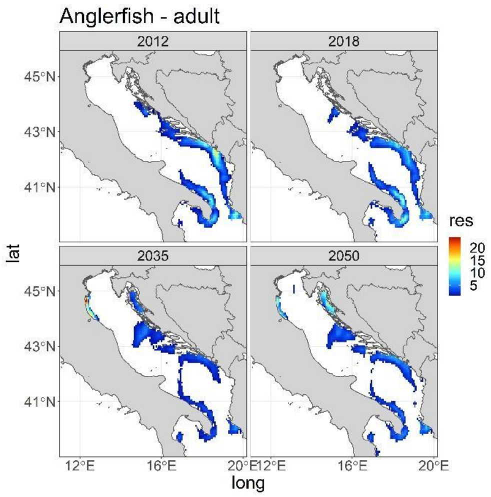
Figure S5.3: density (n/km2) difference between scenario 2018 and future scenarios 2025 and 2050, for each species and life stage (see plot's title)

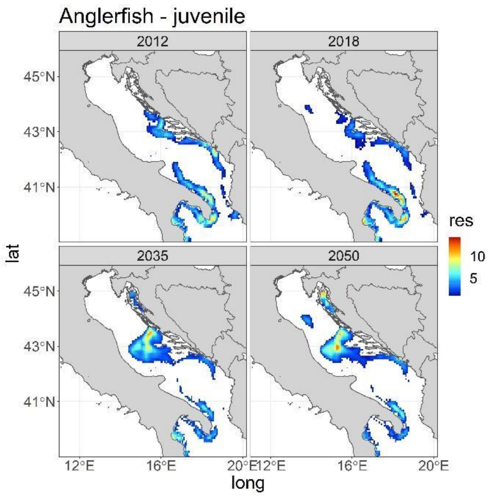

European hake - adult
2012
2018
2035
2050
lat
45°N
43°N
41°N
res
20
10
12°E
16°E
20°E
long

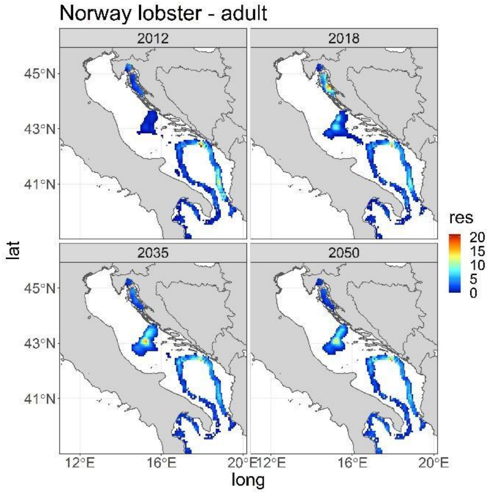

European hake - juvenile
2012
2018
2035
2050
lat
45°N
43°N
41°N
res
15
10
5
12°E
16°E
20°E
long

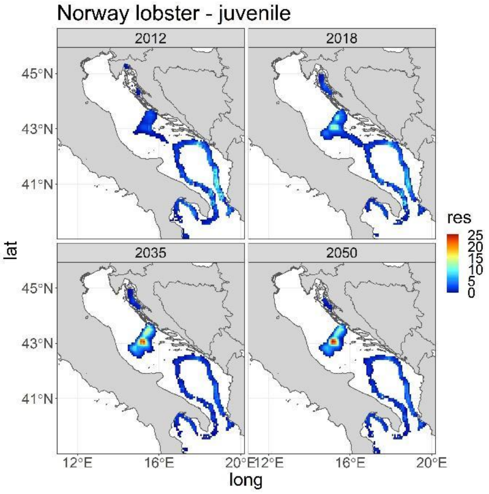

South. squid - adult
2012
2018
2035
2050
lat
45°N
43°N
41°N
res
16
12
8
4
12°E
16°E
20°E
long

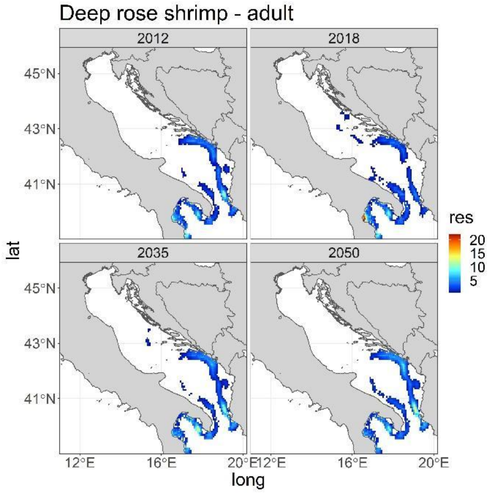

South. squid - juvenile
2012
2018
2035
2050
lat
45°N
43°N
41°N
res
20
15
10
5
12°E
16°E
20°E
long

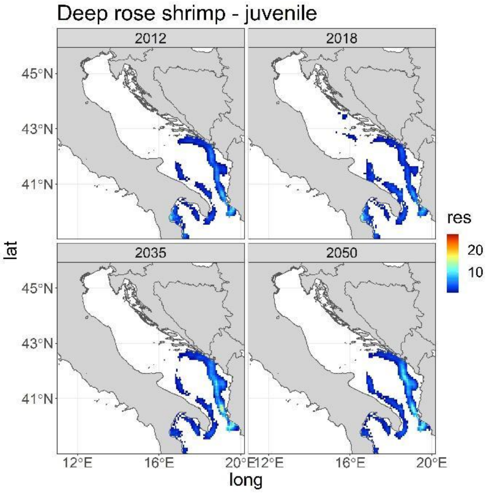

Anglerfish - adult
2012
2018
2035
2050
lat
45°N
43°N
41°N
res
20
15
10
5
12°E
16°E
20°E
long

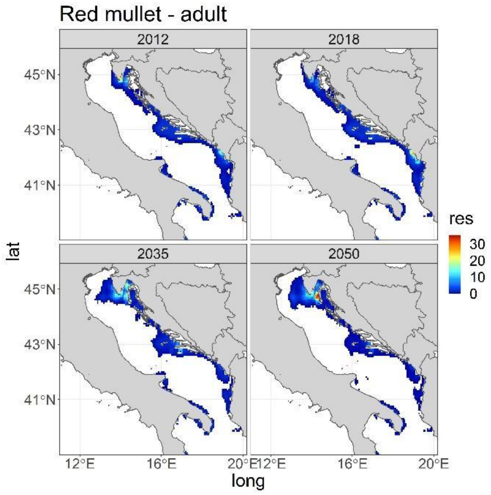

Anglerfish - juvenile
2012
2018
2035
2050
lat
45°N
43°N
41°N
res
10
5
12°E
16°E
20°E
long

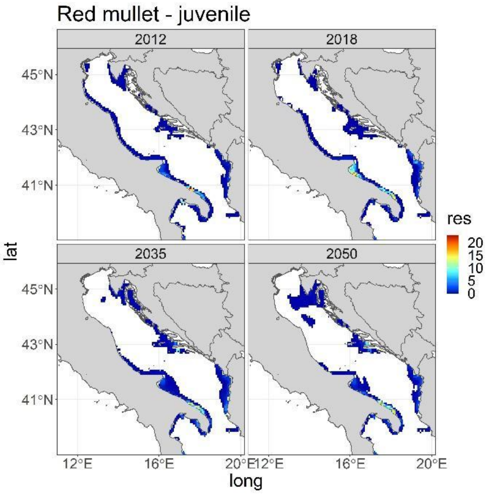

Norway lobster - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
20
15
10
5
0

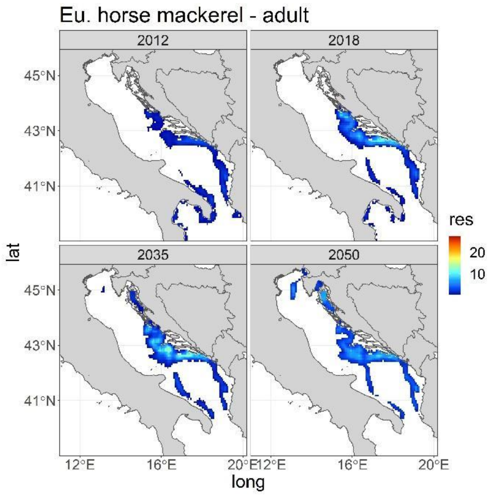

Norway lobster - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
25
20
15
10
5
0

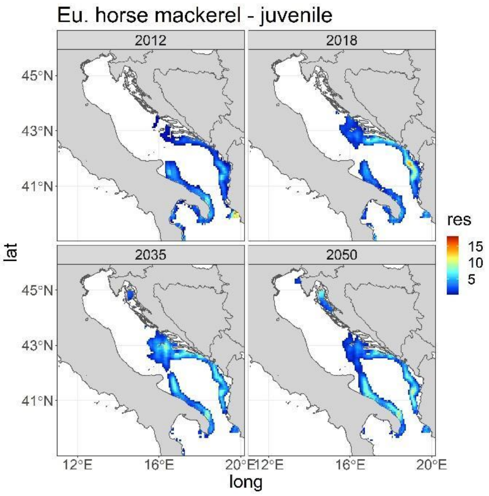

Deep rose shrimp - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
20
15
10
5

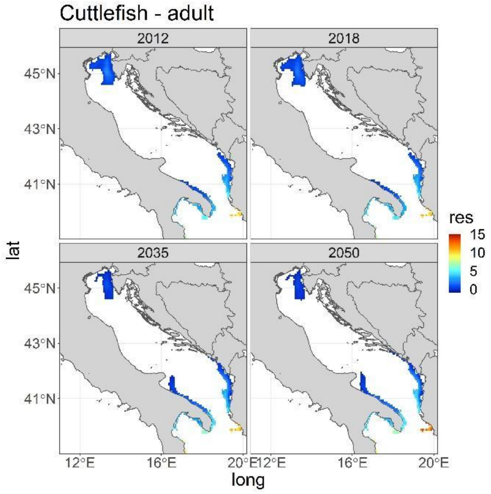

Deep rose shrimp - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
20
10

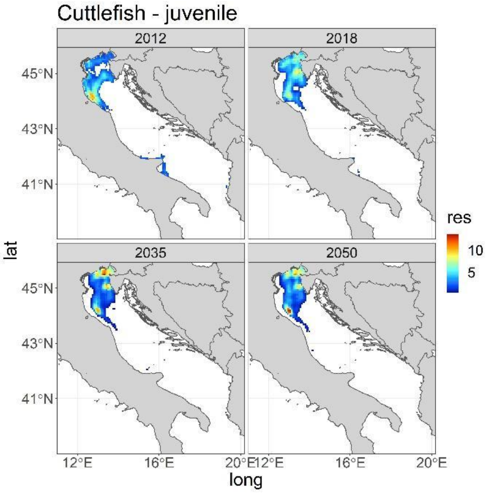

Red mullet - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
30
20
10
0

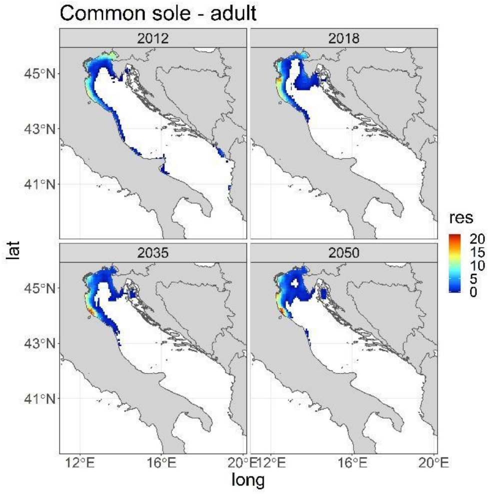

Red mullet - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
20
15
10
5
0

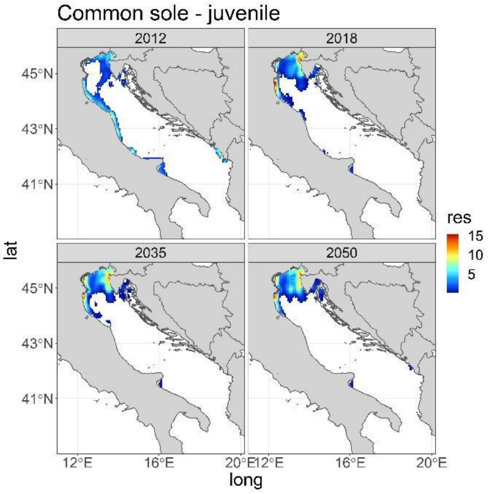

Eu. horse mackerel - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
20
10


Eu. horse mackerel - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
15
10
5


Cuttlefish - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
15
10
5
0


Cuttlefish - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
10
5


Common sole - adult
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
20
15
10
5
0


Common sole - juvenile
2012
2018
2035
2050
45°N
43°N
41°N
lat
12°E
16°E
20°E
long
res
15
10
5

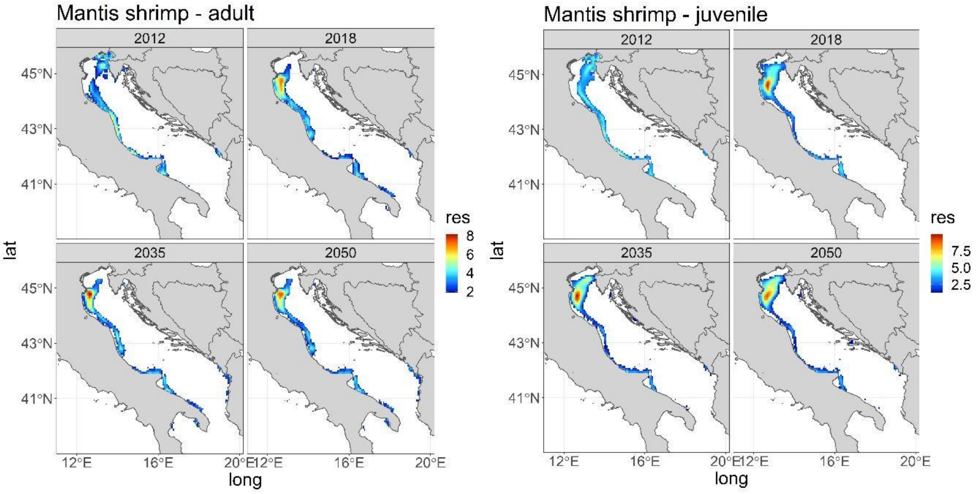


Figure S5.4: hot spot identified by Getis ord-gi and filtered over the third quartile, for each scenario (2012, 2018, 2035, and 2050), species, and life stage (see plot' title).*