



Universitat
de les Illes Balears



DOCTORAL THESIS
2019

**DIVERSITY OF DEMERSAL FISH ASSEMBLAGES
IN THE MEDITERRANEAN**

A handwritten signature in blue ink, which appears to read "M. Teresa Farriols Garau", is written over a circular stamp.

Maria Teresa Farriols Garau



Universitat
de les Illes Balears



**DOCTORAL THESIS
2019**

Doctoral Programme of Marine Ecology

**DIVERSITY OF DEMERSAL FISH ASSEMBLAGES
IN THE MEDITERRANEAN**

Maria Teresa Farriols Garau

**Thesis Supervisor: Dr. Enric Massutí Sureda
Thesis Supervisor: Dr. Francesc Ordinas Cerdà
Thesis Supervisor: Dr. Manuel Hidalgo Roldán
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Doctor by the Universitat de les Illes Balears

CRITERIS DE FORMAT DE LA TESI DOCTORAL A la UNIVERSITAT DE LES ILLES
BALEARS

Annex 3: Model de certificat de director de tesi i de doctorat internacional



**Universitat de les
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Dr. Enric Massutí Sureda, del Centre Oceanogràfic de Balears del *Instituto Español de Oceanografía*

DECLARO:

Que la tesi doctoral que porta per títol *Diversity of demersal fish assemblages in the Mediterranean*, presentada per Maria Teresa Farriols Garau per a l'obtenció del títol de doctor, ha estat dirigida sota la meva supervisió i que compleix amb els requisits necessaris per optar al títol de Doctor Internacional.

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A la meva família

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List of manuscripts

The four chapters containing original research (Chapters 4-7) are present as a collection of four papers, two already published and two others currently submitted, preceded by a general Introduction, Objectives, and Materials and Methods, and followed by a General Discussion, Conclusions and References. For this reason, each chapter can be read separately, because it has its own Summary, Introduction, Materials and Methods, Results and Discussion. The following scientific papers are partially or totally reflected in the Thesis.

Farriols M.T., Ordines F., and Massutí E. (Submitted). N_{90} : a halfway between alpha and gamma diversity. (Chapter 4).

Farriols M.T., Ordines F., Hidalgo M., Guijarro B., and Massutí E. 2015. N_{90} index: A new approach to biodiversity based on similarity and sensitive to direct and indirect fishing impact. *Ecological Indicators*, 52: 245–255. (Chapter 5).

Farriols M.T., Ordines F., Somerfield P.J., Pasqual C., Hidalgo M., Guijarro B., and Massutí E. 2017. Bottom trawl impacts on Mediterranean demersal fish diversity: not so obvious or are we too late?. *Continental Shelf Research*, 137: 84–102. (Chapter 6).

Farriols M.T., Ordines F., Carbonara P., Casciaro L., Di Lorenzo M., Esteban A., Follesa C., García-Ruiz C., Isajlovic I., Jadaud A., Ligas A., Manfredi C., Marceta B., Peristeraki P., Vrgoc N., and Massutí E. (Submitted). Spatio-temporal trends in diversity of demersal fish assemblages along the Mediterranean. (Chapter 7).

Acronyms and abbreviations

AIC	Akaike Information Criterion
ANOVA	Analysis of variance
EA	East Atlantic pattern
EAF	Ecosystem Approach to Fisheries
GAM	Generalized Additive Modeling
GCV	Generalized Cross-Validation
GFCM	General Fisheries Commission for the Mediterranean
GPS	Global Positioning System
GSA	Geographical Sub-Area
HLFI	High Level of Fishing Impact
LFE	Levels of Fishing Effort
LIW	Levantine Intermediate Water
LLFI	Low Level of Fishing Impact
MEDITS	Mediterranean International bottom Trawl Surveys
SIMPER	Similarity Percentage
STECF	Scientific, Technical and Economic Committee for Fisheries
VMS	Vessel Monitoring by satellite System
WIW	Winter Intermediate Waters
WMDW	Western Mediterranean Deep Water

Summary

The present Thesis is a multidimensional study of demersal fish diversity in the Mediterranean. Its main aim is the study of Mediterranean demersal fish diversity and the detection of the effects of fishing on it. To do this, different spatial and temporal scales and different continuous and stratified approaches to explain the diversity patterns observed were considered. Data obtained from Mediterranean International bottom Trawl Surveys (MEDITS) developed during the last two decades in the area and information about the bottom trawl fishing effort were used. A new diversity index, N_{90} , was developed from the results of the Similarity Percentage (SIMPER) analysis. The N_{90} represents the number of species contributing up to the ninety percent of within-group similarity in a group of samples. Its units, expressed as number of species, and the corresponding SIMPER tables, summarizing each species contribution to within-group similarity, facilitate its interpretability. N_{90} is at halfway between alpha Shannon's H' and gamma species richness S diversities, being also correlated, to a lesser extent, to beta S . The R script for the calculation of the index was also developed. The usefulness of N_{90} to detect changes in fish diversity due to fishing impacts was assessed on the deep shelf of the Balearic Islands using data collected during the MEDITS. To do that, N_{90} and other 'traditional' diversity indices (S , H' , Pielou's evenness J' , Margalef's d and Simpson's $1 - \lambda'$) were estimated in two groups of samples subjected to contrasting levels of fishing effort. While N_{90} displayed a clear response to fishing pressure, with lower values in impacted communities, 'traditional' diversity indices showed almost null sensitivity. N_{90} also showed a response to environmental changes in communities subjected to high levels of fishing pressure, showing the sensitivity of this index to the synergistic effects of climate and fishing. The analysis of MEDITS data between 50 and 800 m depth allowed the identification of a minimum set of indices that provide a good representation of the different aspects of demersal fish diversity in the Balearic Islands. Species richness, evenness and the taxonomic and functional breadth of the species gave complementary information and displayed different responses to fishing pressure. While the impact of fishing on fish communities was detected on the continental shelf, no differences between distinct levels of fishing effort were detected on the slope. That could be due to the demersal fish communities of the middle slope have been subjected to high levels of fishing pressure for a long period, and hence, the vulnerable species could have been replaced by species better adapted to fishing impacts long time before the onset of the monitoring of the fishery. MEDITS data were also used to analyse the spatial and temporal patterns of demersal fish diversity in the whole northern Mediterranean during the last twenty years. The results showed that the diversity of demersal fish assemblages can be explained by the spatial distribution and the temporal trend of the bottom trawl fishing effort in the area. Higher values of diversity were found on the continental shelf of Sicily, the Balearic Islands, Sardinia and Aegean Sea. These last three areas also coincide with low trawl fishing effort values. The consideration of species other than target ones through diversity indices is relevant for the implementation of the Ecosystem Approach to Fisheries (EAF). The new developed N_{90} diversity index is an alternative to 'traditional' diversity indices when trying to monitor fishing impacts and the effects of environmental changes. The easy interpretability of its results can contribute to improve the transfer of scientific knowledge to managers and stakeholders.

Resum

Aquesta Tesi presenta un estudi multidimensional de la diversitat de peixos demersals a la Mediterrània. El seu principal objectiu és estudiar la diversitat d'aquests peixos a la Mediterrània i detectar els efectes de la pesca sobre ella. Per explicar els patrons de diversitat observats es consideraren escales temporals i espacials diferents i aproximacions contínues i estratificades. S'utilitzaren dades de campanyes científiques MEDITS, amb art d'arrossegament de fons, realitzades en aquesta àrea durant les dues darreres dècades i informació de l'esforç de la pesquera d'arrossegament de fons. Un nou índex de diversitat, l' N_{90} , es desenvolupà a partir dels resultats de l'anàlisi SIMPER. L' N_{90} representa el nombre d'espècies que contribueixen fins al noranta per cent de la semblança intragrup en un conjunt de mostres. Les seves unitats, nombre d'espècies, i la taula SIMPER corresponent, resumint la contribució de cada espècie a la semblança intragrup, en faciliten la interpretació. L' N_{90} es troba a mig camí entre la diversitat alfa de Shannon H' i gamma de la riquesa específica S , mostrant també una menor correlació amb la diversitat beta d' S . També es desenvolupà l'script d'R per a calcular l' N_{90} . Mitjançant dades MEDITS de la plataforma profunda de les Illes Balears s'avaluà la utilitat de l' N_{90} per a la detecció de canvis en la diversitat dels peixos deguts a l'impacte de la pesca. Per fer això, s'estimaren l' N_{90} i altres índexs de diversitat 'tradicionals' (S , H' , equitativitat de Pielou J' , de Margalef d i de Simpson $1 - \lambda'$) en dos grups de mostres sotmeses a nivells d'esforç pesquer contrastats. L' N_{90} mostrà una clara resposta a la pressió pesquera amb valors més baixos a comunitats impactades mentre que la dels índexs de diversitat 'tradicionals' fou pràcticament nul·la. L' N_{90} també respongué a canvis ambientals a comunitats sotmeses a alts nivells de pressió pesquera, mostrant la seva sensibilitat als efectes sinèrgics del clima i la pesca. L'anàlisi de dades MEDITS entre 50 i 800 m de profunditat permeté la identificació d'un grup mínim d'índexs que representen diferents aspectes de la diversitat de peixos demersals a les Illes Balears. La riquesa específica, l'equitativitat i l'amplitud taxonòmica i funcional de les espècies donaren informació complementària i mostraren respostes diferents enfront de la pressió pesquera. L'impacte de la pesca a les comunitats de peixos demersals fou detectada a la plataforma continental mentre que no es detectaren diferències entre nivells d'esforç pesquer al talús. Això podria ser degut a que les comunitats del talús mitjà han estat sotmeses a alts nivells de pressió pesquera durant un llarg període de temps i, per tant, les espècies vulnerables podrien haver estat substituïdes per espècies més ben adaptades a l'impacte de la pesca abans del monitoratge d'aquesta pesquera. Per analitzar patrons espacials i temporals de diversitat de peixos demersals a tota la Mediterrània nord s'utilitzaren dades MEDITS dels darrers vint anys. Els resultats mostraren que la diversitat de peixos demersals es pot explicar mitjançant la distribució espacial i la tendència temporal de l'esforç de la pesquera d'arrossegament de fons d'aquesta àrea. Valors superiors de diversitat foren trobats a la plataforma continental de Sicília, Illes Balears, Sardenya i la mar Egea. Les darreres tres àrees coincideixen amb valors baixos d'esforç pesquer. La consideració d'espècies a més de les objectiu mitjançant índexs de diversitat és rellevant per a la implementació de l'aproximació ecosistèmica a les pesqueres. L' N_{90} és una alternativa als índexs de diversitat 'tradicionals' per al monitoratge dels impactes de la pesca i els efectes dels canvis mediambientals. La facilitat d'interpretació dels resultats poden contribuir a millorar la transferència de coneixement científic a gestors i parts interessades.

Resumen

Esta Tesis presenta un estudio multidimensional de la diversidad de peces demersales en el Mediterráneo. Su objetivo es estudiar la diversidad de estos peces en el Mediterráneo y detectar los efectos de la pesca sobre ella. Para explicar los patrones de diversidad observados se consideraron escalas temporales y espaciales diferentes y aproximaciones continuas y estratificadas. Se utilizaron datos de campañas científicas MEDITS, con arte de arrastre de fondo, realizadas en esta área durante las dos últimas décadas e información del esfuerzo de la pesquería de arrastre de fondo. Un nuevo índice de diversidad, el N_{90} , se desarrolló a partir de los resultados del análisis SIMPER. N_{90} representa el número de especies que contribuyen hasta el noventa por ciento de la similaridad intragrupo en un conjunto de muestras. Sus unidades, número de especies, y la tabla SIMPER correspondiente, resumiendo la contribución de cada especie a la similaridad intragrupo, facilitan su interpretación. N_{90} se encuentra a medio camino entre la diversidad alfa de Shannon H' y gamma de la riqueza específica S , mostrando también una menor correlación con la diversidad beta de S . También se desarrolló el script de R para calcular N_{90} . Mediante datos MEDITS de la plataforma profunda de las Islas Baleares se evaluó la utilidad de N_{90} para la detección de cambios en la diversidad de peces debido al impacto de la pesca. Para ello, se estimaron N_{90} y otros índices de diversidad ‘tradicionales’ (S , H' , equitatividad de Pielou J' , de Margalef d y de Simpson $1 - \lambda'$) en dos grupos de muestras sometidas a niveles de esfuerzo pesquero contrastados. N_{90} mostró una clara respuesta a la presión pesquera con valores menores en comunidades impactadas mientras que los índices de diversidad ‘tradicionales’ no. N_{90} también respondió a cambios ambientales en comunidades sometidas a altos niveles de presión pesquera, mostrando su sensibilidad a los efectos sinérgicos del clima y la pesca. El análisis de datos MEDITS entre 50 y 800 m de profundidad permitió identificar un grupo mínimo de índices que representan distintos aspectos de la diversidad de peces demersales en las Islas Baleares. La riqueza específica, equitatividad y amplitud taxonómica y funcional de las especies dieron información complementaria y mostraron respuestas diferentes frente a la presión pesquera. El impacto de la pesca en las comunidades de peces demersales fue detectada en la plataforma continental mientras que no se detectó en el talud. Ello podría ser debido a que las comunidades del talud medio han sido sometidas a altos niveles de presión pesquera durante un largo periodo de tiempo y, por tanto, especies vulnerables podrían haber sido reemplazadas por especies mejor adaptadas al impacto de la pesca antes del monitoreo de esta pesquería. Para analizar patrones espaciales y temporales de diversidad en todo el Mediterráneo norte se utilizaron datos MEDITS de los últimos veinte años. Los resultados mostraron que la diversidad de peces demersales se puede explicar mediante la distribución espacial y la tendencia temporal del esfuerzo de la pesquería de arrastre de fondo en esta área. Valores superiores de diversidad se encontraron en la plataforma continental de Sicilia, Islas Baleares, Cerdeña y el mar Egeo. Estas últimas tres áreas coinciden con valores bajos de esfuerzo pesquero. La consideración de especies además de las objetivo mediante índices de diversidad es relevante para la implementación de la aproximación ecosistémica a las pesquerías. N_{90} da una alternativa a los índices de diversidad ‘tradicionales’ para el monitoreo de los impactos de la pesca y los efectos de los cambios medioambientales. La facilidad de interpretación de los resultados puede contribuir a mejorar la transferencia de conocimiento científico a gestores y partes interesadas.

Chapter 1

INTRODUCTION



Chapter 1. Introduction

1.1 The Mediterranean

1.1.1 Geomorphology and oceanography

The Mediterranean is the largest semi-enclosed sea in the world. With a total area of 2,969,000 km² and a maximum depth of 5,267 m, this sea represents the 0.82% of the ocean surface of the planet and 0.32% of the world water volume. It is connected to the Atlantic Ocean through the Strait of Gibraltar, the Black Sea through the Strait of the Dardanelles and the Red Sea through the Suez Channel that was built in 1869. The Strait of Sicily, a shallow ridge at 400 m depth, separates the island of Sicily from the coast of Tunisia and divides the sea into two basins: the western, with an area of 0.85 million km², and the eastern, which presents the maximum depth of the Mediterranean (5,267 m) and an area of 1.65 million km². These basins can be divided in several sub-basins: Alboran, Algerian, Balearic, Liguro-Provençal and Tyrrhenian sub-basins in the western basin; and Adriatic, Ionian, Levantine and Aegean sub-basins in the eastern basin (Figure 1.1).



Figure 1.1: Map of the Mediterranean showing its main basins. The location of the Strait of Gibraltar (a), the Strait of Sicily (b), the Strait of the Dardanelles (c) and the Suez Channel (d) are also shown.

Taking the large areas of open sea and its narrow continental shelves into account a large part of the Mediterranean basin can be classified as deep sea (Sardà et al., 2004). Shelves in the northern shore are relatively wider than those in southern coasts which are narrow and steep (Pinardi et al., 2004). However narrow shelves are also found in the northern Alboran coast, in the Ligurian Sea and in the Tyrrhenian Sea in the western basin, and in the Adriatic, Aegean and the Levant coasts in the eastern basin (Pinardi et al., 2004). By contrast most extended shelves are found along the Tunisian shelf and near the Nile Delta (Pinardi et al., 2004). The slope is a relatively narrow zone, in which the change from 200 m to around 2,500 m depth occurs within a few tens of km. Overall, the continental shelf, slope and the abyssal plains cover about 20, 60 and 15% of the Mediterranean bottoms, respectively (Sardà et al., 2004).

The Mediterranean is considered an extremely oligotrophic sea, which circulation and productivity is highly influenced by the Strait of Gibraltar. Since the evaporation is

higher than precipitation, the Mediterranean acts as a concentration basin in which the Strait of Gibraltar plays a key role in the exchange of water with the Atlantic Ocean that maintains the water balance. Due to evaporation is higher in its eastern basin, the water level decreases while salinity and temperature increase from west to east (Brankart and Brasseur, 1998). Besides there is an eastwards decreasing trend in surface productivity, organic matter availability at the seafloor and the biomass of megabenthic fauna of deep ecosystems (Bouchet and Taviani, 1992; Danovaro et al., 1999; Bosc et al., 2004; Tecchio et al., 2011). The general circulation in the Mediterranean has a high spatial and temporal variability at all scales, from small turbulence to basin scale processes. This variability is the result of the interaction of topographic and coastal influences and internal dynamic processes at three prevailing spatial scales: basin, sub-basin and mesoscale (Robinson et al., 2001).

The Mediterranean thermohaline circulation is typically defined by an open vertical cell that evolves the Atlantic Water, spreading in the surface layer from the Strait of Gibraltar to the eastern Mediterranean, into LIW due to evaporation and cooling in the northeastern Levantine basin. Then, LIW spreads in the opposite direction at intermediate depths throughout the whole basin to finally overflow into the Atlantic Ocean through the Strait of Gibraltar. In the western basin there is also an additional intermediate water mass, the WIW, formed from north winds driven evaporation and cooling of surface waters during the winter over the continental shelf and slope of the Gulf of Lions (Vargas-Yáñez et al., 2012). Two closed thermohaline cells are driven by deep water formation in the eastern and western basins: the WMDW, formed during winter mainly in the cyclonic gyre of the Gulf of Lions, and the Eastern Mediterranean Deep Water, formed in the Southern Adriatic cyclonic gyre (Skirris, 2014).

1.1.2 Biodiversity

Despite of representing a small part of the world's oceans, the Mediterranean hosts an unusually rich and diverse biota. Not in vain the Mediterranean is considered one of the world's biodiversity hotspots due to its high species richness, coupled with an important proportion of endemisms (Boudouresque, 2004; Moranta et al., 2008a; Lejeusne et al., 2010). It is inhabited by approximately 17,000 species, representing 4-18% of the world's marine biodiversity, and includes temperate, cosmopolitan, subtropical, Atlantic and Indo-Pacific taxa (Bianchi and Morri, 2000; Coll et al., 2010). The Mediterranean endemisms represent up to 20-30% of its species (Boudouresque, 2004).

The geological history along with the numerous climatic and hydrologic events occurred in the Mediterranean Sea have been pointed as probable reasons for its high marine biodiversity (Bianchi and Morri, 2000). Such events led to the co-occurrence of temperate and subtropical species in the area, which during the glacial periods hosted cold-water species from the northern Atlantic (Kettle et al., 2011). Some of these glacial period refugees are still present in the Mediterranean such as the boreal fish species *Sprattus sprattus*, *Molva molva*, *Merlangius merlangus* and *Buenia lombartei* (Fernandes et al., 2015; Quignard and Raibaut, 1993; Kovačić et al., 2018). The construction of the Suez Channel aided by a rise in sea temperature also led to the migration and settlement of species from the Red Sea known as 'Lessepsian migrants' (named after Ferdinand de Lesseps, the designer of the Suez Channel) or 'Erythrean aliens' (Pso-madakis et al., 2012). Sea warming is also responsible for the increase in the migration of Atlantic thermophilic species into the Mediterranean through the Strait of Gibraltar

(Mannino et al., 2017). Hence, the Mediterranean Sea biota is more influenced by the Atlantic Ocean in its western part and by the Red Sea in the Levant. From 165 exotic fish species listed by Golani et al. (2017) in the Mediterranean, 46 are of Atlantic origin and recorded after 1960, whereas 106 are of Indo-Pacific origin and recorded after 1920.

The species composition between the western and eastern basins of the Mediterranean shows a high heterogeneity. The highest species richness is found in the western Mediterranean followed by the Adriatic and Aegean Seas, and the Levantine basin, which displays the lowest values (Boudouresque, 2004). In fact, the low biodiversity of the deep sea in the Eastern basin led Forbes (1844) to introduce the ‘azoic zone’ theory which, based on samples from the Eastern Mediterranean, supposed that life in the oceans went extinct below 550 m depth. Some authors argue that the low abundance and diversity in the deep sea in that basin is caused by the episodic anoxic events that have affected the eastern Mediterranean during the quaternary, from which biota is still recovering. Endemic marine species in the Mediterranean either consist of rare paleo-endemisms of Tethyan origin (i.e. they precede the Messinian Salinity Crisis) and of more frequent neo-endemisms of Pliocenic origin (Mannino et al., 2017, Ramírez-Amaro et al., 2018). The western basin seems to be an active centre of endemism showing a higher rate of endemism than the eastern one (Boudouresque, 2004).

Environmental variables like temperature and productivity as well as distance to the Strait of Gibraltar are reported to cause differences in fish biodiversity distribution (Ben Rais Lasram et al., 2009; Meléndez et al., 2017). There is a large-scale eastwards decreasing trend in fish species richness that has been primarily related to the similar decreasing west-east gradient of productivity (Quignard and Tomasini, 2000; Coll et al., 2010; Bosc et al., 2004). However this trend is not always confirmed from works studying demersal fish species diversity of the Mediterranean based on bottom trawl scientific surveys (Gaertner et al., 2013; Granger et al., 2015; Peristeraki et al., 2017).

The number of Mediterranean fish species has been concerning many authors especially since digital databases became available in the mid-1980s (Goren, 2014). Estimates are similar in consecutive studies providing a list of species or just numbers. For example, Fredj and Maurin (1987) listed 638 species; Bianchi and Mori (2000) 613 species; Quignard and Tomasini (2000) 664 species; Coll et al. (2010) 650 species and Coll et al. (2012) 625 species. In a global context, this fish biodiversity estimates are far from those from other areas considered fish biodiversity hotspots. For example, Allen (2008) defined megadiversity countries, based just on coral reef species, as countries with more than 1000 species. Fricke et al. (2011) listed 2328 fish species from New Caledonia whereas Golani and Bogorodsky (2010) listed 1078 for fish species from the Red Sea. Larson et al. (2008), just for gobioid fishes, listed 149 species from Singapore. In this context, the number of fish species in the Mediterranean is more similar to areas like the European Atlantic waters where up to 995 fish species have been listed (Quéro et al., 2003), and where relatively small regions as the Galician Bank can host up to 398 fish species (Bañón et al., 2010). Therefore, although the Mediterranean has been cited as a hotspot of marine diversity that term is, at least, controversial when referred to fish species.

1.1.3 Fisheries

The natural resources of the Mediterranean have been subject to human exploitation since ancient times, when coastal communities started to use different fishing gears, some of which are still in use (Farrugio et al., 1993). Until the XVI century, the Mediterranean fisheries were essentially developed at a small scale and targeted mainly pelagic species, such as Atlantic bluefin tuna, sardine, anchovy and horse mackerel. An important technological innovation occurred in the XVII century with the introduction of the first trawl nets, locally known as ‘Tartana’ (in Italy) or ‘Bous’ (in Catalonia), that were towed by sailing vessels (Osio, 2012). However, the most important technological improvement was represented by the introduction of the steam trawler at the end of the XIX century (Roberts, 2007). The first diesel engine trawlers appeared in Italy and Spain in 1920s, and after the Second World War all trawlers were equipped with motor engines.

Until the industrialization of fisheries occurred in the 1950s, the exploitation of Mediterranean resources was limited to fishing areas generally located at depths shallower than 200 m. In the 1960s, with the decline of stocks on the continental shelf, increasing market demand and the introduction of new technologies, trawl fisheries expanded offshore towards the deeper waters of the continental slope (Roberts, 2002; Morato et al., 2006). In these bottoms, the trawl fleet began to target valuable resources such as the blue and red shrimp, the giant red shrimp, or the Norway lobster (Demestre and Martín, 1993; Maynou, 2008; Cartes et al., 2011; Orsi Relini et al., 2013; Masnadi et al., 2018). Since then, the engine power coupled with a progressive improvement of fishing capacity, technology and catchability has continuously increased to nowadays. The introduction of the radar, GPS, echo-sounder and the real time fishing gear monitoring systems are some of those improvements.

Most Mediterranean fisheries are multispecific with main target species exploited by more than one fishing technique, leading to a high interaction between gears and fleet segments (Ulrich et al., 2012). The presence of a high diversity of species and the absence of large monospecific stocks comparable to those inhabiting some wide areas of the open oceans, is a characteristic of the Mediterranean demersal fisheries, from which more than 100 abundant species are commercialized (Farrugio et al., 1993; Lleonart and Maynou, 2003; Figure 1.2). On the other hand, the high diversity of the communities exploited also leads to high rates of discarded catches (Carbonell et al., 1998; Sánchez et al., 2004).



Figure 1.2: Bottom trawler and example of catch from the bottom trawl fishery in the Balearic Islands (western Mediterranean) on the continental shelf.

In the Mediterranean, the assessment of fisheries is developed within the framework of the GFCM, the regional fisheries management organization of the Mediterranean. The GFCM has established thirty GSAs to assess and manage the marine resources and fisheries (Figure 1.3). This classification is based on political and statistical considerations rather than biological or economic factors (Lleonart and Maynou, 2003). According to the last report of the Working Group on Stock Assessment of Demersal Species, which assessed thirty seven stocks of Mediterranean demersal species, only seven were found to be exploited in a sustainable way, whereas the rest were diagnosed as overexploited (GFCM, 2017).

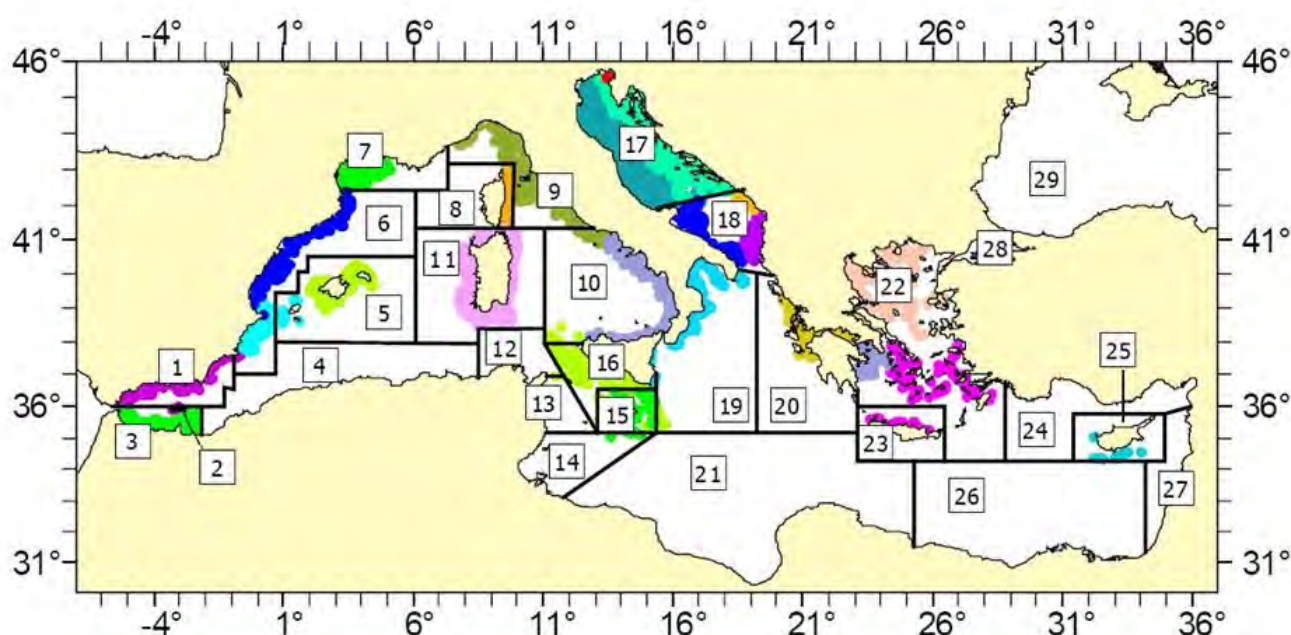


Figure 1.3: Map of the thirty Geographical Sub-Areas (GSAs) established by the General Fisheries Commission for the Mediterranean (GFCM): (01) Northern Alboran Sea; (02) Alboran Island; (03) Southern Alboran Sea; (04) Algeria; (05) Balearic Islands; (06) Northern Spain; (07) Gulf of Lions; (08) Corsica Islands; (09) Ligurian and North Tyrrhenian Sea; (10) South and Central Tyrrhenian Sea; (11) Sardinia; (12) Northern Tunisia (13) Gulf of Hammamet; (14) Gulf of Gabes; (15) Malta Island; (16) South of Sicily; (17) Northern Adriatic Sea; (18) Southern Adriatic Sea; (19) Western Ionian Sea; (20) Eastern Ionian Sea; (21) Southern Ionian Sea; (22) Aegean Sea; (23) Crete; (24) North Levant; (25) Cyprus Island; (26) South Levant; (27) Levant; (28) Marmara Sea; (29) Black Sea; (30) Azov Sea. Modified from: <http://www.sibm.it/MEDITS/%202011/principalegeo.htm>.

1.2 The ecosystem approach to fisheries (EAF)

The conventional management of the Mediterranean bottom trawl fisheries, based on monospecific stocks, has been moving forward during the last years to an EAF. The most specific issues in EAF relate to the impact of fisheries on the environment, including biodiversity and habitat, and the impact of the environment on fisheries, including natural variability and climate change (Garcia and Cochrane, 2005). In this new direction for fisheries management, priority is given to the ecosystem instead of the target species (Pikitch et al., 2004).

It is well known that fisheries have profoundly modified the structure of marine ecosystems (Dayton et al., 1995; Hall, 1999; Kaiser and de Groot, 2000). Effects of fishing on marine ecosystems include: changes in predator-prey relationships leading to shifts in food-web structure not necessarily reversed by the reduction of fishing pressure (alternative stable states; Kaiser et al., 2002); changes in size structure due to vulnerability and selection of fishing for large individuals (Gislason, 2002; Jennings and Dulvy, 2005; Daan et al., 2005); genetic selection of species with particular life-history

traits, like higher growth rate and earlier age-at-maturity (Fromentin and Fonteneau, 2001; Jørgensen et al., 2007); changes in the spatial distribution of target species (e.g. Ciannelli et al., 2013); effects on population of non-target species (Pranovi et al., 2001; Ordines et al., 2014); and decrease of the presence of biogenic habitats, leading to a reduction of the biodiversity of exploited bottoms (Jones, 1992; Engel and Kvitek, 1998; Norse and Watling, 1999; Smith et al., 2000; Hiddink et al., 2006).

The multiple effects of fishing on ecosystems makes the assessment at a community level crucial, particularly due to the multispecific character of the bottom trawl fishery developed along the Mediterranean, and also because a decline in the diversity of demersal assemblages has been reported due to fishing exploitation (Ungaro et al., 1998; Sabatini et al., 2013).

1.3 The diversity measures

Biodiversity and diversity concepts have sometimes been used indistinctly in the scientific literature, mainly because the word biodiversity was originally used in political debate rather than science (Ghilarov, 1996). However, both concepts are complementary (Margalef, 1997). While biodiversity means the total specific, taxonomic or genetic richness contained in nature or in any local or taxonomic part of it, without bothering about differences and possible mathematical relations among the representation of the different taxonomic forms, diversity is referred to actual distributions of individuals or biomasses among species (Margalef, 1997).

The study of the distribution of biodiversity together with its rate of recovery or decline needs biodiversity to be quantified. The most commonly considered measure of biodiversity is the species richness (S), i.e. the count of the number of species in a site, habitat or clade (Purvis and Hector, 2000). Diversity, however takes not only into account species richness but also the relative distribution of abundance among the species, also known as evenness or its opposite dominance, which leads to a plethora of indices, each of them computing and giving different relative weights to these properties (Jost, 2010). In this sense, the ambiguity of some of the indices has led to criticism from several authors (Hurlbert, 1971; Peet, 1974; May, 1975; Hamilton, 2005). Besides S , the more simple diversity index, which gives the same weight to all species, some of the most used diversity indices are Margalef's (d), Simpson's ($1 - \lambda'$), Shannon's (H') and Pielou's evenness (J').

After S , other species richness indices appeared that tried to compensate for sampling effects by dividing S by the total number of individuals in the sample. One of the best known of these indices is d (Margalef, 1958; Clifford and Stephenson, 1975). $1 - \lambda'$ (Simpson, 1949) makes no assumption about the underlying species abundance distribution and it measures the probability that two individuals randomly selected from a sample will belong to the same species. H' diversity index (Shannon and Weaver, 1949) has its origins in the information theory field and is associated with the entropy concept. Since it was thereafter adopted for ecologists, its use has become popular. The index is based on the idea that the diversity, or information, in a natural system can be measured in a similar way to the information contained in a code or a message (Magurran, 2004). It assumes that individuals are randomly sampled from an infinitely large community (Pielou, 1975), and that all species are represented in the sample. However, the use of H' as a diversity index is controversial mainly due to its origins in a non-

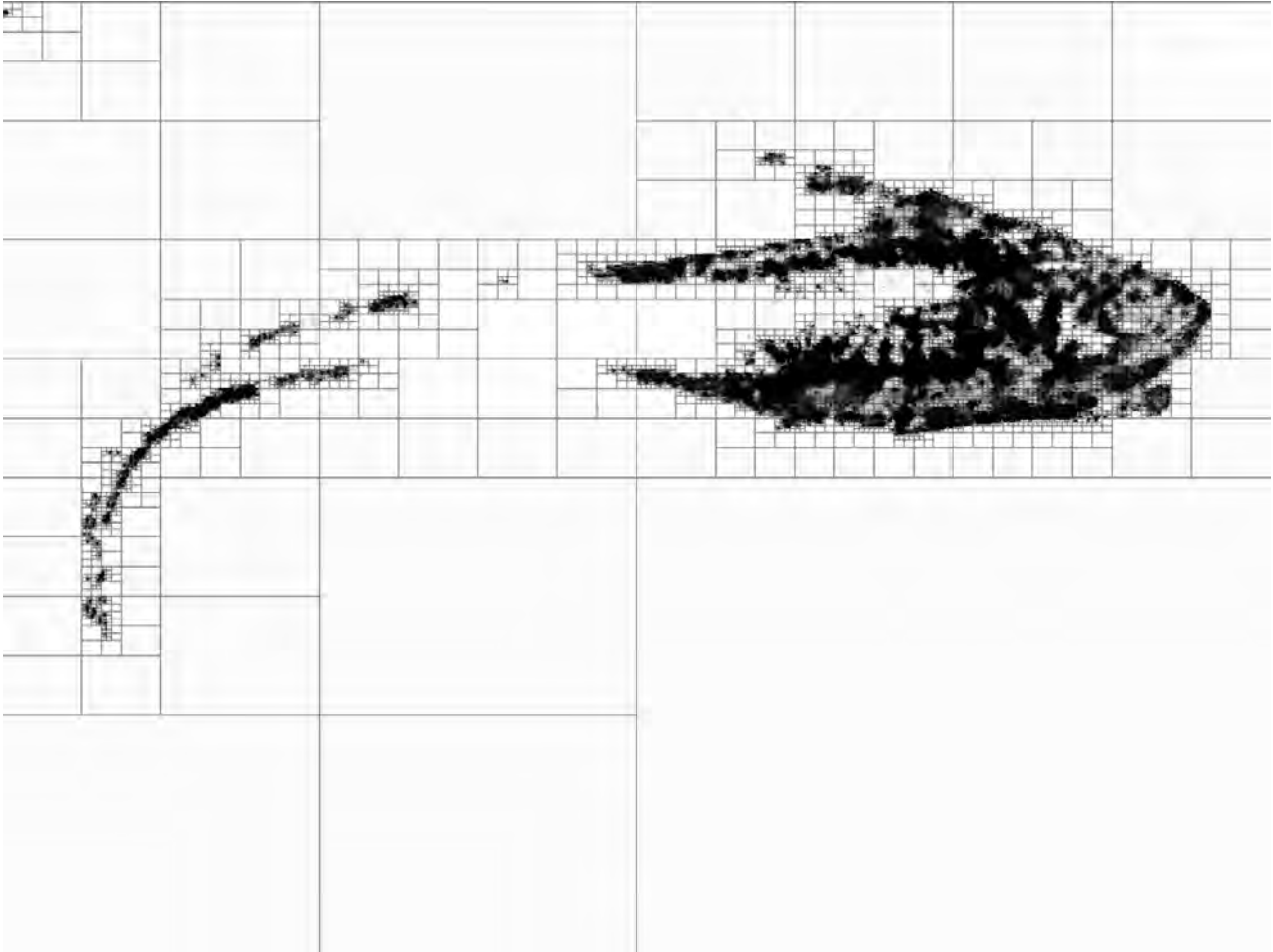
ecology field and its difficult interpretation confounding species richness and evenness aspects (Magurran, 2004). J' evenness (Pielou, 1966) attempts to calculate a separate evenness measure based on H' and represents the ratio of observed diversity to maximum diversity (Pielou, 1969, 1975). To do that it assumes that maximum diversity (H_{max}) that could possibly occur would be found in a situation where all species had equal abundances (Magurran, 2004).

Differentiation diversity describes the degree of change in diversity over space, along transects or between habitats (Hamilton, 2005). Whittaker (1960, 1977) outlined three spatial-levels of differentiation diversity that correspond to his inventory diversity: alpha diversity, beta diversity, and gamma diversity. Total diversity (gamma) can be decomposed into its within-community component (alpha) and among community component (beta). Of these, beta diversity describes the change in diversity along a transect or the difference between habitats (Mumby, 2001; Vellend, 2001; Crist et al., 2003).

New diversity indices have recently appeared taking other aspects of the community structure into account. Contrary to ‘traditional’ diversity indices, only using number of species and/or their relative abundances, these indices also consider the taxonomic or functional relations between them (Magurran, 2004). Considering that the relationships among species could provide additional information, taxonomic diversity indices were developed which reflect the relatedness among taxa in a group of samples representing a community or area (Warwick and Clarke, 1995; Clarke and Warwick, 1998, 2001). These give complementary information to ‘traditional’ diversity indices (Warwick and Clarke, 2001; Leonard et al., 2006). More recently, interest has grown in indices reflecting the functional composition of assemblages in some way. Although there is no standard methodology for their calculation, they generally use information about the biological and functional traits of the species to inform about the functional complexity of a community (e.g. Tilman et al., 1997; Petchey and Gaston, 2002; Villéger et al., 2008; Laliberté and Legendre, 2010). Finally, morphological diversity indices have been developed (Zelditch et al., 2003; Recasens et al., 2006; Lombarte et al., 2012; Farré et al., 2013). These indices assume that morphological traits are considered good predictors of the ecological habits of species (Farré et al., 2016), due to the direct link of the phenotype of species to the use of resources they make, that is the key of their adaptation to the environment (Gatz Jr., 1979; Douglas and Matthews, 1992; Walker, 2010; Farré et al., 2015).

Chapter 2

OBJECTIVES



Chapter 2. Objectives

The main objective of the present Thesis is the study of the Mediterranean demersal fish diversity and the detection of the effects of fishing on it.

The specific objectives of the Thesis are the following:

2.1. To develop a new diversity index (N_{90}) based on the Similarity Percentage (SIMPER) analysis.

2.2. To frame the N_{90} index in the concepts of alpha, beta and gamma diversity.

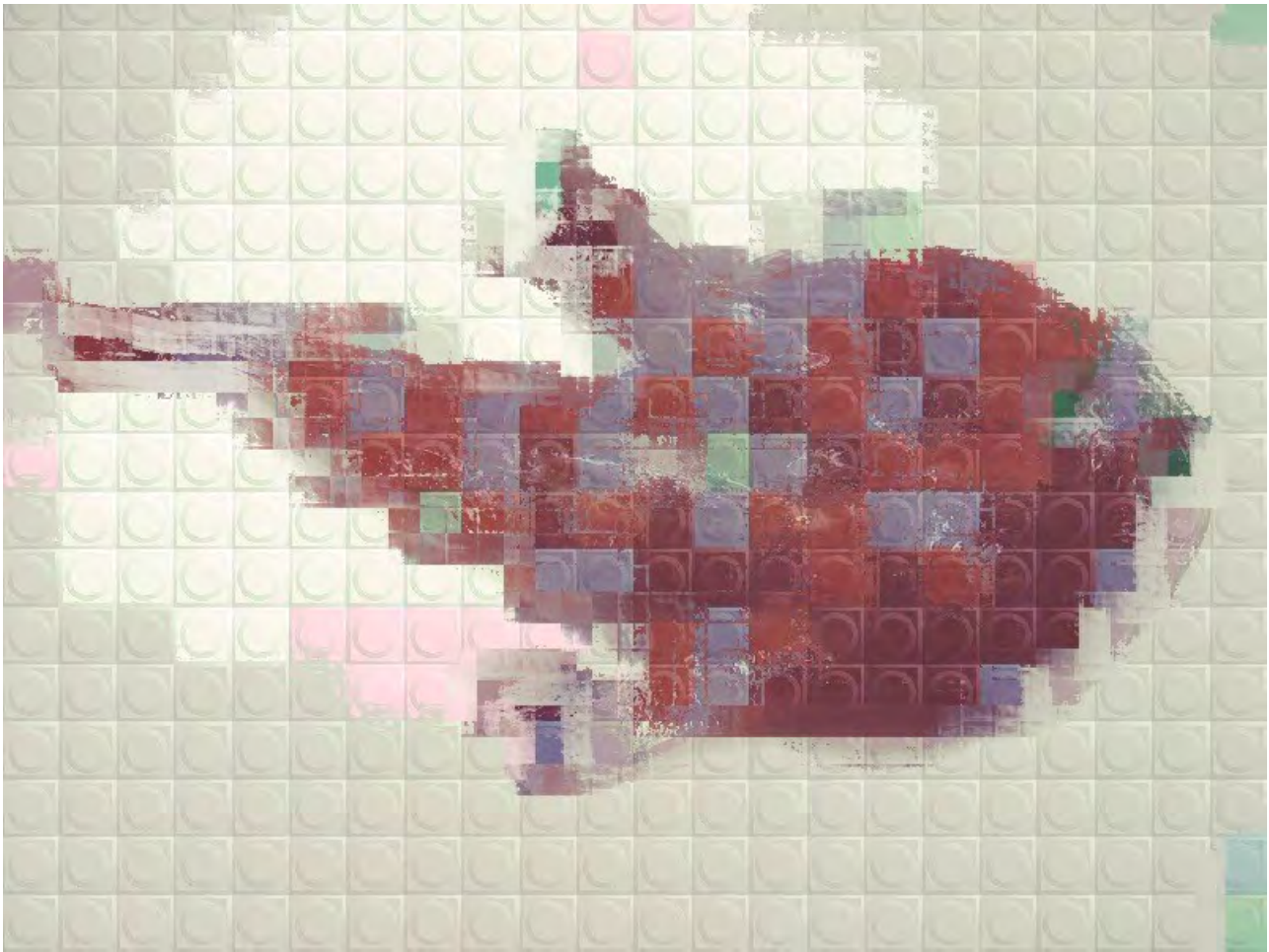
2.3. To assess the suitability of N_{90} to detect the effects of fishing on demersal fish communities and to compare its performance with that of the most used diversity indices.

2.4. To describe the diversity of the demersal fish communities of the Balearic Islands and to assess the effect of the fishing activities on it from an integrative approach including complementary aspects of diversity such as species richness, evenness, and taxonomic and functional diversities, along with the new N_{90} index.

2.5. To study the demersal fish diversity in the northern Mediterranean Sea and through areas with different oceanographic characteristics and subject to different levels of fishing pressure.

Chapter 3

MATERIALS AND METHODS



Chapter 3. Materials and Methods

3.1 MEDITS data

The biological data used in this Thesis were obtained from MEDITS. The MEDITS project (<http://www.sibm.it/MEDITS/%202011/principalemedits.htm>) started in 1994 from the coordination between several research centers from France, Greece, Italy and Spain. Later more institutes from Mediterranean Member states were joining the Project until reaching the cooperation of the 10 riparian countries of the European Union nowadays. The aim of MEDITS Project is to obtain fishery independent data on demersal species and their distribution with a common sampling strategy and protocol in the whole Mediterranean. The surveys intend to include as much as possible all the trawlable areas over the shelves and the upper slopes from 10 to 800 m depth off the coast of the partner countries.

The MEDITS are conducted at daylight hours in spring or early summer depending on the GSA. An experimental bottom trawl GOC73 is used, equipped with a 20 mm mesh codend and with average horizontal and vertical net openings of 17 and 3 m, respectively. The efficiency of the GOC73 experimental gear for catching demersal species have been tested by Fiorentini et al. (1999) and Dremière et al. (1999). The towing speed is around 3.0 knots to ensure the net proportions are maintained during trawling. The effective trawling duration varies between 20 and 60 min depending on the depth strata. The sampling stations follow a depth stratified sampling scheme with random drawing of the positions within each stratum, which are common for all GSAs: A (10-50 m), B (51-100 m), C (101-200 m), D (201-500 m) and E (501-800 m). The number of hauls in each stratum is proportional to the area occupied by the strata in each GSA, and their position is the same from year to year.

In each haul, all species captured are sorted, weighed and individuals counted (Figure 3.1). The body length of fishes, cephalopods and decapods crustaceans is also measured. The data of demersal fish species and their abundances from MEDITS for all GSAs specified in Annex 1 were used to calculate diversity indices from Chapters 4, 5, 6 and 7. Species with a markedly pelagic or mesopelagic habit were excluded from the analyses. Some functional traits of demersal fish species, such as length, weight and shape were also used to calculate functional diversity indices from Chapter 6. For more details about the sampling strategy and protocol see Bertrand et al. (2002) and MEDITS handbook, instruction manual version 9 (AAVV, 2017).

3.2 Diversity indices

This Thesis studies the demersal fish diversity of the Mediterranean using ‘traditional’ diversity indices such as species richness (S), Margalef’s richness (d), Pielou’s evenness (J'), Brillouin, Fisher’s ($Fisher$), Rarefaction 10 ($ES(10)$), Rarefaction 20 ($ES(20)$), Shannon’s (H'), Simpson’s ($1 - \lambda'$), and Hill’s $N1$, $N2$ and N_∞ diversity. The calculation of each ‘traditional’ diversity index is specified in Table 3.1. Which of those ‘traditional’ diversity indices have been calculated is stated in each specific chapter.



Figure 3.1: Mediterranean International Bottom Trawl Surveys (MEDITS) around the Balearic Islands in 2014: a) capture; b) gear; c) sampling.

Taxonomic and functional diversity indices are also calculated in Chapter 6 (Table 3.1). Taxonomic diversity (Δ) and taxonomic distinctness (Δ^*) require taxonomic information, i.e. the taxonomic hierarchy among the species involved, for the estimation of the path or taxonomic branch lengths between each pair of species (Warwick and Clarke, 1995; see Annex 1). Six taxonomic levels were considered: species, genera, families, orders, classes and phylum. The weights given to each level ω_{ij} were equidistant, being 20 for different species belonging to same genera, 40 for species belonging to different genera and same family, 60 for species belonging to different family and same order, 80 for species belonging to different order but same class, and 100 for species belonging to different class and same phylum.

Somerfield et al. (2008) describe how the relatedness indices of Warwick and Clarke (1995) may be adapted to give information about how the average functional breadth of a community may vary. Then, and following Somerfield et al. (2008), functional versions of taxonomic diversity ($F\Delta$) and taxonomic distinctness ($F\Delta^*$) were also calculated in Chapter 6. These indices are based on functional similarities between species instead of taxonomic ones (Table 3.1). For their calculation a resemblance matrix among species derived from a functional traits matrix is used. The measure used to define functional resemblance among species was the simple matching coefficient:

$$f_{ij} = 100 * \left(1 - \frac{a + d}{a + b + c + d}\right)$$

where a is the number of traits common to species i and j ; b the number possessed by i and not j ; c the number possessed by j and not i ; and d the number possessed by neither.

Table 3.1: Diversity indices analysed in this Thesis. $x_i (i = 1, \dots, S)$ denotes the number of individuals of the i th species, $N (= \sum_{i=1} x_i)$ is the total number of individuals in the sample, $p_i (= x_i/N)$ is the proportion of all individuals belonging to species i , N_{max} is the abundance of the species that are most representative in the sample, ω_{ij} is the taxonomic path length between species i and j , f_{ij} is the functional dissimilarity between species i and j .

Diversity index	Formula	Symbol	Description	References
Species richness	Number of species	S	Total number of species	-
Fisher's α	$S = \alpha * Ln(1 + \frac{N}{\alpha})$	$Fisher$	Shape parameter under the assumption that species abundance distribution follows a log series distribution	Fisher et al. (1943)
Simpson	$1 - \lambda' = 1 - \frac{\sum_{i=1}^S x_i(x_i-1)}{N(N-1)}$	$1 - \lambda'$	Probability that two individuals drawn at random from an infinite community belong to the same species	Simpson (1949)
Shannon	$H' = -\sum_{i=1}^S p_i Ln p_i$	H'	Measure of the uncertainty about the species of the nearest neighbour of an individual from the community	Shannon and Weaver (1949)
Margalef's richness	$d = \frac{S-1}{LnN}$	d	Number of species adjusted to the number of individuals	Margalef (1958)
Pielou's evenness	$J' = \frac{H'}{LnS}$	J'	Equitability in the distribution of abundances of species in a community	Pielou (1966)
Rarefaction 10	$ES_{10} = \sum_{i=1}^S [1 - \frac{(N-x_i)!(N-10)!}{(N-x_i-10)!N!}]$	$ES(10)$	Expected number of species in 10 individuals	Sanders (1968) and Hurlbert (1971)
Rarefaction 20	$ES_{20} = \sum_{i=1}^S [1 - \frac{(N-x_i)!(N-20)!}{(N-x_i-20)!N!}]$	$ES(20)$	Expected number of species in 20 individuals	Sanders (1968) and Hurlbert (1971)
Reciprocal Berger-Parker	$N_{\infty} = \frac{N}{N_{max}}$	N_{∞}	Inverse of the dominance of species	Hill (1973)
Hills N1	$N1 = exp H'$	$N1$	Exponential of Shannon	Hill (1973)
Hills N2	$N2 = \frac{1}{\sum_{i=1}^S p_i^2}$	$N2$	Reciprocal of Simpson	Hill (1973)
Brillouin	$Brillouin = \frac{Ln(\frac{N!}{(x_1!x_2!x_3! \dots x_S!)})}{N}$	$Brillouin$	Finite population size version of Shannon	Pielou (1975)
Taxonomic diversity	$\Delta = 2 \frac{\sum \sum_{i < j} (\omega_{ij} x_i x_j)}{N(N-1)}$	Δ	Taxonomic distance expected between two individuals randomly selected	Warwick and Clarke (1995)
Taxonomic distinctness	$\Delta^* = \frac{\sum \sum_{i < j} (\omega_{ij} x_i x_j)}{\sum \sum_{i < j} (x_i x_j)}$	Δ^*	Taxonomic distance expected between two individuals randomly selected, considering that they belong to different species	Warwick and Clarke (1995)
Functional diversity	$F\Delta = 2 \frac{\sum \sum_{i < j} (f_{ij} x_i x_j)}{N(N-1)}$	$F\Delta$	Functional distance expected between two individuals randomly selected	Modified from Somerfield et al. (2008)
Functional distinctness	$F\Delta^* = \frac{\sum \sum_{i < j} (\omega_{ij} x_i x_j)}{\sum \sum_{i < j} (x_i x_j)}$	$F\Delta^*$	Functional distance expected between two individuals randomly selected, considering that they belong to different species	Modified from Somerfield et al. (2008)

3.3 Fishing effort

Both spatial distribution and temporal series of bottom trawl fishing effort have been used to study the effects of fishing on demersal fish diversity.

VMS technology is based on the presence on board of each fishing vessel of an automatic transmitting station (the so-called ‘blue box’), which periodically sends information about vessel position, speed, and prow heading (Russo et al., 2013). The geographic distribution of the fishing effort in the Balearic Islands was assessed through the

analysis of the VMS data of the bottom trawl fleet that operates in this area (Chapters 5 and 6). These data consist of records which contain information on the geographic position, date, time and instantaneous velocity for each boat approximately every two hours. For the bottom trawl fleet that operates in the Balearic Islands this information is available since 2005, the year in which this fleet was required to install VMS.

In the Balearic Islands trawlers are only allowed to work 12 hours per day (from 05:00 am to 05:00 pm) and 5 days per week (from Monday to Friday). In order to limit the VMS positions to when vessels were fishing, only the signals from this time period with an instantaneous velocity from 2 to 3.5 knots were selected to remove VMS signals from boats transiting to fishing grounds or ports. Then, a VMS grid was created taking into account the mean number of VMS signals present on each of the 0.01x0.01 degrees cells in which the area of study was divided.

Temporal series of fishing effort from the whole Mediterranean were collected from GFCM (<http://www.fao.org/gfcm/data/safs/en/>) and STECF (<https://stecf.jrc.ec.europa.eu/reports/medbs>) working groups reports (Chapter 7). Fishing effort data were compiled by trawl fleet targeting different species. The units vary between the different reports, being mainly provided in terms of number of vessels, kilowatt per days at sea and gross tonnage per days at sea. These fishing effort estimations are associated to the main target species of the bottom trawl fleet of the Mediterranean (see Annex 2).

Chapter 4

RESULTS 1. N_{90} INDEX

N_{90} : a halfway between alpha and gamma diversity



Chapter 4. Results 1. N_{90} : a halfway between alpha and gamma diversity

SUMMARY

Diversity is a founding but at the same time complex concept in ecology, related to the number and abundance of species in the community. Taking into account changes of diversity along transects or across environmental gradients, diversity is also classified in alpha, beta or gamma diversity. N_{90} is a recently developed diversity index based on the results of the SIMPER analysis that represents the number of species contributing up to the ninety percent of the within-group similarity in a group of samples. The calculation of N_{90} involves number of species and abundances in a group of samples and it is based on the Bray-Curtis similarity distance. We want to see if N_{90} is related to alpha, beta or gamma versions of indices involving number of species and/or abundances in their calculus, like species richness (S), Shannon's (H') and Pielou's evenness (J'). To do this, we correlated the values of N_{90} to alpha, beta and gamma versions of S , H' and J' by means of linear regression analysis. Having N_{90} at halfway between alpha H' and gamma S favours the detection of the diversity loss due to the fishing-induced retreatment of species populations to localities presenting the most favourable ecological conditions. We also present an R script for the calculation of the N_{90} index and its variability, which allows the calculation of the N_{90} diversity from groups of samples. An example analysis is shown, using a non-real data set included in this Chapter.

4.1 Introduction

4.1.1 The diversity

Diversity is a founding, but at the same time, complex concept in ecology. For most scientists, diversity has to do with number and abundance of species in the community, and a lot of attempts have been done to materialize this concept in a number. Because of this, a high number of diversity indices have been proposed showing different aspects of the community structure, taking into account from the number of species in the community, to the relative abundance or biomass of these species or the taxonomic or functional relations between them (Magurran, 2004). Although it is generally agreed that diversity is a multidimensional concept and the use of diversity indices depend on what effect on diversity you want to detect, there is no consensus about the indices that should be used in each case. Because of that, 'traditional' or classical diversity indices such as species richness (S), Shannon (H') or Pielou's evenness (J'), are usually chosen to describe biological communities because, at least, they are easy to calculate and allow comparisons with previous works.

At a higher level of complexity and taking into account changes of diversity along transects or across environmental gradients, the concept of beta diversity emerges. Although there is some controversy about it (Jurasinski et al., 2009), it is generally agreed that beta diversity is a way of measure the species that change between samples or sites composing a community. The concept of beta diversity was originally proposed by Whitakker (1960, 1972) and their measures were summarized by Chao and Chiu (2016) in two major approaches: i) the diversity decomposition approach that consist in

decomposing the total diversity (gamma) into its within-community component (alpha) and among community component (beta), and it can be applied to species richness as well as other diversity indices involving abundances in their calculations; and ii) the variance framework that consist in computing beta diversity from a dissimilarity index between pairs of communities.

4.1.2 N_{90} diversity index

N_{90} is a diversity index based on the results of the SIMPER analysis (Clarke, 1993) that represents the number of species contributing up to the ninety percent of within-group similarity in a group of samples. It uses the Bray-Curtis similarity index as proposed by Clarke (1993) for the SIMPER analysis. The calculus of the index is completed with a jack-knife resampling routine allowing to get the mean and the variability of N_{90} in the group of samples analysed, usually representing the biodiversity in a given area, a community or an ecosystem.

The hypotheses behind the index is that impacted communities may see reduced both the frequency of occurrence and the evenness of the distribution of species abundances among samples due to the retreatment of species populations to the localities presenting the most favourable ecological conditions.

The species' contribution to the similarity within a group of samples is sensitive to both frequency of occurrence and differences in abundance among samples. Hence, in its first applications, the N_{90} index showed its suitability to detect the impact of bottom trawling on both demersal fish and epibenthic communities (Ordines et al., 2017; Chapters 5, 6 and 7), as well as the indirect effects of fishing on demersal species by-catch (Gorelli et al., 2016). Besides, the N_{90} index has shown some advantages when compared to other diversity indices: (i) easy interpretation, units are number of species as in species richness (S), but, at the same time, N_{90} is less dependent on sample size than S (Hill, 1973; Noss, 1990; Gotelli and Chao, 2013), due to rare species are not usually among the main contributors to within-group similarity; (ii) more sensitivity to anthropogenic impacts and environmental variability and their synergistic effects; (iii) it assesses the diversity for the whole set of samples in the group (usually representing a community or ecosystem) instead of operating at sample level and averaging values afterwards, or alternatively, pooling data from different samples (e.g. an S value taking into account all species appeared in all samples); and (iv) species identity is preserved because the N_{90} index is accompanied by a SIMPER table showing within-group species contribution to the ninety percent similarity.

4.1.3 Objectives

The aim of this Chapter is to frame the N_{90} index in a diversity aspect. To do so, because the calculation of N_{90} involves number of species and abundances, we assessed its correlation with the alpha, beta or gamma versions of indices involving number of species and/or abundances in their calculus, such as species richness (S), Shannon (H') and Pielou's evenness (J'). The R script for the calculation of the N_{90} index and its variability is also presented.

4.2 Materials and Methods

4.2.1 N_{90} diversity index

4.2.1.1 Calculation

The calculation of N_{90} starts with the calculation of the contribution of each species to the within-group similarity using the Bray-Curtis similarity index (Bray and Curtis, 1957) as proposed by Clarke (1993):

$$S_{jk}(i) = 100 * \frac{2 * \min(y_{ij}, y_{ik})}{\sum_{i=1}^p (y_{ij} + y_{ik})}$$

where y_{ij} is the abundance of the species i in the sample j ; y_{ik} , is the abundance of the species i in the sample k ; p is the total number of species in j and k ; and $\min(y_{ij}, y_{ik})$ is the minimum value of the abundance of species i between the samples j and k , taking zero into account. The contribution of each species i to the total similarity of the group S_i is the mean value of $S_{jk}(i)$ for a species in all the sample comparisons in the group. And the total similarity in a group (Sim) is the addition of S_i for all the species in the group:

$$Sim = \sum_{i=1}^p S_i$$

Then the contribution of S_i to Sim is referred to 100%. This procedure is repeated for each resampling in a jack-knife routine, which removes a sample each time. At the end of the procedure, there are as many lists of contribution to similarity by species as number of resamplings. The N_{90} diversity index is the mean number of species which accumulates up to 90% of within-group similarity in all the resamplings.

4.2.1.2 N_{90} script

Data sets

N_{90} was calculated using an R script, version 3.1.1 (R Core Team, 2014) that can be found in the Supplementary data of this Chapter. The data needed to work with the N_{90} script consist in two ‘.csv’ files. The first one includes the abundances of each species. In this data file columns are labelled with the species names and each row corresponds to a sample. The other file includes, in the same order than the previous one, a column, named *Group*, indicating the group to which each sample belongs. These data sets must be imported with the name of *af* (i.e. abundance file) and *gf* (i.e. groups file). The structure of *af* and *gf* can be seen in Table 4.1. Vegan package (Oksanen et al., 2013) is required to carry out all the analyses.

Exploring data

Data_explore (*af*, *gf*, *perc*, *perc2*) function allows the exploration of the data previously to apply the jack-knife resampling routine. For each *Group* given in *gf* it returns: 1) the number of samples in each group (n); 2) the number of samples that will be removed in

each resampling (n_1) for a specified percentage of samples to be removed (*perc*; if *perc* accounts for less than one sample, the function will consider $n_1= 1$ by default); and 3) the maximum number of samples in n_1 that can be repeated in the next resampling for a specified percentage *perc2*. Both *perc* and *perc2* are implemented as integer divisions in the script. The function allows users exploring the samples replaced in each jack-knives using different values of *perc* and *perc2*.

Table 4.1: Abundance data by species and sample for each *Group* of samples used in the example. The columns under *af* show the data included in the abundance file, whereas the column under *gf* shows the data included in the groups file. A, B, C, D, E, F, G, H, I, J, K, L and M are the names of the species.

<i>af</i>													<i>gf</i>	
A	B	C	D	E	F	G	H	I	J	K	L	M	Group	
0	0	0	23	23	0	0	0	0	0	0	235	0	gA	
0	0	0	0	0	0	0	0	0	148	0	49	0	gA	
0	0	0	47	0	24	0	0	284	0	24	0	0	gA	
0	0	0	22	0	0	22	0	66	0	66	22	0	gA	
0	0	0	0	0	0	0	0	578	0	46	0	0	gA	
415	0	0	0	0	0	0	0	394	0	0	109	0	gA	
0	0	175	0	0	0	0	0	0	197	197	372	0	gA	
0	0	0	215	0	0	0	0	882	0	473	0	1269	gA	
41	0	20	41	0	0	20	0	569	203	996	41	0	gA	
39	0	20	20	0	0	0	0	255	0	39	79	1336	gA	
43	0	43	299	0	0	0	0	2542	0	2392	0	0	gB	
22	0	0	90	0	112	0	0	4969	0	627	0	67	gB	
0	0	0	172	0	0	0	0	6919	0	57	0	96	gB	
0	0	0	169	0	0	19	0	226	0	414	19	0	gB	
0	21	21	63	126	0	0	0	0	0	820	147	84	gB	
19	0	0	58	0	0	0	0	1451	0	0	19	0	gB	
0	0	81	0	0	0	61	0	0	606	20	323	0	gB	
0	0	0	74	0	18	0	0	129	18	147	0	0	gB	
38	0	19	208	0	0	0	0	5179	0	151	0	1115	gB	
72	0	0	192	0	0	0	48	3006	0	577	0	24	gB	
56	0	37	111	0	0	0	37	130	19	167	93	501	gB	
0	0	37	130	0	0	0	0	5329	0	3182	0	0	gB	
18	0	165	202	0	0	0	0	3813	0	1540	0	1228	gB	
55	0	92	18	0	0	18	0	4055	110	1468	0	18	gB	
0	0	538	0	0	0	36	0	18	341	72	269	18	gB	
0	0	805	98	39	0	0	0	20	393	1374	569	2061	gB	
273	0	243	273	0	0	30	0	1031	0	576	121	909	gB	
60	0	0	80	0	0	20	40	40	60	498	179	0	gB	
19	0	0	93	0	0	0	75	1325	0	523	0	0	gB	
19	0	0	19	0	0	0	0	8519	0	167	0	1318	gB	
18	0	0	0	0	0	18	0	733	0	72	0	0	gB	
0	0	0	0	0	0	0	0	0	425	0	58	0	gB	
0	0	0	0	38	0	19	0	0	0	303	114	132	gB	
0	0	0	37	0	0	0	18	3118	0	1339	0	18	gB	
0	0	0	59	0	0	0	59	2121	0	238	0	1407	gB	
21	0	0	21	0	0	0	0	2987	0	165	0	0	gB	
0	0	370	0	0	0	0	0	0	206	62	637	0	gB	
0	0	40	20	20	0	0	0	0	0	418	358	219	gB	
0	0	20	40	0	0	0	81	161	20	1732	624	20	gB	
24	0	235	400	0	0	0	71	3695	0	1695	47	4590	gB	

Resampling N_{90}

$N_{90_resampling}(af, gf, cutoff=90, perc, perc2, jkmax)$ function executes the jack-knife resampling routine and returns the value of the N_{90} index. With the value of *jkmax*, the user can specify the number of resamples to be done. The maximum value of *jkmax* permitted for the script is 9999. If this value is overtaken, the function will return a ‘WARNING’ message. The argument *cutoff* allows specifying a different cutoff percentage of accumulated species contribution to within-group similarity than the 90% used by default in the N_{90} diversity index (i.e. *cutoff*= y then N_y). The use of the arguments *perc* and *perc2* has been already explained for *Data_explore* (*af*, *gf*, *perc*, *perc2*)

function.

At the end of the calculation, the *N90_resampling* (*af*, *gf*, *cutoff*=90, *perc*, *perc2*, *jk-max*) function returns a list with 3 objects. The *\$N90_jackknifes* object reports the value of the N_{90} index (*N90.jackknife*) and the within-group total similarity (*Sim.jackknife*) obtained in each resampling for each *Group* given in *gf*. The *\$N90_mean_values* object reports the mean value of the N_{90} index (*Av.N90*) and its standard deviation (*SD.N90*), and the mean within-group total similarity (*Av.Sim*) and its standard deviation (*SD.Sim*), both calculated taking into account all the values obtained in each resampling for each *Group* given in *gf*. And finally, the *\$SIMPER_table* object includes a SIMPER table for each *Group* given in *gf* that shows the contribution of all the species included in the group of samples. These SIMPER tables are generated taking into account all the samples (i.e. without resampling). For each species in a *Group* the table shows: the mean abundance (*Av.Abund*) and its standard deviation (*SD.Abund*), the mean contribution (*Av.Si*) and its standard deviation (*SD.Si*) to within-group similarity, the percentage contribution to within-group similarity (*Contr*), and the cumulative contribution to within-group similarity (*Cum*).

Example

As an example we have applied the N_{90} script functions to a non-real data set. Table 4.1 shows the abundances of 13 species (A, B, C, D, E, F, G, H, I, J, K, L, and M) in two unique groups of samples named as gA and gB. The data must be imported with the name of *af* and *gf* from 2 ‘.csv’ files as has been already explained in Section 4.2.1.2.

4.2.2 Framing N_{90} into alpha, beta or gamma diversity

4.2.2.1 Data

In order to frame the N_{90} index in alpha, beta or gamma diversity, the data collected during the MEDITS on demersal fish communities of the Balearic Islands was used. This scientific survey has been conducted annually since 2001, during late spring in the Balearic Islands, covering the soft bottoms of the continental shelf and slope between 50 and 800 m depth. According to the MEDITS protocol, four depth strata were taken into account: (i) shallow shelf from 50 to 100 m; (ii) deep shelf from 101 to 200 m; (iii) upper slope from 201 to 500 m; and (iv) middle slope from 501 to 800 m. A total of 650 hauls (around 50 per year) carried out between 2002 and 2015 were analysed. In each haul, fish species were sorted and individuals were counted and weighed. Abundances of fish species were standardized to one square km, using the horizontal opening of the net and the distance covered in each haul, obtained using the SCANMAR system and GPS, respectively. The species included in the analyses are specified in Annex 1. For more details on the sampling strategy and protocol, and gear characteristics, see Chapter 3 (Section 3.1).

4.2.2.2 Diversity indices

Following the multiplicative partitioning approach (Whittaker, 1960), alpha, beta and gamma versions of S , H' and J' were calculated. See Chapter 3 (Section 3.2; Table 3.1) for more details on the calculation of ‘traditional’ diversity indices. In the case of S : (i) alpha diversity was calculated as the mean number of species among the samples of

each group; (ii) gamma diversity was calculated as the total number of species for the whole group; and (iii) beta diversity was calculated as gamma diversity divided by alpha diversity. See examples of alpha, beta and gamma versions of S in Figure 4.1. Following the calculation for S , alpha, beta and gamma versions of H' and J' were calculated as follows: (i) alpha diversity was calculated as the mean value of each index among all the samples in each group; (ii) gamma diversity was calculated from the mean values of abundances for each species in the group of samples and then calculating each diversity index for the whole group; and (iii) beta diversity was calculated as gamma diversity divided by alpha diversity.

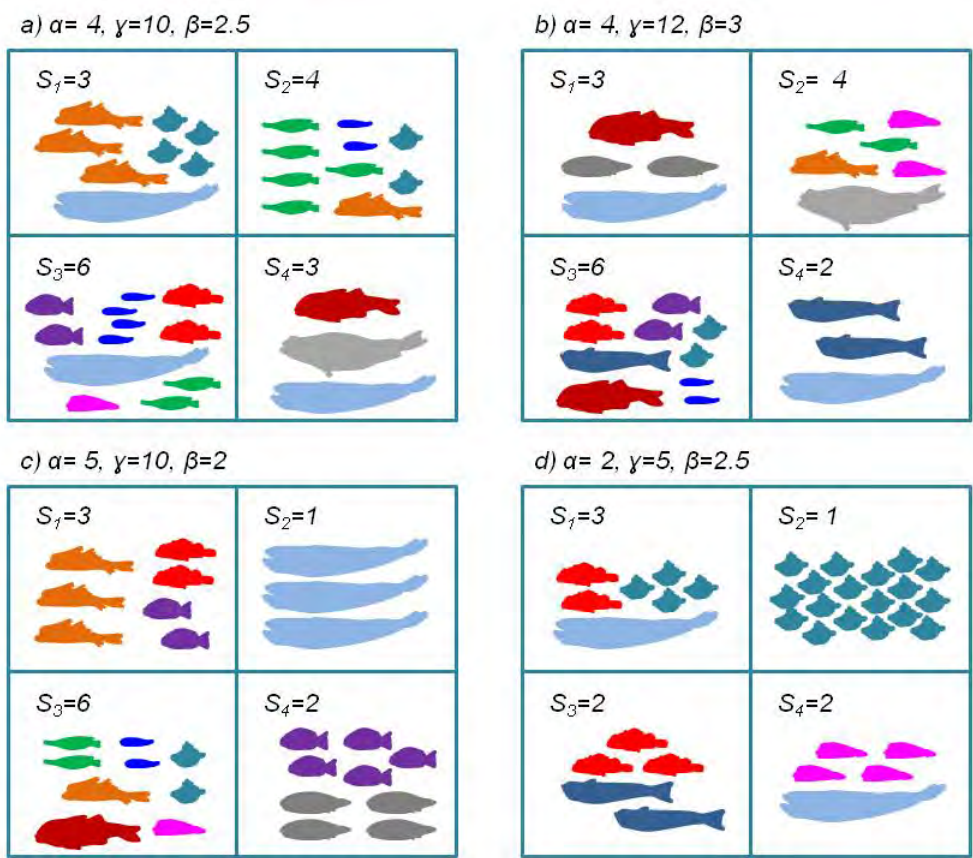


Figure 4.1: Examples of alfa (α), beta (β) and gamma (γ) versions of species richness (S) for four communities of fish (a, b, c, d) with four samples each.

The groups of samples considered for the calculation of N_{90} , as well as for the alpha, beta and gamma versions of S , H' and J' , were defined by the MEDITS depth strata (see Section 4.2.2.1) and the sampling year. Because the number of samples in any group was lower than twenty, a single sample was removed for each jack-knife in the calculus of N_{90} (see about *perc* and *perc2* in Section 4.2.1.2). Once all the indices were calculated, we correlated the values of N_{90} to alpha, beta and gamma versions of S , H' and J' by means of linear regression analysis.

4.3 Results

4.3.1 N90 script

4.3.1.1 Exploring data

The first step is the application of the *Data_explore* (*af*, *gf*, *perc*, *perc2*) function in which a 10 percent of samples is removed in each resampling (*perc*) and a 70 percent of the samples removed can be repeated from the previous resampling (*perc2*):

```
Data_explore (af, gf, perc=10, perc2=70)
```

For our example data set the output will be:

```
Group: "1"
Name of the group: "gA"
Number of samples of the group: "10"
Number of samples removed: "1"
Maximum number of repeated samples from removed: "0"

Group: "2"
Name of the group: "gB"
Number of samples of the group: "30"
Number of samples removed: "3"
Maximum number of repeated samples from removed: "2"
```

It shows that in the first group (gA) there are 10 samples and that the number of samples removed in each resampling with the given percentage ($perc=10$) is $n_1=1$ of which none of them should be repeated according to the given $perc2$ ($perc2=70$). In the second group (gB) there are 30 samples and the number of samples removed in each resampling with the given percentage ($perc=10$) is $n_1=3$. The number of samples that can be repeated according $perc2$ ($perc2=70$) is 2.

4.3.1.2 Resampling N_{90}

For the present example, the $perc=10$ and $perc2=70$ previously explored, are used:

```
N90_resampling (af, gf, cutoff=90, perc=10, perc2=70, jkmax=9999)
```

The main output of this function consists in a list with 3 objects. The $\$N90_jackknifes$ object summarizing the results of N_{90} value and the mean within-group similarity in each resampling (Table 4.2). The $\$N90_mean_values$ object summarizing the N_{90} value and the mean within-group similarity, with their standard deviations for all groups in gf (Table 4.3). And finally the $\$SIMPER_table$ object summarizing the SIMPER analysis results for each group of samples (Table 4.4). This table will allow identifying the species accounting for the N_{90} value due to they are ordered by their contribution to within-group similarity.

Table 4.2: Jack-knife results table obtained using the $N90_resampling$ function for group A (gA) from the $\$N90_jackknifes$ object. $N90_jackknife$ and $Sim_jackknife$ are the values of the N_{90} and the total similarity values in each resampling step, respectively.

Group	N90_jackknife	Sim_jackknife
gA	5	23.727
gA	4	24.326
gA	5	20.527
gA	5	22.314
gA	5	19.980
gA	5	20.616
gA	4	22.541
gA	4	21.070
gA	4	20.011
gA	4	21.217

Table 4.3: Average results table obtained using the $N90_resampling$ function from the $\$N90_mean_values$ object. Av.N90 and the SD.N90 are the N_{90} value and its standard deviation, respectively; Av.Sim and SD.Sim are the average and the standard deviation values of the within-group similarity.

Group	Av.N90	SD.N90	Av.Sim	SD.Sim
gA	4.5	0.527	21.633	1.529
gB	4.395	0.490	29.631	1.201

Table 4.4: Similarity Percentage (SIMPER) analysis table obtained using the $N90_resampling$ function from the $\$SIMPER_table$ object. Av.Abund and SD.Abund are the average and standard deviation values of the abundance, respectively; Av.Si and SD.Si are the mean and standard deviation of the contribution of each species to the within-group similarity; Contr is the percentage contribution to within-group similarity; and Cum is the cumulative percentage contribution.

Group	Species	Av.Abund	SD.Abund	Av.Si	SD.Si	Contr	Cum
gA	I	302.8	302.612	11.120	15.557	51.403	51.403
gA	L	90.7	122.035	3.964	7.167	18.325	69.727
gA	K	184.1	320.450	2.795	4.442	12.919	82.646
gA	M	260.5	549.409	1.219	8.177	5.635	88.281
gA	J	54.8	89.375	1.192	4.754	5.510	93.791
gA	D	36.8	64.966	1.039	2.092	4.805	98.596
gA	A	49.5	129.497	0.175	0.668	0.807	99.403
gA	C	21.5	54.572	0.087	0.334	0.404	99.807
gA	G	4.2	8.867	0.042	0.280	0.193	100
gB	I	2050.533	2371.281	14.989	21.685	50.584	50.584
gB	K	693.2	796.607	8.342	9.584	28.153	78.737
gB	L	119.233	194.182	1.769	4.734	5.970	84.708
gB	M	460.833	957.334	1.665	4.667	5.618	90.326
gB	D	97.533	101.775	1.265	1.801	4.269	94.594
gB	J	73.267	157.214	0.687	3.979	2.318	96.912
gB	C	91.533	184.478	0.522	1.992	1.763	98.675
gB	A	25.233	51.494	0.182	0.470	0.613	99.288
gB	G	7.367	14.454	0.096	0.414	0.323	99.611
gB	H	14.3	26.373	0.088	0.398	0.298	99.909
gB	E	7.433	24.624	0.026	0.253	0.087	99.996
gB	F	4.333	20.599	0.001	0.028	0.004	100

4.3.2 Framing N_{90} into alpha, beta or gamma diversity

It is seen from the results that the highest correlations with N_{90} are related to the gamma version of S ($R=0.761$ and $R^2=0.579$; Figure 4.2) and the alpha version of H' ($R=0.691$ and $R^2=0.477$; Figure 4.2).

N_{90} also showed a positive correlation with beta S ($R=0.577$ and $R^2=0.333$; Figure 4.2).

4.4 Discussion

The high correlation between N_{90} and the gamma version of S and the alpha version of H' means that N_{90} is related to both total number of species in the whole group of samples or community and mean values of H' . The difference between alpha, beta and gamma S is that alpha S takes the mean number of species in the community, beta S the replacement of species between samples of the community and gamma S is the total number of species in the community. So, the high correlation of N_{90} with gamma S has an easy explanation because the species identity is not lost and the total number of species in the community is taken into account during the calculation of N_{90} . However

N_{90} is not equal to gamma S because it just takes into account the species that contribute to 90% similarity in the group of samples; or in other words the species that are more representative in terms of frequency of appearance and abundance from the group of samples in the community. That is also seen in the correlation of N_{90} with alpha H' , that shows that values of N_{90} , which calculus is based in the comparison of the abundances of each pair of samples composing the group or community, are more similar to a mean value of H' in the samples of the group or the community (alpha H') than H' calculated for the whole community (gamma H'). That means, the abundance of a species is just relevant for N_{90} when the species is frequent in the group or community more than when is just abundant in the whole community. Having N_{90} at halfway between alpha H' and gamma S diversities may favour the detection of the reduction in total (gamma) S through the reduction in the frequency of occurrence, and on mean (alpha) H' through the reduction in the evenness of the distribution of species abundances among samples in impacted communities. Altogether, would allow the detection of the diversity loss due to the fishing-induced retreatment of species populations to localities presenting the most favourable ecological conditions.

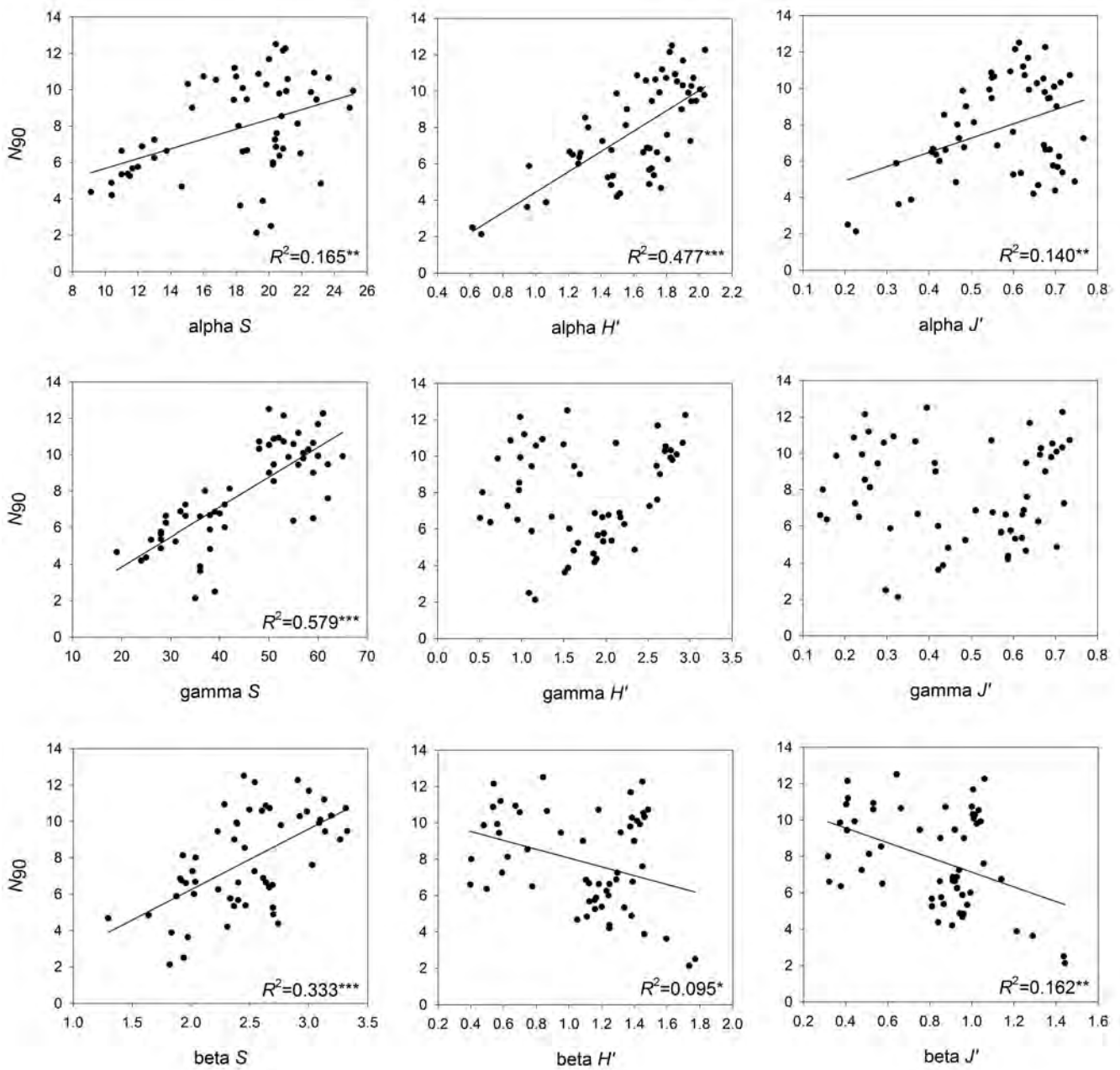


Figure 4.2: Results of the linear regressions analysis of N_{90} with alpha, beta and gamma versions of species richness (S), Shannon (H') and Pielou's evenness (J'). Adjusted R-squared values (R^2) and p-values are presented. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$.

The positive correlation of N_{90} with beta S means that beta S would increase due to an increase in the total number of species (gamma S), not compensated by an increase in mean S (alpha S). However, at least some of the species increasing gamma S , although not frequent enough to change the mean S , would be enough evenly distributed to account in the value of the N_{90} , allowing this index to account for some portion of the beta diversity.

The within-group similarity is an output of the SIMPER analysis which is also obtained when calculating the N_{90} . Following the variance framework, within-group similarity could be interpreted as an inverse measure of beta diversity. However we have not explored this relationship due to the high number of ways proposed to calculate beta diversity from the variance approach that include from dissimilarity measures between pairs of samples to clustering or ordination analysis (e.g. Magurran, 2004; Legendre et al., 2005; Anderson et al., 2006). Nevertheless, the equivalence between within-group similarity and inverse beta diversity seems reasonable from a theoretical point of view.

Supplementary data. N90 script used to calculate N_{90} diversity index and its variability.

```
#####
#####
##### LIBRARIES #####

library (vegan)

#####
##### DATA EXPLORATION #####

Data_explore<-function (af, gf, perc, perc2) {

group<-as.character (unique (gf$Group))
i<-1
  for (g in group){

    message ("Group: \", \", \", \n")

    dbg<- af [gf$Group == g, ]
    n<-nrow (dbg)

    sum<-summary (dbg)

    message ("Name of the group: \", \", \n")
    message ("Number of samples of the group: \", \", \n")

    n1<-(n*perc)/%100 #number of samples removed in each jackknife
    if (n1==0) {n1<-1} else {n1<-n1}

    message ("Number of samples removed in each jack-knife: \", \", \n")

    rep1<-(perc2*n1)/%100
    message ("Maximum number of samples repeated: \", \", \n")

    i<-(i+1)
  }
}

#####
##### SIMILARITY FUNCTION #####

Similarity<-function (dbg, contr) {

  #### combinations within group
  take <- t (combn (1:nrow (dbg), 2))
  take

  md<-numeric (ncol (dbg))
  me<-numeric (ncol (dbg))

  contr <- matrix (nrow = nrow (take), ncol = ncol (dbg+2))
  for (j in 1:nrow (take)) {
    for (i in 1:ncol (dbg)) {
      md[i] <- 2*min (dbg[take[j, 1], i], dbg[take[j, 2], i])
      me <- dbg[take[j, 1], ] + dbg[take[j, 2], ]
      contr[j, ] <- 100*(md / sum(me))
    }
  }
  contr<-data.frame (contr)
  colnames (contr)<-c (names (dbg))
  return (contr)
}

#####
##### CUMULATIVE NUMBER OF SPECIES #####

###cutoff to obtain all the species contributing to similarity is 99

N90<-function (contr, dbg, cutoff, n90){

  ndbg<-ncol (dbg)
  x<- colMeans (contr)
  df<-data.frame (x)
  x<-c (names (dbg))
  y<-df$x

  z1<-data.frame (Species=rep (NA, ndbg), Similarity=rep (NA, ndbg))

  z1$Species<-x
  z1$Similarity<-y

  z1$Similarity <- as.numeric (as.character (z1$Similarity))

  db<-z1[order (z1$Similarity, decreasing = TRUE),]
  b<-sum (db$Similarity)

  ##calculus of contribution to mean similarity
```

```

db$contribution<-((100*db$Similarity)/b)

##calculus of accumulated mean similarity \% and cut according to cutoff

d<-0
for (i in 1:ncol(dbg)){
  d<-(db$contribution[i]+d)
  db$acum[i]<-d
}

table<-db[which(db$acum<=cutoff & db$contribution >0),]
n90in<-nrow(table)
n90<-n90in+1
return(n90)
}

#####
#####
#####              SIMPER TABLE              #####

###cutoff to obtain all the species contributing to similarity is 99

SIMPER_table<-function (contr, dbg, cutoff, table){
  ndbg<-ncol(dbg)
  x1<-colMeans(contr)
  x2<-apply(contr, 2, sd)
  df1<-data.frame(x1)
  df2<-data.frame(x2)
  x<-c(names(dbg))
  y1<-df1$x1
  y2<-df2$x2

  z2<-data.frame(Species=rep(NA, ndbg), Similarity=rep(NA, ndbg), SD=rep(NA, ndbg))

  z2$Species<-x
  z2$Similarity<-y1
  z2$SD<-y2

  ##ordenation of species by similarity

  z2$Similarity <- as.numeric(as.character(z2$Similarity))

  db<-z2[order(z2$Similarity,decreasing = TRUE),]
  b<-sum(db$Similarity)

  ##contribution to mean similarity

  db$contribution<-((100*db$Similarity)/b)

  ##calculus of accumulated mean similarity \% and cut according to 90\%

  d<-0
  for (i in 1:ncol(dbg)){
    d<-(db$contribution[i]+d)
    db$acum[i]<-d
  }

  r<-db[which(db$acum<=cutoff & db$contribution >0),]

  Abundance0<-apply(dbg,2,mean)
  Ab_SD0<-apply(dbg,2,sd)
  Ab_SD10<-data.frame(Ab_SD0)
  Ab0<-data.frame(Abundance0)
  x0<-c(names(dbg))
  y0<-Ab0$Abundance0
  w0<-Ab_SD10$Ab_SD0
  z0<-cbind(x0,y0,w0)
  rb0<-merge(z0, r, by.x = "x0", by.y = "Species")
  table<-rb0[order(rb0$Similarity,decreasing = TRUE),]
  names(table)<-c("Species", "Av.Abund", "SD.Abund", "Av.Si", "SD.Si", "Contr", "Cum")
  return(table)
}

#####
#####
#####              N90 RESAMPLING FUNCTION              #####

N90_resampling<-function(af, gf, cutoff, perc, perc2, jkmax, r5, my_list){

  if (jkmax>9999){
    warning("the maximum number of jackknives must be lower than 10000")
  }

  group<-as.character(unique(gf$Group))

  SIMPERdf=data.frame()
  r5_df<-data.frame()
  r5_df_total<-data.frame()
  r6_df<-data.frame()
  r6_df_total<-data.frame()

  ext<-0

  #### cta is the accumulated contribution percentage or cutoff

```

```

for (g in group){
  ext<-ext+1

  dbg<- af[ gf$Group == g, ]
  message("group: \", \g, \"\n")

  n<-nrow(dbg)
  contr<-Similarity(dbg)

  r<-SIMPER_table(contr, dbg, 101)
  rt<-cbind(g,r)
  colnames(rt)<-c("Group", "Species", "Av.Abund", "SD.Abund", "Av.Si", "SD.Si", "Contr", "Cum")

  rtdf<-data.frame(rt)

  SIMPERdf<-rbind(SIMPERdf, rtdf)

  ### jack-knife for number of species and similarity in the group of samples

  take1 <- t(combn(1:n, 2))
  mf <- data.frame(take1)

  #n1 is the number of samples replaced in each jack-knife

  n1<-(n*perc)%/%100

  if (n1==0) {n1<-1} else {n1<-n1}

  max1<-jkmax*10
  a3<-0
  m1<-1

  rep1<-(perc2*n1)%/%100

  if (n1==1){
    if (jkmax<n) {
      Nsp<-numeric(jkmax)
      Sim<-numeric(jkmax)
      vec<-sample(1:n, jkmax, replace=FALSE)

      for (i in 1:jkmax){
        dbg2<-dbg[c(-vec[i]),]
        aux<-numeric(n-1)
        aux = which(mf[, 'X1'] == vec[i] |mf[, 'X2'] == vec[i])
        contraux<-contr[c(-aux),]
        Nsp[i]<-N90(contraux, dbg2, cutoff)
        Sim[i]<-(100-(100*mean(vegdist(dbg2, method='bray'))))
      }
      message ("Number_of_jack-cknives: \", \jkmax, \"\n")
    } else {
      Nsp<-numeric(n)
      Sim<-numeric(n)
      take <- t(combn(1:n, n1))
      for (i in 1:n) {
        k<-take[i, 1:n1]
        k<-data.frame(k)
        dbg2<-dbg[c(-take[i, 1:n1]),]
        aux<-matrix(nrow=n1, ncol=(n-1))
        for (j in 1:n1){
          aux[j,] = which(mf[, 'X1'] == k[j,1] |mf[, 'X2'] == k[j,1])
        }
        contraux<-contr[c(-aux),]
        contraux
        Nsp[i]<-N90(contraux, dbg2, cutoff)
        Sim[i]<-(100-(100*mean(vegdist(dbg2, method='bray'))))
      }
      message ("Number_of_jack-cknives: \", \n, \"\n")
    }
  } else {
    Nsp<-numeric(jkmax)
    Sim<-numeric(jkmax)
    matr<-matrix(ncol=n1, nrow=jkmax)

    for(k in 1:max1){
      m<-m1
      if (m==(jkmax+1)) break
      samp<-sample(1:n, n1, replace=F)
      if (m==1){
        matr[m,]<-samp
        j2<-data.frame(samp)
        dbg2<-dbg[c(-samp),]
        aux<-matrix(nrow=n1, ncol=(n-1))
        for (l in 1:n1){
          aux[l,] = which(mf[, 'X1'] == j2[l,1]
            |mf[, 'X2'] == j2[l,1])
        }
        contraux<-contr[c(-aux),]
        Nsp[m]<-N90(contraux, dbg2, cutoff)
        Sim[m]<-(100-(100*mean(vegdist(dbg2, method='bray'))))
      }
      m1<-(m+1)
    } else {
      matr2<-matrix(nrow=(m-1), ncol=n1)

```

```

    if (m==2) {
      matr2a<-matr[1,]
      matr2<-as.matrix(t(matr2a))
    } else {
      matr2<- matr[c(1:(m-1)), c(1:n1)]
    }
    res <- matrix(0, nrow =(m-1) , ncol = n1)
    for (i in 1:(m-1)){
      for (j in 1:n1){
        c<-matr2[i,j]
        for (k2 in 1: n1){
          d<-samp[k2]
          if (d==c) {
            res[i,j]<-(res[i,j]+1)
          } else {res[i,j]<-(res[i,j]+0)}
        }
      }
    }
    res2<-apply(res , 1, sum)
    if (any(res2 > repl)) {
      m1<-m
      next
    } else {
      matr[m,]<-samp
      j2<-data.frame(samp)
      dbg2<-dbg[c(-samp),]
      aux<-matrix(nrow=n1 , ncol=(n-1))
      for (l in 1:n1){
        aux[l,] = which(mf[, 'X1'] == j2[l,1]
          |mf[, 'X2'] == j2[l,1])
      }
      contraux<-contr[c(-aux),]
      Nsp[m]<-N90(contraux , dbg2, cutoff)
      Sim[m]<-(100-(100*mean(vegdist(dbg2, method='bray'))))
      m1<-(m+1)
      Nsp<-Nsp[1:m]
      Sim<-Sim[1:m]
    }
  }
}
message("Number_of_jack-knives:\n", m-1, "\n\n")
}
### calculus of mean value and standar deviation of the number of species
### and the total similarity of the group

r5_df<-cbind(g, Nsp, Sim)
colnames(r5_df)<-c("Group", "N90_jackknife", "Sim_jackknife")
r5_df_total<-rbind(r5_df_total, r5_df)

Nsp_sd<-sd(Nsp)
Nsp_mean<-mean(Nsp)
Sim_sd<-sd(Sim)
Sim_mean<-mean(Sim)

r6_df<-cbind(g, Nsp_mean, Nsp_sd, Sim_mean, Sim_sd)
colnames(r6_df)<-c("Group", "Av.N90", "SD.N90", "Av.Sim", "SD.Sim")
r6_df_total<-rbind(r6_df_total, r6_df)

}

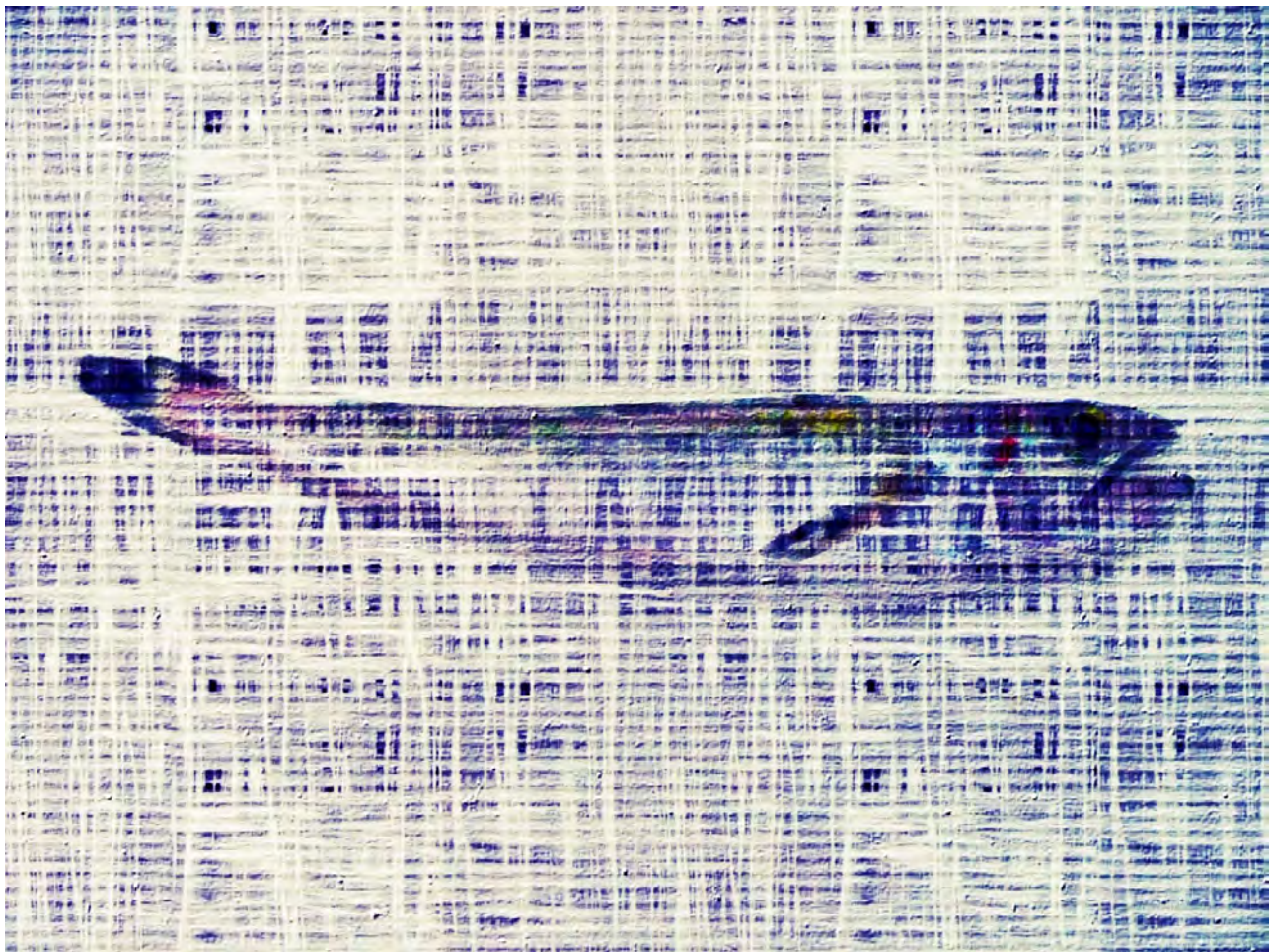
my_list <- list(r5_df_total , r6_df_total , SIMPERdf)
names(my_list) <- c('N90_jackknives', 'N90_mean_values', 'SIMPER_table')
return(my_list)
}
#####
#####

```

Chapter 5

RESULTS 2. DEEP SHELF

N_{90} index: a new approach to biodiversity based on similarity and sensitive to direct and indirect fishing impact



Chapter 5. Results 2. N_{90} index: a new approach to biodiversity based on similarity and sensitive to direct and indirect fishing impact

SUMMARY

An important effort has been made to develop diversity indices suitable to monitor the loss of biodiversity due to anthropogenic impacts in an accurate and comprehensible way. Here, N_{90} , a diversity index based on the species' contribution to the similarity between samples in a group, is presented. N_{90} uses the results of the classic SIMPER analysis and a jack-knife routine to calculate the average and a dispersion value of the number of species contributing up to the ninety percent of the within-group similarity in a group of samples. N_{90} is applied to two groups of samples subjected to contrasting levels of bottom trawl fishing pressure using time series of experimental bottom trawl surveys of the Balearic Islands. The results are compared to those obtained using more 'traditional' diversity indices such as species richness, Shannon's, Simpson's, Pielou's evenness, and Margalef's diversity indices. The N_{90} diversity index displayed a clear response to fishing pressure with significantly lower values in impacted communities, while the 'traditional' diversity indices showed almost null sensitivity to fishing pressure. In addition, N_{90} also detects indirect fishing impacts by fluctuating in response to environmental variation in impacted areas, making this index sensitive to the synergies between climate and fishing impact at community level. The application of the N_{90} diversity index to the case study shows that it may be an alternative to 'traditional' diversity indices when trying to monitor fishing impacts and the effects of environmental changes. Its units, number of species, and the corresponding summary list of species facilitate the interpretability of the results, improving the communication to managers and stakeholders.

5.1 Introduction

Biodiversity on Earth is declining fast due to anthropogenic impacts, with rates of loss of biodiversity that have accelerated since the second half of the 20th century (Millennium Ecosystem Assessment, 2005). In this context, an important effort has been made to develop diversity indices suitable to monitor this loss in an accurate and comprehensible way (Balmford et al., 2005). The main forums engaged in preservation of biodiversity, such as the global Convention on Biological Diversity and the pan-European initiative called Streamlining European 2010 Biodiversity Indicators stressed the need for rigorous, repeatable, widely accepted and easily understood biodiversity indicators that could easily be communicated to decision makers and stakeholders (Feld et al., 2009).

'Traditional' diversity indices as species richness (S), Shannon's (H') and Simpson's ($1 - \lambda'$), have been widely used in ecology. Among them, S (which is simply the count of species present) is the simplest one and it gives an intuitive interpretation of biodiversity because its units are presented in terms of number of species (Purvis and Hector, 2000; Magurran, 2004). However, these indices are very dependent on sample size (Hill, 1973; Noss, 1990; Hewitt et al., 2005; Gotelli and Chao, 2013), and do not take into account the species structure present in the set of surrounding samples

analysed. Instead, they calculate diversity values in individual samples (Gray, 2000; Legendre et al., 2005). These values need to be averaged if the objective is to evaluate diversity in the whole set of samples (usually representing a community or ecosystem), or alternatively, data from the different samples have to be previously pooled in some way (e.g. an S value taking into account all species appeared in all samples). Moreover, their interpretation is not always straightforward since information on species identity is lost, and hence, they cannot be used to monitor species turnover (Lamb et al., 2009).

In the marine environment, one of the main causes of biodiversity loss is the exploitation of fishing resources (Worm et al., 2009). In this sense, there is currently a consensus to develop fishing policies (e.g. Marine Strategy Framework Directive; Directive 2008/56/EC of the European Parliament and of the Council, of 17 June 2008, establishing a framework for Community action in the field of marine environmental policy) that take into account not only the state of the exploited populations of marine resources but also the entire ecosystem, i.e. the so-called EAF management (Pikitch et al., 2004), which emphasizes the need to protect marine ecosystems and their biodiversity. With this objective, the monitoring of the implementation of these policies will need the use of diversity indices that: (i) take into account the community structure; but also (ii) are sensitive to the fishing impact.

In the present study the use of N_{90} , a diversity index based on the species' contribution to the similarity between samples in a group, is proposed. Specifically, N_{90} uses the results of the SIMPER analysis as proposed by Clarke (1993) and a jack-knife routine to calculate the average and a dispersion value of the number of species contributing up to the ninety percent of the similarity in a group of samples. Hence, N_{90} units are as simple to interpret as those of S , but the species taken into account in this case are only those that are important components to define the community present in the set of samples analysed.

The aim of this Chapter is to assess the usefulness of N_{90} to detect changes in fish diversity due to fishing effects. The initial hypotheses is that communities affected by fishing impacts may see reduced both the frequency of occurrence and the evenness of their abundance distributions among samples due to the retreatment of specimens to local optima or areas presenting the most favorable ecological conditions. The species' contribution to the similarity within a group of samples is sensitive to both frequency of occurrence and differences in abundance among samples, and hence, N_{90} is expected to be sensitive as well. To check this hypothesis, biodiversity has been monitored in two groups of samples subjected to contrasting levels of bottom trawl fishing pressure through a time series of experimental bottom trawl surveys in the Balearic Islands (western Mediterranean). The results are compared to those obtained using more 'traditional' diversity indices such as S , H' , Pielou's evenness J' , Margalef's d and Simpson's $1 - \lambda'$. Moreover, the relationships between the time series of the diversity indices and the possible driving factors causing their variability are also explored.

5.2 Materials and Methods

5.2.1 Data

The data set used to assess the performance of N_{90} , and the 'traditional' diversity indices was collected during the MEDITS, carried out annually during spring in the Balearic

Islands since 2001. These surveys cover the bathymetric range between 50 and 800 m. The analyses were focused on the fishing grounds exploited by the bottom trawl fishery targeted to hake (*Merluccius merluccius*), that takes place on the deep shelf, between 100 and 200 m depth (Palmer et al., 2009). From the fishing effort perspective, this fishery was chosen because the bathymetric range includes fishing grounds subjected to well-differentiated levels of fishing pressure (see Section 5.2.2) that have been sampled during the MEDITS since 2003. In addition, the deep shelf is characterized by a common community structure of fish species (Massutí and Reñones, 2005) and is uniformly affected by the same water masses all over the study area during the sampling period (López-Jurado et al., 2008). A total number of 149 experimental hauls, corresponding to a maximum of 14 sampling stations per year, were analysed (Table 5.1; Figure 5.1). In each haul, species were sorted and individuals counted. Abundance was standardized to one square km, by using the horizontal opening of the net and the distance covered in each haul, obtained with a SCANMAR system attached to the net and a GPS, respectively. The species included in the analyses are specified in Annex 1. For more details on the sampling strategy and protocol, and gear characteristics, see Chapter 3 (Section 3.1).

Table 5.1: Number of samples in each fishing impact group by year. HLFi and LLFi indicate high or low level of foshing impact.

Group	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013
HLFi	5	6	5	5	6	6	6	6	6	6	6
LLFi	7	8	8	8	8	8	8	8	8	7	8

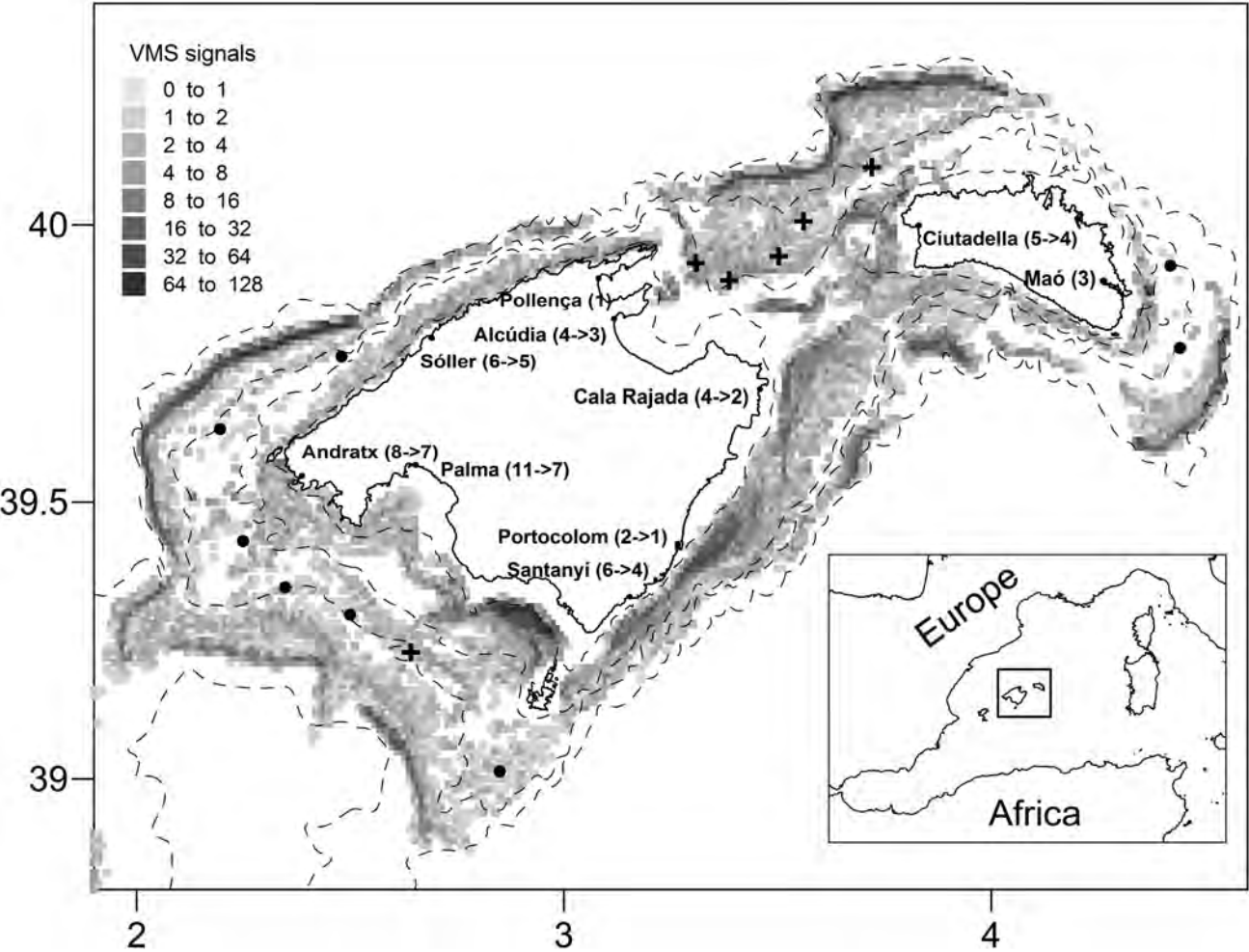


Figure 5.1: Map of the Balearic Islands, showing the mean value of Vessel Monitoring by satellite System (VMS) signals per year in 0.01 x 0.01 degrees cells during the period 2005-2012, and the number of bottom trawlers by port from 2000 to 2013 (between brackets). Stations corresponding to the high and low levels of fishing impact (black crosses and black dots, respectively) are displayed. The isobaths represent 50, 100, 200 and 800 m depth.

5.2.2 Fishing effort

The geographic distribution of the fishing effort in the Balearic Islands was assessed through the analysis of the VMS data of the bottom trawl fleet that operates in this area. The temporal series of VMS used went from 2005 (the year in which the bottom trawl fleet operating in the Balearic Islands began to install the VMS in their boats) to 2012 (the last year for which VMS data were available when the analyses of the present study were carried out). The records in which the fleet was not fishing were removed from the VMS data set by following the procedure explained in Chapter 3 (Section 3.3). Then, a VMS map was created taking into account the mean number of VMS signals present on each of the 0.01×0.01 degrees cells in which the area of study was divided (Figure 5.1). According to this map, and depending on the number of VMS signals recorded, each sampling station was included either in a HLFi or LLFi.

The classification of sampling stations was consistent throughout the time period analysed, with stations classified in both the HLFi and LLFi being always the same ones, independently of the year. The HLFi group included 63 samples from 6 sampling stations in which the number of VMS signals during the period 2005-2012 ranged from 21 to 52 signals/year, whereas the LLFi group included 86 samples from 8 sampling stations where VMS signals ranged from 0 to 12 signals/year (Table 5.1; Figure 5.1).

In the years 2003, 2004 and 2013, for which no VMS data were available, the classification of sampling stations in their corresponding fishing impact level was assumed to be the same as for the period 2005-2012 because: (i) in all the stations, the VMS signals ranged for all the years between the definition of HLFi and LLFi (Figure 5.1); (ii) the spatial exploitation pattern in the deep shelf did not change during the period 2005-2012 (Figure 5.2); (iii) the number of bottom trawlers operating from the different harbors remained almost constant between 2000 and 2013 (Figures 5.1 and 5.2); and (iv) since 1990, the fisheries policy for the Spanish Mediterranean only allows bottom trawlers being at sea during 12 h a day, leaving no chances to exploit fishing grounds at large distances from the boat's base harbor, and limiting their operations to the closer fishing areas. Consequently, it is assumed that the spatial pattern of distribution of VMS signals on the deep shelf has not changed during the whole period analysed, remaining as constant as that observed for the period 2005-2012 for which VMS data were available (Figure 5.2).

5.2.3 Diversity indices

5.2.3.1 N_{90}

The diversity index proposed in the present study is based on the number of species contributing up to the 90% of within-group similarity in the SIMPER analysis as proposed by Clarke (1993), but completing it with a jack-knife resampling routine in order to get the average and a dispersion value for the group analysed. More details on the calculation of N_{90} can be found in Chapter 4 (Section 4.2.1.1). This procedure was repeated for each resampling in a jack-knife routine, which removed a sample each time. At the end of the procedure, there are as many lists of contribution to similarity by species as number of samples in the group. The N_{90} diversity index is the average number of species which accumulated up to 90% of within-group similarity in these lists. All these analyses were carried out with the N90 script included in Chapter 4

(Supplementary data).

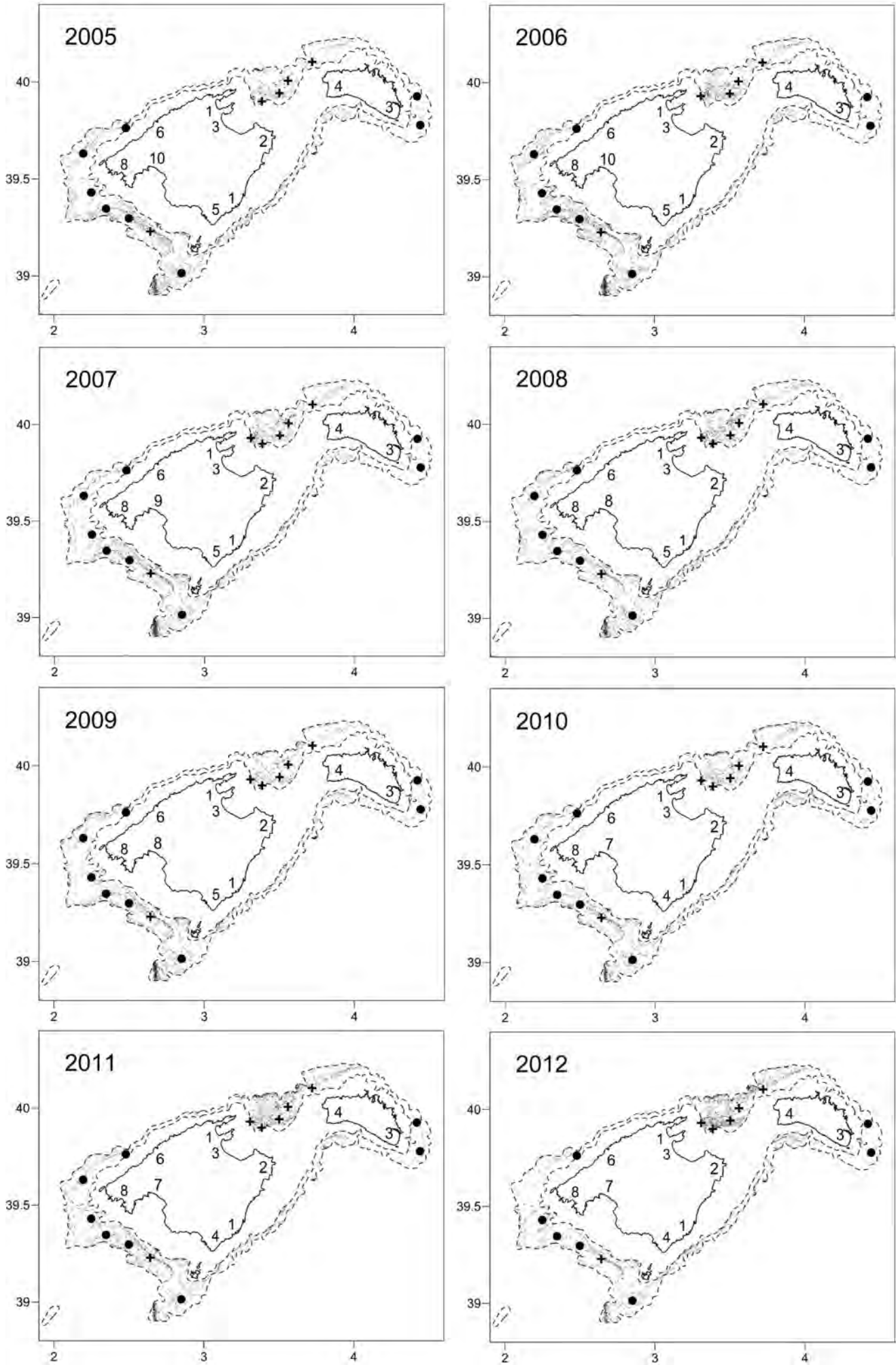


Figure 5.2: Vessel Monitoring by satellite System (VMS) signals and number of boats by port of the bottom trawl fleet of the Balearic Islands during the period 2005-2012. Stations corresponding to the high and low levels of fishing impact (black crosses and black dots, respectively) are displayed. The isobaths represent 100 and 400 m depth.

5.2.3.2 ‘Traditional’ diversity indices

The ‘traditional’ diversity indices analysed were: (i) Species richness (S), defined as the number of species in each sample; (ii) Shannon’s H' ; (iii) Pielou’s evenness J' ; (iv) Margalef’s d ; and (v) Simpson’s $1 - \lambda'$. See Chapter 3 (Section 3.2; Table 3.1) for more details on the calculation of ‘traditional’ diversity indices.

5.2.3.3 Differences between fishing levels throughout the time series

The mean values of all the indices analysed were compared between HLFi and LLFi for each year of the time series using a Student-t test. The p-values were corrected for multiple comparisons using the Bonferroni method. Moreover, for each index, a two-way ANOVA including year and fishing impact level was used to test for the significance of these two factors and their interaction, in the variation of these indices. A significant interaction indicates a different pattern of the mean values of the diversity indices throughout the years depending on fishing impact level.

5.2.4 Driving factors

The fishing effort on the deep shelf and the environmental variability were investigated as possible driving factors explaining the fluctuations observed in the diversity indices.

The fishing effort was computed from the official daily sale bills by boat, supplied by the fishermen association from Mallorca, after assigning them a daily fishing strategy (i.e. the bathymetric stratum exploited: shallow shelf, deep shelf, upper slope and middle slope), for the period 2003-2013, using the discriminant analysis as described in Palmer et al. (2009).

The variables used to study the environmental driving factors were two climatic indices. The IDEA index, is a mesoscale index for the western Mediterranean related to the formation of WIW that affects the regional circulation in the Balearic Islands in spring-summer (Monserrat et al., 2008). The EA is a global climatic model of the atmospheric circulation in the Atlantic that explains the winter (December, January and February) temperature variability in the western Mediterranean (Ulbrich et al., 2012).

In order to study the connection between the driving factors and the diversity indices, the annual fishing effort on the deep shelf and the values of climatic indices affecting the area of study were cross-correlated to those diversity indices with significant differences in their mean annual values. Only lags corresponding to 0, 1 and 2 years were considered because of the short length of the time series analysed (11 years).

5.3 Results

5.3.1 N_{90}

The time series of N_{90} showed that the mean value of number of species in HLFi ranged between 4.40 and 9.00 species, in 2005 and 2008, respectively, whereas in LLFi it ranged between 6.88 and 11.63 species, in 2013 and 2009, respectively (Figure 5.3).

For all the years of the time series analysed except for 2013, N_{90} showed significant differences between HLF and LLFI, the latter showing always the highest number of species (Table 5.2; Figure 5.3). Before 2013, mean values in the LLFI group did not show any temporal trend throughout the time series analysed, whereas in the HLF group, a clear reduction in the number of species occurred between 2004 and 2006, recovering in 2007 with no further clear changes in the rest of the time series (Figure 5.3). In the year 2013, both HLF and LLFI showed a decrease in the number of species, more pronounced in the case of LLFI (Figure 5.3).

The two-way ANOVA showed significant differences in N_{90} for both year and fishing impact level factors and a significant interaction between them (Table 5.3), indicating that HLF and LLFI had a different pattern of mean values of N_{90} depending on the year (Figure 5.3).

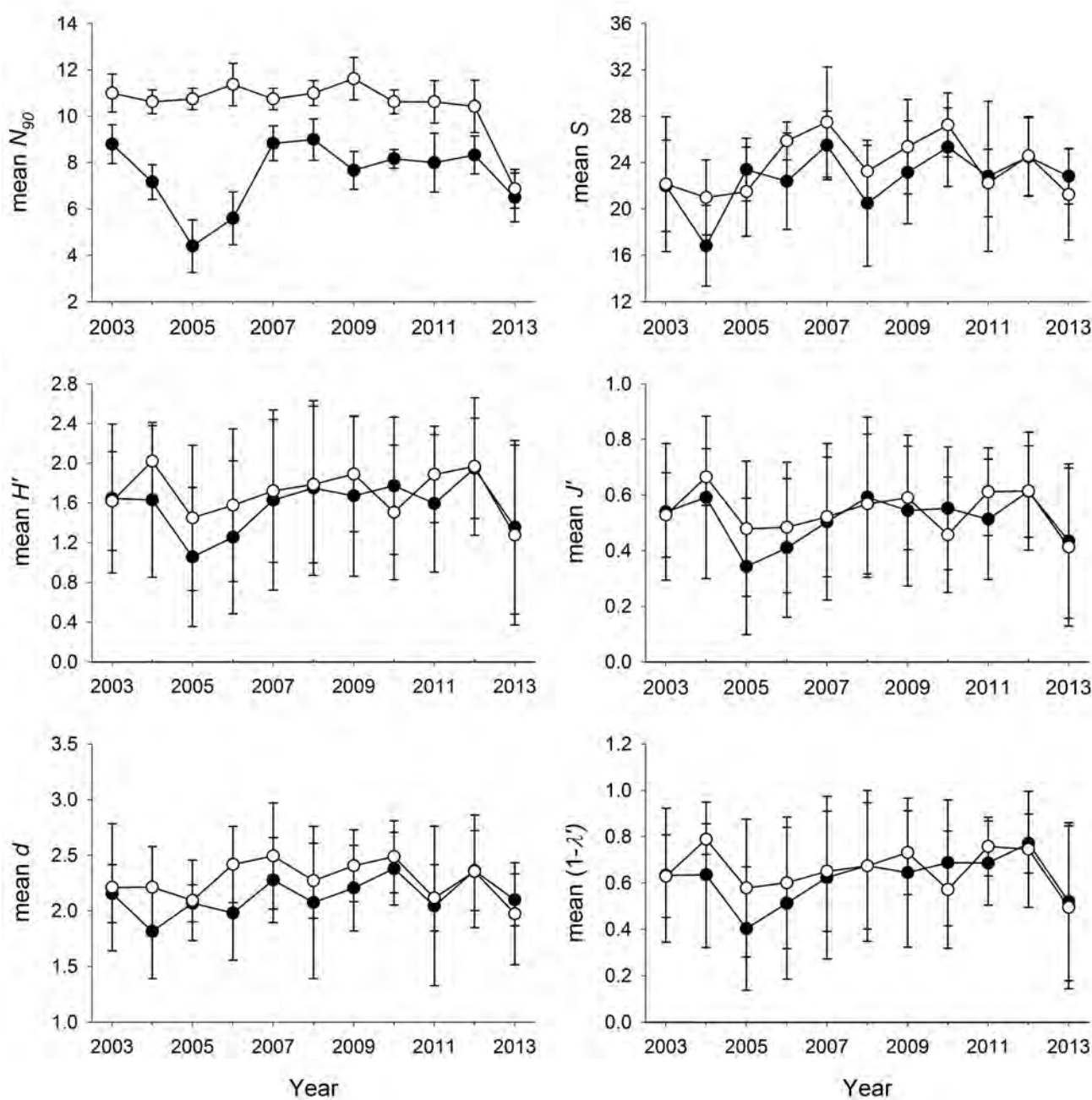


Figure 5.3: Annual mean values and standard deviation of the diversity indices analysed (N_{90} , S , H' , J' , d and $1-\lambda'$) during the period 2003-2013. Black dots: high level of fishing impact; white dots: low level of fishing impact.

Table 5.2: t-Test values comparing high and low levels of fishing impact of the N_{90} , S , H' , J' , d and $1 - \lambda'$ diversity indices. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$. p-values adjusted with the Bonferroni method.

Index	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013
N_{90}	-4.56 *	-10.22 ***	-14.27 ***	-10.01 ***	-5.91 ***	-5.24 **	-8.37 ***	-9.58 ***	-4.52 **	-3.76 *	-0.75
S	-0.05	-2.30	0.96	-2.15	-0.90	-1.30	-0.97	-1.17	0.23	-0.04	0.87
H'	0.07	-1.26	-0.96	-0.73	-0.21	-0.08	-0.60	0.72	-0.93	-0.05	0.16
J'	0.10	-0.66	-0.97	-0.54	-0.13	0.17	-0.38	0.83	-0.99	-0.01	0.14
d	-0.20	-1.88	-0.15	-2.05	-0.91	-0.71	-1.06	-0.62	-0.26	0.03	0.60
$1 - \lambda'$	0.03	-1.37	-1.07	-0.52	-0.17	0.00	-0.64	0.82	-0.87	0.22	0.13

Table 5.3: Results of the two-way Analysis of variance (ANOVA) testing the effects of year, fishing impact (FI), and the interaction between both factors in the variation of each of the diversity indices analysed (N_{90} , S , H' , J' , d and $1 - \lambda'$). df and MS are the degrees of freedom and mean square values, respectively. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$.

Factor	df	N_{90}			S			H'			J'			d			$1 - \lambda'$		
		MS	F	p	MS	F	p	MS	F	p	MS	F	p	MS	F	p	MS	F	p
Year	10	14.36	20.31	***	65.15	4.44	***	0.63	1.24	0.27	0.07	1.36	0.21	0.29	1.69	0.09	0.10	1.43	0.17
FI	1	330.68	467.72	***	47.96	3.27	0.07	0.58	1.12	0.29	0.03	0.49	0.48	0.75	4.32	*	0.06	0.80	0.37
Year*FI	10	9.91	14.01	***	13.62	0.93	0.51	0.15	0.30	0.98	0.01	0.28	0.99	0.09	0.54	0.86	0.02	0.35	0.97
Error	127	0.71			14.67			0.51			0.05			0.17			0.07		

SIMPER summary tables showed that the species ranking first in terms of contribution to the total similarity vary depending on the year (Table 5.4). Within HLFi these species were, *M. merluccius*, *Serranus hepatus* and *Glossanodon leioglossus*, whereas in LLFI they were *Lepidotrigla cavillone*, *Capros aper*, *Chelidonichthys cuculus* and *G. leioglossus*. Species like *Citharus linguatula* and *Trisopterus minutus* only appeared as contributors to N_{90} in HLFi, whereas *Denteltosteus quadrimaculatus*, *Mullus surmuletus*, and *Raja clavata* appeared only in LLFI. The only year in which the most important species in terms of within-group similarity was the same for both HLFi and LLFI was 2005, with *G. leioglossus*. However, the contribution of the species to the similarity was higher in HLFi (68%) than in LLFI (19%; Table 5.4). The only shark species, *Scyliorhinus canicula*, appeared in N_{90} in all the years of the time series for LLFI. In the case of HLFi, *S. canicula* disappeared after the first year of the period of N_{90} low values (2004-2006) and appeared again the year of the recovery (i.e. 2007), being found in the rest of the time series (Table 5.4; Figure 5.3).

5.3.2 ‘Traditional’ diversity indices

The time series of mean values of S showed that the number of species in HLFi ranged between 16.83 and 25.50, in 2004 and 2007, respectively, whereas in LLFI it ranged between 21.00 and 27.50, in 2004 and 2007, respectively (Figure 5.3). The mean values of H' in HLFi ranged between 1.06 and 1.95, in 2005 and 2012, respectively, whereas in LLFI values ranged between 1.28 and 2.02, in 2013 and 2004, respectively (Figure 5.3). The mean values of J' in HLFi ranged between 0.34 and 0.61, in 2005 and 2012, respectively, whereas in LLFI values ranged between 0.41 and 0.66, in 2013 and 2004, respectively (Figure 5.3). The mean values of d in HLFi ranged between 1.82 and 2.38, in 2004 and 2010, respectively, whereas in LLFI values ranged between 1.98 in 2013 and 2.49 in 2007 and 2010 (Figure 5.3). The time series of $1 - \lambda'$ showed mean values in HLFi ranging between 0.40 and 0.77, in 2005 and 2012, respectively, whereas in

LLFI values ranged between 0.50 and 0.79 in 2013 and in 2004, respectively (Figure 5.3).

Table 5.4: Similarity Percentage (SIMPER) analysis summary table of species appearing in the 90% cutoff of within-group similarity. A is the mean abundance (individuals/km²) of each species, and %C is the percentage contribution of each species to within-group similarity. Sim is the within-group similarity by year and high or low level of fishing impact (HLFI and LLFI, respectively).

A			%C		
2003 HLFI; mean Sim = 20.15%			2003 LLFI; mean Sim = 16.74%		
<i>Merluccius merluccius</i>	867	16	<i>Lepidotrigla cavillone</i>	997	21
<i>Capros aper</i>	2713	16	<i>Macroramphosus scolopax</i>	2025	16
<i>Macroramphosus scolopax</i>	1026	15	<i>Serranus hepatus</i>	894	12
<i>Serranus hepatus</i>	1422	13	<i>Chelidonichthys cuculus</i>	1367	9
<i>Scyliorhinus canicula</i>	972	12	<i>Scyliorhinus canicula</i>	996	8
<i>Lepidotrigla cavillone</i>	1156	8	<i>Capros aper</i>	2897	7
<i>Trisopterus minutus</i>	301	5	<i>Trachinus draco</i>	199	5
<i>Chelidonichthys cuculus</i>	384	3	<i>Serranus cabrilla</i>	316	4
<i>Arnoglossus rueppelii</i>	111	3	<i>Mullus surmuletus</i>	3821	3
			<i>Arnoglossus rueppelii</i>	517	3
			<i>Merluccius merluccius</i>	195	3
2004 HLFI; mean Sim = 25.13%			2004 LLFI; mean Sim = 25.29%		
<i>Merluccius merluccius</i>	1388	36	<i>Capros aper</i>	1358	19
<i>Scyliorhinus canicula</i>	536	16	<i>Scyliorhinus canicula</i>	1051	18
<i>Lepidotrigla cavillone</i>	518	16	<i>Merluccius merluccius</i>	589	12
<i>Serranus hepatus</i>	204	7	<i>Lepidotrigla cavillone</i>	1175	7
<i>Trisopterus minutus</i>	213	5	<i>Chelidonichthys cuculus</i>	486	7
<i>Mullus barbatus</i>	612	5	<i>Macroramphosus scolopax</i>	865	7
<i>Trachinus draco</i>	77	3	<i>Mullus surmuletus</i>	249	6
<i>Capros aper</i>	220	3	<i>Trachinus draco</i>	333	4
			<i>Mullus barbatus</i>	803	4
			<i>Arnoglossus rueppelii</i>	170	3
			<i>Raja clavata</i>	171	3
2005 HLFI; mean Sim = 25.82%			2005 LLFI; mean Sim = 14.46%		
<i>Glossanodon leioglossus</i>	52876	68	<i>Glossanodon leioglossus</i>	44907	19
<i>Merluccius merluccius</i>	2851	10	<i>Lepidotrigla cavillone</i>	735	11
<i>Trisopterus minutus</i>	9138	8	<i>Capros aper</i>	1262	11
<i>Serranus hepatus</i>	1814	6	<i>Scyliorhinus canicula</i>	840	10
			<i>Merluccius merluccius</i>	543	9
			<i>Chelidonichthys cuculus</i>	1036	9
			<i>Serranus hepatus</i>	821	8
			<i>Macroramphosus scolopax</i>	1178	5
			<i>Raja clavata</i>	185	3
			<i>Trachinus draco</i>	130	3
			<i>Arnoglossus rueppelii</i>	240	2
2006 HLFI; mean Sim = 21.73%			2006 LLFI; mean Sim = 19.61%		
<i>Merluccius merluccius</i>	6762	46	<i>Glossanodon leioglossus</i>	47622	24
<i>Trisopterus minutus</i>	2425	18	<i>Capros aper</i>	7288	19
<i>Serranus hepatus</i>	2791	12	<i>Merluccius merluccius</i>	1268	8
<i>Lepidotrigla cavillone</i>	2382	9	<i>Chelidonichthys cuculus</i>	1694	7
<i>Glossanodon leioglossus</i>	202568	4	<i>Deltentosteus quadrimaculatus</i>	920	7
<i>Trachinus draco</i>	475	2	<i>Scyliorhinus canicula</i>	1034	6
			<i>Lepidotrigla cavillone</i>	793	6
			<i>Serranus hepatus</i>	1015	5
			<i>Mullus barbatus</i>	305	3
			<i>Mullus surmuletus</i>	431	3
			<i>Trachinus draco</i>	288	3
			<i>Arnoglossus rueppelii</i>	525	3
2007 HLFI; mean Sim = 26.90%			2007 LLFI; mean Sim = 24.10%		
<i>Serranus hepatus</i>	4448	31	<i>Chelidonichthys cuculus</i>	3650	17
<i>Lepidotrigla cavillone</i>	2454	16	<i>Capros aper</i>	20190	15
<i>Merluccius merluccius</i>	4076	16	<i>Deltentosteus quadrimaculatus</i>	1798	11
<i>Trisopterus minutus</i>	1865	10	<i>Lepidotrigla cavillone</i>	2064	11
<i>Glossanodon leioglossus</i>	166569	5	<i>Glossanodon leioglossus</i>	27166	9
<i>Chelidonichthys cuculus</i>	1369	4	<i>Serranus hepatus</i>	1803	8
<i>Trachinus draco</i>	1581	3	<i>Merluccius merluccius</i>	1055	7
<i>Capros aper</i>	2378	3	<i>Scyliorhinus canicula</i>	1112	4
<i>Scyliorhinus canicula</i>	783	3	<i>Macroramphosus scolopax</i>	1168	4
			<i>Mullus surmuletus</i>	4420	3
			<i>Arnoglossus rueppelii</i>	308	2

Table 5.4: Similarity Percentage (SIMPER) analysis summary table of species appearing in the 90% cutoff of within-group similarity. A is the mean abundance (individuals/km²) of each species, and %C is the percentage contribution of each species to within-group similarity. Sim is the within-group similarity by year and high or low level of fishing impact (HLFI and LLFI, respectively).

	A	%C		A	%C
2008 HLFI; mean Sim = 19.40%			2008 LLFI; mean Sim = 19.43%		
<i>Serranus hepatus</i>	543	25	<i>Capros aper</i>	10372	25
<i>Merluccius merluccius</i>	536	16	<i>Scyliorhinus canicula</i>	1097	13
<i>Scyliorhinus canicula</i>	865	15	<i>Lepidotrigla cavillone</i>	711	13
<i>Lepidotrigla cavillone</i>	720	11	<i>Chelidonichthys cuculus</i>	1544	8
<i>Trachinus draco</i>	402	8	<i>Serranus hepatus</i>	261	7
<i>Trisopterus minutus</i>	593	5	<i>Trachinus draco</i>	287	6
<i>Mullus barbatus</i>	610	3	<i>Merluccius merluccius</i>	413	5
<i>Chelidonichthys cuculus</i>	260	3	<i>Mullus barbatus</i>	440	4
<i>Capros aper</i>	1770	3	<i>Deltentosteus quadrimaculatus</i>	1086	4
<i>Serranus cabrilla</i>	136	3	<i>Mullus surmuletus</i>	1816	3
			<i>Macroramphosus scolopax</i>	2394	3
2009 HLFI; mean Sim = 26.96%			2009 LLFI; mean Sim = 24.55%		
<i>Serranus hepatus</i>	1636	27	<i>Lepidotrigla cavillone</i>	1847	19
<i>Merluccius merluccius</i>	5517	22	<i>Chelidonichthys cuculus</i>	2025	18
<i>Lepidotrigla cavillone</i>	1737	16	<i>Merluccius merluccius</i>	1411	11
<i>Scyliorhinus canicula</i>	1553	11	<i>Scyliorhinus canicula</i>	1743	10
<i>Capros aper</i>	1398	6	<i>Serranus hepatus</i>	962	9
<i>Trachinus draco</i>	503	4	<i>Mullus surmuletus</i>	929	6
<i>Chelidonichthys cuculus</i>	659	3	<i>Deltentosteus quadrimaculatus</i>	625	5
<i>Trisopterus minutus</i>	242	2	<i>Capros aper</i>	1606	4
			<i>Trachinus draco</i>	673	3
			<i>Arnoglossus rueppelii</i>	197	3
			<i>Glossanodon leioglossus</i>	28011	2
			<i>Raja clavata</i>	161	2
2010 HLFI; mean Sim = 28.08%			2010 LLFI; mean Sim = 19.59%		
<i>Serranus hepatus</i>	3360	36	<i>Chelidonichthys cuculus</i>	4030	27
<i>Merluccius merluccius</i>	4127	15	<i>Glossanodon leioglossus</i>	21281	11
<i>Lepidotrigla cavillone</i>	1251	9	<i>Serranus hepatus</i>	1711	10
<i>Scyliorhinus canicula</i>	1689	8	<i>Lepidotrigla cavillone</i>	1607	9
<i>Chelidonichthys cuculus</i>	1706	8	<i>Scyliorhinus canicula</i>	1619	9
<i>Glossanodon leioglossus</i>	42597	7	<i>Capros aper</i>	12826	8
<i>Capros aper</i>	1656	4	<i>Merluccius merluccius</i>	764	5
<i>Trachinus draco</i>	474	2	<i>Mullus surmuletus</i>	828	4
<i>Trisopterus minutus</i>	362	2	<i>Deltentosteus quadrimaculatus</i>	2636	4
			<i>Trachinus draco</i>	667	3
			<i>Macroramphosus scolopax</i>	508	2
2011 HLFI; mean Sim = 17.89%			2011 LLFI; mean Sim = 28.78%		
<i>Serranus hepatus</i>	1787	20	<i>Chelidonichthys cuculus</i>	3048	24
<i>Glossanodon leioglossus</i>	72733	15	<i>Lepidotrigla cavillone</i>	1896	14
<i>Macroramphosus scolopax</i>	18368	14	<i>Capros aper</i>	10476	13
<i>Lepidotrigla cavillone</i>	1346	12	<i>Scyliorhinus canicula</i>	824	9
<i>Capros aper</i>	30906	10	<i>Macroramphosus scolopax</i>	4863	8
<i>Merluccius merluccius</i>	2375	8	<i>Serranus hepatus</i>	1015	7
<i>Scyliorhinus canicula</i>	964	6	<i>Glossanodon leioglossus</i>	7909	4
<i>Citharus linguatula</i>	281	3	<i>Mullus surmuletus</i>	509	4
			<i>Merluccius merluccius</i>	325	3
			<i>Deltentosteus quadrimaculatus</i>	794	2
			<i>Mullus barbatus</i>	331	2
2012 HLFI; mean Sim = 31.66%			2012 LLFI; mean Sim = 29.00%		
<i>Merluccius merluccius</i>	6802	33	<i>Chelidonichthys cuculus</i>	3098	20
<i>Serranus hepatus</i>	1587	15	<i>Lepidotrigla cavillone</i>	2931	18
<i>Macroramphosus scolopax</i>	1987	11	<i>Serranus hepatus</i>	1521	14
<i>Scyliorhinus canicula</i>	1624	11	<i>Scyliorhinus canicula</i>	1968	12
<i>Lepidotrigla cavillone</i>	1235	9	<i>Mullus surmuletus</i>	746	5
<i>Glossanodon leioglossus</i>	11887	7	<i>Capros aper</i>	5660	5
<i>Capros aper</i>	3394	2	<i>Merluccius merluccius</i>	670	5
<i>Citharus linguatula</i>	240	2	<i>Trachinus draco</i>	527	5
<i>Chelidonichthys cuculus</i>	513	2	<i>Deltentosteus quadrimaculatus</i>	776	3
			<i>Macroramphosus scolopax</i>	1453	2
			<i>Serranus cabrilla</i>	241	2
2013 HLFI; mean Sim = 23.56%			2013 LLFI; mean Sim = 20.44%		
<i>Merluccius merluccius</i>	8140	49	<i>Glossanodon leioglossus</i>	132945	34
<i>Serranus hepatus</i>	1594	13	<i>Chelidonichthys cuculus</i>	2452	22
<i>Glossanodon leioglossus</i>	40565	13	<i>Lepidotrigla cavillone</i>	1119	13
<i>Scyliorhinus canicula</i>	1554	6	<i>Scyliorhinus canicula</i>	1123	9
<i>Trisopterus minutus</i>	508	4	<i>Serranus hepatus</i>	1135	6
<i>Lepidotrigla cavillone</i>	552	4	<i>Merluccius merluccius</i>	555	5
<i>Chelidonichthys cuculus</i>	1068	2	<i>Capros aper</i>	2251	2

None of the ‘traditional’ diversity indices showed significant differences between HLFi and LLFi for any year of the time series analysed (Table 5.2, Figure 5.3). S and d showed a similar trend, with both HLFi and LLFi showing low values at the beginning of the time series (2003 and 2004, Figure 5.3). They increased afterwards until 2007, with oscillatory pattern until the end of the series for HLFi, and a slight decrease for LLFi in the last years, more pronounced for S (Figure 5.3). H' , J' and $1 - \lambda'$ also showed similar trends, for both HLFi and LLFi. Their mean values dropped in 2005, suffered an increase until 2007 and an oscillation afterwards around the same value obtained at the beginning of the time series, in 2003. For all these indices and both HLFi and LLFi a decrease occurred in 2013, that in the case of LLFi was the year showing the minimum mean value of the whole time series (Figure 5.3). The results of the two-way ANOVA did not show a significant interaction between year and fishing impact for any of the ‘traditional’ diversity indices. Differences between years were only significant in the case of S , whereas fishing impact level was only significant for d (Table 5.3).

5.3.3 Driving factors

The cross-correlations between time series of fishing effort on the deep shelf and annual values of N_{90} and S in both HLFi and LLFi groups did not show any correlation for any index and for any temporal lag. However, a significant correlation was detected at lag 0 when analysing the time series of both the IDEA and EA climatic indices and the mean values of N_{90} in the HLFi group (IDEA: $r = 0.628$; $p < 0.05$; EA: $r = 0.619$; $p < 0.05$) (Figure 5.4). These correlation coefficients increase to 0.648 and 0.716 for IDEA and EA, respectively, when excluding 2013. No significant correlation was observed for any other temporal lag.

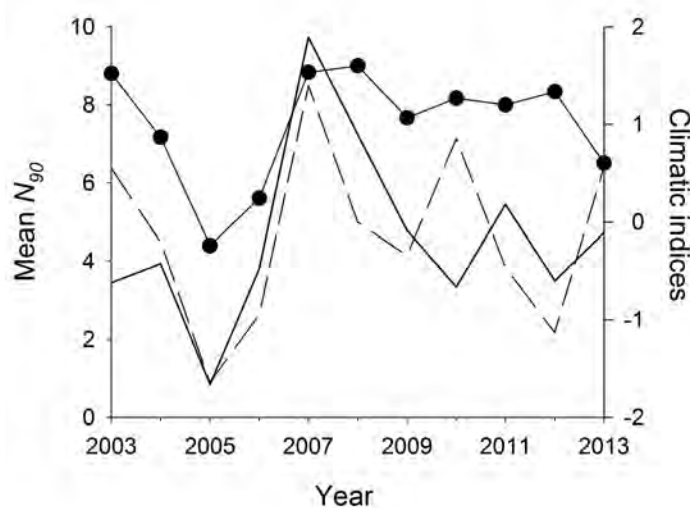


Figure 5.4: Mean values of the N_{90} and the IDEA and Eastern Atlantic pattern (EA) indices during the period 2003-2013. Black dots: annual mean values of N_{90} in the high level of fishing impact group; continuous line: values of the IDEA regional index; dashed line: mean winter values of the EA index.

5.4 Discussion

Fishing activities are reducing biodiversity of the seas worldwide (Worm et al., 2009). Among the multiple fishing techniques, bottom trawling is among the most impacting ones. Its low selectivity and damaging collateral effects on seabed communities is decreasing the presence of biogenic habitats, and leading to a reduction of the biodiversity

of exploited bottoms (Jones, 1992; Engel and Kvitek, 1998; Norse and Watling, 1999; Smith et al., 2000; Hiddink et al., 2006).

The magnitude of the effects of bottom trawling has led to compare them with those of forest clear-cutting, considered as one of major impacts on biodiversity on land (Watling and Norse, 1998). However, the impact on biodiversity is not easily monitored using indicators based on the composition of species assemblages such as ‘traditional’ diversity indices (e.g. S , H' and d , among others) because they are difficult to interpret and the effect of fishing on them is not easily predictable (Rochet and Trenkel, 2003). In fact, some attempts to monitor differences among the biodiversity of areas subjected to different fishing pressures using diversity indices have failed or even found unexpected results not easily interpretable (Bianchi et al., 2000; D’Onghia et al., 2003). Similarly, in the present study, the ‘traditional’ diversity indices analysed showed almost null sensitivity to fishing pressure, reduced inter-annual variation and high dispersion throughout the time series analysed. However, the N_{90} diversity index showed a clear response to fishing pressure, and considerable inter-annual variability in communities highly impacted by fishing.

This higher sensitivity of N_{90} , based on the outputs of species contributions to the similarity within a group of samples from a SIMPER analysis, is in agreement with the initial hypothesis of the present study: assemblages subjected to fishing impacts may see reduced the frequency of occurrence and the evenness of the distribution of species abundances due to retreatment to areas presenting the most favorable environmental conditions.

The differences found between the two levels of fishing pressure are in agreement with the negative effects of fishing on biodiversity (Norse and Watling, 1999; Pauly et al., 2002; Worm et al., 2009). However, the N_{90} diversity index was also able to detect different patterns throughout the time series depending on the level of exploitation. The samples in the low fishing pressure group showed, except for the last year of the series, higher and more stable N_{90} values than in the high fishing pressure one, whose values reached a minimum in 2005 that did not recover until 2007. This drop is coincident with the severe colder-than-normal 2004-2005 and 2005-2006 winters’ conditions in the north-western Mediterranean. Particularly the 2004-2005 winter has been considered an extreme oceanographic episode that triggered an outstanding formation of deep waters, resulting in the emergence of a thermohaline anomaly (López-Jurado et al., 2005) called Western Mediterranean Transition (CIESM, 2009). The WMDW is originated in the area of the Gulf of Lions and the Ligurian Sea, and is characterized by a minimum of temperature with values lower than 13°C. This water mass is located in the lowest part of the water column (from the bottom up to 900-1000 m depth), except in 2005 when it occupied shallower depths up to 600-700 m in the Balearic Islands, modifying the usual distribution of the water masses throughout the whole water column. Although the effect of these changes in other water masses and the whole water column has not been described yet, it is expected that changes in the distribution of water masses above WMDW (i.e. LIW, WIW and Atlantic Water) can impact the distribution of the most sensitive species within the deep shelf community.

The time series of N_{90} in the high fishing pressure group showed significant correlations with the values of the IDEA index (Monserrat et al., 2008), related to the formation of WIW (located above LIW when it appears in the system, López-Jurado et al., 2008) and the mean winter values of the EA, a climatic index that explains the

winter temperature variability in the western Mediterranean (Ulbrich et al., 2012), what will determine water masses formation. This result suggests that the N_{90} diversity index is able to reflect the response of fish assemblages to a marked change in climate and oceanographic conditions. The areas subjected to the higher fishing pressure were sensitive to environmental changes, whereas the areas with lower fishing pressure did not show this sensitivity. A lower fishing pressure may allow populations in a better state to buffer the effects of adverse environmental conditions at community level. Hence, N_{90} is not only able to detect the direct fishing effects on the mean biodiversity but also the effects of marked climate changes, at least in fishing-impacted communities with potentially increased sensitivity to adverse environmental conditions.

Several studies have shown that fishing impact can indirectly affect marine populations by increasing their sensitivity to environmental variation (Perry et al., 2010; Planque et al., 2010). Although this has been recently demonstrated for several species worldwide (Botsford et al., 2011; Rouyer et al., 2011; Botsford et al., 2014) and at the study area (Hidalgo et al., 2011; Quetglas et al., 2013), any study has still identified synergistic effects of fishing and climate at the biodiversity level. Supporting evidence of this synergy can be inferred from the summary list of species corresponding to the N_{90} value. For instance, the only shark species which appears all the years in the low fishing pressure grounds, *S. canicula*, disappeared in the high fishing pressure ones in the year of the period with the lowest value of N_{90} , 2005, and appeared again the year of the recovery, in 2007. Elasmobranchs are considered to be especially vulnerable to the impact of fishing activities (Stevens et al., 2000). *S. canicula* is among the species that did not count for N_{90} when a severe environmental change took place in coincidence with high fishing pressure. Several teleost species disappeared as well from the N_{90} diversity index during the low value period, pointing out that combined effects of fishing and a change of environment conditions did not exclusively affect the most vulnerable species. For instance, this was the case for *C. cuculus*, a species always present in the low fishing pressure group but irregularly present in the high fishing pressure scenario, which did not contribute to N_{90} in the period 2004-2006. The estate of exploitation of this species has been recently assessed in the Balearic Islands and was found to be overexploited (Ordines et al., 2014). Similarly, the same overexploitation state has been observed for *Trachinus draco*, a species found only during six years in the high fishing pressure group and absent from the N_{90} diversity index in 2005. By contrast, *M. merluccius*, a species overexploited in the area (GFCM, 2013), contributed to the N_{90} values of the high fishing pressure group every year of the time series analysed. However, the *M. merluccius*' contribution to N_{90} exclusively depends on recruits and juveniles. Moderate abundance of young hake make this species the main target among the species in the deep shelf off the Balearic Islands (Palmer et al., 2009), though highly fluctuating and sensitive to environmental variability (Massutí et al., 2008) due to its truncated demography and the high dependence upon young classes (Hidalgo et al., 2011). This suggests that both species-specific life history traits and density-dependent aggregation patterns may play an important role in its response to fishing and environmental drivers to fully understand and interpret biodiversity variation.

Although no correlation was detected between fishing effort and N_{90} nor S , there is a drop of diversity in 2013, observed not only for N_{90} and S , but for all the indices analysed. This drop could be related to the clear increasing trend of the fishing effort experienced on the deep shelf during the years 2009-2013 (Figure 5.5). This is the opposite to what occurred at the end of the last century, when the bottom trawl fleet

displaced its fishing effort towards greater depths (upper and middle slope) to exploit highly valuable decapod crustaceans (Hidalgo et al., 2009). But, as a consequence of the current economic crisis, this fleet has changed again its fishing strategy, coming back to the shelf and targeting species of lower commercial value (sold cheaper) as demersal fish and cephalopods (Figure 5.5).

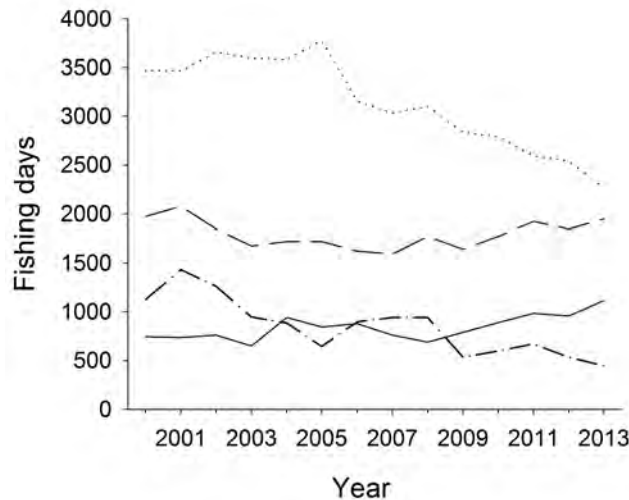


Figure 5.5: Number of fishing days of the bottom trawl fleet of the Balearic Islands operating on the shallow shelf (dashed line), deep shelf (continuous line), upper slope (dash-dotted line) and middle slope (dotted line) fishing grounds between 2000 and 2013, estimated from the analysis of daily sales bills (see Section 5.2.4).

N_{90} shows some improvements when compared to the ‘traditional’ diversity indices. The value of the N_{90} diversity index is calculated taking into account all samples, whereas the value for ‘traditional’ diversity indices is calculated at a sample level and, thus, has to be averaged if one is interested in the biodiversity of a given area/community. In this last case, two samples with completely different species composition may have similar diversity values, even more similar than if the contrary occurs. Instead, N_{90} reports the number of the most important species structuring the community and is assumed to be higher in communities with higher biodiversity, i.e. with higher number of species and individuals more evenly distributed among them. The ninety percent contribution cutoff allows excluding the species more irregularly distributed among the samples and/or whose presence does not characterize the community. It may represent a loss of information but it also minimizes the sample-size dependence affecting ‘traditional’ diversity indices (Hill, 1973; Noss, 1990; Hewitt et al., 2005; Gotelli and Chao, 2013).

The interpretability is also a major drawback for most of ‘traditional’ diversity indices (Gray, 2000; Purvis and Hector, 2000; Lamb et al., 2009; Zhao et al., 2014). This is why one of the most used diversity indices is the simplest one, S , which is simply the count of species present and has a direct interpretation of its units (Gray, 2000; Purvis and Hector, 2000). The interpretability of N_{90} is also straightforward as it has the same units as S , number of species. Finally, whereas ‘traditional’ diversity indices loose species identity making difficult to distinguish whether changes in biodiversity are related to specific species or to community composition (Lamb et al., 2009; Zhao et al., 2014), the N_{90} value is provided with a list of contributing species. This allows a traceability of species turnover and may be relevant to monitor the spreading of non-indigenous species (Galil, 2007; Lamb et al., 2009), a global phenomenon that is especially important in the Mediterranean (Galil, 2007; Golani and Appelbaum-Golani, 2010). The application of the N_{90} diversity index to the case study showed that it may

be an alternative to ‘traditional’ diversity indices when trying to monitor fishing impacts and the effects of environmental changes. The study shows that this novel index is likely to provide new knowledge, even for highly well-studied communities and systems, of high impact and relevance for management purposes. Particularly, it may improve the communication to managing organisms and stakeholders due to a better interpretability of the diversity metrics and its temporal and spatial patterns.

Chapter 6

RESULTS 3. BALEARIC ISLANDS

Bottom trawl impacts on Mediterranean demersal fish diversity: not so obvious or are we too late?



Chapter 6. Results 3. Bottom trawl impacts on Mediterranean demersal fish diversity: not so obvious or are we too late?

SUMMARY

Measures of biodiversity change may be useful as indicators if they are responsive to manageable drivers of biodiversity loss. However, there are many candidate indicators that are considered to be robust to survey artifacts and sensitive to manageable impacts. Using extensive survey data on demersal fish assemblages around the Balearic Islands (western Mediterranean) we analyse relationships among ‘traditional’, taxonomic and functional diversity indices, to identify a minimum set of indices that provide a good representation of the different aspects of diversity. Secondly we model the responses of the demersal fish community diversity to bottom trawl fishing pressure. To do so, we used two different approaches: (i) considering fishing effort and depth as continuous explanatory variables; and (ii) grouping samples according to bathymetric sampling strata and contrasting levels of fishing effort. The results show that diversity can be described using different complementary aspects such as species richness, evenness, and the taxonomic and functional breadth of the species present in a given community, displaying different responses to fishing pressure. However, the changes in diversity in response to fishing may only be detectable in those communities where the levels of fishing pressure have remained relatively low. When communities have been exposed to high levels of fishing pressure for a long period, the relevant changes in diversity may have happened long before the onset of monitoring of the fishery, and hence it may be too late to detect differences between levels of fishing effort. This seems to be the case on the middle slope of the Balearic Islands, where vulnerable species have disappeared or are very infrequent, and have been replaced by species better adapted to fishing impacts.

6.1 Introduction

Within the context of the EAF (Pikitch et al., 2004), indicators of biodiversity are needed to assess fisheries and to monitor progress, in relation to management objectives, particularly those related to the integration of concerns about environmental and anthropogenic impacts (Balmford et al., 2005; Garcia and Cochrane, 2005; Rice and Rochet, 2005; Sutherland et al., 2006). However, there are many candidate indicators that are thought to be robust to survey artifacts such as sampling methods and measurement uncertainty, and yet sensitive to manageable impacts such as fishing or pollution (Rice, 2003; Fulton et al., 2005).

‘Traditional’ diversity measures, like species richness (S), Shannon (H') or Pielou’s evenness (J'), measure the number of objects (species, taxa), reflect the relative abundances of objects within samples (dominance, evenness), or attempt to combine the two, and they assume that all species are equally important (Magurran, 2004; Mouchet et al., 2010). An alternative type of diversity index N_{90} was described in Chapter 4. It is based on SIMPER analysis (Clarke, 1993) and is defined as the mean number of species contributing up to 90% of within-group similarity in a group of samples. In Chapter 5 it was considered to be more sensitive to the synergistic effects of fishing impact and

environmental variability than the ‘traditional’ diversity indices.

Considering that the relationships among species could provide additional information, taxonomic diversity indices were developed which reflect the relatedness among taxa in samples (Warwick and Clarke, 1995; Clarke and Warwick, 1998, 2001). These give complementary information to ‘traditional’ diversity indices (Warwick and Clarke, 2001; Leonard et al., 2006). More recently interest has grown in indices which reflect the functional composition of assemblages in some way. Although there is no standard methodology for their calculation, they generally use information about the biological and functional traits of species identified in samples to inform about how the overall assemblage may ecologically function (e.g. Tilman et al., 1997; Petchey and Gaston, 2002; Villéger et al., 2008; Laliberté and Legendre, 2010). Somerfield et al. (2008) describe how the relatedness indices of Warwick and Clarke (1995) may be adapted to give information about how the average functional breadth of a community may vary.

Several studies have addressed patterns in the diversity of fishes in the Mediterranean based on field surveys, the majority of them analysing bathymetric patterns (Stefanescu et al., 1993; Moranta et al., 1998; Kallianiotis et al., 2000; Mérigot et al., 2007a, 2007b; Ordines et al., 2011), some analysing spatial patterns (Gaertner et al., 2007, 2010, 2013; Granger et al., 2015; García-Ruiz et al., 2015; Navarro et al., 2015), but only a few studies analysing temporal patterns (Gaertner et al., 2007, 2013; Granger et al., 2015). Although habitat loss and degradation, followed by exploitation, pollution, climate change, eutrophication and species invasions, maritime traffic and aquaculture, have all been identified as conspicuous threats to marine diversity in the Mediterranean (Coll et al., 2010), trawl fishing has been identified as one of the most important factors that could impact the diversity of demersal fish assemblages (Coll et al., 2012). However, studies focused on this impact are scarce (Rochet et al., 2010; Navarro et al., 2015) and, as Granger et al. (2015) concluded, in the absence of knowledge based on data, specific modeling to analyse the effect of fishing effort on demersal fish diversity are necessary and need to be performed in forthcoming studies.

The high multispecificity of the bottom trawl fishery in the Mediterranean (Caddy, 1993; Lleonart and Maynou, 2003) highlights the importance of the use of diversity indices to study the effects of fishing on demersal communities. In this area, the Balearic Islands (western Mediterranean) represent a spot of maximum diversity (Granger et al., 2015). The marine ecosystems along the continental shelf and slope of this archipelago and their benthic and demersal communities have been subjected to regular trawl fishing since the middle of the 20th century (Oliver, 1983; Quetglas et al., 2013). Since the 1960s, when the deep-water trawl fishery started (Oliver, 1983), fishing effort has moved from the continental shelf to the slope to exploit the more-highly valued decapods crustaceans (Moranta et al., 2008b; Hidalgo et al., 2009). Thus, the middle slope has been subjected to the highest level of fishing effort in the archipelago for at least four decades. Even so, the overall activity of the trawl fishery around the Balearic Islands has historically been lower than in adjacent areas, resulting in less impacted ecosystems and target resources off the archipelago, compared to those off the Iberian Peninsula (Quetglas et al., 2012).

Using extensive survey data from the Balearic Islands, in this Chapter we analyse relationships among ‘traditional’, taxonomic and functional diversity indices to identify a minimum set of indicators that provide a good representation of changes in assemblages, taking into account the different aspects of diversity. We then model the

responses of the demersal fish community diversity to bottom trawl fishing pressure using two different approaches: (i) considering fishing effort and depth as continuous explanatory variables; and (ii) considering bathymetric sampling strata and contrasting levels of fishing effort. The second approach allows us to analyse the performance of diversity indices in defined levels of fishing effort (low, medium, high and very high). The same indices were used for both approaches, except one (N_{90}) which could only be used in the second one as this index cannot be computed at sample level but needs a set of samples within a group.

6.2 Materials and Methods

6.2.1 Data sources

6.2.1.1 Fish assemblages

Data were collected during the MEDITS. This scientific survey has been conducted annually since 2001, during late spring in the Balearic Islands, covering the soft bottoms of the continental shelf and slope between 50 and 800 m depth. According to the MEDITS protocol, four depth strata were taken into account: (i) shallow shelf from 50 to 100 m; (ii) deep shelf from 101 to 200 m; (iii) upper slope from 201 to 500 m; and (iv) middle slope from 501 to 800 m. A total of 439 hauls (around 50 per year) carried out between 2006 and 2014 were analysed (Table 6.1; Figure 6.1). In each haul, fish species were sorted and individuals were counted and weighed. Abundances of fish species were standardized to one square km, using the horizontal opening of the net and the distance covered in each haul, obtained using the SCANMAR system (Catch Control Systems, Scanmar AS, Åsgårdstrand, Norway) and GPS, respectively. Species with a markedly pelagic or mesopelagic habit were excluded from the analyses. The species included in the analyses are specified in Annex 1. For more details on the sampling strategy and protocol, and gear characteristics, see Chapter 3 (Section 3.1).

6.2.1.2 Fishing effort

For the bottom trawl fleet that operates in the Balearic Islands VMS data from 2006 to 2014 were used to model the geographic distribution of fishing effort in the area and to estimate the fishing effort by fishing ground. Once the data were filtered as explained in Chapter 3 (Section 3.3), a total of 553,526 signals were analysed to define fishing grounds of the bottom trawl fishery in the Balearic Islands (Table 6.1). Then VMS signals were assigned to a points net defined from a 0.01 degrees resolution grid using Matlab R2013a and the different fishing grounds were inferred from VMS density contours assigned at each grid point (Figure 6.1). Finally, using expert knowledge of the bottom trawl fishery in the Balearic Islands, each fishing ground was checked in order to differentiate adjacent fishing grounds and delimit fishing grounds with low densities of VMS. Once the boundary of each fishing ground had been defined, the fishing effort was calculated as the number of boat fishing trips to each fishing ground per year during the period 2006-2014. Each MEDITS sampling station was associated to a fishing ground and consequently to its fishing effort. Thus, within each fishing ground, all sampling stations were assigned the same fishing effort. The sampling stations that were not associated to a fishing ground (8, 10 and 21; Figure 6.1) were matched to the lowest fishing effort value in each depth strata.

Table 6.1: Number of samples analysed to calculate diversity indices from Mediterranean International Bottom Trawl Surveys (MEDITS) and number of signals of Vessel Monitoring by Satellite System (VMS) analysed to associate fishing effort to each sampling station by year from the Spanish Ministry of Agriculture, Food and Environment.

	2006	2007	2008	2009	2010	2011	2012	2013	2014
Samples	44	50	50	50	48	48	49	50	50
VMS	59234	57828	61649	58589	59413	62150	69744	59779	65140

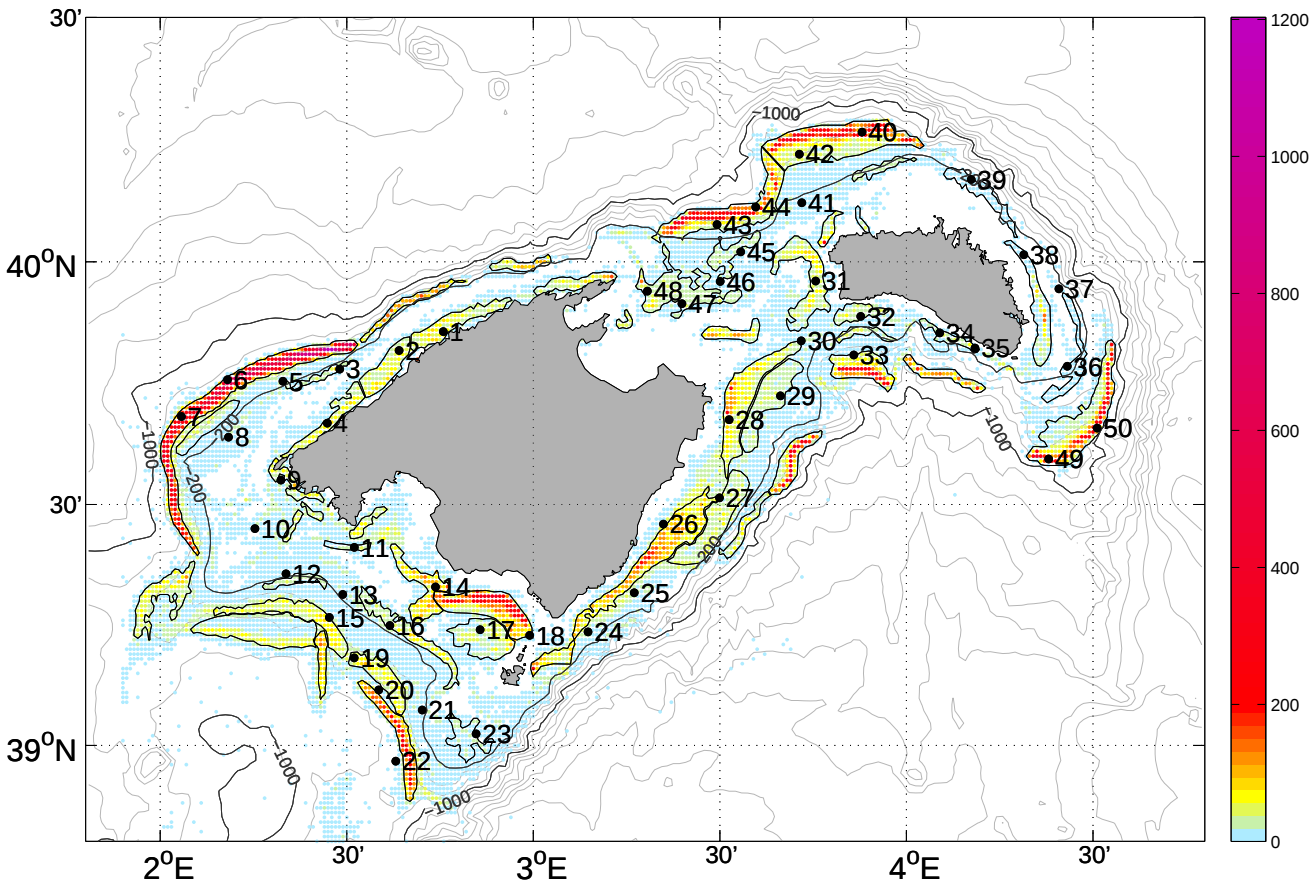


Figure 6.1: Map of the Balearic Islands, showing the Mediterranean International Bottom Trawl Surveys (MEDITS) sampling stations (black dots) and the fisheries grounds identified (black contours). The points represent the 0.01 resolution grid used to assign the Vessel Monitoring by satellite System (VMS) signals. The color bar represents the intensity of VMS signals during the period 2006-2014.

6.2.2 Data analysis

6.2.2.1 Diversity indices

Seventeen diversity indices were calculated. They all were calculated at sample level, except N_{90} that it is calculated from groups of samples (see below). ‘Traditional’ diversity measures were species richness (S), Margalef’s richness (d), Pielou’s evenness (J'), *Brillouin*, Fisher’s α (*Fisher*), Rarefaction 10 ($ES(10)$), Rarefaction 20 ($ES(20)$), Shannon’s (H'), Simpson’s ($1 - \lambda'$), and Hill’s $N1$, $N2$ and $N\infty$ diversity indices (Magurran, 2004). See Chapter 3 (Section 3.2; Table 3.1) for more details on the calculation of ‘traditional’ diversity indices.

Taxonomic diversity (Δ) and taxonomic distinctness (Δ^*) were calculated using a taxonomic hierarchy (see Annex 1) derived from World Register of Marine Species (WoRMS Editorial Board, 2015) based on six taxonomic levels: species, genera, families, orders, classes and phylum. The weights given to each level ω_{ij} are explained with more detail in Chapter 3 (Section 3.2; Table 3.1).

Following Somerfield et al. (2008), functional versions of taxonomic diversity ($F\Delta$)

and taxonomic distinctness ($F\Delta^*$) were also calculated. The resemblance matrix among species was derived from a functional traits matrix (Table 6.2). A presence/absence traits matrix was constructed using; (i) data on fish shape, mean weight and maximum length from MEDITS in the Balearic Islands; and (ii) data on reproduction from literature (Serena, 2005; Coll, 2006) and FishBase (Froese and Pauly, 2015). The measure used to define functional resemblance among species was the simple matching coefficient as specified in Chapter 3 (Section 3.2; Table 3.1).

Table 6.2: Functional traits for the fish species used to calculate functional diversity ($F\Delta$) and functional distinctness ($F\Delta^*$) indices. Species are grouped according to; (i) their reproductive characteristics as: external fertilization (EF1); external fertilization forming a mucilage (EF2); internal fertilization, egg layers (IF1); internal fertilization, viviparous or ovoviviparous (IF2); (ii) shape: Flat (F); Elongate (E); Laterally Flat (LF); Rounded (R); (iii) Mean weight: > 10 g (MW1); > 100 g (MW2); > 500 g (MW3); > 1000 g (MW1): and (iv) Maximum length: > 15 cm (MxL1); > 30 cm (MxL2); > 60 cm (MxL3); > 120 cm (MxL4). Information of shape, mean weight and maximum length from Mediterranean International Bottom Trawl Surveys (MEDITS). Information on reproduction from literature (Serena, 2005; Coll, 2006) and FishBase (Froese and Pauly, 2015)

Species	Reproduction				Shape				Mean Weigh				Maximum Length			
	EF1	EF2	IF1	IF2	F	E	LF	R	MW1	MW2	MW3	MW4	MxL1	MxL2	MxL3	MxL4
<i>Chlopsis bicolor</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0
<i>Conger conger</i>	1	0	0	0	0	1	0	0	1	1	0	0	1	1	1	1
<i>Gnathophis mystax</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0
<i>Nemichthys scolopaceus</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	1
<i>Facciolella oxyrhyncha</i>	1	0	0	0	0	1	0	0	1	1	0	0	1	1	1	0
<i>Nettastoma melanurum</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0
<i>Echelus myrus</i>	1	0	0	0	0	1	0	0	1	1	0	0	1	1	1	0
<i>Ophichthus rufus</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0
<i>Ophisurus serpens</i>	1	0	0	0	0	1	0	0	1	1	0	0	1	1	1	1
<i>Aulopus filamentosus</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Chlorophthalmus agassizi</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Evermannella balbo</i>	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Bathypterois mediterraneus</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Synodus saurus</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Hoplostethus mediterraneus</i>	1	0	0	0	0	0	1	0	1	0	0	0	1	1	0	0
<i>Gadiculus argenteus</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Micromesistius poutassou</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Trisopterus minutus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Gaidropsarus biscayensis</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Molva dypterygia</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0
<i>Coelorinchus caelorhincus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Hymenocephalus italicus</i>	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
<i>Nezumia aequalis</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Trachyrincus scabrus</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	0	0	0
<i>Merluccius merluccius</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0
<i>Gadella maraldi</i>	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Lepidion lepidion</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0
<i>Mora moro</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Phycis blennoides</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Phycis phycis</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Lophius budegassa</i>	1	0	0	0	1	0	0	0	1	1	0	0	1	1	1	0
<i>Lophius piscatorius</i>	1	0	0	0	1	0	0	0	1	1	1	0	1	1	1	0
<i>Notacanthus bonaparte</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0
<i>Polyacanthonotus rissoanus</i>	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
<i>Cataetys allenii</i>	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0
<i>Benthocometes robustus</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Ophidion barbatum</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0
<i>Ophidion rochei</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0
<i>Alepocephalus rostratus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Argentina sphyraena</i>	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
<i>Glossanodon leioglossus</i>	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
<i>Nansenia oblita</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Gymnammodytes cicereus</i>	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
<i>Blennius ocellaris</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Parablennius tentacularis</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Callanthias ruber</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Callionymus maculatus</i>	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
<i>Synchiropus phaeton</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Centrolophus niger</i>	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	0
<i>Schedophilus medusophagus</i>	1	0	0	0	0	0	0	1	1	1	1	0	1	1	1	0
<i>Cepola macrophthalmia</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0
<i>Epigonus constanciae</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Epigonus denticulatus</i>	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
<i>Epigonus telescopus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Deltentosteus collonianus</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Deltentosteus quadrimaculatus</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Lesueurigobius friesii</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Lesueurigobius sanzi</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Coris julis</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Mullus barbatus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Mullus surmuletus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0

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Species	Reproduction				Shape				Mean Weigh				Maximum Length			
	EF1	EF2	IF1	IF2	F	E	LF	R	MW1	MW2	MW3	MW4	MxL1	MxL2	MxL3	MxL4
<i>Polyprión americanum</i>	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1
<i>Anthias anthias</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Serranus cabrilla</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Serranus hepatus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Dentex dentex</i>	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	0
<i>Diplodus annularis</i>	1	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
<i>Diplodus vulgaris</i>	1	0	0	0	0	0	1	0	1	1	0	0	1	1	0	0
<i>Pagellus acarne</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Pagellus bogaraveo</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Pagellus erythrinus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Pagrus pagrus</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Spondyliósoma cantharus</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Trachinus draco</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Trachinus radiatus</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Lepidopus caudatus</i>	1	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0
<i>Uranoscopus scaber</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Melanostigma atlanticum</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Arnoglossus imperialis</i>	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0
<i>Arnoglossus laterna</i>	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Arnoglossus rueppelii</i>	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
<i>Arnoglossus thori</i>	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Bothus podas</i>	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0
<i>Citharus linguatula</i>	1	0	0	0	1	0	0	0	1	0	0	0	1	1	0	0
<i>Symphurus ligulatus</i>	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Symphurus nigrescens</i>	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Lepidorhombus boscii</i>	1	0	0	0	1	0	0	0	1	0	0	0	1	1	0	0
<i>Lepidorhombus whiagonis</i>	1	0	0	0	1	0	0	0	1	1	0	0	1	1	0	0
<i>Zeugopterus regius</i>	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
<i>Microchirus ocellatus</i>	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0
<i>Microchirus variegatus</i>	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0
<i>Monochirus hispidus</i>	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
<i>Pegusa lascaris</i>	1	0	0	0	1	0	0	0	1	1	0	0	1	1	0	0
<i>Solea vulgaris</i>	1	0	0	0	1	0	0	0	1	1	0	0	1	1	0	0
<i>Dactylopterus volitans</i>	1	0	0	0	0	0	0	1	1	1	1	0	1	1	0	0
<i>Peristedion cataphractum</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Scorpaena elongata</i>	0	1	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Scorpaena loppei</i>	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0
<i>Scorpaena notata</i>	0	1	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Scorpaena porcus</i>	0	1	0	0	0	0	0	1	1	1	0	0	1	0	0	0
<i>Scorpaena scrofa</i>	0	1	0	0	0	0	0	1	1	1	0	0	1	1	0	0
<i>Helicolenus dactylopterus</i>	0	0	1	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Chelidonichthys cuculus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Chelidonichthys lucerna</i>	1	0	0	0	0	0	0	1	1	1	0	0	1	1	1	0
<i>Chelidonichthys obscurus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Eutrigla gurnardus</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Lepidotrigla cavillone</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Lepidotrigla dieuzeidei</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
<i>Trigla lyra</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Trigloporus lastoviza</i>	1	0	0	0	0	0	0	1	1	0	0	0	1	1	0	0
<i>Syngnathus acus</i>	0	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0
<i>Zeus faber</i>	1	0	0	0	0	0	1	0	1	1	0	0	1	1	1	0
<i>Galeus melastomus</i>	0	0	1	0	0	0	0	1	1	1	0	0	1	1	1	0
<i>Scyliorhinus canicula</i>	0	0	1	0	0	0	0	1	1	1	0	0	1	1	1	0
<i>Mustelus asterias</i>	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	1
<i>Mustelus mustelus</i>	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	1
<i>Dasyatis centroura</i>	0	0	0	1	1	0	0	0	1	1	1	1	1	1	1	1
<i>Dasyatis pastinaca</i>	0	0	0	1	1	0	0	0	1	1	1	1	1	1	1	0
<i>Myliobatis aquila</i>	0	0	0	1	1	0	0	0	1	1	1	1	1	1	1	1
<i>Dipturus oxyrinchus</i>	0	0	1	0	1	0	0	0	1	1	1	0	1	1	1	1
<i>Leucoraja circularis</i>	0	0	1	0	1	0	0	0	1	1	1	1	1	1	1	0
<i>Leucoraja naevus</i>	0	0	1	0	1	0	0	0	1	1	0	0	1	1	1	0
<i>Raja brachyura</i>	0	0	1	0	1	0	0	0	1	1	1	1	1	1	1	0
<i>Raja clavata</i>	0	0	1	0	1	0	0	0	1	1	1	0	1	1	1	0
<i>Raja miraletus</i>	0	0	1	0	1	0	0	0	1	1	0	0	1	1	0	0
<i>Raja polystigma</i>	0	0	1	0	1	0	0	0	1	1	0	0	1	1	1	0
<i>Raja radula</i>	0	0	1	0	1	0	0	0	1	1	1	0	1	1	1	0
<i>Rostroraja alba</i>	0	0	1	0	1	0	0	0	1	1	1	1	1	1	1	1
<i>Centrophorus granulosus</i>	0	0	0	1	0	0	0	1	1	0	0	0	1	1	1	0
<i>Dalatias licha</i>	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	0
<i>Etmopterus spinax</i>	0	0	0	1	0	0	0	1	1	0	0	0	1	1	0	0
<i>Oxynotus centrina</i>	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	0
<i>Squalus blainville</i>	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	0
<i>Torpedo marmorata</i>	0	0	0	1	1	0	0	0	1	1	0	0	1	1	0	0
<i>Chimaera monstrosa</i>	0	0	1	0	0	0	0	1	1	1	1	0	1	1	0	0

The N_{90} diversity index is the mean number of species contributing up to the 90% of within-group similarity calculated from abundance data for samples assigned a priori to groups. Species contributions are calculated for each resampling in a jack-knife routine, which removes a sample each time, producing lists of contribution to similarity by species for each. The N_{90} diversity index is the mean number of species which accumulates up to 90% of within-group similarity in all the resamplings. More details on the calculation of N_{90} can be found in Chapter 4 (Section 4.2.1.1).

SIMPER analysis for each group of samples was also undertaken to see their species composition. The percentage of contribution of each species to within-group similarity was calculated as the mean value of species contributions to similarity taking all jack-knives made by group of samples into account.

All diversity measures were calculated using PRIMER 7 (Clarke et al., 2014), except N_{90} which was calculated using the with the N90 script included in Chapter 4 (Supplementary data).

6.2.2.2 Relationships among diversity indices

The relationships among diversity indices calculated using sample data were quantified using the coefficient of determination (R^2) between the indices. This measure was preferred to correlation as it accounts for positive and negative relationships. Relationships among indices were visualized by hierarchical agglomerative clustering with group-average linkage. N_{90} was not included in this analysis, because it cannot be calculated from single samples.

This analysis was used to select a subset of indices to study the impact of trawling on fish diversity. One index corresponding to each group detected in the cluster analysis was selected. When several indices gave similar information, the simplest and most meaningful index was chosen (Mérigot et al., 2007b).

6.2.2.3 Trawling impacts on fish diversity

Two different approaches were applied. The first approach considered fishing effort as a continuous variable (number of fishing trips), while in the second it was treated as a discrete variable, taking LFE into account. This second approach allows us to analyse the performance of indicators in extreme values of fishing effort.

Continuous approach

GAM modeling (Hastie and Tibshirani, 1986) was applied to analyse the effect of fishing effort and depth, included in the models as continuous variables, on the selected demersal fish diversity indices. Sampling year was included as a factor in the models to take into account the inter-annual variability. This technique is a non-parametric regression, used to inspect the non-linear relationships between dependent (response variable: diversity indices) and explanatory (covariates: depth and fishing effort) variables. The GAM models were formulated as follows:

$$Y_i = s(\text{Depth}) + s(\text{FE}) + \text{year}$$

where Y_i are diversity indices selected from Section 6.2.2.2, and FE is the fishing effort as number of fishing trips. Minimization of both the GCV and the AIC were used to select the best model. For all models, the assumptions of variance homogeneity and normal distribution of residuals were checked and confirmed from residual plots. All GAM analysis were carried out with R using the *mgcv* library (Wood, 2004).

Stratified approach

The diversity indices selected were the same as those used in the continuous approach plus N_{90} . For this approach each sampling station was classified according to a four LFE scale established from the range of fishing effort detected in the study area. Sampling stations located in fishing grounds subjected to < 75 , $76-375$, $376-675$ and > 676 fishing trips per year were assigned to the low, medium, high and very high LFE, respectively. Analyses were done within each bathymetric strata considered in the sampling scheme (see Section 6.2.1.1), because they are coincident with the main bathymetric communities of demersal species and resources on the continental shelf and slope of the western and central Mediterranean (e.g. Massutí and Reñones, 2005; Biagi et al., 2002; Colloca et al., 2003). Sampling station 14, originally assigned to the medium LFE, was re-assigned to the high LFE because, particularly in the shallow shelf it showed a larger difference with the rest of sampling stations belonging to the medium LFE than to those in the high LFE (Figure 6.2).

A two way ANOVA was applied to test for significant effects of LFE and year on the diversity indices. In the case of the N_{90} , the values used in the two-way ANOVA were the number of species contributing up to the 90% of within-group similarity in each jack-knife done in the calculation routine of the N_{90} within each year, depth stratum and LFE. In the middle slope the calculation of N_{90} was not possible, because the number of samples per year in the very high LFE group (2 samples) was insufficient to calculate mean and standard deviation from a jack-knife routine, so the number of species which accumulates up to 90% of within-group similarity in the SIMPER analysis was used. For all indices that showed a significant interaction between year and LFE, LFE within each year were compared using Students t-test. SIMPER was used to compare the composition of communities in samples from different LFE within each depth stratum.

6.3 Results

6.3.1 Relationships among diversity indices

Cluster analysis separated four groups of diversity measures at a level of $R^2=0.45$, corresponding to a correlation of 0.67 (Figure 6.3): (i) indices that are mainly influenced by the number of species (S , d and $Fisher$); (ii) indices that are influenced by the relative abundance distribution of species ($N1$, $N2$, H' , $Brillouin$, $ES(10)$, $ES(20)$, $1 - \lambda'$, J' , Δ , N_∞ and $F\Delta$); (iii) indices that are mainly influenced by taxonomic information about the species (Δ^*); and (iv) indices that are mainly influenced by functional information about the species ($F\Delta^*$). Some indices showed high within-group correlations. This was the case of $Fisher$ and d ($R^2 \geq 0.98$) in the (i) group, and $ES(10)$, $ES(20)$, $Brillouin$, H' , $N1$ and $N2$ ($R^2 \geq 0.89$), and J' , $1 - \lambda'$ and Δ ($R^2 \geq 0.89$) in the (ii) group.

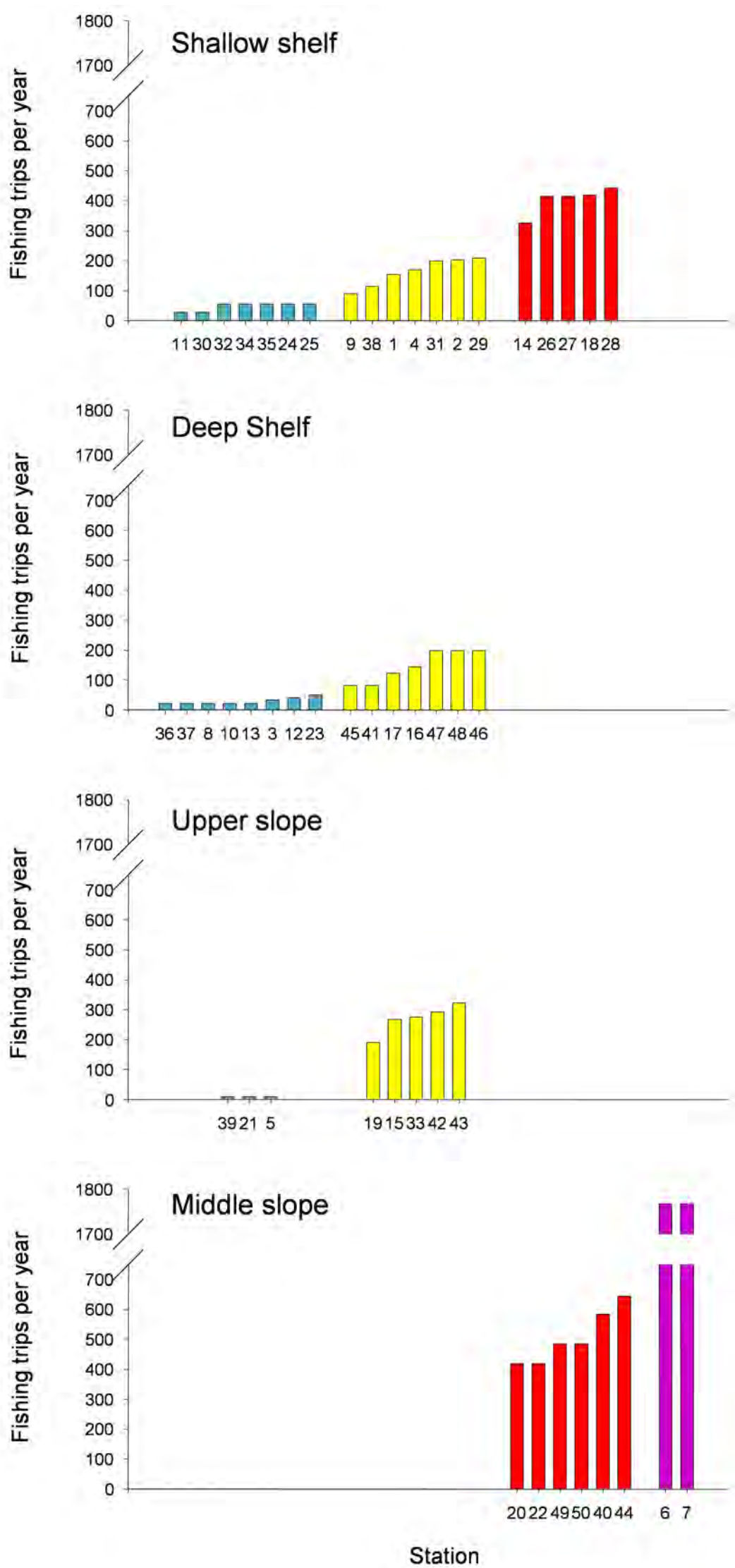


Figure 6.2: Mean annual fishing effort at each sampling station by depth strata used to the classification of each sampling station into levels of fishing effort (LFE). Blue bar: low LFE; yellow bar: medium LFE; red bar: high LFE; and purple bar: very high LFE.

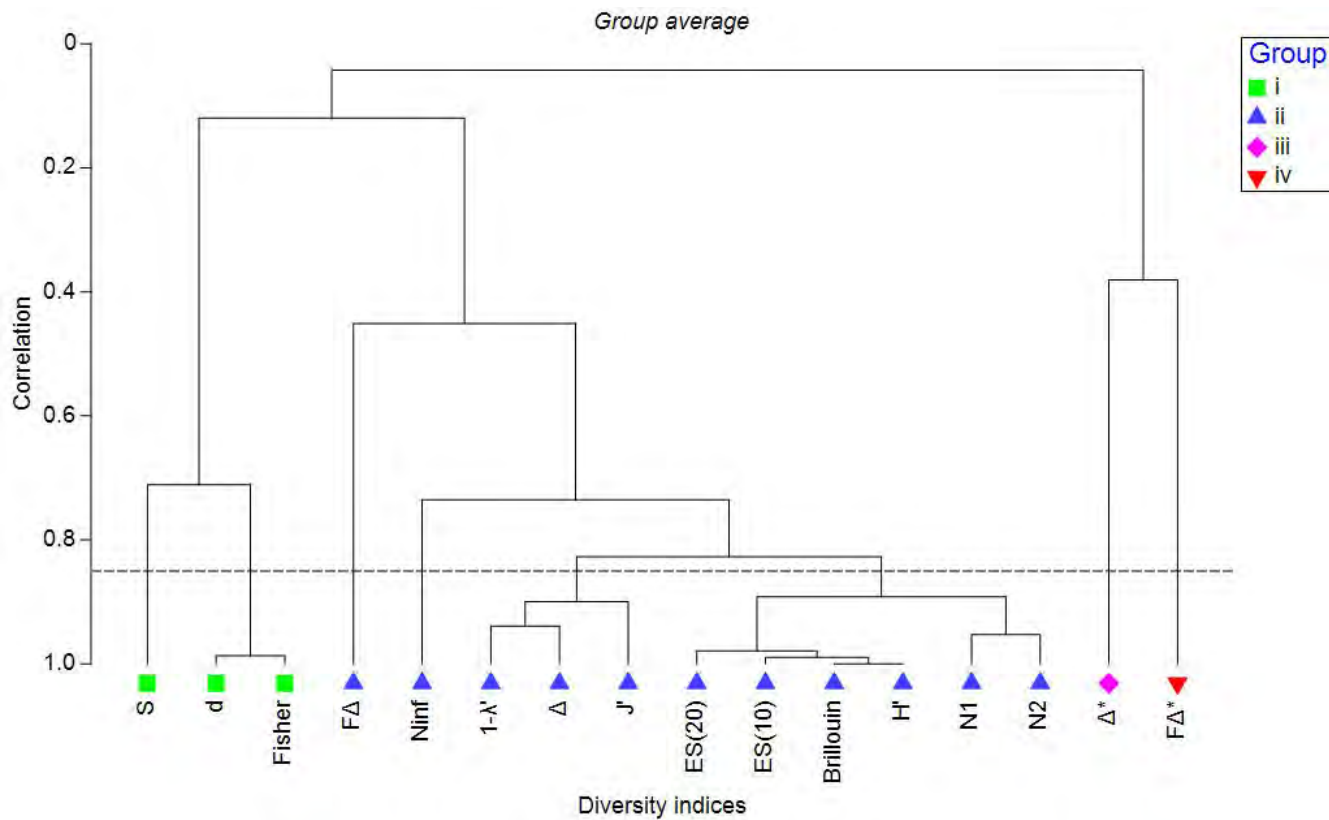


Figure 6.3: Relationships between the sixteen diversity indices analysed based on the coefficient of determination R^2 . The data used for the cluster analysis were the values of the indices for each sample during the sampling period (2006-2014). The legend shows the groups that represent complementary aspects of diversity: (i) species richness; (ii) evenness; (iii) taxonomy; and (iv) functionality. The dashed line shows the correlation level ($R^2=0.85$) used to select the diversity indices used in the analysis: S , d , J' , H' , N_∞ ($Ninf$), Δ^* , $F\Delta$ and $F\Delta^*$.

In order to simplify the analyses and considering the high correlation showed by some of the indices, only one index from each group with $R^2 \geq 0.85$ in the cluster analysis was selected. These indices were S , d , J' , H' , N_∞ , Δ^* , $F\Delta$ and $F\Delta^*$, plus the N_{90} diversity index in the case of the stratified approach.

6.3.2 Trawling impacts on fish diversity

6.3.2.1 Continuous approach

The final models for each diversity index were the most complete ones where all the covariates were significant. GCV and AIC values for final models are presented in Table 6.3. Residual plots from Generalized Additive Model (GAM) analysis showing the residuals deviation from normality for each diversity index selected from the cluster analysis are presented in Figure 6.4.

GAM modeling showed that some years had significant effect on S , d , J' , N_∞ , Δ^* and $F\Delta$ during the period under consideration (Table 6.4; Figure 6.5). All the indices were significantly influenced by the bathymetry (Table 6.4; Figure 6.5). S and d , increased from 50 to around 200 m, and then decreased to around 600 m, remaining constant to 800 m. Both J' and H' showed a similar pattern, as expected from their high correlation ($R^2 \geq 0.83$; Figure 6.3), and their values decreased from 50 to a minimum around 300 m, from where they increased to around 600 m and remained constant between 600 and 800 m. Both Δ^* and $F\Delta^*$ showed a continuous increase with depth. Fishing effort only showed a significant effect on J' , Δ^* and $F\Delta^*$ (Table 6.4; Figure 6.5). J' was positively and linearly influenced by fishing effort, whereas Δ^* and $F\Delta^*$ were negatively influenced.

Table 6.3: Results of the Generalized Cross-Validation (GCV) and the Akaike Information Criterion (AIC) of the final Generalized Additive Models (GAMs) for the diversity indices selected from the cluster analysis: S , d , J' , H' , N_∞ , Δ^* , $F\Delta$ and $F\Delta^*$. Covariates are Depth and Fishing Effort (FE). Year is included as a factor in the model. All variables shown in the model formulations were significant.

	GCV	AIC
$S = s(\text{Depth}) + \text{year}$	17.71	2516.94
$d = s(\text{Depth}) + \text{year}$	0.18	508.36
$J' = s(\text{Depth}) + s(\text{FE}) + \text{year}$	0.03	343.04
$H' = s(\text{Depth})$	0.27	671.32
$N_\infty = s(\text{Depth}) + \text{year}$	1.23	1342.25
$\Delta^* = s(\text{Depth}) + s(\text{FE}) + \text{year}$	41.21	2888.46
$F\Delta = s(\text{Depth}) + \text{year}$	24.06	2651.80
$F\Delta^* = s(\text{Depth}) + s(\text{FE})$	26.98	2702.54

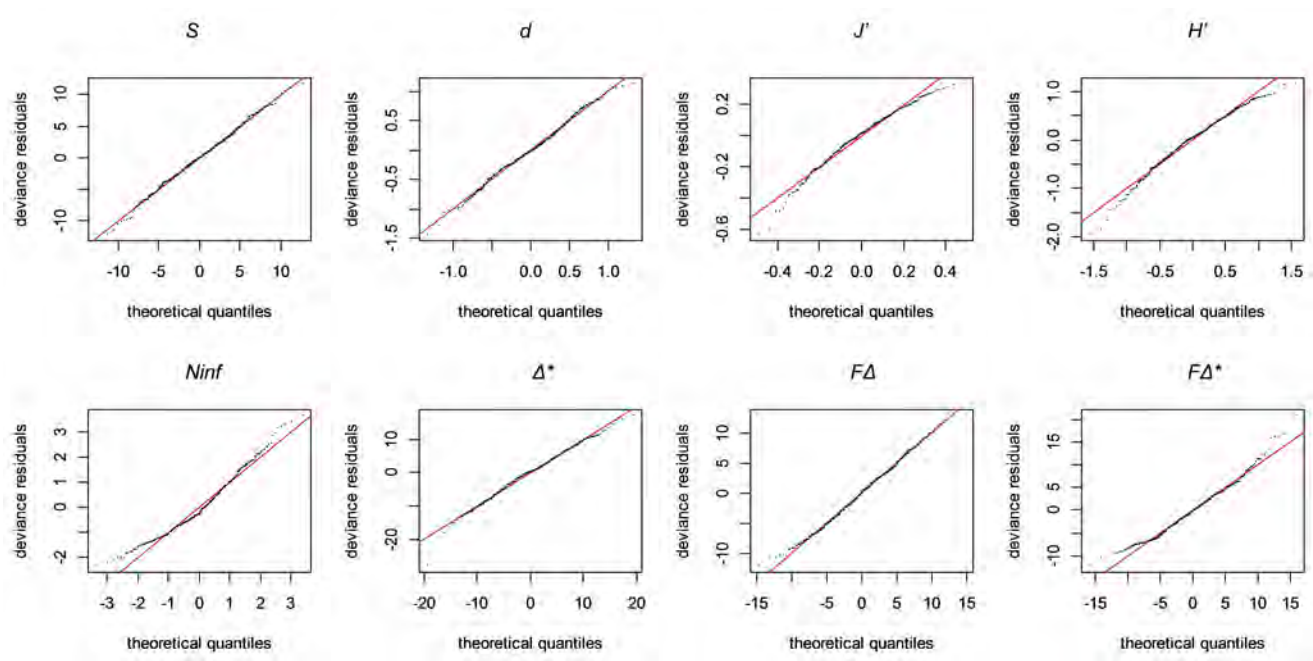


Figure 6.4: Residual plots from Generalized Additive Model (GAM) analysis showing the residuals deviation from normality for each diversity index selected from the cluster analysis (S , d , J' , H' , N_∞ ($Ninf$), Δ^* , $F\Delta$ and $F\Delta^*$).

Table 6.4: Results of Generalized Additive Model (GAM) analysis for the diversity indices selected from the cluster analysis: S , d , J' , H' , N_∞ , Δ^* , $F\Delta$ and $F\Delta^*$. Covariates are Depth and Fishing Effort. Years showing a significant effect on each variable are included. The deviance explained for the final model is also included.

	Variables			Definitive model
	Depth	Fishing effort	Year	Deviance (%)
S	***	ns	2007*, 2010*, 2013**	49.50%
d	***	ns	2010*, 2013**	21.80%
J'	***	**	2008*	41.90%
H'	***	ns	ns	28.30%
N_∞	***	ns	2008*	22.80%
Δ^*	***	**	2013*	9.71%
$F\Delta$	***	ns	2008*	19.10%
$F\Delta^*$	***	*	ns	14.90%

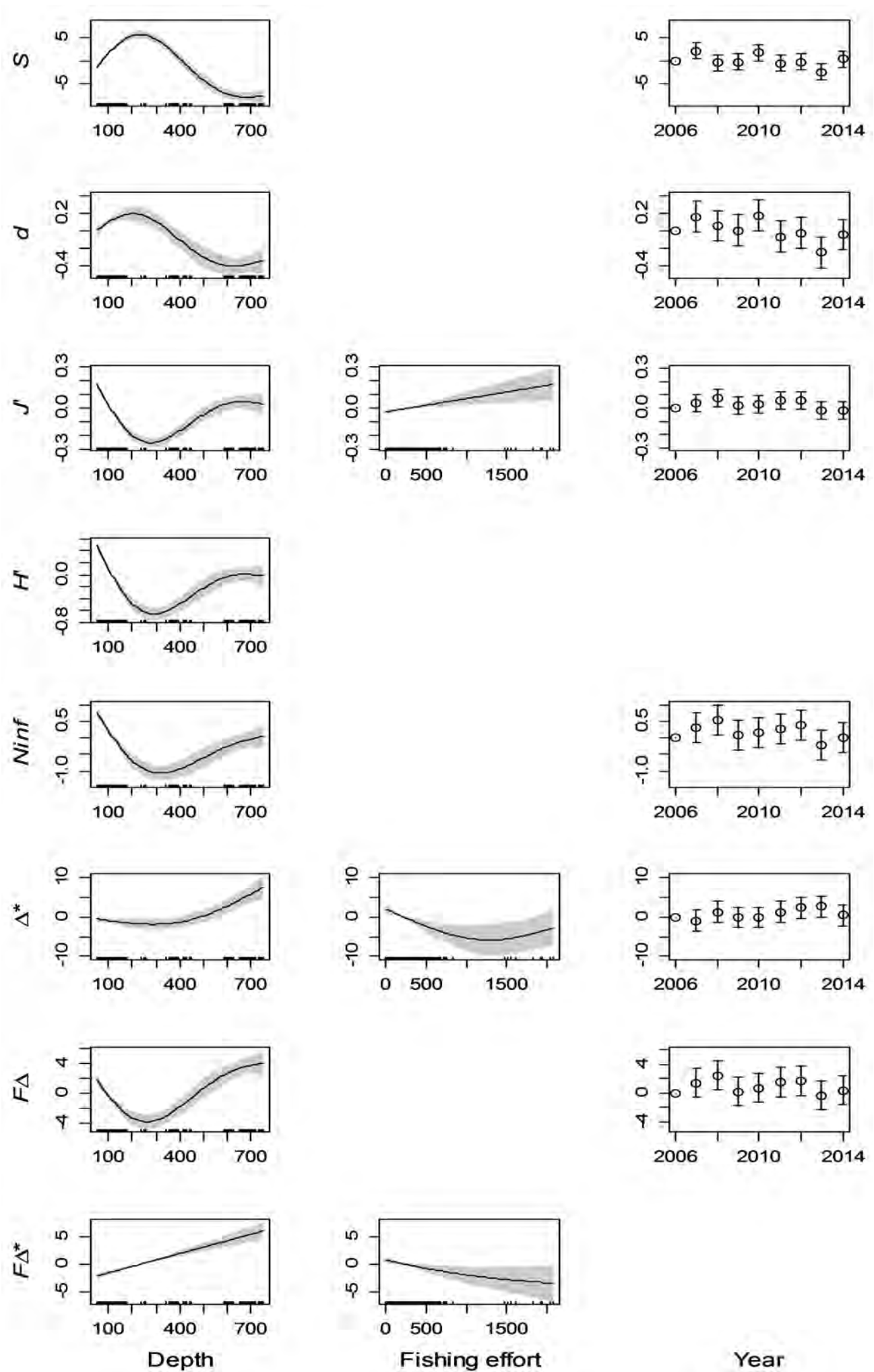


Figure 6.5: Results of Generalized Additive Model (GAM) analysis showing the responses of the diversity indices selected from the cluster analysis (S , d , J' , H' , N_{∞} (N_{inf}), Δ^* , $F\Delta$ and $F\Delta^*$) to depth and fishing effort. Responses for year factor are also presented. Shaded areas and dispersion values represent 95% confidence intervals.

6.3.2.2 Stratified approach

The two-way ANOVA showed significant inter-annual differences for S , d and N_{90} on the shallow and deep shelf, $F\Delta$ and N_{90} on the upper slope and S and d on the middle slope (Table 6.5). The LFE had a significant effect on J' and N_{90} on the shallow shelf, S , d and N_{90} on the deep shelf, S , J' , H' and $F\Delta$ on the upper slope and J' and H' on the middle slope (Table 6.5). When significant differences appeared, S , d and N_{90} showed higher values in the lower LFE of each particular bathymetric stratum, whereas contrary, J' , H' and $F\Delta$ showed higher values in the higher LFE of each particular bathymetric stratum (Figure 6.6). N_{90} was the only index showing a significant interaction between year and LFE (Table 6.5), indicating that inter-annual fluctuations do not follow the same pattern in the areas with different LFE. Despite this interaction on both the shallow and the deep shelf the values of N_{90} in the lower LFE were significantly higher than values in the higher LFE for most years (Table 6.6; Figure 6.7).

Table 6.5: Results of two-way Analysis of variance (ANOVA) testing the effects of year and level of fishing effort (LFE) and the interaction of both factors in the variation of each of the diversity indices analysed (S , d , J' , H' , N_{∞} , Δ^* , $F\Delta$, $F\Delta^*$ and N_{90}). df and MS are the degrees of freedom and mean square values, respectively. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$.

		Shallow shelf				Deep shelf				Upper slope				Middle slope			
		df	MS	F	p	df	MS	F	p	df	MS	F	p	df	MS	F	p
S	Year	8	84.55	3.57	***	8	48.30	3.22	**	8	12.97	1.45	0.20	8	17.12	2.42	*
	LFE	2	53.86	2.27	0.11	1	161.78	10.78	**	1	51.46	5.75	*	1	8.44	1.19	0.28
	Year*LFE	16	11.64	0.49	0.95	8	15.51	1.03	0.42	8	5.86	0.65	0.73	8	9.62	1.36	0.24
	Error	139	23.68			116	15.01			51	8.96			52	7.08		
d	Year	8	0.59	2.73	**	8	0.35	2.07	*	8	0.16	2.13	0.05	8	0.34	3.11	**
	LFE	2	0.15	0.71	0.50	1	1.17	6.82	*	1	0.12	1.60	0.21	1	0.02	0.14	0.71
	Year*LFE	16	0.13	0.61	0.88	8	0.16	0.95	0.48	8	0.01	0.18	0.99	8	0.21	1.87	0.09
	Error	139	0.22			116	0.17			51	0.07			52	0.11		
J'	Year	8	0.02	0.89	0.53	8	0.06	1.13	0.35	8	0.04	1.45	0.20	8	0.01	0.39	0.92
	LFE	2	0.11	5.74	**	1	0.04	0.80	0.37	1	0.21	7.44	**	1	0.23	11.15	**
	Year*LFE	16	0.01	0.63	0.86	8	0.02	0.36	0.94	8	0.03	0.89	0.54	8	0.01	0.63	0.75
	Error	139	0.02			116	0.05			51	0.03			52	0.02		
H'	Year	8	0.12	0.63	0.75	8	0.61	1.23	0.29	8	0.42	1.65	0.14	8	0.16	1.08	0.39
	LFE	2	0.59	3.07	0.05	1	0.05	0.10	0.75	1	1.61	6.33	*	1	0.99	6.68	*
	Year*LFE	16	0.14	0.75	0.74	8	0.20	0.41	0.91	8	0.21	0.82	0.59	8	0.13	0.84	0.57
	Error	139	0.19			116	0.50			51	0.25			52	0.15		
N_{∞}	Year	8	0.88	0.66	0.72	8	2.70	1.41	0.20	8	0.59	1.37	0.23	8	0.76	0.87	0.55
	LFE	2	3.58	2.70	0.07	1	0.82	0.43	0.51	1	1.61	3.73	0.06	1	3.05	3.50	0.07
	Year*LFE	16	1.19	0.89	0.58	8	0.43	0.22	0.99	8	0.27	0.63	0.75	8	1.06	1.22	0.31
	Error	139	1.33			116	1.91			51	0.43			52	0.87		
Δ^*	Year	8	95	1.62	0.12	8	18.10	1.41	0.20	8	35.12	1.08	0.39	8	29.87	0.36	0.94
	LFE	2	166	2.83	0.06	1	30.20	2.34	0.13	1	12.66	0.39	0.54	1	0.07	0.00	0.98
	Year*LFE	16	7	0.11	1.00	8	2.80	0.21	0.99	8	36.96	1.13	0.36	86	39.18	0.47	0.87
	Error	139	59			116	12.90			51	32.65			52	83.84		
$F\Delta$	Year	8	24.43	1.09	0.37	8	50.06	1.80	0.08	8	52.68	2.61	*	8	29.89	1.39	0.22
	LFE	2	14.49	0.65	0.53	1	4.94	0.18	0.67	1	168.47	8.33	**	1	39.91	1.85	0.18
	Year*LFE	16	10.66	0.47	0.96	8	21.02	0.75	0.64	8	24.27	1.20	0.32	8	28.85	1.34	0.25
	Error	139	22.45			116	27.86			51	20.22			52	21.57		
$F\Delta^*$	Year	8	37.64	1.19	0.31	8	20.22	0.93	0.50	8	30.42	1.34	0.25	8	33.32	1.13	0.36
	LFE	2	48.64	1.53	0.22	1	64.91	2.98	0.09	1	40.24	1.77	0.19	1	6.01	0.20	0.65
	Year*LFE	16	19.83	0.62	0.86	8	14.96	0.69	0.70	8	15.88	0.70	0.69	8	33.96	1.15	0.34
	Error	139	31.75			116	21.77			51	22.75			52	29.43		
N_{90}	Year	8	6.00	7.68	***	8	23.69	41.98	***	8	13.84	6.00	***				
	LFE	2	18.24	23.34	***	1	214.45	380.00	***	1	0.56	0.24	0.62				
	Year*LFE	16	3.94	5.05	***	8	17.58	31.15	***	8	6.42	2.78	*				
	Error	139	0.78			116	0.56			51	2.31						

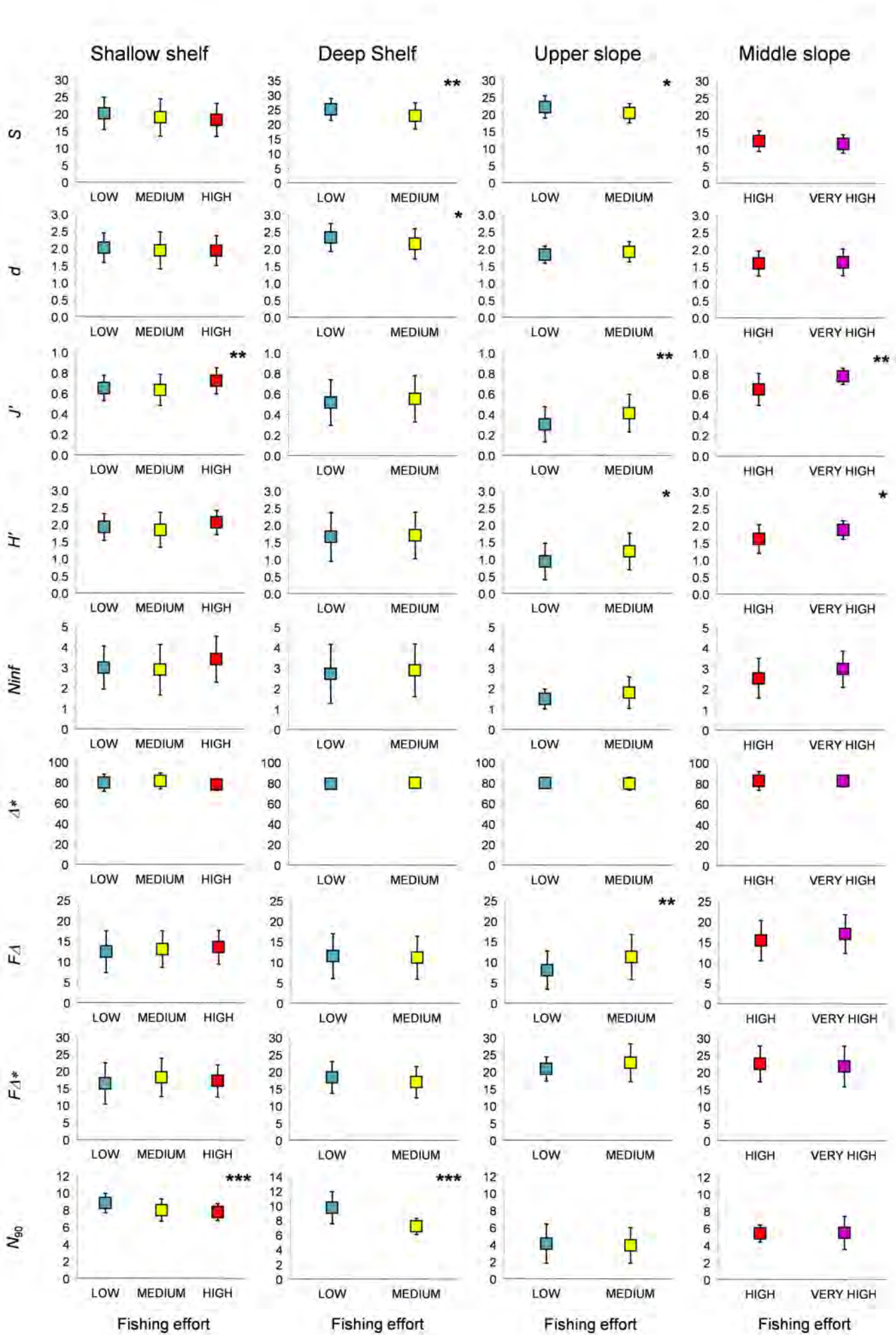


Figure 6.6: Mean values and standard deviation of the diversity indices selected from the cluster analysis (S , d , J' , H' , N_{∞} (N_{inf}), Δ^* , $F\Delta$, $F\Delta^*$ and N_{90}). Blue square: low level of fishing effort; yellow square: medium level of fishing effort; red square: high level of fishing effort; and purple square: very high level of fishing effort. The levels of significance obtained from the Analysis of variance (ANOVA) for the fishing effort factor are also represented. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$.

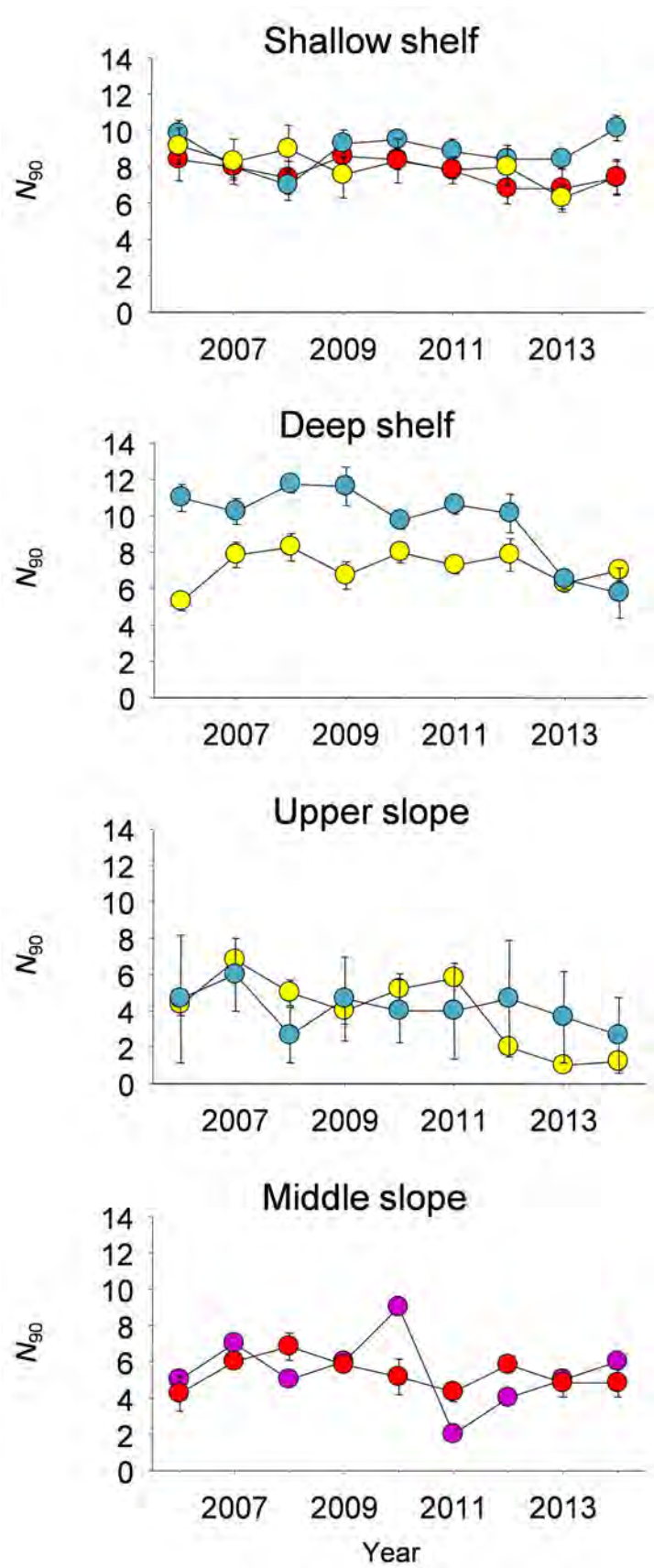


Figure 6.7: Mean values and standard deviation of the N_{90} diversity index during the period 2006-2014. Blue dots: low level of fishing effort; yellow dots: medium level of fishing effort; red dots: high level of fishing effort; and purple dots: very high level of fishing effort.

Table 6.6: t-Test values comparing levels of fishing effort (LFE) of the N_{90} diversity index for each depth strata. L, M, H and VH are low, medium, high and very high LFE, respectively. SS, DS, US and MS are shallow shelf, deep shelf, upper slope and middle slope, respectively. The levels of significance obtained from the student-t for the fishing effort factor for each year are also represented. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$.

		2006	2007	2008	2009	2010	2011	2012	2013	2014
SS	L-M	1.32	-0.55	-3.46**	3.06**	2.15	2.56*	0.89	6.12***	6.01***
	H-M	-1.20	-0.46	-2.38*	1.68	0.11	-0.09	-2.18	0.97	-0.05
	H-L	-2.51*	0	0.81	-1.72	-3.32**	-2.99*	-3.45**	-3.45**	-6.02***
DS	L-M	17.09***	6.61***	10.87***	10.18***	6.52***	12.80***	4.33***	0.81	-2.21*
US	L-M	-0.16	0.9	3.03*	-0.63	1.36	1.57	-1.97	-2.51*	-1.60
MS	H-VH	-	-	-	-	-	-	-	-	-

The species contributing to N_{90} varied markedly between LFE (Table 6.7). Some species contributed to N_{90} in one LFE but not in the other. On the shallow shelf *Lepidotrigla cavillone* only contributed to N_{90} in the low LFE, whereas *Pagellus acarne* and *Mullus barbatus* only contributed in the medium LFE. On the deep shelf *Deltentosteus quadrimaculatus*, *Mullus surmuletus*, *M. barbatus* and *Raja clavata* only contributed to N_{90} in the low LFE, whereas *Trisopterus minutus* only contributed in the medium LFE. On the upper slope, *Glossanodon leioglossus*, *Scyliorhinus canicula*, *Trigla lyra*, *Synchiropus phaeton*, *Helicolenus dactylopterus* and *Merluccius merluccius* only contributed to N_{90} in the low LFE whereas *Galeus melastomus*, *Coelorinchus caelorhinchus* and *Phycis blennoides* only contributed in the medium LFE. On the middle slope *Hymenocephalus italicus* and *Etmopterus spinax* only contributed to N_{90} in the high LFE whereas *Notacanthus Bonaparte*, *Polyacanthonotus rissoanus*, *Lepidion lepidion* and *Mora moro* only contributed in the very high LFE.

Table 6.7: Similarity Percentage (SIMPER) analysis summary table of species appearing in the 90% of within-group similarity. A is the mean abundance (individuals/km²) of each species, and %C is the mean value of the percentage contribution of each species to within-group similarity, taking into account all the jack-knives made by group of depth strata, level of fishing effort (LFE) and year. Sim is the within-group similarity by depth strata subjected to different LFE. L, M, H and VH are low, medium, high and very high LFE, respectively. SS, DS, US and MS are shallow shelf, deep shelf, upper slope and middle slope, respectively.

A			%C			A			%C			A			%C		
SS L; mean Sim=30.38%						SS M; mean Sim=26.38%						SS H; mean Sim=34.82%					
<i>Scyliorhinus canicula</i>	1768	25	<i>Scyliorhinus canicula</i>	1787	32	<i>Serranus cabrilla</i>	1504	31	<i>Scyliorhinus canicula</i>	692	16	<i>Trigloporus lastoviza</i>	1168	14	<i>Trachinus draco</i>	707	14
<i>Serranus cabrilla</i>	1620	19	<i>Serranus cabrilla</i>	1252	15	<i>Scyliorhinus canicula</i>	692	16	<i>Trigloporus lastoviza</i>	1168	14	<i>Trachinus draco</i>	707	14	<i>Trachinus draco</i>	707	14
<i>Trachinus draco</i>	1257	12	<i>Mullus surmuletus</i>	2793	14	<i>Trigloporus lastoviza</i>	1168	14	<i>Trigloporus lastoviza</i>	1168	14	<i>Trachinus draco</i>	707	14	<i>Trachinus draco</i>	707	14
<i>Mullus surmuletus</i>	2152	8	<i>Trigloporus lastoviza</i>	823	10	<i>Trachinus draco</i>	707	14	<i>Trachinus draco</i>	707	14	<i>Trachinus draco</i>	707	14	<i>Trachinus draco</i>	707	14
<i>Trigloporus lastoviza</i>	1012	7	<i>Trachinus draco</i>	527	8	<i>Scorpaena notata</i>	418	4	<i>Scorpaena notata</i>	418	4	<i>Scorpaena notata</i>	418	4	<i>Scorpaena notata</i>	418	4
<i>Serranus hepatus</i>	1800	6	<i>Serranus hepatus</i>	1518	3	<i>Serranus hepatus</i>	683	4	<i>Serranus hepatus</i>	683	4	<i>Serranus hepatus</i>	683	4	<i>Serranus hepatus</i>	683	4
<i>Chelidonichthys cuculus</i>	489	4	<i>Scorpaena notata</i>	174	2	<i>Arnoglossus thori</i>	309	3	<i>Arnoglossus thori</i>	309	3	<i>Arnoglossus thori</i>	309	3	<i>Arnoglossus thori</i>	309	3
<i>Lepidotrigla cavillone</i>	570	3	<i>Pagellus acarne</i>	737	2	<i>Pagellus erythrinus</i>	363	3	<i>Pagellus erythrinus</i>	363	3	<i>Pagellus erythrinus</i>	363	3	<i>Pagellus erythrinus</i>	363	3
<i>Scorpaena notata</i>	390	3	<i>Chelidonichthys cuculus</i>	267	2	<i>Mullus surmuletus</i>	482	2	<i>Mullus surmuletus</i>	482	2	<i>Mullus surmuletus</i>	482	2	<i>Mullus surmuletus</i>	482	2
<i>Arnoglossus thori</i>	280	3	<i>Pagellus erythrinus</i>	377	2	<i>Scorpaena scrofa</i>	99	2	<i>Scorpaena scrofa</i>	99	2	<i>Scorpaena scrofa</i>	99	2	<i>Scorpaena scrofa</i>	99	2
<i>Scorpaena scrofa</i>	235	2	<i>Mullus barbatus</i>	472	1												
DS L; mean Sim=20.80%						DS M; mean Sim=28.17%											
<i>Chelidonichthys cuculus</i>	2887	22	<i>Merluccius merluccius</i>	4213	26	<i>Merluccius merluccius</i>	4213	26	<i>Merluccius merluccius</i>	4213	26	<i>Merluccius merluccius</i>	4213	26	<i>Merluccius merluccius</i>	4213	26
<i>Glossanodon leioglossus</i>	48175	18	<i>Serranus hepatus</i>	2467	26	<i>Serranus hepatus</i>	2467	26	<i>Serranus hepatus</i>	2467	26	<i>Serranus hepatus</i>	2467	26	<i>Serranus hepatus</i>	2467	26
<i>Scyliorhinus canicula</i>	1291	11	<i>Lepidotrigla cavillone</i>	1496	11	<i>Lepidotrigla cavillone</i>	1496	11	<i>Lepidotrigla cavillone</i>	1496	11	<i>Lepidotrigla cavillone</i>	1496	11	<i>Lepidotrigla cavillone</i>	1496	11
<i>Serranus hepatus</i>	1115	8	<i>Scyliorhinus canicula</i>	1115	8	<i>Scyliorhinus canicula</i>	1115	8	<i>Scyliorhinus canicula</i>	1115	8	<i>Scyliorhinus canicula</i>	1115	8	<i>Scyliorhinus canicula</i>	1115	8
<i>Lepidotrigla cavillone</i>	1135	8	<i>Glossanodon leioglossus</i>	61339	6	<i>Glossanodon leioglossus</i>	61339	6	<i>Glossanodon leioglossus</i>	61339	6	<i>Glossanodon leioglossus</i>	61339	6	<i>Glossanodon leioglossus</i>	61339	6
<i>Merluccius merluccius</i>	782	7	<i>Trisopterus minutus</i>	802	5	<i>Trisopterus minutus</i>	802	5	<i>Trisopterus minutus</i>	802	5	<i>Trisopterus minutus</i>	802	5	<i>Trisopterus minutus</i>	802	5
<i>Deltentosteus quadrimaculatus</i>	1002	5	<i>Trachinus draco</i>	686	5	<i>Trachinus draco</i>	686	5	<i>Trachinus draco</i>	686	5	<i>Trachinus draco</i>	686	5	<i>Trachinus draco</i>	686	5
<i>Mullus surmuletus</i>	1163	4	<i>Chelidonichthys cuculus</i>	1018	3	<i>Chelidonichthys cuculus</i>	1018	3	<i>Chelidonichthys cuculus</i>	1018	3	<i>Chelidonichthys cuculus</i>	1018	3	<i>Chelidonichthys cuculus</i>	1018	3
<i>Trachinus draco</i>	433	4															
<i>Mullus barbatus</i>	289	2															
<i>Raja clavata</i>	205	2															
US L; mean Sim=20.40%						US M; mean Sim=40.20%											
<i>Glossanodon leioglossus</i>	147998	29	<i>Gadiculus argenteus</i>	30376	70	<i>Gadiculus argenteus</i>	30376	70	<i>Gadiculus argenteus</i>	30376	70	<i>Gadiculus argenteus</i>	30376	70	<i>Gadiculus argenteus</i>	30376	70
<i>Scyliorhinus canicula</i>	1646	16	<i>Galeus melastomus</i>	2322	11	<i>Galeus melastomus</i>	2322	11	<i>Galeus melastomus</i>	2322	11	<i>Galeus melastomus</i>	2322	11	<i>Galeus melastomus</i>	2322	11
<i>Micromesistius poutassou</i>	8619	10	<i>Coelorinchus caelorhincus</i>	1203	4	<i>Coelorinchus caelorhincus</i>	1203	4	<i>Coelorinchus caelorhincus</i>	1203	4	<i>Coelorinchus caelorhincus</i>	1203	4	<i>Coelorinchus caelorhincus</i>	1203	4
<i>Gadiculus argenteus</i>	11201	10	<i>Micromesistius poutassou</i>	847	3	<i>Micromesistius poutassou</i>	847	3	<i>Micromesistius poutassou</i>	847	3	<i>Micromesistius poutassou</i>	847	3	<i>Micromesistius poutassou</i>	847	3
<i>Trigla lyra</i>	603	8	<i>Phycis blennoides</i>	429	3	<i>Phycis blennoides</i>	429	3	<i>Phycis blennoides</i>	429	3	<i>Phycis blennoides</i>	429	3	<i>Phycis blennoides</i>	429	3
<i>Synchiropus phaeton</i>	654	7															
<i>Helicolenus dactylopterus</i>	332	7															
<i>Merluccius merluccius</i>	2169	5															
MS H; mean Sim=35.62%						MS VH; mean Sim=40.27%											
<i>Phycis blennoides</i>	369	33	<i>Nezumia aequalis</i>	112	25	<i>Nezumia aequalis</i>	112	25	<i>Nezumia aequalis</i>	112	25	<i>Nezumia aequalis</i>	112	25	<i>Nezumia aequalis</i>	112	25
<i>Galeus melastomus</i>	408	25	<i>Galeus melastomus</i>	163	23	<i>Galeus melastomus</i>	163	23	<i>Galeus melastomus</i>	163	23	<i>Galeus melastomus</i>	163	23	<i>Galeus melastomus</i>	163	23
<i>Nezumia aequalis</i>	170	16	<i>Phycis blennoides</i>	116	12	<i>Phycis blennoides</i>	116	12	<i>Phycis blennoides</i>	116	12	<i>Phycis blennoides</i>	116	12	<i>Phycis blennoides</i>	116	12
<i>Hymenocephalus italicus</i>	134	9	<i>Notacanthus bonaparte</i>	84	11	<i>Notacanthus bonaparte</i>	84	11	<i>Notacanthus bonaparte</i>	84	11	<i>Notacanthus bonaparte</i>	84	11	<i>Notacanthus bonaparte</i>	84	11
<i>Symphurus ligulatus</i>	35	4	<i>Polyacanthonotus rissoanus</i>	24	8	<i>Polyacanthonotus rissoanus</i>	24	8	<i>Polyacanthonotus rissoanus</i>	24	8	<i>Polyacanthonotus rissoanus</i>	24	8	<i>Polyacanthonotus rissoanus</i>	24	8
<i>Etmopterus spinax</i>	33	3	<i>Lepidion lepidion</i>	59	6	<i>Lepidion lepidion</i>	59	6	<i>Lepidion lepidion</i>	59	6	<i>Lepidion lepidion</i>	59	6	<i>Lepidion lepidion</i>	59	6
			<i>Symphurus ligulatus</i>	57	5	<i>Symphurus ligulatus</i>	57	5	<i>Symphurus ligulatus</i>	57	5	<i>Symphurus ligulatus</i>	57	5	<i>Symphurus ligulatus</i>	57	5
			<i>Mora moro</i>	25	5	<i>Mora moro</i>	25	5	<i>Mora moro</i>	25	5	<i>Mora moro</i>	25	5	<i>Mora moro</i>	25	5

The contribution to similarity and the abundance of the elasmobranch *S. canicula* were higher in the low and medium LFE on the shallow shelf and in the low LFE on the deep shelf (Table 6.7). The contribution to similarity of the teleost *M. surmuletus*

was higher in the low and medium LFE on the shallow shelf. *Serranus hepatus*, *L. cavillone* and *M. merluccius* showed low contributions in the low LFE on the deep shelf but they were the most highly contributing species in the medium LFE. On the upper slope the most highly contributing species were also different between LFE, with *G. leioglossus* accounting for 29% of the similarity in the low LFE but not appearing in the medium LFE, in which *Gadiculus argenteus* accounted for 70% of the similarity. On the middle slope, *P. blennoides* and *G. melastomus* showed the highest contributions and abundances in the high LFE whereas in the very high LFE the highest contribution was given by *Nezumia aequalis*, also followed by *G. melastomus*.

6.4 Discussion

This Chapter studies biodiversity from a comprehensive and integrated point of view and highlights the importance of detecting the effects of fishing on diversity when monitoring and managing bottom trawl fisheries. Although it is well known that biodiversity is a multidimensional concept (Purvis and Hector, 2000; Mérigot et al., 2007a, 2007b), the comparison of sixteen diversity indices developed in the present study shows that some of them are highly correlated. However, there is a clear differentiation between the indices related to species counts, including their relative abundance or not, and those incorporating information about taxonomy or functionality of the species. Four groups of indices measuring complementary aspects of diversity are identified: (i) species richness, represented by indices highly influenced by the number of species; (ii) evenness, represented by indices that take into account the relative abundance of the species; (iii) taxonomy, represented by indices mainly influenced by taxonomic information; and (iv) functionality, represented by indices mainly influenced by functional information about species.

As expected, taxonomic diversity (Δ) groups with Simpson (and therefore other evenness measures) as there is a strong mechanistic relationship between these measures (Clarke and Warwick, 1998). What is more, if all species are in one genus all those indices collapse to the same measure. The index Δ can be highly influenced by the relative abundances of species, leading to situations in which the evenness component may mask the taxonomic or functional aspects of interest. This was the motivation for the development of Δ^* , which can be seen as a measure of pure taxonomic relatedness. Our results demonstrate a similar performance for the functional versions of these measures, $F\Delta$ and $F\Delta^*$. A recent study on the diversity of demersal fish in the Mediterranean (Granger et al., 2015) has shown that both functional and taxonomic diversity indices were highly correlated with Simpson's diversity index. In that sense, it is important that general statements, such as the finding by Granger et al. (2015), are understood in the context of the exact measures used and how they are related to each other mathematically, not just ecologically.

A clear relationship between demersal fish diversity and depth is shown, but with different, and even opposite, trends for some groups of indices. Although the relationships between depth and diversity of demersal fish assemblages have not always a straightforward interpretation (Gaertner et al., 2013), our results are in agreement with those found both in western (Mérigot et al., 2007a, 2007b) and eastern (Labropoulou and Papaconstantinou, 2004) Mediterranean. In this area species abundance is higher on the continental shelf, coinciding with lower evenness (higher dominance). These bathymetric differences in fish diversity also coincide with changes in the composition

of demersal assemblages with depth (e.g. Massutí and Reñones, 2005; Biagi et al., 2002; Colloca et al., 2003).

A clear effect of fishing effort on evenness (J') is detected in both the continuous and the stratified approaches. This index increases with increasing fishing effort and its mean value is higher at the higher level of fishing effort than at the lower levels in all bathymetric strata, except for the deep shelf. In the second approach, the indices H' and $F\Delta$, which are highly correlated with J' , also show similar results as might be expected. While this may suggest that fishing exploitation works as a factor that increases the evenness of the communities and decreases the dominance of species (Zhou et al., 2010), it is also worth noticing that fishing pressure is not an independent process. Fishers choose where to go, and differences in diversity among fishing grounds may not be a result of fishing effort, but a cause. Fishermen choose grounds to fish on the basis of their knowledge of the species that inhabit them, and it is possible that grounds with more diverse assemblages are more attractive for fishing. However, the decrease on indices like Δ^* , $F\Delta^*$, S and N_{90} with the increasing fishing effort points to the removal of dominant species of the community as the most likely explanation.

The continuous decreasing trend of Δ^* with increasing fishing effort, i.e. in heavily fished areas the members of assemblages tend to be more closely related to each other taxonomically, supports the hypothesis that taxonomic indices may be more sensitive to community changes than ‘traditional’ ones (Hall and Greenstreet, 1998; Rogers et al., 1999; Leonard et al., 2006). In our case, the increased sensitivity of Δ^* could detect the small differences in fish diversity due to trawling during the relatively short study period (2006-2014). The reduction of $F\Delta^*$ with respect to the increasing fishing effort, i.e. in heavily fished assemblages the fish are more similar functionally, implies that one effect of fishing is to remove functional variety. Further research would be necessary to determine whether changes in the functional components of the communities represent the organisms adaptations to the environment or their response to stress (de Juan et al., 2007). These results are not fully confirmed from the stratified approach, in which significant differences between levels of fishing effort for $F\Delta^*$ and Δ^* are not detected. However, it should be recognized that in such situations it is to be expected that correlational statistical approaches will have more power to detect change than categorical ones, and the lack of significance in a test should not be interpreted as the absence of an effect (Somerfield et al., 2002).

Although there is an increasing general concern about the importance of the role played by species in the ecosystems, there is no consensus about how functions (or ‘functioning’) should be quantified (Tilman et al., 1997; Petchey and Gaston, 2002; Villéger et al., 2008; Laliberté and Legendre, 2010). Functional diversity indices do not always have a straightforward interpretation. Leaving aside the important differences in the ways in which indices may be formulated (Somerfield et al., 2008), the values of functional diversity indices are highly dependent on the functional traits chosen to calculate the functional similarities between species, the weights given to each trait and the quality of the data that traits rely on (Petchey and Gaston, 2006; Somerfield et al., 2008). Although we have selected a few relevant functional traits based on reliable data, mainly from bottom trawl surveys conducted in the area, several variations in these factors could influence the results. In the present Chapter, the similarity between the definition of $F\Delta^*$ and Δ^* leads to a similar interpretation, with $F\Delta^*$ seen as ‘the expected (weighted) functional distance between any two randomly chosen individuals of the sample, considering that they belong to different species’. Hence, lower values of

$F\Delta^*$ with high levels of fishing effort correspond to shorter average functional distance among species living in the most impacted areas. However, we found higher values of $F\Delta^*$ on the middle slope, where levels of fishing pressure are the highest. This stratum has the lowest number of species, but they display large functional differences. Thus, the increase in functional diversity could be due to the absence of species with intermediate functional distances in the community (that would decrease $F\Delta^*$) or to disappearance of this species due to fishing. Nevertheless the role of some functions in ecosystems, along with the importance of functional redundancy, still remains unclear (Tilman et al., 1997; Levin and Lubchenco, 2008). For a given number of species, assemblages with higher functional trait dispersion are expected to result in greater ecosystem adaptability, but they may also show greater vulnerability since any species loss will result in the loss of more functions (Wiedmann et al., 2014).

Although the continuous approach does not show a significant effect of fishing effort on S , the stratified approach shows significantly lower values of S at medium levels of fishing effort compared to low ones on the deep shelf and the upper slope. While it is true that a loss in species richness can occur only if species disappear, they may appear to do so if they become rare and are not sampled. The decrease of S observed in this study apparently relate primarily to changes in the frequency of occurrence of some species.

The index N_{90} also shows significant lower values at higher levels of fishing effort compared to the lower ones on the shallow and deep shelf. This result is in accordance with those from Chapter 5, where the only index that showed a significant response of diversity to fishing effort was N_{90} . Like mean S , N_{90} is also sensitive to the frequencies of occurrence of species in samples. The sensitivity of N_{90} to fishing effort is due to reductions in the frequency of occurrence and in the evenness of species among samples in communities affected by fishing impacts. The significant interaction detected between fishing effort and year for N_{90} indicates that there is a different response of the index depending on the level of fishing effort. As suggested in Chapter 5, this effect could be related to a different response of the communities to environmental changes, with higher sensitivity to these changes in communities more impacted by fishing (Perry et al., 2010; Planque et al., 2010; Navarro et al., 2015).

The contrasting results obtained in the shelf and the slope of the Balearic Islands give relevant information about the current state of the demersal fish communities inhabiting these depths and habitats. Except for differences in evenness, in the middle slope there are no clear differences in fish diversity between different levels of fishing effort. Trawl fishing effort is the highest in this depth stratum, showing areas subject to high and very high levels of fishing effort, due to the displacement of the bottom trawl fishery from the shelf to the slope (Moranta et al., 2008b; Hidalgo et al., 2009) that started in the middle of the 20th century (Oliver, 1983). Even the lowest fishing effort level associated to this stratum may have been too high for the most vulnerable components of the fish community. These species may have experienced the effects of trawl fishing (i.e. removing or decreasing frequency of occurrence of the most vulnerable species) long before the period analysed in the present Chapter.

Early descriptions of these trawl fishing grounds by Maurin (1968) from bottom trawl surveys showed the regular presence of vulnerable species, such as the deep water corals *Funiculina quadrangularis* and *Isidella elongata*, which now have almost disappeared in the area. Works on the ichthyofauna of the Balearic Islands repeatedly

recorded the presence of demersal elasmobranchs such as *Scyliorhinus stellaris*, *Galeorhinus galeus*, *Rhinobathos* spp. and *Squatina* spp. (Ferrer, 1930; de Buen, 1935; Oliver, 1944; Maurin, 1968), that are no longer present in survey catches (Table 6.2). In fact these, and other vulnerable species such as *Squalus acanthias* and *Torpedo torpedo*, which do not appear in survey catches either, have been catalogued as extinct, critically endangered or endangered in the red lists of fishes of the Balearic Islands (Mayol et al., 2000; Grau et al., 2015). The disappearance of these top predators indicates that major changes in the fish communities studied may have happened long before the period of the present study (2006–2014), during which there have been no clear changes in the fishing effort of the bottom trawl fleet.

On the other hand, the benthic communities of the fishing grounds on the Balearic shelf do not seem to be as transformed as those on the slope, probably due to their greater extent and the lower fishing effort received. In fact, some of these fishing grounds overlap with sensitive habitats such as m  erl and crinoids beds (Ordines and Massut  , 2009). This lower fishing impact still allows the presence on the shelf of some vulnerable fish species, not only those adapted to the highest levels of fishing pressure. On the slope, fish species are few and scarce and represent only a small percentage of the abundance of the demersal fauna, which is clearly dominated by decapods crustaceans (Guijarro et al., 2011). However, on the shelf the vulnerable fish species should be even more abundant in the areas subjected to low fishing pressure, leading to detectable differences of fish diversity between the higher and the lower levels of fishing effort in this stratum. In the strata showing significant differences in fish diversity using N_{90} , the SIMPER results show differences in species contribution of demersal fish species between levels of fishing effort. Some elasmobranchs, considered highly vulnerable to fishing impacts (Stevens et al., 2000; Quetglas et al., 2016), are more abundant and contribute more to within-group similarity in the areas with low levels of fishing effort. Examples include *Scyliorhinus canicula* on the shallow shelf, deep shelf and upper slope, and *Raja clavata* on the deep shelf. *Galeus melastomus* shows the opposite pattern in the upper slope, but this could be due to the distinct mean depth of the groups of samples associated to medium (408 m) and low (286 m) levels of fishing effort, and the bathymetric distribution of this species in the area, which only starts to be abundant below 350–400 m depth (Ram  rez-Amaro et al., 2015).

On the middle slope, differences in N_{90} could not be tested due to the low number of sampling stations in the very high level of fishing effort. However SIMPER results show that the vulnerable species *Etmopterus spinax*, is only present in the high level of fishing effort. By contrast, whereas the abundance of the elasmobranch *G. melastomus* is higher in the high level of fishing effort, differences in contributions to similarity from the high and very high levels of fishing effort are less evident. The scavenging and opportunistic behaviour of *G. melastomus* (Fanelli et al., 2009; Anastasopoulou et al., 2013) could counteract its vulnerability to fishing exploitation through its feeding on animals damaged by the trawl or on other scavengers (Kaiser and Spencer, 1994). There is also a high contribution to within-group similarity of opportunistic species like *Nezumia aequalis* and *Nothacanthus bonaparte* (Iwamoto, 2015; Mauchline and Gordon, 1986), in the very high level of fishing effort. *N. aequalis* exhibits a benthopelagic behaviour, searching in the sediment with a diet consisting largely of epibenthic and infaunal invertebrates (e.g. polychaetes and amphipods; Macpherson, 1979), whose availability could be favoured by trawl fishing. *N. bonaparte* has also been considered to be a benthic scavenger (Tecchio, 2012).

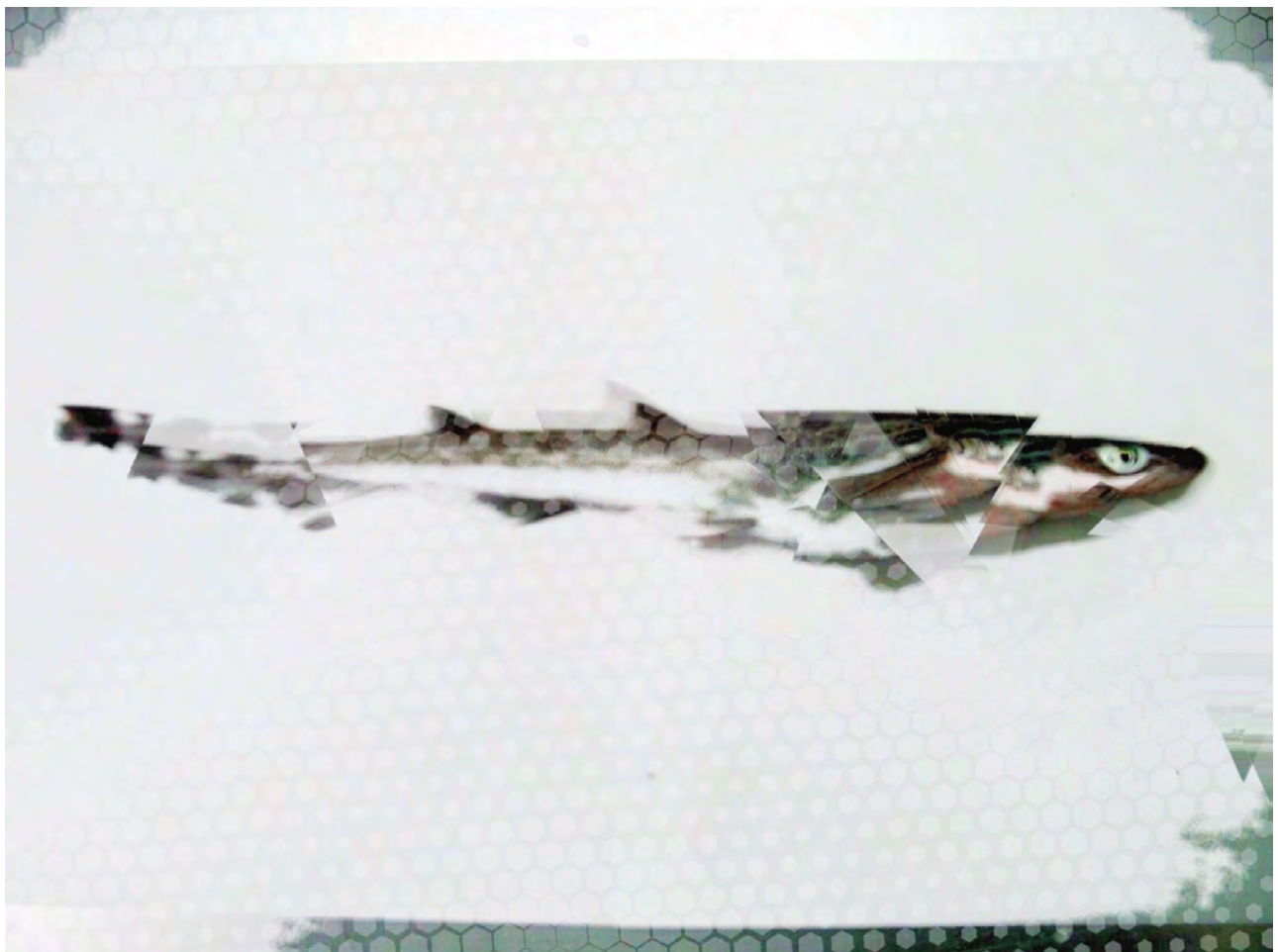
Our results have shown changes in fish diversity due to the effect of fishing effort on demersal fish communities, but not for all depth strata and diversity indices analysed. That could be due to the continuous exploitation of the studied area for a long period of time which may have prevented to detect those changes during the relatively short time period analysed (2006-2014). To assess the whole potential of those diversity indices to monitor the effects of fishing on fish communities, a longer time-series preferably closer to the start of the fishing activity in the area, would be needed. However, achieving such a time series may be difficult and an alternative could be the study of time-series collected following a decline in fishing effort, perhaps through the closure of a fishery. The comparison of results obtained from other Mediterranean areas with different ranges of fishing effort would also achieve this purpose. Although in the present study we have distinguished four levels of trawl fishing effort, low, medium, high and very high, we must be aware that the effort in the Balearic Islands is lower than that exerted on adjacent areas off Iberian coast (Quetglas et al., 2012). Thus higher differences in fish diversity would be expected from the comparison of these more contrasting areas, which would be highly valuable for the assessment of the effects of fishing on fish communities.

The study of demersal fish diversity from a comprehensive and integrated point of view shows that diversity can be described using different complementary aspects such as species richness, evenness, and taxonomic and functional breadth of the species present in a given community. Each one of them may have a different response to fishing impact. However, changes in diversity may only be detectable in those communities where the levels of fishing pressure have remained relatively low. When they have been exposed for a long period to high levels of fishing pressure, the changes in diversity attributable to fishing may have happened long before the start of monitoring of the fishery and therefore it is too late to detect differences between different levels of fishing effort. This seems to be the case on the middle slope of the Balearic Islands, where vulnerable species have disappeared or are very infrequent, and have been replaced by species more adapted to the impacts of fishing.

Chapter 7

RESULTS 4. MEDITERRANEAN

Spatio-temporal trends in diversity of demersal fish assemblages along the Mediterranean



Chapter 7. Results 4. Spatio-temporal trends in diversity of demersal fish assemblages along the Mediterranean

SUMMARY

The high species richness, coupled with an important proportion of endemisms, makes the Mediterranean one of the world's biodiversity hotspots. However, the continuous increase of fisheries in the last decades has led to the overexploitation of their main commercial stocks. Using fishery independent data collected under the framework of the MEDITS developed during the last two decades we study the demersal fish diversity pattern in the Mediterranean at a large spatial and temporal scale to assess if this pattern is being affected by the general fishing overexploitation of their demersal resources. Then, detected trends on diversity are compared to the spatio-temporal variation in bottom trawl fishing effort along the Mediterranean. Our results show a stability and even recovery of demersal fish diversity of the Mediterranean together with higher values of diversity on the continental shelves of the Balearic Islands, Sardinia, Sicily and the Aegean Sea. Both at large temporal and spatial scale the high diversity of demersal assemblages in the Mediterranean is associated to a reduction in bottom trawl fishing effort. The inclusion of species other than target ones through diversity indices is relevant in the implementation of an ecosystem based fisheries management.

7.1 Introduction

The Mediterranean is considered one of the Large Marine Ecosystems of the World, owing to its bathymetry, hydrography, productivity and trophic webs (Duda and Sherman, 2002). It is a semi-enclosed sea connected to the Atlantic Ocean through the Strait of Gibraltar, the Black Sea through the Strait of the Dardanelles and the Red Sea through the artificial Suez Channel (Figure 7.1). It acts as a concentration basin, where evaporation is higher in its eastern basin, causing the water level to decrease and salinity to increase from west to east (Coll et al., 2010). While temperature also increases eastwards, surface productivity, organic matter availability at the seafloor and the biomass of megabenthic fauna of deep ecosystems decrease eastwards (Brankart and Brasseur, 1998; Bosc et al., 2004; Danovaro et al., 1999; Tecchio et al., 2011). The Mediterranean has narrow continental shelves and a large area of open sea. In fact the continental shelf covers about 20% of the Mediterranean bottoms whereas the slope covers about 60% (Sardá et al., 2004). Therefore, a large part of this basin can be classified as deep sea (Coll et al., 2010).

The high species richness, coupled with an important proportion of endemisms, makes the Mediterranean one of the world's biodiversity hotspots (Moranta et al., 2008a; Boudouresque, 2004; Lejeusne et al., 2010). Environmental variables like temperature and productivity as well as distance to Strait of Gibraltar have been shown to be causes of fish species richness distribution (Ben Rais Lasram et al., 2009; Meléndez et al., 2017). However, this high biodiversity is presently threatened by the combined action of anthropogenic impacts, introduction of alien species and climate change (Bianchi et al., 2012). Among human activities, fisheries are one of the most important factors affecting marine resources and ecosystems.

Fishing activities can lead to changes in the structure of marine habitats. They

include: effects on populations of target (e.g. Vasilakopoulos et al., 2014) and non-target species (e.g. Ordines et al., 2014); shifts in food-web structure due to changes in predator-prey relationships (Kaiser et al., 2002); changes in body-size distributions due to the size-selection of fisheries (e.g. Daan et al., 2005); genetic selection of species with physical characteristics and reproductive traits more compatible with fishing (e.g. Fromentin and Fonteneau, 2001); resuspension of superficial sediments (e.g. Smith et al., 2003), and habitat modification (e.g. Callaway et al., 2002).

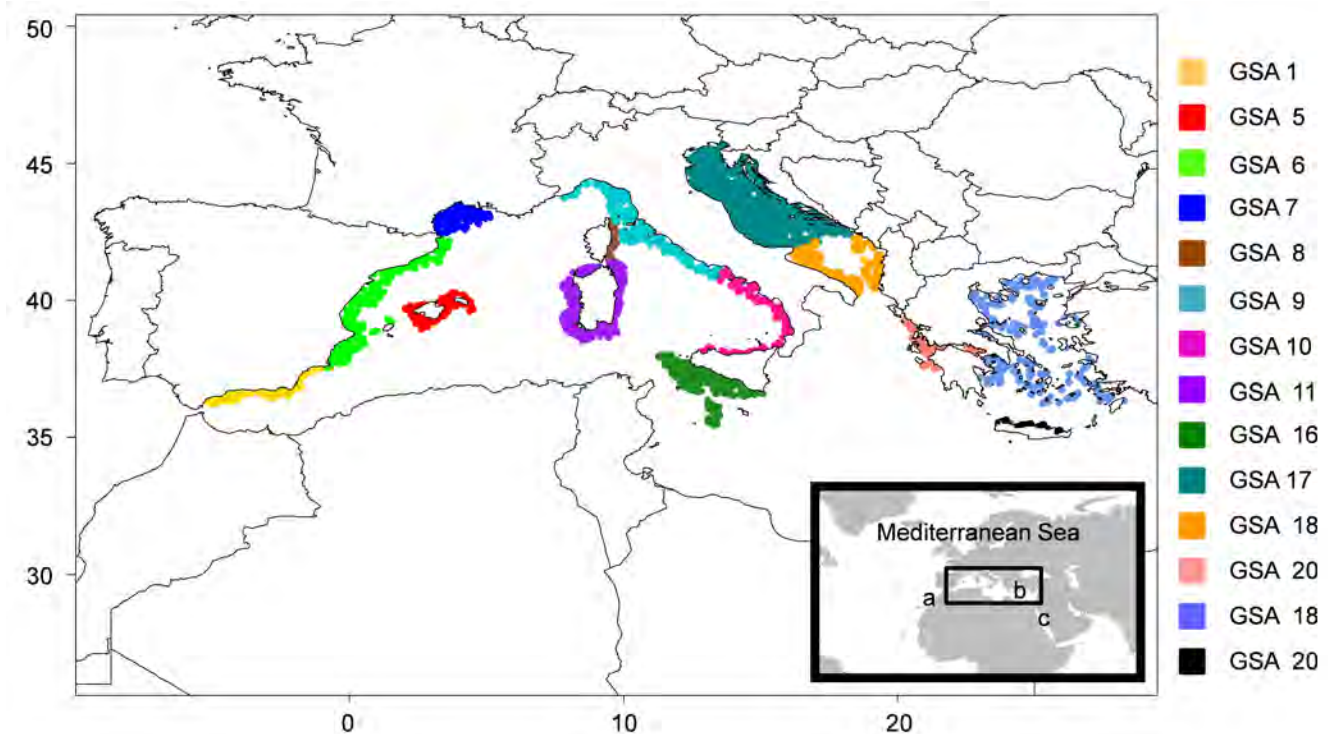


Figure 7.1: Map of the study area showing the 17,540 hauls sampled between 1994 and 2015 in 15 Geographical Sub-Areas (GSAs). Each colour corresponds to one of the GSAs defined by the General Fisheries Commission for the Mediterranean (GFCM; www.gfcm.org). The smaller map shows the location of the Mediterranean and its connections to the Atlantic Ocean through the Strait of Gibraltar (a), the Black Sea through the Strait of the Dardanelles (b) and the Red Sea through the artificial Suez Channel (c).

The natural resources of the Mediterranean have been subject to human exploitation since ancient times, when coastal communities started to use different fishing gears, some of which still in use (Farrugio et al., 1993). Dramatic long-term changes in marine communities took place before the industrialization of fisheries that occurred in the 1950s, and have already been documented in some areas, such as the Adriatic Sea (Fortibuoni et al., 2010). Until 1950, the exploitation of Mediterranean resources was limited to fishing areas shallower than 200 m depth. In the last decades, with the decline of stocks on the continental shelf, increasing market demand, and the introduction of new technologies, trawl fisheries have expanded offshore and towards the deeper waters of the continental slope (Roberts, 2002; Morato et al., 2006) to target valuable resources such as red shrimps (e.g. Demestre and Martín, 1993; Guijarro et al., 2008; Masnadi et al., 2018).

In this area, the assessment of fisheries is developed within the framework of the GFCM, the regional fisheries management organization of the Mediterranean. Out of the 27 Mediterranean stocks of fishing target species assessed by the GFCM in its last report, about 80% were assessed as overexploited (GFCM, 2016). The presence of a high diversity of species and the absence of large monospecific stocks comparable to those inhabiting some wide areas of the open oceans, is a characteristic of the Mediterranean demersal fisheries (Farrugio et al., 1993). Then, the assessment at a community level is crucial, particularly due to the multispecific character of the bottom trawl fishery,

and also because a decline in the diversity of demersal assemblages has been reported due to fishing exploitation (Ungaro et al., 1998; Sabatini et al., 2013). The assessment at a community level is also a requirement for the implementation of an ecosystem based management of fisheries (Browman and Stergiou, 2004).

The aim of this Chapter is to study the demersal fish diversity pattern in the Mediterranean at a large spatial and temporal scale and to assess if this pattern is being affected by the general fishing overexploitation of demersal resources in the area. To do so, we have used fishery independent data collected under the framework of the MEDITS trawl surveys developed during the last two decades. The detected trends were compared to the spatio-temporal variation in bottom trawl fishing effort along the Mediterranean Sea.

7.2 Materials and Methods

7.2.1 Data

Demersal fish were collected during MEDITS bottom trawl surveys conducted from 1994 to 2015 in 14 Geographic Sub Areas (GSAs) along the European coasts of the Mediterranean Sea. Some GSAs have gaps in their sampling years: i) GSA 5 started sampling in 2001; ii) there are no data in 2002 for GSA 8 (technical problem of the boat); and iii) there are no data for 2002, 2007, 2009-2013 and 2015 for GSAs 20, 22 and 23. For more details on the sampling strategy and protocol, and gear characteristics, see Chapter 3 (Section 3.1).

A total of 17,540 hauls performed between 46 and 866 m depth were analysed (Table 7.1; Figure 7.1). Hauls shallower than 46 m depth were excluded from the analysis because they could not be found for all GSAs. A species accumulation curve for each GSA was performed and we confirmed that differences in number of species were not due to differences in the number of hauls considered for each GSA (Table 7.1; Figure 7.2). The catch of each sample was sorted, identified to species level, counted, weighed and standardized to square km by using the horizontal opening of the net and the distance covered in each haul. Species with a pelagic or mesopelagic behaviour, like most species of the families Myctophidae (e.g. *Ceratoscopelus maderensis*) and Cupleidae (e.g. *Engraulis encrasicolus*), were excluded from the analyses. The species included in the analyses are specified in Annex 1.

Table 7.1: Name of the areas and number of samples analysed for each Geographical Sub-Area (GSA).

GSA	Area	Samples
GSA 1	Northern Alboran Sea	743
GSA 5	Balearic Islands	650
GSA 6	Northern Spain	1459
GSA 7	Gulf of Lions	1143
GSA 8	Corsica	451
GSA 9	Ligurian, North and Central Tyrrhenian Sea	2468
GSA 10	Central and Southern Tyrrhenian Sea	1333
GSA 11	Sardinia	1811
GSA 16	Strait of Sicily	1492
GSA 17	Northern Adriatic Sea	2296
GSA 18	South Adriatic Sea	1684
GSA 20	Eastern Ionian Sea	308
GSA 22	Aegean Sea	1427
GSA 23	Crete	175

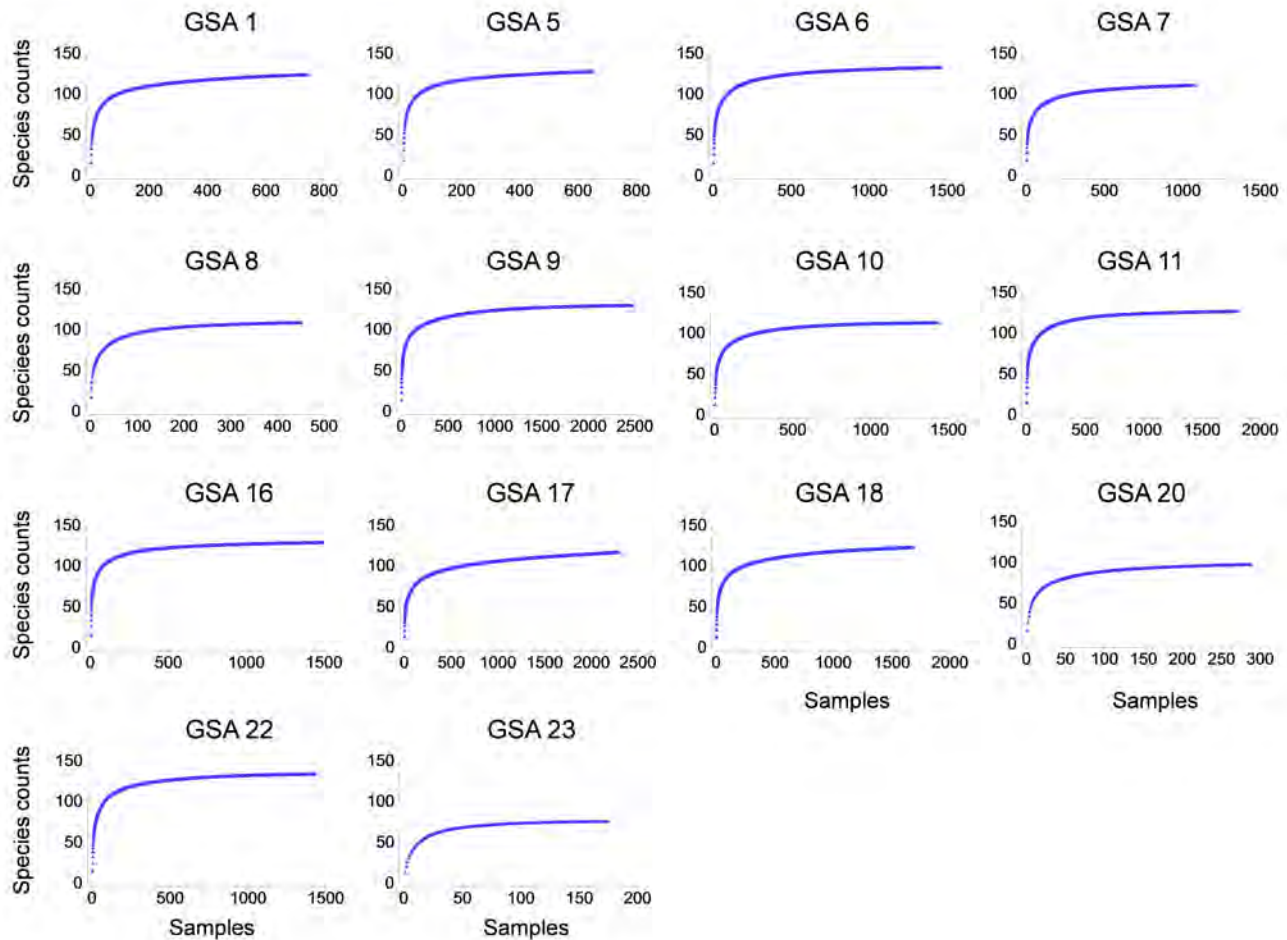


Figure 7.2: Species accumulation curves for each GSA. Note that for all GSAs asymptotic values of species counts are reached.

7.2.2 Fish assemblages and diversity

Cluster analysis was used to analyse the structure of demersal fish assemblages and to identify different assemblages according to depth strata in each GSA. Relationships among samples were detected by hierarchical agglomerative clustering with group-average linkage after a fourth root transformation of the data. The distance used to make groups was the Bray-Curtis Similarity. These analyses were performed using PRIMER 7 (Clarke et al., 2014). The calculus of diversity indices explained below was made taking into account the groups of samples obtained from the cluster analysis.

The N_{90} diversity index was calculated following the procedure described in Chapter 4 (Section 4.2.1.1). Species contributions are calculated for each resampling in a jack-knife routine, which removes a number of samples each time, producing lists of contribution to similarity by species in each resampling. Because the groups of samples for each GSA, strata and year were large, we removed a 10% of samples in each resampling (*perc*) with a 50% of replacement. That is, a 50% of samples removed in a resampling (*perc2*) must be different from previous ones. In this way, we obtain values of deviation for N_{90} other than 0 for groups with a lot of observations. The use of the arguments *perc* and *perc2* are explained with more detail in Chapter 4 (Section 4.2.1.2). The N_{90} diversity index is the mean number of species which accumulates up to 90% of within-group similarity in all the resamplings. SIMPER analysis for each group of samples was also undertaken to see their species composition. All these analyses were carried out with the N90 script included in Chapter 4 (Supplementary data).

Diversity indices, such as species richness (S) and Pielou's evenness (J') that have shown some kind of response by demersal fish assemblages in the Mediterranean to

fishing impact (Chapter 6), have also been included in this Chapter. These ‘traditional’ diversity indices are also helpful for comparison with previous works. See Chapter 3 (Section 3.2; Table 3.1) for more details on the calculation of ‘traditional’ diversity indices.

7.2.3 Fishing effort

Information on annual fishing effort was collected from GFCM (<http://www.fao.org/gfcm/data-/safs/en/>) and STECF (<https://stecf.jrc.ec.europa.eu/reports/medbs>) working groups reports (see Chapter 3; Section 3.3). Fishing effort data have been compiled by trawl fleet targeting different species. The units vary between the different reports, being mainly provided in terms of number of vessels, kilowatt per days at sea and gross tonnage per days at sea (see Annex 2).

To estimate fishing effort in each depth stratum obtained from cluster analysis, the strata were associated to the main target species of the fleets. Because target species varied between GSAs, we considered: i) *Mullus barbatus* or *Mullus surmuletus* for the continental shelf; ii) *Nephrops norvegicus* or *Parapenaeus longirostris* for the shelf break/upper slope; and iii) *Aristeus antennatus* or *Aristaeomorpha foliacea* for the lower slope.

To compare temporal trends in fishing effort and demersal fish diversity, the longest series of fishing effort available for each GSA and depth stratum regardless the kind of units were selected. When we did not find values of fishing effort for a certain GSA, experts were contacted to obtain a trend in number of vessels in that area.

7.2.4 Temporal and spatial analysis

In order to analyse temporal trends in diversity, linear regressions were fit to the mean values of S , J' and N_{90} for each year, GSA and depth stratum. Linear regression analyses with the annual values of fishing effort in each GSA and depth stratum were also performed. The exploration of the scatter plots of the time series together with the comparison of Pearson (assuming linear pattern) and Spearman (suitable also for other monotonic patterns than the linear) correlation coefficients were done. The values of both correlation coefficients were similar, indicating that the detected trends could be fitted using a simple linear model. Thus the linear regression and the Pearson coefficient of correlation were presented along with the coefficient of determination (i.e. variance explained). Trends in diversity of GSAs 20, 22 and 23 excluding 2014 have also been calculated to avoid gaps on those time series (see Section 7.2.1). These analyses were carried out with R, version 3.1.1 (R Core Team 2014).

In order to observe spatial differences in diversity by GSA, time series of mean values and standard deviation of each diversity index (see Section 7.2.1 for years included in each GSA) were plotted. For those series with a significant temporal trend, the diversity values at the beginning and the end of the time series were plotted instead of mean values and standard deviation.

SIMPER analysis for each group of samples from N_{90} was also performed to see differences in species composition in each GSA. The percentage of contribution of each species to within-group similarity was calculated as the mean value of species contributions to similarity taking all groups of observations by year and stratum for each GSA

into account.

7.3 Results

7.3.1 Community structure

Results from cluster analysis detecting main fish assemblages for each GSA are shown in Figure 7.3. Three groups of samples were selected from most GSAs, corresponding to a level of similarity between 30% and 40%. Maximum, minimum and mean depths of each cluster group by GSA were obtained. According to these depth values, samples were grouped in three different depth strata: shelf, shelf break/upper slope and lower slope (Table 7.2; Figure 7.3). For GSAs 17 and 23 only two groups were selected. GSA 17 does not present samples below 350 m while negligible sample number exists for GSA 23 over 496 m (Table 7.2). For GSAs 7 and 20, even there are samples in the lower slope group, there were not enough to calculate the N_{90} along all the time series. So, both lower slope groups were omitted from the temporal and spatial analysis.

In 9 out of the 12 GSAs presenting lower slope samples, samples from shelf break/upper slope clustered with samples from lower slope. The exceptions were GSAs 6, 11 and 22, where samples from shelf break/upper slope clustered with those from the continental shelf. Minimum, maximum and mean depths for each group of samples from cluster analysis are shown in Table 7.2. Mean depth of continental shelf samples ranged from 76 m in GSA 1 to 125 m in GSA 10, while for the shelf break/upper slope they ranged from 180 m in GSA 17 to 421 m in GSA 7, and for the lower slope between 496 m in GSA 11 and 699 m in GSA 7.

7.3.2 Temporal trends

Although the analysis of temporal evolution for N_{90} , S and J' did not show any significance in most GSAs and depth strata (Table 7.3; Figures 7.4-7.7), some trends were detected. N_{90} increased in the continental shelf of GSAs 1, 8 and 20, the shelf break/upper slope of GSAs 7, 11 and 18, and the lower slope of GSA 11, while it only decreased in the shelf break/upper slope of GSA 5 (Table 7.3; Figures 7.4 and 7.7). S increased in the continental shelf of GSAs 8 and 10, the shelf break/upper slope of GSAs 7, 8, 10 and 22, and the lower slope of GSAs 8, 10, 11, 16 and 18, while it decreased in the shelf break/upper slope of GSA 17 and the lower slope of GSA 9 (Table 7.3; Figures 7.5 and 7.7). J' increased in the continental shelf of GSA 7, the shelf break/upper slope of GSAs 7 and 8, and the lower slope of GSA 11, while it decreased in the continental shelf of GSAs 10 and 16, the shelf break/upper slope of GSAs 5 and 22, and the lower slope of GSAs 1 and 8 (Table 7.3; Figures 7.6 and 7.7). Those trends are confirmed when excluding the last year of time series (2014) for GSAs 20, 22 and 23 (Table 7.3).

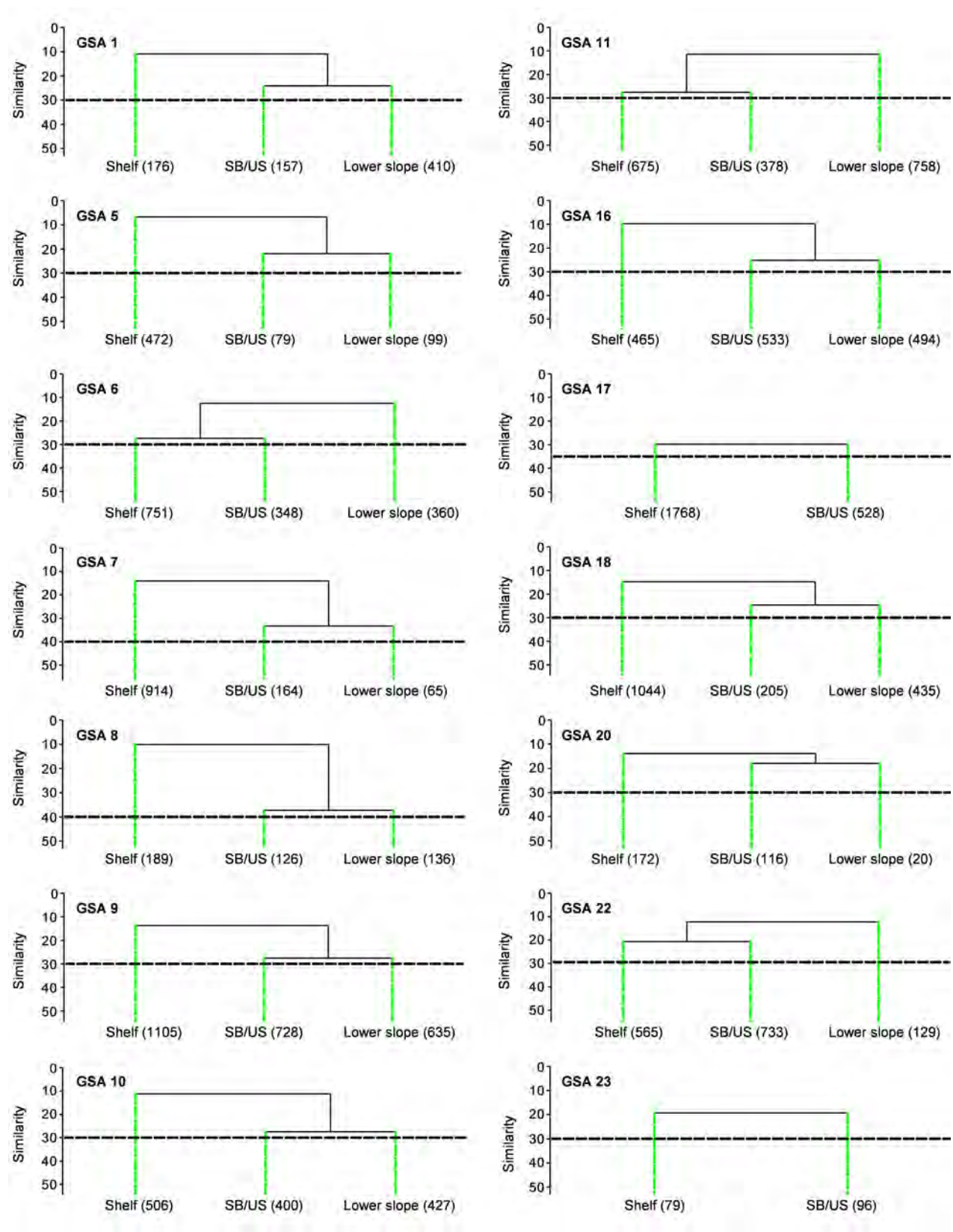


Figure 7.3: Cluster of samples obtained from Mediterranean International Bottom Trawl Surveys (MED-ITS). The data used for the cluster analysis were the double root transformation of abundances of demersal fish species for each sample during the sampling period of each Geographical Sub-Area (GSA). The dashed line shows the similarity level used to classify the depth strata: shelf, shelf break/upper slope (SB/US) and lower slope. The number in brackets represents the number of samples in each depth stratum.

Table 7.2: Minimum, Maximum and Mean depth of samples grouped in each depth stratum (shelf, shelf break/upper slope and lower slope) from cluster analysis for each Geographical Sub-Area (GSA).

GSA	Strata	Minimum depth	Maximum depth	Mean depth
GSA 1	Shelf	50	168	76
	Shelf break/upper slope	118	373	203
	Lower slope	219	807	519
GSA 5	Shelf	46	258	108
	Shelf break/upper slope	316	698	402
	Lower slope	581	756	678
GSA 6	Shelf	50	147	84
	Shelf break/upper slope	82	392	183
	Lower slope	257	798	505
GSA 7	Shelf	55	155	93
	Shelf break/upper slope	214	705	421
	Lower slope	414	866	699
GSA 8	Shelf	56	158	94
	Shelf break/upper slope	261	510	350
	Lower slope	405	583	510
GSA 9	Shelf	50	399	118
	Shelf break/upper slope	141	640	340
	Lower slope	364	757	559
GSA 10	Shelf	50	350	125
	Shelf break/upper slope	170	616	365
	Lower slope	339	693	594
GSA 11	Shelf	50	292	97
	Shelf break/upper slope	109	357	198
	Lower slope	219	725	496
GSA 16	Shelf	51	220	94
	Shelf break/upper slope	108	654	333
	Lower slope	436	794	630
GSA 17	Shelf	50	235	91
	Shelf-break/upper slope	62	332	180
GSA 18	Shelf	50	349	104
	Shelf-break/upper slope	111	397	270
	Lower-slope	247	732	501
GSA 20	Shelf	55	189	94
	Shelf break/upper slope	149	664	379
	Lower slope	483	800	654
GSA 22	Shelf	50	340	109
	Shelf break/upper slope	107	708	336
	Lower slope	337	791	579
GSA 23	Shelf	57	155	91
	Shelf break/upper slope	115	496	245

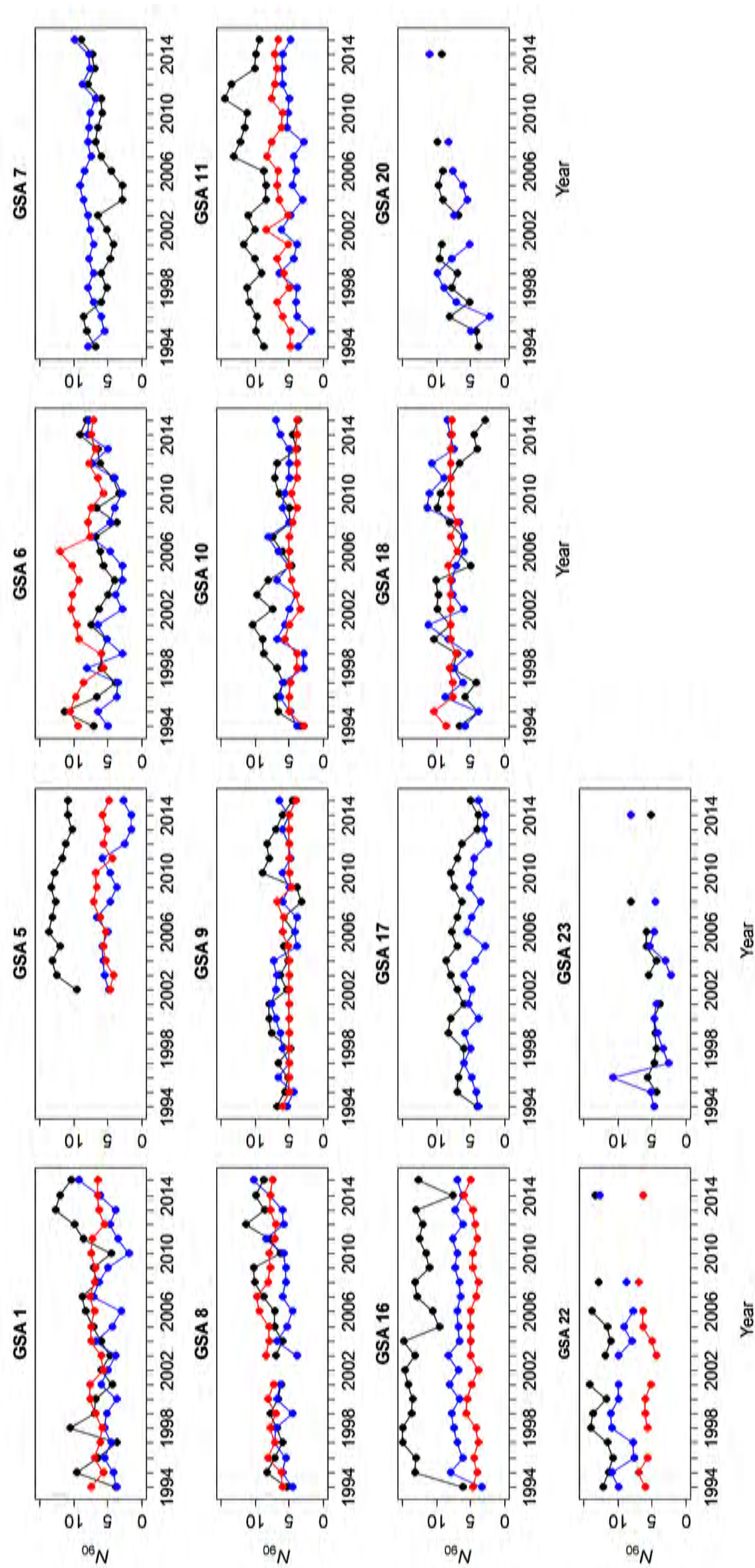


Figure 7.4: Mean values of N_{90} diversity index during the period 1994–2015 for each Geographical Sub-Area (GSA) and depth strata. Black dots: shelf; blue dots: shelf break/upper slope; and red dots: lower slope.

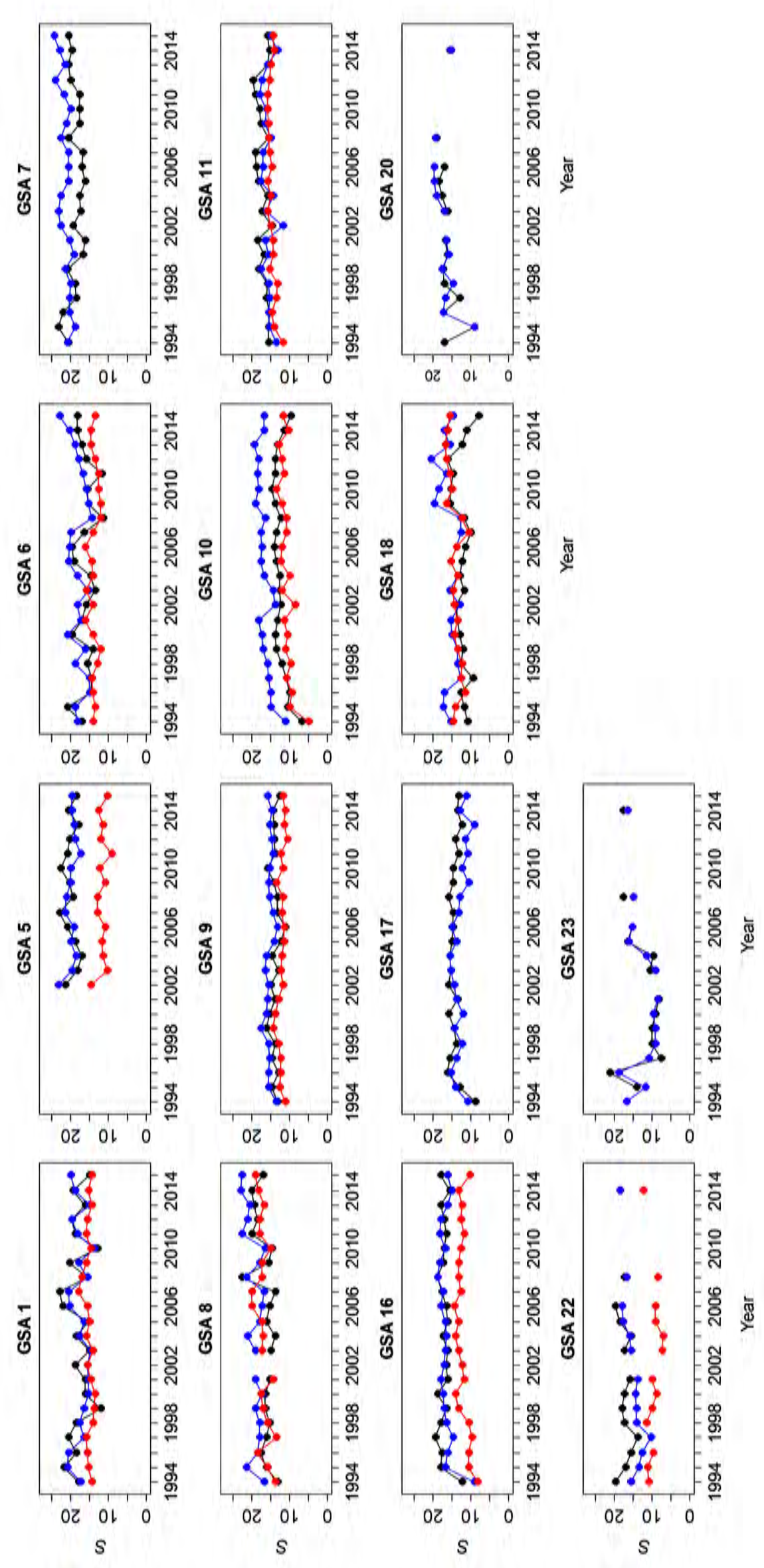


Figure 7.5: Mean values of species richness (S) during the period 1994–2015 for each Geographical Sub-Area (GSA) and depth strata. Black dots: shelf; blue dots: shelf break/upper slope; and red dots: lower slope.

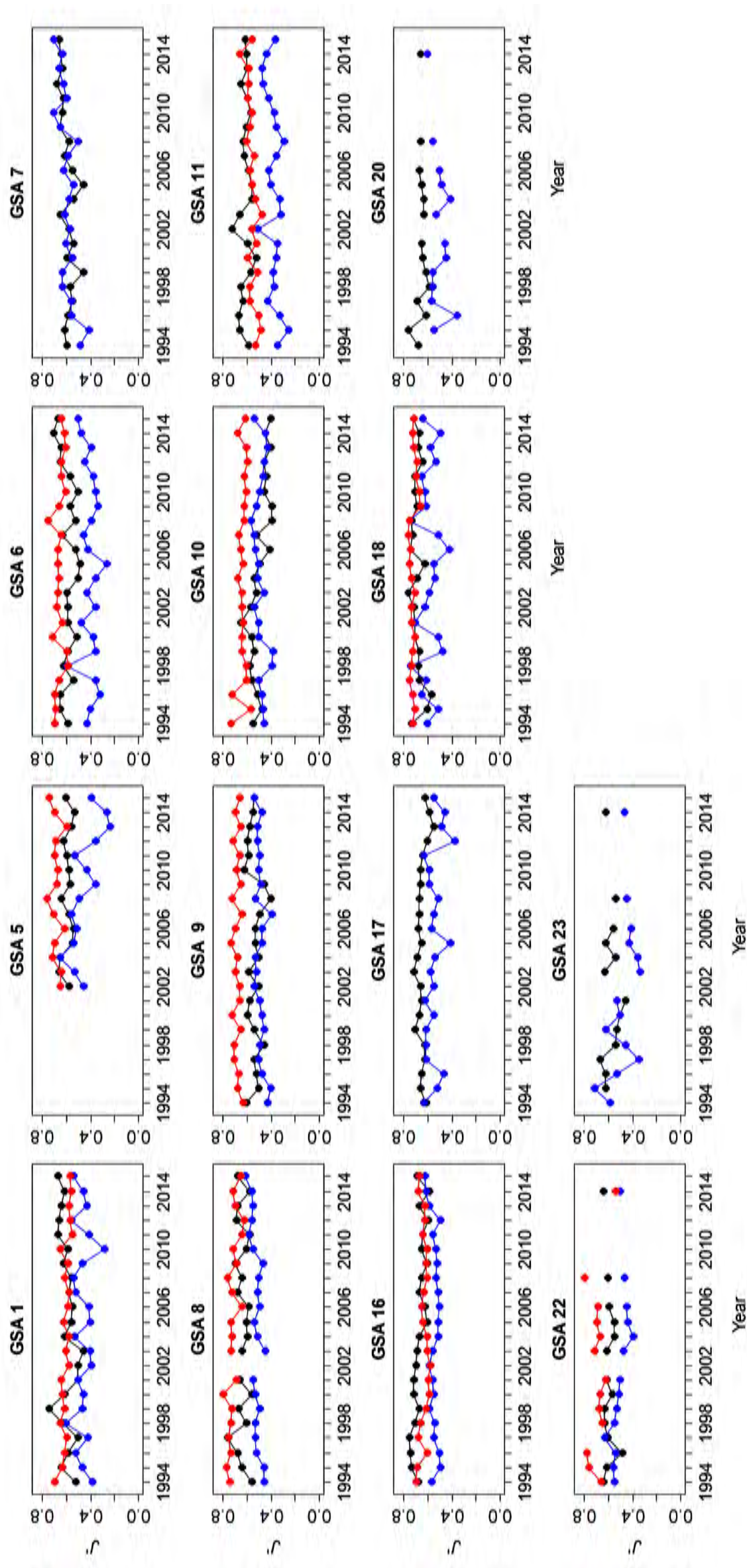


Figure 7.6: Mean values of Pielou's evenness (J') during the period 1994–2015 for each Geographical Sub-Area (GSA) and depth strata. Black dots: shelf; blue dots: shelf break/upper slope; and red dots: lower slope.

When quantitative analysis in temporal evolution of fishing effort could be made, the detected significance mainly showed a decreasing trend (Table 7.4; Figure 7.7). That is the case of the continental shelf in GSAs 1, 5, 6 and 7, the shelf break/upper slope in GSAs 1, 11, 17 and 18, and the lower slope in GSAs 5 and 11. It increased only in the continental shelf and the lower slope of GSA 18. Expert knowledge suggested increasing trends in fishing effort for the lower slope in GSAs 20, 22 and 23, and decreasing trends in the continental shelf of GSAs 8, 9, 16, 20, 22 and 23, and in the lower slope of GSAs 1, 7 and 8 (Table 7.4; Figure 7.7).

Table 7.3: Results of linear regressions analysis of the time series for N_{90} , species richness (S) and Pielou’s evenness (J') for each Geographical Sub-Area (GSA) and depth stratum (shelf, shelf break/upper slope and lower slope). Slope values of the adjusted linear regressions (b), adjusted R-squared values and p-values (p) are presented. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$. For GSAs 20, 22 and 23: a) results for time series 1994-2006; and b) results for time series 1994-2014.

index	GSA	Shelf			Shelf break/upper slope			Lower slope		
		b	Adjusted R-squared	p	b	Adjusted R-squared	p	b	Adjusted R-squared	p
N_{90}	GSA 1	0.209	0.051	*	0.047	-0.050	0.383	0.001	0.430	0.955
	GSA 5	-0.090	-0.010	0.287	-0.286	0.473	**	0.037	-0.052	0.565
	GSA 6	-0.027	-0.029	0.683	0.063	-0.034	0.321	-0.112	0.031	0.059
	GSA 7	0.041	0.200	0.462	0.079	0.391	*			
	GSA 8	0.195	-0.052	**	0.089	0.294	0.070	0.041	0.376	0.175
	GSA 9	-0.005	-0.044	0.923	-0.027	0.105	0.483	-0.013	-0.049	0.493
	GSA 10	-0.101	0.463	0.128	0.068	0.005	0.121	-0.014	0.025	0.523
	GSA 161	0.084	-0.031	0.136	0.090	0.119	*	0.083	0.338	*
	GSA 16	-0.066	0.455	0.398	0.019	0.025	0.593	0.012	-0.044	0.540
	GSA 17	0.012	0.088	0.540	0.013	0.083	0.798			
	GSA 18	-0.036	0.004	0.647	0.141	-0.046	*	-0.036	0.031	0.111
	GSA 20a	0.487	0.503	**	0.115	-0.066	0.553			
	GSA 20b	0.315	-0.066	**	0.225	0.007	0.069			
	GSA 22a	0.054	-0.065	0.577	-0.110	0.023	0.289	-0.053	-0.003	0.351
	GSA 22b	0.064	-0.070	0.279	0.044	0.344	0.579	0.015	0.045	0.706
	GSA 23a	0.075	0.061	0.231	-0.156	-0.007	0.360			
	GSA 23b	0.099	-0.090	0.098	0.038	0.152	0.740			
S	GSA 1	-0.044	-0.040	0.658	0.010	-0.049	0.898	0.036	0.005	0.305
	GSA 5	0.013	-0.082	0.914	-0.136	0.092	0.154	-0.089	-0.005	0.351
	GSA 6	-0.030	-0.044	0.728	0.090	0.018	0.254	-0.017	-0.041	0.674
	GSA 7	-0.055	-0.017	0.427	0.142	0.331	**			
	GSA 8	0.161	0.169	*	0.149	0.180	*	0.134	0.203	*
	GSA 9	-0.027	-0.026	0.504	-0.023	-0.026	0.505	-0.061	0.151	*
	GSA 10	0.122	0.138	*	0.197	0.411	***	0.165	0.336	**
	GSA 11	0.064	0.026	0.226	0.041	-0.017	0.433	0.080	0.227	*
	GSA 16	0.026	-0.035	0.600	0.112	0.101	0.082	0.105	0.145	*
	GSA 17	0.010	-0.048	0.861	-0.130	0.196	*			
	GSA 18	0.041	-0.031	0.550	0.109	0.055	0.152	0.142	0.278	**
	GSA 20a	0.297	0.149	0.118	0.582	0.492	**			
	GSA 20b	0.166	0.072	0.182	0.230	0.117	0.136			
	GSA 22a	0.099	-0.042	0.471	0.359	0.410	*	-0.251	0.465	*
	GSA 22b	0.089	0.019	0.286	0.304	0.546	**	-0.031	-0.077	0.712
	GSA 23a	-0.021	-0.111	0.957	-0.095	-0.088	0.742			
	GSA 23b	0.274	0.035	0.257	0.134	-0.034	0.466			
J'	GSA 1	0.003	0.051	0.160	0.000	-0.050	0.988	-0.004	0.430	***
	GSA 5	-0.003	-0.010	0.370	-0.020	0.473	**	0.002	-0.052	0.562
	GSA 6	0.001	-0.029	0.533	0.001	-0.034	0.589	-0.002	0.031	0.210
	GSA 7	0.004	0.200	*	0.007	0.391	**			
	GSA 8	0.000	-0.052	0.937	0.004	0.294	**	-0.004	0.376	**
	GSA 9	0.001	-0.044	0.745	0.002	0.105	0.077	0.000	-0.049	0.874
	GSA 10	-0.008	0.463	***	0.002	0.005	0.304	-0.002	0.025	0.229
	GSA 11	-0.001	-0.031	0.554	0.004	0.119	0.064	0.004	0.338	**
	GSA 16	-0.005	0.455	***	0.002	0.025	0.230	0.000	-0.044	0.729
	GSA 17	-0.002	0.088	0.098	-0.004	0.083	0.104			
	GSA 18	0.002	0.004	0.312	-0.001	-0.046	0.790	-0.001	0.031	0.211
	GSA 20a	-0.003	-0.023	0.406	-0.003	-0.090	0.688			
	GSA 20b	-0.001	-0.066	0.663	0.004	0.007	0.320			
	GSA 22a	-0.002	-0.059	0.549	-0.013	0.673	***	-0.003	-0.042	0.461
	GSA 22b	0.001	-0.070	0.710	-0.007	0.344	*	-0.004	0.045	0.237
	GSA 23a	-0.004	-0.065	0.548	-0.018	0.329	*			
	GSA 23b	0.000	-0.090	0.937	-0.009	0.152	0.093			

In 6 of the 7 cases in which an increment of N_{90} was detected, it coincided with a decrease in fishing effort (Tables 7.3 and 7.4; Figure 7.7). Out of the 11 cases showing increments in S , only in 3 cases the increase of S was coupled with a decrease in fishing effort. In 5 cases there was no trend in fishing effort, while in only one case the increase of S was coupled with increasing fishing effort. In 2 cases, no information on the temporal evolution of fishing effort was available (Tables 7.3 and 7.4; Figure 7.7).

10 GSAs showed significant trends in J' ; in 2 of them J' increased and fishing effort decreased, while 3 GSAs showed a decrease in both J' and fishing effort. 2 GSAs showed a decrease in J' coupled with no trend in fishing effort, while no information on fishing effort trend was available in 3 cases (Tables 7.3 and 7.4; Figure 7.7).

Table 7.4: Results of linear regression analysis of the time series of fishing effort of the longest series available for each Geographical Sub-Area (GSA) and depth stratum (shelf, shelf break/upper slope and lower slope). Slope values of the adjusted linear regressions (b), adjusted R-squared values and p-values (p) are presented. Qualitative values of slopes are obtained from expert knowledge. *: $p < 0.05$; **: $p < 0.01$; and ***: $p < 0.001$, ns: non-significant.

GSA	Shelf			Shelf break/upper slope			Lower slope		
	b	Adjusted R-squared	p	b	Adjusted R-squared	p	b	Adjusted R-squared	p
GSA 1	-8.800	0.717	*	-10.890	0.865	***	Decreasing		
GSA 5	-5.118	0.898	***	7.500	0.163	0.175	-7.530	0.526	**
GSA 6	-11.659	0.808	***	3.248	0.071	0.204	0.000	0.510	0.117
GSA 7	-13.821	0.765	**				Decreasing		
GSA 8	Decreasing						Decreasing		
GSA 9	Decreasing			1.820	-0.081	0.874	8.109	-0.088	0.669
GSA 10	Increasing		ns	-7.385	0.197	0.063	Decreasing		ns
GSA 11	63.572	0.390	0.058	-13.226	0.372	*	-25.227	0.867	***
GSA 16	Decreasing						-4.700	0.167	0.272
GSA 17	9.617	-0.054	0.467	-6.822	0.360	*	Decreasing		ns
GSA 18	75.448	0.644	**	-14.548	0.581	*	29.516	0.301	*
GSA 20	Decreasing						Increasing		
GSA 22	Decreasing						Increasing		
GSA 23	Decreasing						Increasing		

	Shelf				Shelf break/upper slope				Lower slope			
	N_{90}	S	J'	FE	N_{90}	S	J'	FE	N_{90}	S	J'	FE
GSA 1		n.s.	n.s.		n.s.	n.s.	n.s.		n.s.	n.s.		
GSA 5	n.s.	n.s.	n.s.			n.s.		n.s.	n.s.	n.s.	n.s.	
GSA 6	n.s.	n.s.	n.s.		n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
GSA 7	n.s.	n.s.						-	-	-	-	
GSA 8			n.s.		n.s.			-	n.s.			
GSA 9	n.s.	n.s.	n.s.		n.s.	n.s.	n.s.	n.s.	n.s.		n.s.	n.s.
GSA 10	n.s.			n.s.	n.s.		n.s.	n.s.	n.s.		n.s.	n.s.
GSA 11	n.s.	n.s.	n.s.	n.s.		n.s.	n.s.					
GSA 16	n.s.	n.s.			n.s.	n.s.	n.s.	-	n.s.		n.s.	n.s.
GSA 17	n.s.	n.s.	n.s.	n.s.	n.s.		n.s.		-	-	-	n.s.
GSA 18	n.s.	n.s.	n.s.			n.s.	n.s.		n.s.		n.s.	
GSA 20		n.s.	n.s.		n.s.	n.s.	n.s.	-	-	-	-	
GSA 22	n.s.	n.s.	n.s.		n.s.			-	n.s.	n.s.	n.s.	
GSA 23	n.s.	n.s.	n.s.		n.s.	n.s.	n.s.	-	-	-	-	

Figure 7.7: Trends obtained from linear regression of N_{90} , species richness (S), Pielou’s evenness (J') and fishing effort (FE) for Geographical Sub-Areas (GSA) and depth stratum (shelf, shelf break/upper slope and lower slope). Trends obtained from the analysis are in continuous lines and trends from expert knowledge in discontinuous line and gray background. n.s.: non-significant trends. -: no data available. For GSAs 20, 22 and 23 trends of time series 1994-2014 are presented.

7.3.3 Spatial patterns

Mean values of N_{90} , S and J' showed differences between GSAs and depth strata (Figure 7.8). Regarding N_{90} , the continental shelf of GSAs 5, 11, 16 and 22 showed higher values than the rest of GSAs in this depth stratum and even than the shelf break/upper

slope and lower slope. Within the shelf break/upper slope, the highest values of N_{90} were estimated in GSAs 7, 16, 17, 18, 20 and 22, while on the lower slope the highest values were for GSAs 6, 8 and 18. S showed similar values on the continental shelf of all GSAs, with the exception of GSA 10 that showed a lower value. A similar situation was observed on the shelf break/upper slope, with similar values of S in all GSAs, except for GSA 17 with a lower value, and GSAs 7 and 8 that showed the highest values. On the lower slope, the values of S were similar in all GSAs, with the exception of GSAs 9, 10 and 16 that showed lower values. J' showed similar values on the continental shelf in all GSAs, except GSAs 9 and 10 which showed lower values. The same scenario was observed on the shelf break/upper slope, with similar values of J' in all GSAs, with the exception of GSAs 1, 5, 6 and 11 that showed lower values. On the lower slope, GSA 11 showed the lowest value of J' , while similar values were obtained in the rest of GSAs.

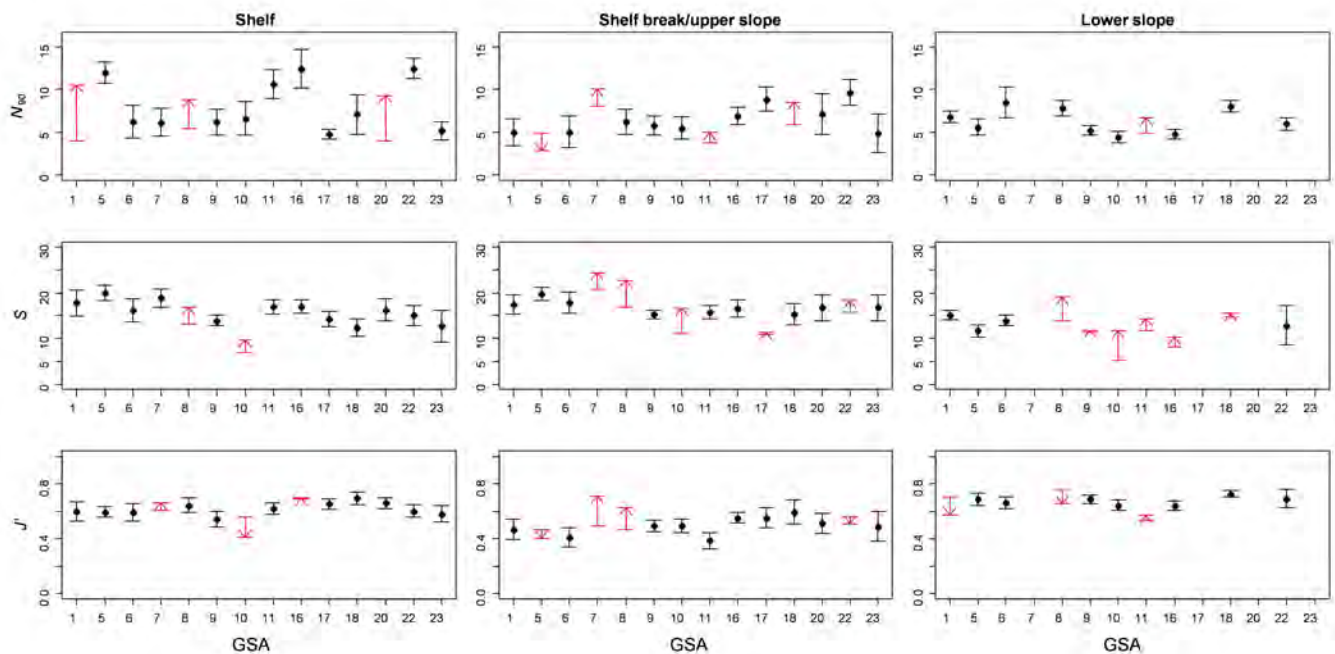


Figure 7.8: Mean values and standard deviations of N_{90} , species richness (S) and Pielou's evenness (J') during the whole times series considered for each Geographical Sub-Area (GSA) and strata (shelf, shelf break/upper slope and lower slope). In series with a significant temporal trend, values at the beginning and the end of the time series are presented in red. Red arrows point to the last value of the time series. Note that in some cases the trend of time series do not match with the arrows direction (see Figure 7.6). For GSAs 20, 22 and 23 the whole time series 1994-2014 have been considered.

The SIMPER analysis also showed differences in the species contribution between GSAs and depth strata (Tables 7.5 and 7.6). The species with the highest percentage contribution to within-group similarity on the continental shelf, shelf break/upper slope and lower slope, respectively, were the following: *Serranus hepatus*, *Gadiculus argenteus* and *Galeus melastomus* in GSA 1; *Scyliorhinus canicula*, *G. argenteus* and *Phycis blennoides* in GSA 5; *Merluccius merluccius*, *Micromesistius poutassou* and *P. blennoides* in GSA 6; *Mullus barbatus*, *G. argenteus* and *G. melastomus* in GSA 8; *M. merluccius*, *G. argenteus* and *P. blennoides* in GSA 9; *Glossanodon leioglossus*, *Chlorophthalmus agassizi* and *Hymenocephalus italicus* in GSA 10; *S. hepatus*, *G. leioglossus* and *P. blennoides* in GSA 11; *M. merluccius*, *G. argenteus* and *Nezumia sclerorhynchus* in GSA 16; *M. merluccius*, *Helicolenus dactylopterus* and *P. blennoides* in GSA 18; and *S. hepatus*, *Argentina sphyraena* and *N. sclerorhynchus* in GSA 22 (Table 7.5). The species with the highest percentage contribution to within-group similarity in GSA 7 were *T. minutus* on the continental shelf and *G. argenteus* on the shelf break/upper slope, *Lepidotrigla cavillone* on the continental shelf and *C. agassizi* on

the shelf break/upper slope in GSA 20, and *L. cavillone* on the continental shelf and *A. sphyraena* on the shelf break/upper slope in GSA 23. In GSA 17, *M. merluccius* was the species with the highest contribution on both the continental shelf and the shelf break/upper slope.

Table 7.5: Similarity Percentage (SIMPER) analysis summary table of species appearing in the 90% cutoff of within-group similarity. A is the mean abundance (individuals/km²) of each species, and %C is the mean value of the percentage contribution of each species to within-group similarity, taking into account each SIMPER made by group of Geographical Sub-Area (GSA), depth strata and year. Depth strata are: shelf, shelf break/upper slope (SB/US) and lower slope.

	A	%C		A	%C		A	%C
GSA 1 Shelf			GSA 1 SB/US			GSA 1 Lower slope		
<i>Serranus hepatus</i>	1629	31	<i>Gadiculus argenteus</i>	7829	37	<i>Galeus melastomus</i>	2533	26
<i>Pagellus acarne</i>	4684	24	<i>Helicolenus dactylopterus</i>	2509	16	<i>Nezumia aequalis</i>	2046	22
<i>Merluccius merluccius</i>	418	8	<i>Micromesistius poutassou</i>	7519	12	<i>Hoplostethus mediterraneus</i>	1460	15
<i>Cepola macrophthalma</i>	687	6	<i>Lepidopus caudatus</i>	6280	9	<i>Coelorinchus caelorhincus</i>	1315	13
<i>Mullus barbatus</i>	1237	6	<i>Merluccius merluccius</i>	1217	8	<i>Phycis blennoides</i>	364	8
<i>Callionymus maculatus</i>	514	3	<i>Phycis blennoides</i>	706	5	<i>Etmopterus spinax</i>	245	3
<i>Arnoglossus laterna</i>	237	3	<i>Scyliorhinus canicula</i>	491	3	<i>Trachyrincus scabrus</i>	744	2
<i>Serranus cabrilla</i>	338	2	<i>Coelorinchus caelorhincus</i>	873	2	<i>Micromesistius poutassou</i>	299	2
<i>Arnoglossus thori</i>	544	2						
<i>Scyliorhinus canicula</i>	158	2						
<i>Lesueurigobius sanzi</i>	255	1						
<i>Trachinus draco</i>	103	1						
GSA 5 Shelf			GSA 5 SB/US			GSA 5 Lower slope		
<i>Scyliorhinus canicula</i>	1348	25	<i>Gadiculus argenteus</i>	24060	68	<i>Phycis blennoides</i>	425	30
<i>Serranus hepatus</i>	1464	12	<i>Galeus melastomus</i>	2222	9	<i>Galeus melastomus</i>	440	24
<i>Serranus cabrilla</i>	743	11	<i>Coelorinchus caelorhincus</i>	1592	5	<i>Nezumia aequalis</i>	226	19
<i>Trachinus draco</i>	548	9	<i>Chlorophthalmus agassizi</i>	2906	5	<i>Hymenocephalus italicus</i>	174	7
<i>Mullus surmuletus</i>	1163	6	<i>Phycis blennoides</i>	461	3	<i>Notacanthus bonaparte</i>	55	4
<i>Lepidotrigla cavillone</i>	741	5	<i>Helicolenus dactylopterus</i>	506	3	<i>Lepidion lepidion</i>	93	4
<i>Merluccius merluccius</i>	1007	5				<i>Symphurus ligulatus</i>	45	3
<i>Glossanodon leioglossus</i>	28236	5						
<i>Chelidonichthys cuculus</i>	893	5						
<i>Trigloporus lastoviza</i>	448	4						
<i>Scorpaena notata</i>	163	1						
<i>Pagellus erythrinus</i>	179	1						
<i>Mullus barbatus</i>	312	1						
GSA 6 Shelf			GSA 6 SB/US			GSA 6 Lower slope		
<i>Merluccius merluccius</i>	2955	45	<i>Micromesistius poutassou</i>	57532	40	<i>Phycis blennoides</i>	698	43
<i>Trisopterus minutus</i>	2248	19	<i>Gadiculus argenteus</i>	9766	20	<i>Galeus melastomus</i>	381	22
<i>Cepola macrophthalma</i>	514	7	<i>Merluccius merluccius</i>	4285	19	<i>Micromesistius poutassou</i>	300	4
<i>Mullus barbatus</i>	487	7	<i>Trisopterus minutus</i>	1754	6	<i>Nezumia aequalis</i>	79	4
<i>Serranus hepatus</i>	408	7	<i>Helicolenus dactylopterus</i>	914	3	<i>Trachyrincus scabrus</i>	166	4
<i>Lepidotrigla cavillone</i>	250	3	<i>Scyliorhinus canicula</i>	811	3	<i>Hymenocephalus italicus</i>	55	3
<i>Pagellus erythrinus</i>	98	1				<i>Gadiculus argenteus</i>	422	3
<i>Lophius budegassa</i>	56	1				<i>Symphurus nigrescens</i>	67	2
						<i>Scyliorhinus canicula</i>	130	2
						<i>Coelorinchus caelorhincus</i>	128	2
						<i>Gaidropsarus biscayensis</i>	58	2
GSA 7 Shelf			GSA 7 SB/US			GSA 7 Lower slope		
<i>Trisopterus minutus</i>	6435	47	<i>Gadiculus argenteus</i>	6804	39			
<i>Merluccius merluccius</i>	3239	19	<i>Galeus melastomus</i>	1470	11			
<i>Eutrigla gurnardus</i>	1651	12	<i>Micromesistius poutassou</i>	7815	10			
<i>Serranus hepatus</i>	896	5	<i>Phycis blennoides</i>	561	8			
<i>Lepidotrigla cavillone</i>	1297	4	<i>Coelorinchus caelorhincus</i>	1068	7			
<i>Cepola macrophthalma</i>	561	2	<i>Helicolenus dactylopterus</i>	719	7			
<i>Lesueurigobius friesii</i>	513	2	<i>Lepidorhombus boscii</i>	417	6			
			<i>Trigla lyra</i>	565	5			
GSA 8 Shelf			GSA 8 SB/US			GSA 8 Lower slope		
<i>Mullus barbatus</i>	4127	20	<i>Gadiculus argenteus</i>	17009	47	<i>Galeus melastomus</i>	1246	29
<i>Lepidotrigla cavillone</i>	1287	19	<i>Galeus melastomus</i>	2979	11	<i>Hymenocephalus italicus</i>	535	19
<i>Scyliorhinus canicula</i>	941	15	<i>Chlorophthalmus agassizi</i>	4386	9	<i>Coelorinchus caelorhincus</i>	405	12
<i>Serranus hepatus</i>	1157	14	<i>Micromesistius poutassou</i>	2373	8	<i>Phycis blennoides</i>	248	8
<i>Pagellus erythrinus</i>	538	10	<i>Scyliorhinus canicula</i>	1119	7	<i>Helicolenus dactylopterus</i>	169	6
<i>Chelidonichthys cuculus</i>	352	5	<i>Lepidotrigla dieuzeidei</i>	1147	4	<i>Nezumia sclerorhynchus</i>	223	6
<i>Serranus cabrilla</i>	283	3	<i>Argentina sphyraena</i>	842	3	<i>Hoplostethus mediterraneus</i>	254	6
<i>Mullus surmuletus</i>	373	2	<i>Etmopterus spinax</i>	196	4			
<i>Trigloporus lastoviza</i>	162	1	<i>Chlorophthalmus agassizi</i>	280	4			
<i>Lepidotrigla dieuzeidei</i>	432	1						
GSA 9 Shelf			GSA 9 SB/US			GSA 9 Lower slope		
<i>Merluccius merluccius</i>	4334	55	<i>Gadiculus argenteus</i>	5253	52	<i>Phycis blennoides</i>	490	27
<i>Trisopterus minutus</i>	1076	16	<i>Merluccius merluccius</i>	4894	13	<i>Hymenocephalus italicus</i>	527	27
<i>Mullus barbatus</i>	551	8	<i>Phycis blennoides</i>	564	12	<i>Galeus melastomus</i>	439	22
<i>Serranus hepatus</i>	274	4	<i>Chlorophthalmus agassizi</i>	896	6	<i>Nezumia sclerorhynchus</i>	239	9
<i>Lepidotrigla cavillone</i>	271	4	<i>Galeus melastomus</i>	289	4	<i>Etmopterus spinax</i>	105	7
<i>Arnoglossus laterna</i>	110	3	<i>Micromesistius poutassou</i>	1322	4			
<i>Glossanodon leioglossus</i>	4801	2						

Table 7.5: Similarity Percentage (SIMPER) analysis summary table of species appearing in the 90% cutoff of within-group similarity. A is the mean abundance (individuals/km²) of each species, and %C is the mean value of the percentage contribution of each species to within-group similarity, taking into account each SIMPER made by group of Geographical Sub-Area (GSA), depth strata and year. Depth strata are: shelf, shelf break/upper slope (SB/US) and lower slope.

	A	%C		A	%C		A	%C
GSA 10 Shelf			GSA10 SB/US			GSA 10 Lower slope		
<i>Glossanodon leioglossus</i>	16087	12	<i>Chlorophthalmus agassizi</i>	11376	61	<i>Hymenocephalus italicus</i>	1152	49
<i>Merluccius merluccius</i>	2725	57	<i>Phycis blennoides</i>	479	8	<i>Nezumia sclerorhynchus</i>	351	19
<i>Lepidotrigla cavillone</i>	598	3	<i>Hymenocephalus italicus</i>	1128	7	<i>Phycis blennoides</i>	199	11
<i>Mullus barbatus</i>	502	7	<i>Gadiculus argenteus</i>	1290	7	<i>Galeus melastomus</i>	255	10
<i>Serranus hepatus</i>	490	4	<i>Merluccius merluccius</i>	1039	6	<i>Etmopterus spinax</i>	70	4
<i>Lepidopus caudatus</i>	463	2	<i>Helicolenus dactylopterus</i>	226	2			
<i>Trisopterus minutus</i>	236	2						
<i>Cepola macrophthalma</i>	91	3						
<i>Arnoglossus laterna</i>	80	2						
GSA 11 Shelf			GSA11 SB/US			GSA 11 Lower slope		
<i>Serranus hepatus</i>	1751	26	<i>Glossanodon leioglossus</i>	77021	51	<i>Phycis blennoides</i>	879	31
<i>Merluccius merluccius</i>	2903	22	<i>Merluccius merluccius</i>	6301	13	<i>Hymenocephalus italicus</i>	818	20
<i>Lepidotrigla cavillone</i>	1131	9	<i>Trisopterus minutus</i>	5084	11	<i>Gadiculus argenteus</i>	8361	18
<i>Trisopterus minutus</i>	2474	9	<i>Argentina sphyraena</i>	4673	9	<i>Galeus melastomus</i>	987	12
<i>Mullus barbatus</i>	840	7	<i>Lepidotrigla dieuzeidei</i>	1590	5	<i>Chlorophthalmus agassizi</i>	3734	5
<i>Serranus cabrilla</i>	344	4	<i>Scyliorhinus canicula</i>	1175	4	<i>Etmopterus spinax</i>	122	3
<i>Chelidonichthys cuculus</i>	368	3				<i>Merluccius merluccius</i>	848	2
<i>Scyliorhinus canicula</i>	335	3						
<i>Mullus surmuletus</i>	200	2						
<i>Trigloporus lastoviza</i>	191	2						
<i>Trachinus draco</i>	105	2						
<i>Argentina sphyraena</i>	2800	2						
<i>Citharus linguatula</i>	227	1						
GSA 16 Shelf			GSA16 SB/US			GSA 16 Lower slope		
<i>Merluccius merluccius</i>	970	25	<i>Gadiculus argenteus</i>	5100	26	<i>Nezumia sclerorhynchus</i>	982	40
<i>Serranus hepatus</i>	785	11	<i>Merluccius merluccius</i>	1622	20	<i>Hymenocephalus italicus</i>	573	19
<i>Lepidotrigla cavillone</i>	1327	10	<i>Chlorophthalmus agassizi</i>	3368	14	<i>Galeus melastomus</i>	318	17
<i>Chelidonichthys cuculus</i>	548	7	<i>Coelorinchus caelorhincus</i>	1231	10	<i>Nezumia aequalis</i>	383	7
<i>Mullus barbatus</i>	580	7	<i>Hymenocephalus italicus</i>	768	8	<i>Hoplostethus mediterraneus</i>	134	5
<i>Mullus surmuletus</i>	261	5	<i>Phycis blennoides</i>	314	7	<i>Phycis blennoides</i>	79	3
<i>Raja miraletus</i>	302	5	<i>Lepidopus caudatus</i>	2220	6			
<i>Serranus cabrilla</i>	181	4						
<i>Citharus linguatula</i>	234	3						
<i>Argentina sphyraena</i>	912	2						
<i>Trisopterus minutus</i>	280	2						
<i>Trigloporus lastoviza</i>	131	2						
<i>Arnoglossus laterna</i>	116	2						
<i>Lepidotrigla dieuzeidei</i>	588	2						
<i>Scyliorhinus canicula</i>	102	2						
<i>Zeus faber</i>	52	2						
<i>Trachinus draco</i>	77	1						
GSA 17 Shelf			GSA17 SB/US			GSA 17 Lower slope		
<i>Merluccius merluccius</i>	931	28	<i>Merluccius merluccius</i>	2155	43			
<i>Mullus barbatus</i>	1344	20	<i>Micromesistius poutassou</i>	3434	33			
<i>Trisopterus minutus</i>	861	18	<i>Trisopterus minutus</i>	312	5			
<i>Serranus hepatus</i>	1150	13	<i>Lepidopus caudatus</i>	489	5			
<i>Cepola macrophthalma</i>	327	6	<i>Gadiculus argenteus</i>	379	3			
<i>Lepidotrigla cavillone</i>	359	2	<i>Lesueurigobius friesii</i>	201	2			
<i>Merlangius merlangus</i>	161	2						
<i>Eutrigla gurnardus</i>	108	2						
GSA 18 Shelf			GSA18 SB/US			GSA 18 Lower slope		
<i>Merluccius merluccius</i>	939	43	<i>Helicolenus dactylopterus</i>	466	11	<i>Phycis blennoides</i>	405	20
<i>Trisopterus minutus</i>	424	20	<i>Chlorophthalmus agassizi</i>	663	10	<i>Nezumia sclerorhynchus</i>	305	14
<i>Mullus barbatus</i>	317	7	<i>Micromesistius poutassou</i>	823	8	<i>Galeus melastomus</i>	282	13
<i>Serranus hepatus</i>	175	6	<i>Glossanodon leioglossus</i>	2993	7	<i>Hoplostethus mediterraneus</i>	319	11
<i>Lepidotrigla cavillone</i>	376	4	<i>Argentina sphyraena</i>	1378	6	<i>Coelorinchus caelorhincus</i>	318	10
<i>Chelidonichthys cuculus</i>	232	4	<i>Lepidopus caudatus</i>	338	4	<i>Hymenocephalus italicus</i>	254	10
<i>Arnoglossus laterna</i>	106	3	<i>Gadiculus argenteus</i>	587	4	<i>Etmopterus spinax</i>	167	9
<i>Cepola macrophthalma</i>	81	2	<i>Phycis blennoides</i>	109	4	<i>Helicolenus dactylopterus</i>	117	4
<i>Lesueurigobius friesii</i>	74	2	<i>Chelidonichthys cuculus</i>	470	4			
			<i>Scyliorhinus canicula</i>	146	3			
			<i>Lepidorhombus boscii</i>	65	2			
			<i>Arnoglossus rueppelii</i>	153	2			
			<i>Lepidotrigla cavillone</i>	238	2			
			<i>Merluccius merluccius</i>	895	25			

Table 7.5: Similarity Percentage (SIMPER) analysis summary table of species appearing in the 90% cutoff of within-group similarity. A is the mean abundance (individuals/km²) of each species, and %C is the mean value of the percentage contribution of each species to within-group similarity, taking into account each SIMPER made by group of Geographical Sub-Area (GSA), depth strata and year. Depth strata are: shelf, shelf break/upper slope (SB/US) and lower slope.

	A	%C		A	%C		A	%C
GSA 20 Shelf			GSA 20 SB/US			GSA 20 Lower slope		
<i>Lepidotrigla cavillone</i>	1299	26	<i>Chlorophthalmus agassizi</i>	6565	28			
<i>Serranus hepatus</i>	1416	24	<i>Gadiculus argenteus</i>	9073	24			
<i>Mullus barbatus</i>	1145	15	<i>Argentina sphyraena</i>	3257	14			
<i>Merluccius merluccius</i>	527	11	<i>Merluccius merluccius</i>	860	6			
<i>Arnoglossus laterna</i>	329	5	<i>Lepidopus caudatus</i>	444	4			
<i>Trisopterus minutus</i>	359	3	<i>Helicolenus dactylopterus</i>	361	4			
<i>Pagellus erythrinus</i>	272	2	<i>Scyliorhinus canicula</i>	187	3			
<i>Argentina sphyraena</i>	2318	2	<i>Peristedion cataphractum</i>	714	2			
<i>Citharus linguatula</i>	142	2	<i>Coelorinchus caelorhincus</i>	588	2			
			<i>Hymenocephalus italicus</i>	677	2			
			<i>Phycis blennoides</i>	129	2			
GSA 22 Shelf			GSA 22 SB/US			GSA 22 Lower slope		
<i>Serranus hepatus</i>	1774	19	<i>Argentina sphyraena</i>	12691	27	<i>Nezumia sclerorhynchus</i>	626	43
<i>Trisopterus minutus</i>	1666	13	<i>Gadiculus argenteus</i>	5823	18	<i>Hymenocephalus italicus</i>	575	14
<i>Merluccius merluccius</i>	1890	11	<i>Merluccius merluccius</i>	505	10	<i>Trachyrincus scabrus</i>	251	9
<i>Citharus linguatula</i>	569	11	<i>Micromesistius poutassou</i>	2037	7	<i>Phycis blennoides</i>	119	8
<i>Lepidotrigla cavillone</i>	887	10	<i>Chlorophthalmus agassizi</i>	5423	6	<i>Coelorinchus caelorhincus</i>	317	8
<i>Mullus barbatus</i>	785	5	<i>Phycis blennoides</i>	169	5	<i>Hoplostethus mediterraneus</i>	105	6
<i>Chelidonichthys cuculus</i>	968	4	<i>Scyliorhinus canicula</i>	372	5	<i>Etmopterus spinax</i>	66	4
<i>Lophius budegassa</i>	178	4	<i>Lepidorhombus boscii</i>	151	4			
<i>Argentina sphyraena</i>	3244	4	<i>Coelorinchus caelorhincus</i>	1395	4			
<i>Serranus cabrilla</i>	221	3	<i>Hymenocephalus italicus</i>	801	3			
<i>Scyliorhinus canicula</i>	195	3	<i>Helicolenus dactylopterus</i>	148	2			
<i>Arnoglossus laterna</i>	164	2	<i>Lepidopus caudatus</i>	431	2			
<i>Dentex maroccanus</i>	458	2						
<i>Mullus surmuletus</i>	246	1						
GSA 23 Shelf			GSA 23 SB/US			GSA 23 Lower slope		
<i>Lepidotrigla cavillone</i>	2773	38	<i>Argentina sphyraena</i>	16100	49			
<i>Mullus barbatus</i>	3330	21	<i>Chlorophthalmus agassizi</i>	9753	10			
<i>Serranus hepatus</i>	2784	12	<i>Merluccius merluccius</i>	1305	9			
<i>Citharus linguatula</i>	262	7	<i>Chelidonichthys cuculus</i>	758	6			
<i>Pagellus erythrinus</i>	627	6	<i>Coelorinchus caelorhincus</i>	657	6			
<i>Arnoglossus laterna</i>	855	4	<i>Helicolenus dactylopterus</i>	330	5			
<i>Serranus cabrilla</i>	263	3	<i>Lepidotrigla cavillone</i>	400	2			
			<i>Phycis blennoides</i>	109	2			
			<i>Gadiculus argenteus</i>	3003	2			

Some species showed high percentage contribution to within-group similarity during most of the years of the time series and for most of the GSAs (Table 7.6). On the continental shelf, these species were *S. hepatus*, *L. cavillone*, *M. barbatus* and *M. merluccius*. On the shelf break/upper slope, only *G. argenteus* was present in all GSAs, while on the lower slope these species were *P. blennoides*, *G. melastomus* and *Etmopterus spinax*.

7.4 Discussion

The results have shown that demersal fish assemblages are highly structured along the Mediterranean. In fact, we have been able to identify three common assemblages in most GSAs corresponding to the continental shelf, shelf break/upper slope and lower slope strata of each area. There are only two GSAs, the North Adriatic Sea and Crete that did not present lower slope assemblages, due to the shallower depth surveyed in these areas compared to the rest of GSAs. Although the number of samples was not enough to follow their temporal series, the Gulf of Lions and the Eastern Ionian Sea also followed this depth structure. The results confirm the findings of previous works on the structure of demersal assemblages in the Mediterranean, showing that either for fishes (Ungaro et al., 1999; Labropoulou and Papaconstantinou, 2004; García-Ruiz et al., 2015) or/and other taxonomic groups (Tserpes et al., 1999; Colloca et al., 2003;

Massutí and Reñones, 2005) they are strongly organized along a depth gradient.

Table 7.6: Number of years that each species contributed to the 90% cutoff of within-group similarity, taking into account each Similarity Percentage (SIMPER) analysis by Geographical Sub-Area (GSA), depth stratum and year during the time series. Depth strata are: shelf, shelf break/upper slope (SB/US) and lower slope.

		GSA													
	Species	1	5	6	7	8	9	10	11	16	17	18	20	22	23
Shelf	<i>Argentina sphyraena</i>	-	-	-	-	3	4	1	9	13	-	2	9	6	-
	<i>Arnoglossus imperialis</i>	-	-	-	-	-	-	-	-	4	-	-	-	-	-
	<i>Arnoglossus laterna</i>	8	-	3	6	-	12	10	-	10	4	12	11	8	4
	<i>Arnoglossus rueppelii</i>	-	2	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Arnoglossus thori</i>	7	3	-	-	5	-	-	6	4	-	-	-	-	-
	<i>Callionymus maculatus</i>	12	-	1	2	-	-	-	-	-	2	3	-	-	-
	<i>Cepola macrophthalma</i>	16	-	18	11	-	4	13	4	1	18	11	-	3	-
	<i>Chelidonichthys cuculus</i>	-	14	-	-	17	-	1	15	19	3	13	7	12	-
	<i>Chelidonichthys obscurus</i>	-	-	-	-	-	-	-	-	7	-	-	-	-6	-
	<i>Citharus linguatula</i>	-	-	2	1	-	1	-	6	18	1	-	4	14	12
	<i>Deltentosteus collonianus</i>	-	-	-	-	-	-	-	1	-	-	-	-	-	-
	<i>Deltentosteus quadrimaculatus</i>	1	3	1	-	4	-	1	5	-	-	-	-	-	2
	<i>Dentex maroccanus</i>	-	-	-	-	-	-	-	-	-	-	-	-	6	-
	<i>Diplodus annularis</i>	-	-	-	-	-	-	-	1	-	-	-	2	1	-
	<i>Eutrigla gurnardus</i>	-	-	1	22	-	-	-	-	-	5	3	1	3	-
	<i>Glossanodon leioglossus</i>	-	12	-	-	-	8	17	-	-	-	-	-	-	-
	<i>Gymnammodytes cicerelus</i>	-	-	-	-	-	-	-	1	-	-	-	-	-	-
	<i>Helicolenus dactylopterus</i>	-	-	-	-	-	-	2	-	-	-	-	-	-	-
	<i>Lepidopus caudatus</i>	1	-	-	-	-	1	8	-	1	-	2	-	-	-
	<i>Lepidotrigla cavillone</i>	4	14	12	18	20	15	16	22	22	9	15	14	14	13
	<i>Lepidotrigla dieuzeidei</i>	1	-	-	-	4	-	-	1	6	-	-	3	2	-
	<i>Lesueurigobius friesii</i>	-	-	1	7	-	4	1	-	-	2	6	-	3	-
	<i>Lesueurigobius sanzi</i>	6	-	1	-	-	-	-	-	-	-	-	-	-	-
	<i>Lesueurigobius suerii</i>	-	-	-	-	-	-	4	-	-	-	-	-	-	-
	<i>Lophius budegassa</i>	-	-	6	2	-	-	-	-	-	2	6	-	14	1
	<i>Merlangius merlangus</i>	-	-	-	-	-	-	-	-	-	10	-	-	-	-
	<i>Merluccius merluccius</i>	21	14	22	22	2	22	22	22	22	22	22	13	14	1
	<i>Microchirus boscanion</i>	1	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Micromesistius poutassou</i>	-	-	-	1	-	-	-	-	-	-	3	-	-	-
	<i>Mullus barbatus</i>	17	4	20	2	20	21	20	22	19	22	17	14	14	13
	<i>Mullus surmuletus</i>	-	14	-	-	7	-	-	10	17	-	-	-	4	1
	<i>Ophichthus rufus</i>	2	-	2	-	-	-	-	-	-	-	-	-	-	-
	<i>Pagellus acarne</i>	21	-	2	-	2	-	-	-	1	-	-	-	-	4
	<i>Pagellus bogaraveo</i>	5	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Pagellus erythrinus</i>	3	5	3	-	21	-	5	3	4	2	-	8	-	12
	<i>Phycis blennoides</i>	-	-	-	-	-	-	3	-	-	-	1	-	-	-
	<i>Pomatoschistus marmoratus</i>	1	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Pomatoschistus microps</i>	1	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Raja clavata</i>	-	2	-	-	-	-	-	-	-	-	-	-	2	-
	<i>Raja miraletus</i>	-	-	-	-	4	-	-	2	22	-	-	-	-	-
	<i>Scorpaena notata</i>	1	4	-	-	-	-	-	2	-	-	-	-	-	-
	<i>Scorpaena scrofa</i>	-	3	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Scyliorhinus canicula</i>	5	14	-	-	21	-	-	15	12	-	-	-	12	-
	<i>Serranus cabrilla</i>	10	14	-	-	13	-	-	20	21	-	-	2	14	4
	<i>Serranus hepatus</i>	22	14	20	20	20	22	18	22	21	22	18	13	14	5
	<i>Symphurus nigrescens</i>	2	-	1	-	-	-	-	-	-	-	1	-	2	-
	<i>Trachinus draco</i>	6	14	-	-	-	-	-	12	8	-	-	-	-	-
	<i>Trigloporus lastoviza</i>	-	14	-	-	2	-	-	11	11	-	-	-	-	-
	<i>Trisopterus luscus</i>	-	-	1	-	-	-	-	-	-	-	-	-	-	-
	<i>Trisopterus minutus</i>	-	2	20	22	-	22	6	22	5	22	22	7	14	-
	<i>Uranoscopus scaber</i>	-	-	-	-	-	-	-	-	3	-	-	-	-	-
	<i>Zeus faber</i>	-	3	-	-	1	-	-	1	10	-	-	1	-	-
SB/US	<i>Argentina sphyraena</i>	-	-	6	3	10	3	-	19	5	-	6	12	14	14
	<i>Arnoglossus rueppelii</i>	1	-	2	-	-	-	-	-	-	-	10	-	-	1
	<i>Callionymus maculatus</i>	2	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Cepola macrophthalma</i>	-	-	1	-	-	-	-	-	-	3	-	-	-	-
	<i>Chelidonichthys cuculus</i>	-	-	-	-	1	-	-	1	-	1	11	-	1	10
	<i>Chlorophthalmus agassizi</i>	-	12	-	3	18	18	22	-	20	-	15	11	8	6
	<i>Coelorinchus caelorhincus</i>	5	8	-	20	4	3	5	-	20	-	-	3	12	2
	<i>Epigonus denticulatus</i>	1	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Epigonus telescopus</i>	-	-	-	-	-	-	-	-	1	-	-	-	-	-
	<i>Gadiculus argenteus</i>	21	14	20	22	21	22	19	1	21	8	6	12	13	5
	<i>Galeorhinus galeus</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	<i>Galeus melastomus</i>	-	10	-	22	20	15	2	-	-	-	-	1	1	-
	<i>Glossanodon leioglossus</i>	-	-	-	-	2	-	-	22	-	-	7	-	-	-
	<i>Helicolenus dactylopterus</i>	17	4	11	21	1	7	5	-	7	1	22	8	9	5
	<i>Hoplostethus mediterraneus</i>	-	-	-	-	-	-	-	-	-	-	-	1	-	1
	<i>Hymenocephalus italicus</i>	-	2	-	-	-	1	19	-	20	-	-	5	11	2
	<i>Lepidopus caudatus</i>	10	-	1	-	-	1	5	-	15	10	5	5	2	-
	<i>Lepidorhombus boscii</i>	-	2	-	19	5	1	-	-	-	-	7	3	9	2
	<i>Lepidorhombus whiffiagonis</i>	-	-	-	-	-	-	-	-	-	1	1	-	-	-
	<i>Lepidotrigla cavillone</i>	-	-	-	-	-	-	-	-	-	-	2	-	-	3
	<i>Lepidotrigla dieuzeidei</i>	-	-	-	-	9	-	-	9	-	-	3	3	1	1
	<i>Lesueurigobius friesii</i>	-	-	-	-	-	-	-	-	-	7	2	-	-	1
	<i>Lophius budegassa</i>	-	-	1	-	-	-	-	-	-	2	-	-	2	1
	<i>Merluccius merluccius</i>	15	-	22	2	4	22	18	21	22	22	22	10	14	10
	<i>Micromesistius poutassou</i>	10	4	22	21	18	11	3	2	-	22	16	-	10	2
	<i>Mullus barbatus</i>	-	-	3	-	-	-	-	-	-	2	7	-	-	-
	<i>Mullus surmuletus</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	1

Table 7.6: Number of years that each species contributed to the 90% cutoff of within-group similarity, taking into account each Similarity Percentage (SIMPER) analysis by Geographical Sub-Area (GSA), depth stratum and year during the time series. Depth strata are: shelf, shelf break/upper slope (SB/US) and lower slope.

		GSA													
	Species	1	5	6	7	8	9	10	11	16	17	18	20	22	23
	<i>Nezumia sclerorhynchus</i>	-	-	-	-	-	-	-	-	-	-	-	2	1	-
	<i>Pagellus bogaraveo</i>	5	-	-	1	-	-	-	-	-	-	1	-	2	-
	<i>Peristedion cataphractum</i>	-	-	-	-	-	-	-	-	-	-	4	8	-	1
	<i>Phycis blennoides</i>	9	7	4	22	1	21	22	-	21	5	13	4	9	4
	<i>Scorpaena elongata</i>	1	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Scyliorhinus canicula</i>	10	-	8	1	20	-	-	8	-	-	10	4	13	-
	<i>Serranus hepatus</i>	3	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Symphurus nigrescens</i>	1	-	-	-	-	-	1	-	-	-	1	-	-	-
	<i>Synchiropus phaeton</i>	-	1	-	1	-	-	-	-	-	-	-	-	-	-
	<i>Trachyrincus scabrus</i>	-	-	-	1	-	-	-	-	-	-	-	-	-	-
	<i>Trigla lyra</i>	-	-	-	14	1	-	-	-	-	-	2	-	-	-
	<i>Trisopterus minutus</i>	-	-	12	-	-	1	-	19	-	14	-	3	4	-
	<i>Zeus faber</i>	-	-	-	-	-	-	-	-	-	-	1	-	-	1
Lower slope	<i>Alepocephalus rostratus</i>	1	-	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Argentina sphyraena</i>	-	-	-	-	-	-	-	1	-	-	-	-	-	-
	<i>Chimaera monstrosa</i>	-	-	-	-	-	-	-	-	1	-	3	-	2	-
	<i>Chlorophthalmus agassizi</i>	-	-	-	-	10	-	-	16	-	-	6	-	-	-
	<i>Coelorinchus caelorrhincus</i>	22	-	9	-	21	-	1	-	7	-	21	-	10	-
	<i>Epigonus denticulatus</i>	5	-	5	-	-	-	-	-	-	-	-	-	-	-
	<i>Etmopterus spinax</i>	13	7	2	-	13	21	7	16	1	-	20	-	5	-
	<i>Gadiculus argenteus</i>	2	-	15	-	4	-	-	22	-	-	-	-	-	-
	<i>Gaidropsarus biscayensis</i>	-	-	6	-	-	-	-	-	-	-	-	-	-	-
	<i>Galeus melastomus</i>	22	14	22	-	21	22	21	22	22	-	22	-	2	-
	<i>Glossanodon leioglossus</i>	-	-	-	-	-	-	-	1	-	-	-	-	-	-
	<i>Helicolenus dactylopterus</i>	5	-	9	-	19	-	-	7	1	-	16	-	-	-
	<i>Hoplostethus mediterraneus</i>	22	-	1	-	15	2	4	-	17	-	21	-	7	-
	<i>Hymenocephalus italicus</i>	-	11	13	-	21	22	21	22	21	-	20	-	13	-
	<i>Lepidion lepidion</i>	-	6	3	-	-	-	-	-	-	-	-	-	-	-
	<i>Lepidopus caudatus</i>	1	-	1	-	-	-	-	-	-	-	-	-	-	-
	<i>Lepidorhombus boscii</i>	-	-	3	-	1	-	-	1	-	-	-	-	1	-
	<i>Lophius budegassa</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	-
	<i>Merluccius merluccius</i>	-	-	-	-	-	-	-	8	-	-	3	-	1	-
	<i>Micromesistius poutassou</i>	6	-	20	-	-	-	-	-	-	-	1	-	-	-
	<i>Mora moro</i>	-	3	-	-	-	-	-	1	-	-	-	-	-	-
	<i>Nettastoma melanurum</i>	-	-	-	-	-	-	1	-	-	-	-	-	-	-
	<i>Nezumia aequalis</i>	22	14	18	-	-	1	-	-	3	-	-	-	-	-
	<i>Nezumia sclerorhynchus</i>	-	-	-	-	16	21	21	4	19	-	22	-	13	-
	<i>Notacanthus bonaparte</i>	-	5	5	-	-	-	-	-	-	-	-	-	-	-
	<i>Pagellus bogaraveo</i>	-	-	1	-	1	-	-	-	-	-	-	-	-	-
	<i>Phycis blennoides</i>	21	14	22	-	19	22	22	22	13	-	21	-	13	-
	<i>Polyacanthonotus rissoanus</i>	-	1	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Scyliorhinus canicula</i>	-	-	12	-	-	-	-	-	-	-	-	-	-	-
	<i>Symphurus ligulatus</i>	-	3	2	-	-	-	1	-	-	-	-	-	-	-
	<i>Symphurus nigrescens</i>	-	-	8	-	-	-	-	2	-	-	-	-	1	-
	<i>Trachyrincus scabrus</i>	11	-	13	-	2	3	-	-	-	-	1	-	9	-

Despite the similar bathymetric gradient along the Mediterranean, the results have shown differences in the bathymetric limitations and composition of demersal fish assemblages between GSAs. That is not surprising considering that oceanographic conditions vary between GSAs and bathymetric distributions of communities respond according to this variations. In fact we have incorporated cluster analysis to escape from the assumption that communities are structured according to MEDITS strata, and we have made an analysis based on real assemblages for each GSA. Therefore the analysis of demersal fish diversity based on cluster analysis for each particular area of the Mediterranean is more accurate than the generally used beforehand assignation of a depth stratum to the samples analysed for the whole Mediterranean.

Our results show a stability and even recovery of demersal fish diversity in the Mediterranean. Out of the 114 temporal series analysed, only 27% showed a significant trend, with an increasing pattern in 71% of the cases presenting significant trends. N_{90} and species richness (S) have shown increasing trends in most cases (87.5% and 84.6% respectively), while Pielou’s evenness (J') is the indicator that has shown the highest proportion of decreasing trends (60%). This stability has been also shown in the unique study analysing long temporal series from bottom trawl survey data (1994-2012) for

the whole Mediterranean (Granger et al., 2015). These authors took into account three scales of analysis corresponding to 18 GSAs, 7 biogeographical zones and 2 basins, along a depth ranging from 0 to 800 m. The assemblages by depth were not considered, which could explain why they did not detect any recovery.

The continuous increase of fisheries in the last decades has led to the overexploitation of the main commercial stocks in most of the Mediterranean areas (Colloca et al., 2013; Sartor et al., 2014). However, bottom trawl fisheries have suffered a recent decrease in the Mediterranean, due to the economic losses of this activity (Quetglas et al., 2017; Table 7.5) and the implementation of additional management measures, such as the prohibition of bottom trawling within 1.5 nautical miles from the coast (EC Regulation 1967/2006). However, this recent measure has possibly replaced part of the trawl fishing effort from the shelf to deeper bathymetric zones (Tserpes et al., 2011). Our results show that increasing trends in N_{90} and S and decreasing trends in J' coincide in some cases with decreasing trends in bottom trawl fishing effort. It could be, therefore, a cause and effect relation, because it is in accordance with the expected effect of fishing on biodiversity. The increasing trend in N_{90} with decreasing fishing effort reinforces the previous results that confirm the usefulness of this index when detecting the effects of fishing on demersal fish diversity. The increase of evenness with increasing fishing effort has been suggested for some authors (Murawski, 2000; Zhou et al., 2010) due to the reduction of dominant species by fishing (Cury et al., 2000; Rice, 2000) and confirmed from the study of the effects of fishing on evenness indices (D'Onghia et al. 2003; Chapter 6). However, the expected increase in S and decrease in J' with decreasing fishing effort are not always observed in our results. There are some differences in the aspects of diversity that each of these indices capture. Increasing values in N_{90} with decreasing fishing effort indicate an increase in the frequency of occurrence and the evenness of the distribution of species abundances due to expansion to areas presenting the most favourable environmental conditions. On the other hand an increase in S and decrease in J' with decreasing fishing effort implies an increase of the number of species and an increase of the dominance of some species, respectively. Although both components, number of species and evenness, are also affecting N_{90} the calculation of each of those indices are extremely different. N_{90} take into account the homogeneity or heterogeneity of all the samples of a stratum and year for each GSA in its calculation and involves the most frequent and abundant species in the group without losing species identity by the comparison among all the samples in the group. In contrast, S and J' in a group are calculated from their mean values and consequently species identity is lost. That is possibly explaining why extreme values of fishing effort were needed to detect the effects of fishing in S and J' in Chapter 6. In some cases, the N_{90} showed no trend when there was a trend in fishing effort and vice versa. That could be due to different causes. It is either too early to detect the effects of decreasing fishing effort on demersal fish diversity or the decrease is not so important to change the diversity trend. Similarly, increasing trends in fishing effort could not result in a decrease in fish diversity due to the adaptation of demersal fish communities to fishing exploitation.

It must also be considered that there is a high complexity in the evaluation of fishing effort in the whole area. Available temporal series used to analyse fishing effort are not covering the whole time series of demersal fish diversity in all cases (see Annex 2) and the inclusion of more years of the temporal series to the analysis could lead to different trends of fishing effort. In addition, as the nominal fishing effort spatio-temporal pattern on a Mediterranean wide level is not available, the use of different effort esti-

mates by area may increase the uncertainty of the model. Besides number of fishing vessels is a poor proxy for effort, because it is not accounting of other capacity changes (e.g., Lengths over all, or Kw), because it is not accounting of technological creep and because it is not accounting of temporal and spatial changes of fishing operations (Anticamara et al., 2011). For instance, despite the regulation of decrease in fishing capacity is in place since 1991, the GT of the fleets can be increasing because boats are decreasing in number (decommissioning) but increasing in size over time (e.g. Fortibuoni et al., 2017) or due to increased time of vessels trawling. This issue is enormously relevant for the Mediterranean Sea where fisheries are managed by effort control and technical measures in contrast to quotas (Norther EU seas; see Cardinale and Scarcella, 2017) and should be considered when interpreting the results. However in areas like Spanish and French Mediterranean, restrictions on hours of trawling would not permit an unlimited increase of fishing effort with decreasing number of vessels (REAL DECRETO 1440/1999, de 10 de septiembre; Arrêté n° 99-162 du 10 juin 1999). In any case, a more appropriate indicator than number of vessels should be used for fishing effort whenever is possible.

Regarding spatial patterns, we have not found the expected longitudinal decreasing western-eastern pattern in species richness observed in previous works on fish communities (Quignard and Tomasini, 2000; Coll et al., 2010). Moreover, this trend is not either observed for N_{90} and J' in any depth stratum. The absence of a western/eastern decreasing trend further suggests that primary production or temperature regime are possibly not the major factor explaining large scale patterns of diversity in demersal fish assemblages (Gaertner et al., 2007; Granger et al., 2015). However, it is difficult to compare our results to diversity values obtained with non-standardized data mainly collected from fish inventories from other works. Besides, and due to the limited sampling approach (i.e. data concerning only one guild of fishes or limited to specific depths, gear or habitat), some of regional inventories result useless for comparative studies (Psomadakis et al., 2012). Recent studies based mainly on standardized time series data also question the previously considered west-east diversity decreasing trend in the Mediterranean (Gaertner et al., 2013; Granger et al., 2015; Peristeraki et al., 2017).

The higher values of diversity are found on the continental shelf of insular areas, like the Balearic Islands, Sardinia, Sicily and the Aegean Sea. This higher diversity can be explained taking into account the peculiarities of the distinct biogeographic sectors within the Mediterranean (Lejeune et al., 2010) that can be characterized by the shallow water biota (Bianchi et al., 2012). In the Strait of Sicily, for example, the meeting of western and eastern Mediterranean species produces a peak in fish species richness in the central Mediterranean (Ben Rais Lasram et al., 2009; Garofalo et al., 2007). The greater sampling effort of this work compared to previous ones (Morri et al., 1999; Koukouras et al., 2001) could affect the unexpected high diversity values found in the Aegean Sea. The presence of algae facies deeper than 50 m on the Balearic Islands is likely to enhance demersal fish diversity in this area. Coralligenous and mærl communities are very characteristic of the Mallorca-Menorca continental shelf up to 85-90 m depth (Canals and Ballesteros, 1997; Ordines and Massutí, 2009) and it has been pointed out as a plausible reason to explain the differences observed between the coastal demersal resources of the Balearic Islands and the adjacent Iberian Peninsula (Massutí and Reñones, 2005). In fact, habitat type has shown to affect the distribution of demersal species, most of them being more abundant and showing a better condition in mærl and *Peyssonnelia* beds (Ordines and Massutí, 2009; Ordines et al., 2009,

2015), which have also shown high diversity of fish.

The results of SIMPER analysis reinforce the idea of mäerl and Peyssonnelia beds causing high diversity values also in the continental shelves of Sicily, Sardinia and the Aegean Sea. Species like *Serranus cabrilla*, *Scyliorhinus canicula* and *Mullus surmuletus*, whose in the Balearic Islands have shown to be more abundant in those habitats (Ordines and Massutí, 2009), contribute to N_{90} mainly just in this archipelago, Sardinia, Sicily and the Aegean Sea. Similar habitats to those found in the Balearic shelf have been reported in the Aegean sea (Georgiadis et al., 2009). The presence of a higher number of vulnerable species like demersal chondrichthyans in the Balearic Islands, Sardinia, Sicily and the Aegean Sea (Bertrand et al., 2000; Damalas and Vassilopoulou, 2011; Ramírez-Amaro et al., 2015) compared to adjacent areas also contribute to the higher fish diversity values found there.

The spatial distribution of the bottom trawl fishing effort by GSA shows that the number of vessels per km^2 is low on the continental shelf of Balearic Islands, Sardinia and the Aegean Sea (Colloca et al., 2017). The coincidence of areas with a low fishing effort with areas with a high diversity, is in accordance with previous works where higher values of N_{90} and S and lower values of J' were associated to areas with a low fishing effort (Chapter 6). The lower fishing effort exerted by these relatively smaller bottom trawl fleets in these areas could have preserved, at least to some extent, their fish diversity along with a better conservation of their sensitive and essential habitats, like mäerl and Peyssonnelia beds. These habitats are precisely those more affected by the low selectivity and damaging collateral effects of bottom trawling on seabed communities, which decrease the presence of biogenic habitats, leading to a reduction of the biodiversity in exploited bottoms (e.g. Norse and Watling, 1999; Smith et al., 2000; Hiddink et al., 2006).

Spatial patterns of demersal fish diversity on shelf break/upper slope and lower slope along the Mediterranean are different than those detected on the continental shelf. Thus, areas with the highest values of diversity on the continental shelf do not coincide with areas with highest values of diversity on the shelf break/upper slope and lower slope. Although the assignment of depth strata was different in previous works and the comparison is not straightforward, a different pattern on shelf and slope areas was also observed for species richness (Gaertner et al., 2007, 2013). This is likely due to differences on the distribution of cumulative threats to marine biodiversity, that are mainly concentrated in coastal areas and on the continental shelf of the Mediterranean (Coll et al., 2012), and to the presence of particular habitats on the shelf break and slope bottoms which can represent potential hotspots of biodiversity (Danovaro et al., 2010). In that sense, although the distribution of deep-sea diversity is different than the continental shelf one, it is affected by similar factors: changes in spatial distribution of fishing effort together with habitat type. For example, higher values of N_{90} on the slope of Northern Spain could be related to the presence of submarine canyons in the area where high values of biodiversity have been reported (see Fernandez-Arcaya, et al. 2017 for a review). However, the description of deep-sea habitats has just been implemented for some particular areas of the Mediterranean and this information is not exhaustive at all (Danovaro et al., 2010). Moreover, an intensive habitat mapping based on MEDITS samples would be useful to relate demersal fish assemblages to their corresponding habitats as made in some continental shelf areas (e.g. Ordines and Massutí, 2009).

The outcomes of the present study show that both at large temporal and spatial scale

bottom trawl fisheries have reduced diversity of demersal assemblages in the Mediterranean. However, in the recent decades a general stable scenario or even some recovery trend has been highlighted. This result was not expected if the alarming overexploitation status of Mediterranean stocks is taken into account. Besides, the use of diversity indices to study the effects of fishing on demersal assemblages is important mainly regarding the high multispecificity of the bottom trawl fishery in the Mediterranean (Caddy, 1993; Lleonart and Maynou, 2003). In this sense, a change from the assessment of demersal resources based in exploited monospecific stocks to another one based on the study of the whole demersal fish assemblages is needed. Therefore, the inclusion of species other than target ones made in this Chapter through diversity indices is important in the implementation of an EAF (Pikitch et al., 2004).

Chapter 8

GENERAL DISCUSSION



Chapter 8. General discussion

Diversity indices are widely used to describe biological communities and to detect the impact of the environmental factors and anthropogenic activities. This Thesis aimed to detect the impact of fishing activities and environmental variability on the Mediterranean demersal fish diversity. To do so, a multidimensional study of diversity at different spatial and temporal scales was performed using both fishery dependent and independent data. A new diversity index was also developed, called N_{90} , which is based on the species' contribution to the similarity within a group of samples, usually representing a community, as it is calculated from the SIMPER analysis.

The N_{90} diversity index has revealed a consistent response to fishing impacts, always showing lower values in impacted demersal fish communities. It has been confirmed in all chapters of the Thesis, regardless of the communities studied or the approach used. In a first step the effects of fishing and climate and oceanographic conditions on diversity were tested in a single bathymetric stratum, the deep shelf, of the Balearic Islands (Chapter 5). The communities analysed were progressively expanded, first to all the depth strata (shallow shelf, deep shelf, upper slope and middle slope) sampled in this archipelago (Chapter 6) and finally to the northern whole Mediterranean (Chapter 7). In all these cases, the assessment of the effect of fishing activities on diversity needed the quantification of the fishing effort, which has been done using different methodological approaches that included from categorical levels to continuous measures of fishing effort. Differences on diversity due to impacts of fishing effort were found in areas subjected to two (low vs. high levels of fishing effort in Chapter 5) and four (low vs. medium vs. high vs. very high levels of fishing effort in Chapter 6) contrasting levels of fishing effort. Besides, trends of temporal series of N_{90} and other diversity indices were compared to trends of temporal series of fishing effort, from both a quantitative (Chapter 6) and a qualitative (Chapter 7) point of view. The consistency of results support the hypothesis that fish assemblages subjected to fishing impacts reduce both the frequency of occurrence and the evenness of species abundances among samples, due to the retrieval of species populations to the localities presenting the most favourable conditions, reflected in a decrease of N_{90} . In that sense, we have been able to detect the effects of bottom trawl fishing on diversity of Mediterranean demersal fish communities, through changes in the distribution of their most representative species.

This Thesis allowed a complete description of demersal fish diversity in the Mediterranean through the estimation of different and complementary diversity aspects, such as species richness, evenness, and taxonomic and functional breadth of the species present in fish assemblages sampled from MEDITS. Each of these complementary diversity aspects, represented by several diversity indices highly correlated between them, have shown some kind of response to fishing effort, although they have not been confirmed from all approaches. Decreasing diversity with increasing fishing effort is detected in indices related to species, taxonomic and functional dimensions of diversity, meaning that in heavily fished areas reductions in the frequency of occurrence of some species together with a removal of taxonomic and functional variety are detected. In that sense, members of assemblages in impacted areas tend to be more closely related to each other taxonomically and more similar functionally (Martins et al., 2012). Contrary to this effect, an increase of indices related to the evenness component of diversity with increasing fishing effort is also detected, suggesting that fishing exploitation decreases the dominance of species of demersal fish communities (Zhou et al., 2010). N_{90} , S

(species richness) and J' (Pielou's evenness) are the indices that show a higher consistency among the results obtained in this Thesis, which is supported by their relationships among them. However the low correlation between N_{90} and any of the alpha, beta or gamma versions of J' suggests that results are highly dependent on the communities studied and the groups of samples taken into account to explore these relationships.

N_{90} is sensitive to environmental changes in communities impacted by fishing, which suggests the synergistic effects of fishing and climate change on demersal fish communities. This result has been obtained through the detection of more fluctuating dynamics in lower values of N_{90} associated to impacted demersal fish communities of the deep shelf of the Balearic Islands. Extreme climatic events, altogether with the significant interaction detected between fishing effort and year for all depth strata of the Balearic Islands for N_{90} , indicate that there is a contrasting sensitivity of diversity in impacted and non-impacted communities as revealed by a different response of the N_{90} index calculated for different levels of fishing effort. The synergies between the effects of fishing and environmental factors on demersal fish diversity have not been deduced from the study of any of the rest of diversity indices. In that sense, N_{90} has shown to be a very adequate diversity index for the monitoring of the Mediterranean fish communities, under the current context of general overfishing (Colloca et al., 2013; Vasilakopoulos et al., 2014; Cardinale and Scarcella, 2017) and water warming and changing of oceanographic conditions due to climate change in this area (Macias et al., 2013; Cramer et al., 2018; and references cited therein). In any case, the higher effects of environmental conditions on communities impacted by fishing, which are reflected in a decrease of demersal fish diversity, support the hypothesis that communities in a better state of exploitation are more capable to buffer adverse environmental conditions.

This Thesis has shown that differences in demersal fish diversity due to contrasting levels of fishing effort are mainly detected in communities where fishing pressure have remained relatively low: i.e. the continental shelf of the Balearic Islands. Our outcomes have also shown that although present diversity of demersal fish communities is the result of a long-term cumulative effect of fishing activity that has reduced diversity, it seems that a current recovery is taking place in some areas and bathymetric ranges throughout the Mediterranean. Lower levels of demersal fish diversity in highly impacted areas are related to the disappearance of vulnerable species and top predators (e.g. chondrichthyans), together with the regression of essential and sensitive fish habitats, due to the high fishing effort exerted on these grounds. For all that, the recovery of demersal fish diversity, due to the resilience and hence recovery of those vulnerable species and habitats can be attributed to the general decreasing trend of bottom trawl fishing effort during recent years. Trawl fishing activity in the Mediterranean has not been significantly reduced and much less the fishing capacity of this fleet and its fishing gears, that in some cases have increased. However the drastic reduction in the number of trawlers during the last two decades (Quetglas et al., 2017) must have compensated the increase of fishing activity resulting in a general decrease of bottom trawl fishing effort. In this scenario the recovery of vulnerable species is achievable but the possibility that final recovered communities would be very different to the non-impacted ones is also plausible. In that sense, the increase of demersal fish diversity would not mean a recovery of the original fish assemblages, but an adaptation to a new (and therefore transformed) state, with species less sensitive to fishing impacts and more compatible with bottom trawl exploitation.

The use of diversity indices to study the effects of fishing on demersal assemblages

is important, mainly regarding the high multispecificity of the bottom trawl fishery in the Mediterranean (Lleonart and Maynou, 2003). For that, in addition to the current monospecific assessment and advice for the management of trawl fisheries and their resources in the area, a complementary assessment based on the study of the whole demersal fish assemblages is needed. The inclusion of species other than target ones, through diversity indices, is important for the implementation of an ecosystem based fisheries assessment and management. In addition, the ecological sustainability of fisheries is a new demand of the new European Common Fisheries Policy (Regulation No. 1380/2013) that goes in line with the EAF. The use of indicators calculated from fishery independent data, like the obtained from MEDITS, can be also relevant in the context of the Marine Strategy Framework Directive¹, where community indicators like Conservation Status of Fish or Large Fish Indicator, among others, have been used to assess the environmental status of European waters (Directive 2008/56/EC of the European Parliament and of the Council, of 17 June 2008, establishing a framework for Community action in the field of marine environmental policy; IEO, 2012). However, to properly use diversity indices as indicators of the state of exploited communities, it is important to know how and why they respond to fishing effects. In that sense, the sensitivity of N_{90} to fishing effort and environmental factors, together with the traceability of the contributing species and its high interpretability, make this index suitable for the implementation of all these policies and directives.

In the Mediterranean Sea, the management of fisheries is based on the control of fishing capacity of the fleet, gears selectivity and the fishing activity in space and time (Russo et al., 2017). Because it allows for high resolution analyses of fishing activity and quantitative evaluations of fishing effort, at both spatial and temporal scales (Bastardie et al., 2010; Lee et al., 2010), VMS is nowadays a very powerful tool for fisheries assessment and management (Russo et al., 2013). VMS joint with Automatic Identification Systems are the unique sources of data to monitor the dynamics of fishing fleet that provides information at short spatial (e.g. few kilometres) and temporal (e.g. hours) scales. Therefore, these data can be overlapped to the spatio-temporal information obtained from scientific bottom trawl surveys and scientific observers on board fishing fleet. The use of spatial distributions of bottom trawl fishing effort through VMS data is a particularity of the present Thesis. The results have shown that the application of quantitative data to estimate fishing effort has been useful to detect the effects of fishing exploitation on demersal fish diversity. In fact, the estimation of fishing effort by trawl fishing grounds around the Balearic Islands from VMS data, calculated in Chapter 6, has allowed a quantitative and continuous analysis of the effects of bottom trawling on demersal fish diversity. A more detailed approach than in Chapter 7, where data on fishing effort were obtained from GFCM and STEFC working groups reports. Currently this is the only information available in Mediterranean to compare the impact of bottom trawling on demersal fish populations along the whole basin. Indeed, the outcomes of this Thesis are in line with other works, where VMS information has been shown to be the primary source of information to reveal both small and large scale impact of bottom trawling in Atlantic and Mediterranean European waters (Eigaard et al., 2017; Amoroso et al., 2018).

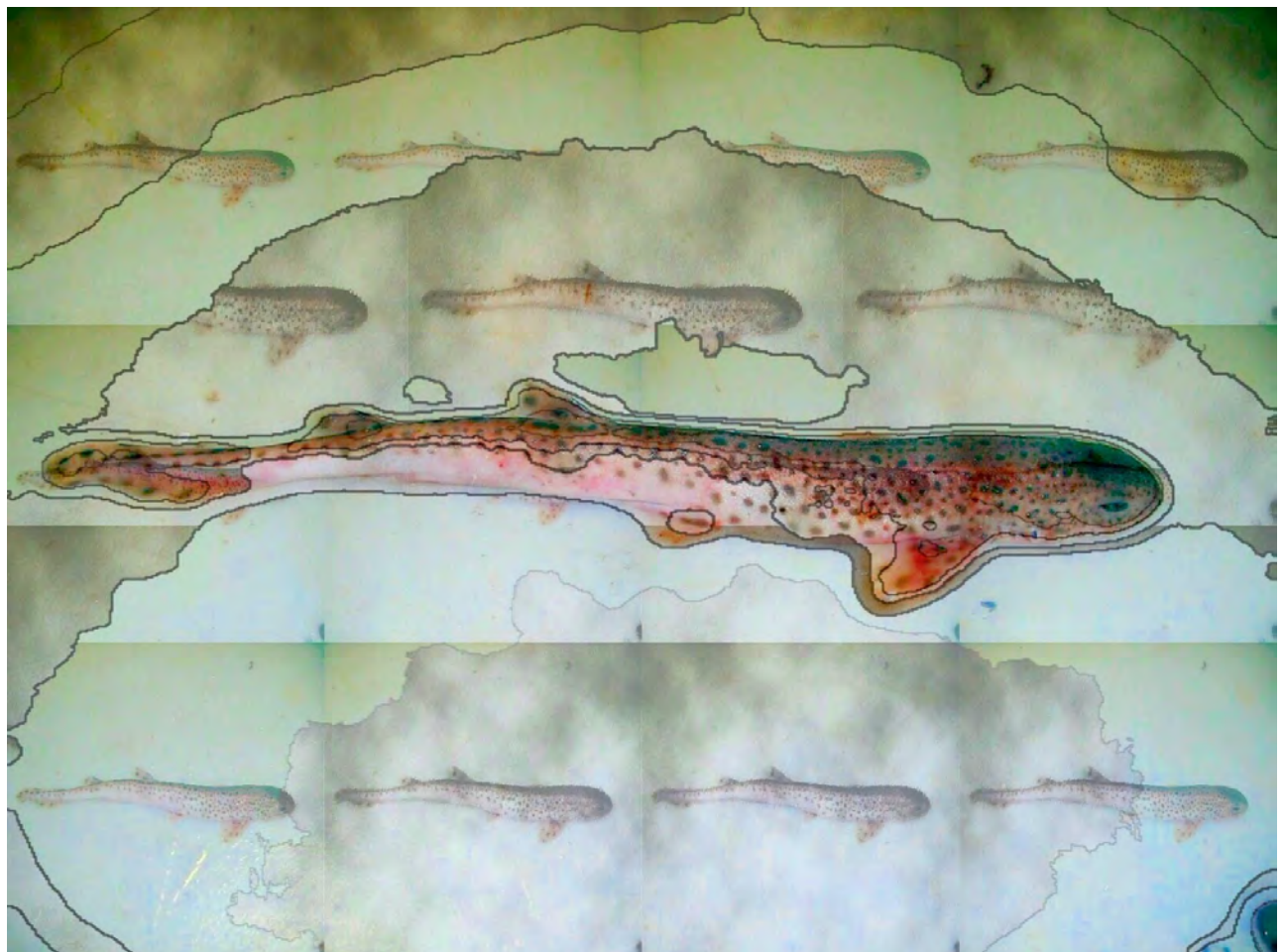
The future extended availability of VMS data and the widespread implementation of Automatic Identification Systems would allow the use of more precise estimations of fishing effort and permit more accurate studies of bottom trawl fishing effects on

¹http://ec.europa.eu/environment/marine/eu-coast-and-marine-policy/marine-strategy-framework-directive/index_en.htm.

demersal fish communities. However the effects of fishing on ecosystems could be also detected through the application of diversity indices to areas closed to bottom trawl fisheries such as Marine Protected Areas. This application would allow, not only avoiding problems related to the estimations of fishing effort, but also studying the evolution of communities from areas recently closed to fisheries. Some of the direct and indirect effects of exploitation may be diminished by fishing closures (Collie et al., 2000; Pipitone et al., 2000); and closed areas are useful in clarifying the recovery of ecosystems from fishing (Murawski et al., 2000; Badalamenti et al., 2002). In that sense, the future application of N_{90} to these protected areas could be usefull to compare communities of non-impacted and impacted areas and to monitor the potential recovery of diversity from fishing effects. Besides, future research is needed to implement the N_{90} index in other communities more than demersal fishes and to explore its response to impacts more than bottom trawl fishing ones.

Chapter 9

CONCLUSIONS



Chapter 9. Conclusions

Diversity index

9.1. A new diversity index based on the hypothesis that ‘communities subjected to fishing impacts may see reduced the frequency of occurrence and the evenness of the distribution of species abundances due to retreatment to areas presenting the most favourable environmental conditions’ was developed. The index, named N_{90} , is based on the results of Similarity Percentage (SIMPER) analysis and represents the number of species contributing up to ninety percent of within-group similarity in a group of samples. N_{90} uses the Bray-Curtis similarity index and its calculation is completed with a jack-knife resampling routine, allowing to get the mean value and its variability in the group of samples analysed. This index reports the number of the most important species structuring the community. The R script for the calculation of the N_{90} index and its variability was developed and also presented in this Thesis.

9.2. The N_{90} index was framed at the halfway between alpha Shannon’s H' and gamma species richness S . This favours the detection of changes in total number of species (gamma S), through variations in their frequency of occurrence, and in mean H' (alpha), through the variation in the evenness of species abundance among samples. N_{90} was also positively correlated to beta S , indicating that the occurrence of some species that would increase gamma diversity, although not being frequent enough to change alpha diversity, could be accounted in the N_{90} .

9.3. N_{90} showed a high sensitivity to the impacts of fishing. It showed significant differences between high and low levels of fishing effort, the latter showing always the highest values. This sensitivity to fishing impact can be also inferred from the summary list of species contributing to N_{90} . Vulnerable and overexploited species, like sharks or teleosts, contributed more to the N_{90} index in the assemblages subjected to lower fishing pressure. N_{90} also showed inter-annual variability in assemblages highly impacted by fishing, which is in agreement with that species and communities subjected to higher fishing pressure are more sensitive to environmental changes. By contrast, ‘traditional’ diversity indices such as species richness S , Shannon’s H' , Pielou’s evenness J' , Margalef’s d and Simpson’s $1 - \lambda'$ showed almost null sensitivity to fishing pressure.

9.4. The application of N_{90} may be an alternative to ‘traditional’ diversity indices to monitor fishing impacts because it displays a clear response, with significantly lower values in impacted assemblages. Contrary to ‘traditional’ diversity indices, N_{90} gives a direct assessment of the diversity, i.e. the whole set of samples is involved in the calculation, instead of operating at sample level and averaging values afterwards or, alternatively, pooling data from different samples. The N_{90} units, number of species, facilitate the interpretability of results at the same time that this index is less dependent on sample size than S , due to rare species are not usually among the main contributors to within-group similarity. Moreover, the species identity is not lost and the SIMPER tables allow an easier interpretation of the evolution of the index through a temporal series and/or between different fishing impact regimes.

Fish diversity

9.5. The analysis of sixteen diversity indices revealed that the demersal fish communities of the Balearic Islands can be described from four groups of indices, each one related to complementary aspects of diversity: (i) species richness, represented by indices highly influenced by the number of species (S , d and $Fisher$); (ii) evenness, represented by indices that take into account the relative abundance of the species ($N1$, $N2$, H' , $Brillouin$, $ES(10)$, $ES(20)$, $1 - \lambda'$, J' , Δ , N_∞ and $F\Delta$); (iii) taxonomy, represented by indices influenced by the taxonomic variability (Δ^*); and (iv) functionality, represented by indices influenced by the functional variability ($F\Delta^*$).

9.6. Fishing impact decreases the value of diversity indices related to species richness, taxonomic and functional aspects, indicating that along with the loss of species, the remaining members of the assemblages in impacted areas tend to be more closely related to each other taxonomically and more similar functionally. The opposite occurs for indices related to the evenness aspect of diversity, i.e. an increase of the evenness with increasing fishing impact, suggesting that fishing exploitation decreases the abundance of the dominant species of demersal fish communities.

9.7. The contrasting results obtained between the continental shelf and the slope gave relevant information about the current state of the demersal fish communities inhabiting these depths and habitats around the Balearic Islands. Except for the evenness, in the middle slope there were no clear differences in fish diversity between different levels of fishing effort. Some vulnerable species of elasmobranchs are no longer present in survey samples, indicating that major changes in demersal fish communities off Balearic Islands may have happened long before the period of the present study (2006-2014). On the other hand, demersal fish communities on the continental shelf do not seem to be as transformed as those on the slope, probably due to their greater extent and the lower fishing effort received. In this sense, changes in diversity are only detectable in those communities where the levels of fishing pressure have remained relatively low.

9.8. The analysis of data from Mediterranean International Bottom Trawl Surveys (MEDITS) developed between 1994 and 2015 at 14 Geographic Sub Areas (GSAs), considered by the General Fisheries Commission for the Mediterranean (GFCM), along the whole northern Mediterranean, allowed to confirm that fish communities are strongly organized along a depth gradient in the whole basin. The fish communities were structured in three bathymetric assemblages that were common to most GSAs: the continental shelf (mean depths: 76-125 m), shelf break/upper slope (mean depths: 180-421 m) and lower slope (mean depths: 496-699 m).

9.9. The temporal evolution of diversity indices showed a general stable scenario or even some recovery trends of demersal fish diversity along the northern Mediterranean during the last two decades. The increasing trends in N_{90} and species richness and decreasing trends in evenness coincided in some cases with a reduction in bottom trawl fishing effort. The expected longitudinal decreasing western-eastern pattern in species richness, observed in previous works on fish communities in the Mediterranean was not detected. This suggests that primary production or temperature regimes are not the major factor explaining large scale patterns of diversity in these communities.

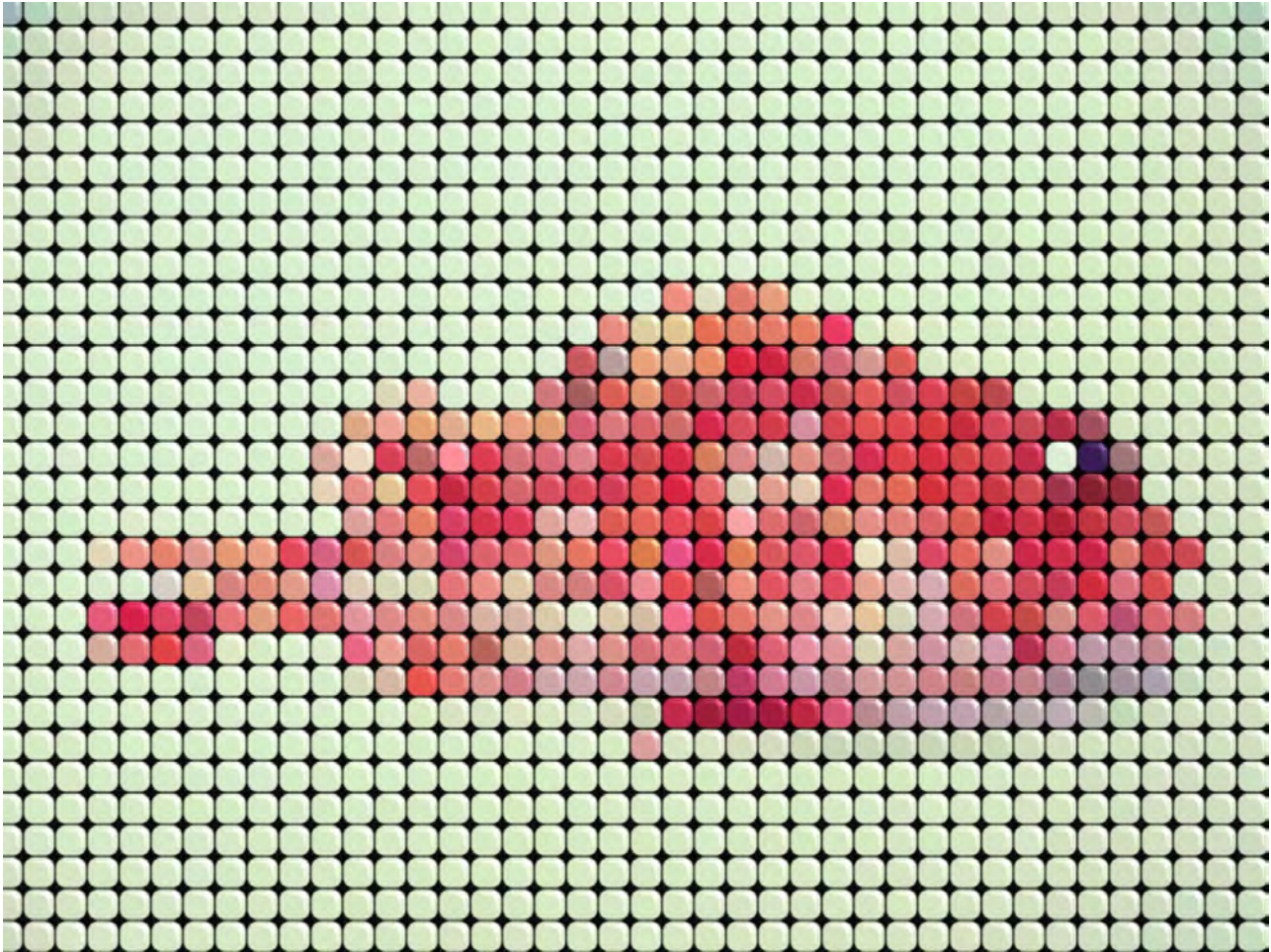
9.10. Higher values of diversity were found on the continental shelf of Sicily,

Balearic Islands, Sardinia, and the Aegean Sea, coinciding for the last three areas with low bottom trawl fishing effort values. Besides, the presence of species like *Serranus cabrilla*, *Scyliorhinus canicula* and *Mullus surmuletus*, more abundant in Mediterranean essential fish habitats and sensitive habitats, contributed to N_{90} especially in all those areas. The presence of a higher number of vulnerable species like demersal chondrichthyans compared to adjacent areas also contribute to the higher fish diversity values found there.

9.11. The ecological sustainability of fisheries is a new demand of the new European Common Fisheries Policy (Regulation No. 1380/2013) that goes in line with the Ecosystem Approach to Fisheries (EAF). In fisheries with a marked multispecies character such as the Mediterranean bottom trawl fishery, incorporating diversity indices to study the effects of fishing on demersal assemblages may be particularly useful to complement the current monospecific assessment of target species populations. However, it is important to know what effect is expected on the selected diversity indices, as they can display different responses to anthropogenic impacts and environmental factors.

Chapter 10

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Chapter 10. References

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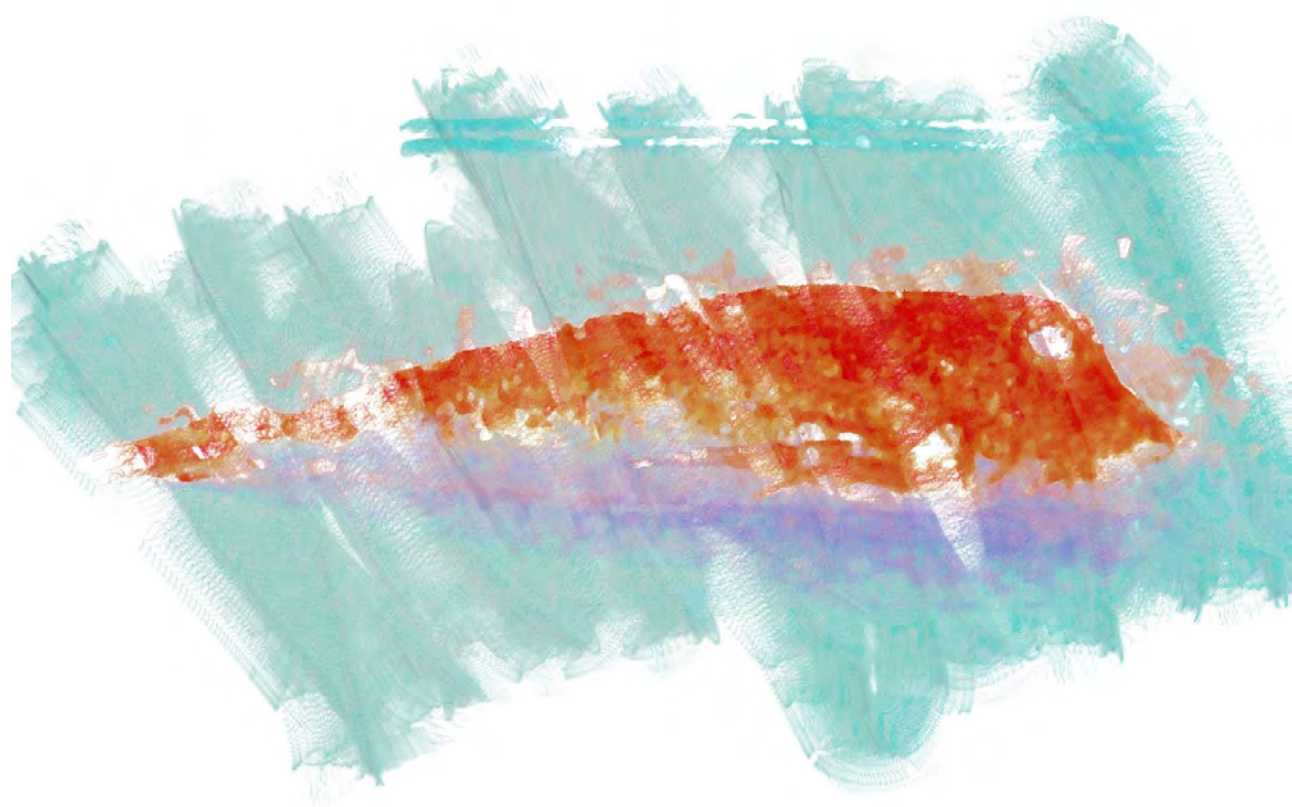
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Chapter 11

Appendix A



Annex 1. Demersal fish species considered for this Thesis by Geographical Sub-Areas (GSA). For Balearic Islands (GSA 5) the chapters in which the species is included are specified: 1) Chapter 4; 2) Chapter 5; 3) Chapter 6; 4) Chapter 7; and x) all chapters

GSA																			
Class	Order	Family	Species	Authority	1	5	6	7	8	9	10	11	16	17	18	20	22	23	
Actinopterygii	Anguilliformes	Congridae	<i>Ariosoma balearicum</i>	(Delaroche, 1809)	-	-	-	-	x	x	x	x	x	x	x	-	x	-	
Actinopterygii	Anguilliformes	Congridae	<i>Conger conger</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Anguilliformes	Congridae	<i>Gnathophis mystax</i>	(Delaroche, 1809)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Anguilliformes	Nemichthyidae	<i>Nemichthys scolopaceus</i>	Richardson, 1848	x	x ^{1,3,4}	x	x	-	x	x	x	x	-	x	-	x	-	
Actinopterygii	Anguilliformes	Netastomatidae	<i>Facciolella oxyrhyncha</i>	(Bellotti, 1883)	x	x ^{3,4}	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Anguilliformes	Netastomatidae	<i>Netastoma melanurum</i>	Rafinesque, 1810	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-	
Actinopterygii	Anguilliformes	Ophichthidae	<i>Apterichthys caecus</i>	(Linnaeus, 1758)	-	x ⁴	x	x	-	x	-	-	-	-	-	-	-	-	
Actinopterygii	Anguilliformes	Ophichthidae	<i>Dalophis imberbis</i>	(Delaroche, 1809)	-	-	-	-	-	x	x	x	x	-	x	-	-	-	
Actinopterygii	Anguilliformes	Ophichthidae	<i>Echelus myrus</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Anguilliformes	Ophichthidae	<i>Ophichthus rufus</i>	(Rafinesque, 1810)	x	x ^{1,3,4}	x	x	x	x	x	x	-	-	x	x	x	-	
Actinopterygii	Anguilliformes	Ophichthidae	<i>Ophisurus serpens</i>	(Linnaeus, 1758)	x	x ⁴	x	x	x	x	x	x	x	-	x	-	x	x	
Actinopterygii	Aulopiformes	Aulopidae	<i>Aulopus filamentosus</i>	(Bloch, 1792)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Aulopiformes	Chlorophthalmidae	<i>Chlorophthalmus agassizi</i>	Bonaparte, 1840	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Aulopiformes	Evermannellidae	<i>Evermannella balbo</i>	(Risso, 1820)	x	x ^{3,4}	x	-	-	x	x	x	x	-	-	-	x	-	
Actinopterygii	Aulopiformes	Ipnopidae	<i>Bathypterois dubius</i>	Vaillant, 1888	-	-	-	x	-	x	x	-	x	-	-	-	x	-	
Actinopterygii	Aulopiformes	Ipnopidae	<i>Bathypterois mediterraneus</i>	Bauchot, 1962	-	-	x	-	-	x	x	-	x	-	-	-	x	-	
Actinopterygii	Aulopiformes	Synodontidae	<i>Synodus saurus</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	-	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Beryciformes	Trachichthyidae	<i>Hoplostethus mediterraneus</i>	Cuvier, 1829	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Clupeiformes	Clupeidae	<i>Sprattus sprattus</i>	(Linnaeus, 1758)	-	-	x	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Gadiformes	Gadidae	<i>Gadiculus argenteus</i>	Guichenot, 1850	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Gadidae	<i>Merlangius merlangus</i>	(Linnaeus, 1758)	-	-	-	-	-	-	-	-	-	x	x	x	x	-	
Actinopterygii	Gadiformes	Gadidae	<i>Micromesistius putassou</i>	(Risso, 1827)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Gadidae	<i>Trisopterus minutus</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Lotidae	<i>Gaidropsarus biscayensis</i>	(Collett, 1890)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	-	x	-	
Actinopterygii	Gadiformes	Lotidae	<i>Gaidropsarus mediterraneus</i>	(Linnaeus, 1758)	-	-	-	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Lotidae	<i>Molva dypterygia</i>	(Pennant, 1784)	x	x ^{1,3,4}	x	-	-	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Lotidae	<i>Molva macrophthalma</i>	(Rafinesque, 1810)	x	-	x	x	-	x	-	x	-	-	-	-	-	-	
Actinopterygii	Gadiformes	Lotidae	<i>Molva molva</i>	(Linnaeus, 1758)	x	-	x	-	-	x	x	x	x	x	x	-	x	x	
Actinopterygii	Gadiformes	Macrouridae	<i>Coelorhynchus caelorhincus</i>	(Risso, 1810)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Macrouridae	<i>Hymenocephalus italicus</i>	Giglioli, 1884	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Macrouridae	<i>Nezumia aequalis</i>	(Günther, 1878)	x	x ^{1,3,4}	x	x	-	x	x	x	x	x	x	-	x	x	
Actinopterygii	Gadiformes	Macrouridae	<i>Nezumia sclerorhynchus</i>	(Valenciennes, 1838)	-	-	-	x	x	x	x	x	x	x	x	x	x	-	
Actinopterygii	Gadiformes	Macrouridae	<i>Trachyrhynchus scabrurus</i>	(Rafinesque, 1810)	x	x ^{1,3,4}	x	x	x	x	-	x	-	x	x	-	x	-	
Actinopterygii	Gadiformes	Merlucciidae	<i>Merluccius merluccius</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Moridae	<i>Gadella mairaldi</i>	(Risso, 1810)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-	
Actinopterygii	Gadiformes	Moridae	<i>Lepidion lepidion</i>	(Risso, 1810)	-	x ^{1,3,4}	x	x	-	x	-	x	-	x	-	-	-	-	
Actinopterygii	Gadiformes	Moridae	<i>Mora moro</i>	(Risso, 1810)	x	x ^{1,3,4}	x	x	-	x	x	x	x	x	x	-	x	-	
Actinopterygii	Gadiformes	Phycidae	<i>Phycis blennoides</i>	(Brünnich, 1768)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Gadiformes	Phycidae	<i>Phycis phycis</i>	(Linnaeus, 1766)	x	x ^{1,3,4}	x	x	-	x	x	x	x	x	x	x	x	x	
Actinopterygii	Lophiiformes	Lophiidae	<i>Lophius budegassa</i>	Spinola, 1807	x	x	x	x	x	x	x	x	x	x	x	x	x	x	

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		GSA																
Class	Order	Family	Species	Authority	1	5	6	7	8	9	10	11	16	17	18	20	22	23
Actinopterygii	Lophiiformes	Lophiidae	<i>Lophius piscatorius</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Notacanthiformes	Notacanthidae	<i>Notacanthus bonaparte</i>	Risso, 1840	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-
Actinopterygii	Notacanthiformes	Notacanthidae	<i>Polyacanthonotus rissoanus</i>	(De Filippi & Verany, 1857)	x	x ^{1,3,4}	x	-	-	x	-	x	-	-	-	-	-	-
Actinopterygii	Ophidiiformes	Bythidae	<i>Bellotia apoda</i>	Giglioli, 1883	x	-	x	-	-	x	-	-	x	-	-	x	x	-
Actinopterygii	Ophidiiformes	Bythidae	<i>Cataetx allenii</i>	(Byrne, 1906)	x	x ^{1,3,4}	x	x	-	x	-	x	-	-	-	-	-	-
Actinopterygii	Ophidiiformes	Ophidiidae	<i>Benthocometes robustus</i>	(Goode & Bean, 1886)	x	x ^{1,3,4}	x	x	x	x	x	x	x	-	x	x	-	-
Actinopterygii	Ophidiiformes	Ophidiidae	<i>Ophidion barbatum</i>	Linnaeus, 1758	x	x ^{1,3,4}	x	x	-	x	x	x	x	x	x	-	x	-
Actinopterygii	Ophidiiformes	Ophidiidae	<i>Ophidion rochei</i>	Müller, 1845	-	x ^{1,3,4}	-	x	-	x	-	-	-	-	-	-	x	-
Actinopterygii	Osmeriformes	Alepocephalidae	<i>Alepocephalus rostratus</i>	Risso, 1820	x	x ^{1,3,4}	x	x	-	x	-	x	x	-	-	-	-	-
Actinopterygii	Osmeriformes	Argentinidae	<i>Argentina sphyraena</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Osmeriformes	Argentinidae	<i>Glossanodon leiglossus</i>	(Valenciennes, 1848)	x	x	x	x	x	x	x	x	x	x	x	x	x	-
Actinopterygii	Perciformes	Ammodytidae	<i>Gymnamodytes cicerelus</i>	(Rafinesque, 1810)	-	x ^{1,3,4}	-	-	-	-	-	x	x	-	-	-	x	-
Actinopterygii	Perciformes	Blenniidae	<i>Blennius ocellaris</i>	Linnaeus, 1758	x	-	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Blenniidae	<i>Parablennius gattorugine</i>	(Linnaeus, 1758)	-	-	-	-	-	-	-	x	-	-	-	-	-	-
Actinopterygii	Perciformes	Blenniidae	<i>Parablennius tentaculatus</i>	(Brünnich, 1768)	-	-	-	-	-	-	-	x	-	x	-	-	-	-
Actinopterygii	Perciformes	Callanthiidae	<i>Callanthias ruber</i>	(Rafinesque, 1810)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Callionymidae	<i>Callionymus lyra</i>	Linnaeus, 1758	x	-	x	x	-	-	-	x	x	x	-	x	x	-
Actinopterygii	Perciformes	Callionymidae	<i>Callionymus maculatus</i>	Rafinesque, 1810	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Callionymidae	<i>Callionymus risso</i>	Lesueur, 1814	x	x ⁴	x	x	-	x	x	-	x	x	-	x	x	x
Actinopterygii	Perciformes	Callionymidae	<i>Synchiropus phaeon</i>	(Günther, 1861)	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Centrolophidae	<i>Centrolophus niger</i>	(Gmelin, 1789)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	-	x	x	-
Actinopterygii	Perciformes	Centrolophidae	<i>Schedophilus medusophagus</i>	(Cocco, 1839)	-	x ^{1,3,4}	-	-	-	-	x	-	x	-	-	-	-	-
Actinopterygii	Perciformes	Centrolophidae	<i>Schedophilus ovatus</i>	(Cuvier, 1833)	x	-	-	-	x	x	x	x	-	x	x	-	-	-
Actinopterygii	Perciformes	Cepolidae	<i>Cepola macrophthalma</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Epigonidae	<i>Epigonus constanciae</i>	(Giglioli, 1880)	x	x ^{1,3,4}	x	x	x	x	x	-	-	-	-	x	x	-
Actinopterygii	Perciformes	Epigonidae	<i>Epigonus denticulatus</i>	Dieuzeide, 1950	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-
Actinopterygii	Perciformes	Epigonidae	<i>Epigonus telescopus</i>	(Risso, 1810)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Epigonidae	<i>Microichthys coccoi</i>	Rüppell, 1852	-	-	-	-	-	x	x	-	-	-	x	-	-	-
Actinopterygii	Perciformes	Gobiidae	<i>Deltentosteus collonians</i>	(Risso, 1820)	-	x ^{1,3,4}	-	-	-	x	-	x	-	-	-	-	x	-
Actinopterygii	Perciformes	Gobiidae	<i>Deltentosteus quadrimaculatus</i>	(Valenciennes, 1837)	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Gobiidae	<i>Lesueurigobius friesii</i>	(Malm, 1874)	x	x	x	x	x	x	x	-	x	x	x	x	x	x
Actinopterygii	Perciformes	Gobiidae	<i>Lesueurigobius sanzi</i>	(de Buen, 1918)	x	x ^{1,3,4}	x	x	-	-	-	-	x	-	x	-	-	-
Actinopterygii	Perciformes	Gobiidae	<i>Lesueurigobius suerii</i>	(Risso, 1810)	x	-	x	x	-	-	x	-	x	x	x	x	-	-
Actinopterygii	Perciformes	Gobiidae	<i>Pomatoschistus marmoratus</i>	(Risso, 1810)	x	-	x	-	-	-	-	-	-	-	-	-	-	-
Actinopterygii	Perciformes	Gobiidae	<i>Pomatoschistus microps</i>	(Kr, 1838)	x	-	x	-	-	-	-	-	-	-	-	-	-	-
Actinopterygii	Perciformes	Labridae	<i>Acantholabrus palloni</i>	(Risso, 1810)	-	-	-	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Labridae	<i>Coris julis</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	-	-	x	-	x	x	-	-	x	x	x
Actinopterygii	Perciformes	Labridae	<i>Lappanella fasciata</i>	(Cocco, 1833)	x	-	x	x	x	x	x	x	x	-	-	x	x	x
Actinopterygii	Perciformes	Moronidae	<i>Dicentrarchus labrax</i>	(Linnaeus, 1758)	-	-	-	-	-	x	x	x	-	-	-	-	-	-
Actinopterygii	Perciformes	Mullidae	<i>Mullus barbatus</i>	Linnaeus, 1758	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x
Actinopterygii	Perciformes	Mullidae	<i>Mullus surmuletus</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x

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GSA																			
Class	Order	Family	Species	Authority	1	5	6	7	8	9	10	11	16	17	18	20	22	23	
Actinopterygii	Perciformes	Polyprionidae	<i>Polyprion americanum</i>	(Bloch & Schneider, 1801)	-	x ^{3,4}	x	x	-	-	x	-	-	-	-	-	x	-	
Actinopterygii	Perciformes	Pomatomidae	<i>Pomatomus saltatrix</i>	(Linnaeus, 1766)	-	-	x	-	-	x	-	-	x	-	-	-	-	-	
Actinopterygii	Perciformes	Sciaenidae	<i>Umbrina cirrosa</i>	(Linnaeus, 1758)	-	-	x	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Perciformes	Serranidae	<i>Anthias anthias</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	-	-	x	-	
Actinopterygii	Perciformes	Serranidae	<i>Serranus cabrilla</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Serranidae	<i>Serranus hepatus</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Serranidae	<i>Serranus scriba</i>	(Linnaeus, 1758)	-	-	-	-	-	x	x	x	x	x	x	x	x	-	
Actinopterygii	Perciformes	Sparidae	<i>Dentex dentex</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-	
Actinopterygii	Perciformes	Sparidae	<i>Dentex gibbosus</i>	(Rafinesque, 1810)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Perciformes	Sparidae	<i>Dentex macrophthalmus</i>	(Bloch, 1791)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Perciformes	Sparidae	<i>Dentex maroccanus</i>	Valenciennes, 1830	x	-	x	-	-	-	-	-	-	-	-	-	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Diplodus annularis</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Diplodus puntazzo</i>	(Walbaum, 1792)	x	x ^{1,4}	x	-	x	x	-	x	x	-	-	-	x	-	
Actinopterygii	Perciformes	Sparidae	<i>Diplodus sargus</i>	(Linnaeus, 1758)	-	-	x	x	x	x	x	x	-	-	x	-	-	-	
Actinopterygii	Perciformes	Sparidae	<i>Diplodus vulgaris</i>	(Geoffroy Saint-Hilaire, 1817)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-	
Actinopterygii	Perciformes	Sparidae	<i>Lithognathus mormyrus</i>	(Linnaeus, 1758)	-	-	x	x	-	x	x	x	x	x	-	-	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Pagellus acarne</i>	(Risso, 1827)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Pagellus bogaraveo</i>	(Brünnich, 1768)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Pagellus erythrinus</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Pagrus pagrus</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Sparidae	<i>Sparus aurata</i>	Linnaeus, 1758	x	-	x	x	-	x	x	x	-	x	x	x	x	-	
Actinopterygii	Perciformes	Sparidae	<i>Spondylotus cantharus</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	-	-	x	x	
Actinopterygii	Perciformes	Trachinidae	<i>Trachinus araneus</i>	Cuvier, 1829	-	-	x	x	x	-	-	x	x	x	-	x	-	-	
Actinopterygii	Perciformes	Trachinidae	<i>Trachinus draco</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Trachinidae	<i>Trachinus radiatus</i>	Cuvier, 1829	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Trichiuridae	<i>Lepidopus caudatus</i>	(Euphrasen, 1788)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Uranoscoptidae	<i>Uranoscopus scaber</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Perciformes	Zoaridae	<i>Melanostigma atlanticum</i>	Koefoed, 1952	-	x ^{3,4}	x	x	-	x	-	-	-	-	-	-	-	-	
Actinopterygii	Pleuronectiformes	Bothidae	<i>Arnoglossus imperialis</i>	(Rafinesque, 1810)	x	x	x	x	x	x	-	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Bothidae	<i>Arnoglossus kessleri</i>	Schmidt, 1915	-	-	-	-	-	-	-	x	-	-	-	-	-	-	
Actinopterygii	Pleuronectiformes	Bothidae	<i>Arnoglossus laterna</i>	(Walbaum, 1792)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Bothidae	<i>Arnoglossus rueppelii</i>	(Cocco, 1844)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Bothidae	<i>Arnoglossus thori</i>	Kyle, 1913	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Bothidae	<i>Bothus podas</i>	(Delaroche, 1809)	x	x ^{1,3,4}	x	x	-	x	x	x	x	-	-	x	x	x	
Actinopterygii	Pleuronectiformes	Citharidae	<i>Citharus linguatula</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Cynoglossidae	<i>Symphurus ligulatus</i>	(Cocco, 1844)	x	x ^{1,3,4}	x	x	x	x	x	x	x	-	-	x	x	-	
Actinopterygii	Pleuronectiformes	Cynoglossidae	<i>Symphurus nigrescens</i>	Rafinesque, 1810	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Scophthalmidae	<i>Lepidorhombus bosci</i>	(Risso, 1810)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Scophthalmidae	<i>Lepidorhombus whiffiagonis</i>	(Walbaum, 1792)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Scophthalmidae	<i>Scophthalmus maximus</i>	(Linnaeus, 1758)	x	-	x	x	x	x	x	x	x	x	x	x	x	-	
Actinopterygii	Pleuronectiformes	Scophthalmidae	<i>Scophthalmus rhombus</i>	(Linnaeus, 1758)	x	-	x	x	x	x	-	x	x	x	x	x	x	-	
Actinopterygii	Pleuronectiformes	Scophthalmidae	<i>Zeugopterus regius</i>	(Bonnaterre, 1788)	-	x ^{3,4}	-	-	-	-	-	-	-	-	-	-	-	-	

Annex 1. Demersal fish species considered for this Thesis by Geographical Sub-Areas (GSA). For Balearic Islands (GSA 5) the chapters in which the species is included are specified: 1) Chapter 4; 2) Chapter 5; 3) Chapter 6; 4) Chapter 7; and x) all chapters

GSA																			
Class	Order	Family	Species	Authority	1	5	6	7	8	9	10	11	16	17	18	20	22	23	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Bathysolea profundicola</i>	(Vaillant, 1888)	x	x ^{1,4}	x	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Buglossidium luteum</i>	(Risso, 1810)	x	-	x	x	x	x	-	x	x	x	x	-	x	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Microchirus boscanion</i>	(Chabanaud, 1926)	x	x ⁴	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Microchirus ocellatus</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	-	-	x	-	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Microchirus variegatus</i>	(Donovan, 1808)	x	x	x	x	x	x	-	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Monochirus hispidus</i>	Rafinesque, 1814	x	x ^{1,3,4}	x	x	-	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Pegusa impar</i>	(Bennett, 1831)	x	-	-	-	-	x	x	x	-	x	x	-	-	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Pegusa lascaris</i>	(Risso, 1810)	x	x ^{1,3,4}	-	-	-	x	x	x	-	x	-	-	-	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Solea senegalensis</i>	Kaup, 1858	x	-	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Solea solea</i>	(Linnaeus, 1758)	x	-	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Solea vulgaris</i>	Quensel, 1806	-	x ^{3,4}	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Pleuronectiformes	Soleidae	<i>Synapturichthys kleinii</i>	(Risso, 1827)	-	x ^{1,4}	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Scorpaeniformes	Dactylopteridae	<i>Dactylopterus volitans</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	-	-	-	-	x	x	-	-	x	x	-	
Actinopterygii	Scorpaeniformes	Lipariidae	<i>Paraliparis leptochirus</i>	(Tortonese, 1959)	x	-	x	-	-	x	-	-	-	-	-	-	-	-	
Actinopterygii	Scorpaeniformes	Peristediidae	<i>Peristedion cataphractum</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Scorpaenidae	<i>Scorpaena elongata</i>	Cadenat, 1943	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Scorpaenidae	<i>Scorpaena loppei</i>	Cadenat, 1943	x	x	x	x	x	x	x	x	x	x	x	x	-	-	
Actinopterygii	Scorpaeniformes	Scorpaenidae	<i>Scorpaena notata</i>	Rafinesque, 1810	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Scorpaenidae	<i>Scorpaena porus</i>	Linnaeus, 1758	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Scorpaenidae	<i>Scorpaena scrofa</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Sebastidae	<i>Helicolenus dactylopterus</i>	(Delaroche, 1809)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Sebastidae	<i>Trachyscorpia cristulata</i>	(Goode & Bean, 1896)	x	-	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Chelidonichthys cuculus</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Chelidonichthys lucerna</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Chelidonichthys obscurus</i>	(Walbaum, 1792)	x	x ^{1,3,4}	x	x	x	x	x	x	x	-	-	x	x	-	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Eutrigla gurnardus</i>	(Linnaeus, 1758)	-	x ^{1,3,4}	x	x	x	x	-	x	x	x	x	x	x	-	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Lepidotrigla cavillone</i>	(Lacepède, 1801)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Lepidotrigla dieuzeidei</i>	Blanc & Hureau, 1973	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Trigla lyra</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Scorpaeniformes	Triglidae	<i>Trigloporus lastoviza</i>	(Bonnaterre, 1788)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Actinopterygii	Syngnathiformes	Syngnathidae	<i>Syngnathus acus</i>	Linnaeus, 1758	x	x ^{1,3,4}	x	x	-	-	x	x	x	x	x	x	x	x	
Actinopterygii	Tetraodontiformes	Tetraodontidae	<i>Sphaeroides pachygaster</i>	(Müller & Troschel, 1848)	x	-	-	-	-	-	-	-	-	-	-	-	-	-	
Actinopterygii	Zeiformes	Zeidae	<i>Zeus faber</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Carcharhiniformes	Pentanchidae	<i>Galeus atlanticus</i>	(Vaillant, 1888)	x	-	-	-	-	-	-	-	-	-	-	-	-	-	
Elasmobranchii	Carcharhiniformes	Pentanchidae	<i>Galeus melastomus</i>	Rafinesque, 1810	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Carcharhiniformes	Scyliorhinidae	<i>Scyliorhinus canicula</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Carcharhiniformes	Scyliorhinidae	<i>Scyliorhinus stellaris</i>	(Linnaeus, 1758)	-	-	x	-	x	x	x	x	x	x	x	-	x	-	
Elasmobranchii	Carcharhiniformes	Triakidae	<i>Galeorhinus galeus</i>	(Linnaeus, 1758)	x	-	-	x	-	-	-	-	-	-	-	-	-	-	
Elasmobranchii	Carcharhiniformes	Triakidae	<i>Mustelus asterias</i>	Cloquet, 1819	-	x ^{1,3,4}	-	-	-	-	-	-	-	-	-	-	-	-	
Elasmobranchii	Carcharhiniformes	Triakidae	<i>Mustelus mustelus</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	-	x	x	x	x	x	x	x	x	x	-	
Elasmobranchii	Carcharhiniformes	Triakidae	<i>Mustelus punctulatus</i>	Risso, 1827	x	-	-	-	-	-	-	-	x	x	-	-	-	-	

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GSA																			
Class	Order	Family	Species	Authority	1	5	6	7	8	9	10	11	16	17	18	20	22	23	
Elasmobranchii	Hexanchiformes	Hexanchidae	<i>Heprtranchias perlo</i>	(Bonnaterre, 1788)	x	-	-	-	-	x	-	x	x	-	x	x	x	x	
Elasmobranchii	Hexanchiformes	Hexanchidae	<i>Hexanchus griseus</i>	(Bonnaterre, 1788)	-	-	x	x	-	x	x	x	x	-	-	-	x	-	
Elasmobranchii	Hexanchiformes	Dasyatidae	<i>Dasyatis centroura</i>	(Mitchill, 1815)	-	x ^{1,3,4}	-	-	x	-	-	x	-	x	-	-	-	-	
Elasmobranchii	Hexanchiformes	Dasyatidae	<i>Dasyatis pastinaca</i>	(Linnaeus, 1758)	-	x ^{1,3,4}	x	x	x	x	x	x	x	x	-	x	x	x	
Elasmobranchii	Hexanchiformes	Dasyatidae	<i>Dasyatis tortonesei</i>	Capapé, 1975	-	-	-	-	-	-	-	-	-	-	-	-	x	x	
Elasmobranchii	Hexanchiformes	Dasyatidae	<i>Pteroplatytrigon violacea</i>	(Bonaparte, 1832)	x	-	x	x	x	x	x	-	x	x	x	-	-	-	
Elasmobranchii	Hexanchiformes	Myliobatidae	<i>Myliobatis aquila</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	-	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Hexanchiformes	Myliobatidae	<i>Pteromylaeus bovinus</i>	(Geoffroy Saint-Hilaire, 1817)	-	-	-	-	-	-	-	-	x	x	-	-	x	-	
Elasmobranchii	Rajiformes	Rajidae	<i>Dipturus oxyrinchus</i>	(Linnaeus, 1758)	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Leucoraja circularis</i>	(Couch, 1838)	x	x	x	x	x	-	x	x	x	x	x	-	x	-	
Elasmobranchii	Rajiformes	Rajidae	<i>Leucoraja fullonica</i>	(Linnaeus, 1758)	-	-	-	x	x	x	-	-	x	x	x	-	-	-	
Elasmobranchii	Rajiformes	Rajidae	<i>Leucoraja melitenensis</i>	(Clark, 1926)	x	-	-	-	-	-	-	-	x	-	-	-	x	-	
Elasmobranchii	Rajiformes	Rajidae	<i>Leucoraja naevus</i>	(Müller & Henle, 1841)	x	x	x	x	x	-	-	-	x	-	-	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja asterias</i>	Delaroche, 1809	x	-	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja brachyura</i>	Lafont, 1871	-	x	-	x	x	-	-	x	x	-	-	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja clavata</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja miraletus</i>	Linnaeus, 1758	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja montagui</i>	Fowler, 1910	x	-	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja polystigma</i>	Regan, 1923	x	x	x	x	x	x	x	x	x	x	x	x	x	-	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja radula</i>	Delaroche, 1809	x	x ^{1,3,4}	x	-	x	-	-	-	x	-	-	x	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Raja undulata</i>	Lacepède, 1802	-	-	-	-	-	-	-	-	-	-	-	-	x	x	
Elasmobranchii	Rajiformes	Rajidae	<i>Rostroraja alba</i>	(Lacepède, 1803)	x	x ^{1,3,4}	-	-	x	x	-	-	x	x	x	-	x	-	
Elasmobranchii	Squaliformes	Centrophoridae	<i>Centrophorus granulosus</i>	(Bloch & Schneider, 1801)	x	x ^{1,3,4}	-	x	x	x	x	x	x	x	x	x	x	-	
Elasmobranchii	Squaliformes	Dalatiidae	<i>Dalatiopsis licha</i>	(Bonnaterre, 1788)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-	
Elasmobranchii	Squaliformes	Etmopteridae	<i>Etmopterus spinax</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Squaliformes	Oxynotidae	<i>Oxynotus centrina</i>	(Linnaeus, 1758)	x	x ^{1,3,4}	-	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Squaliformes	Squalidae	<i>Squalus acanthias</i>	Linnaeus, 1758	x	-	-	-	-	-	-	-	-	-	-	-	-	-	
Elasmobranchii	Squaliformes	Squalidae	<i>Squalus blainville</i>	(Risso, 1827)	-	x	-	-	-	-	-	-	-	-	-	-	-	-	
Elasmobranchii	Squaliformes	Squalidae	<i>Squalus uyato</i>	(Rafinesque, 1810)	x	-	x	x	x	-	x	-	x	-	-	x	-	-	
Elasmobranchii	Torpediniformes	Torpedinidae	<i>Tetronarce nobiliana</i>	(Bonaparte, 1835)	x	-	x	x	x	x	x	x	x	x	x	x	x	-	
Elasmobranchii	Torpediniformes	Torpedinidae	<i>Torpedo marmorata</i>	Risso, 1810	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Elasmobranchii	Torpediniformes	Torpedinidae	<i>Torpedo nobiliana</i>	Bonaparte, 1835	x	-	x	-	-	-	-	-	-	-	-	-	-	-	
Elasmobranchii	Torpediniformes	Torpedinidae	<i>Torpedo torpedo</i>	(Linnaeus, 1758)	x	-	-	x	x	x	x	x	x	x	x	x	x	x	
Holocephali	Chimaeriformes	Chimaeridae	<i>Chimaera monstrosa</i>	Linnaeus, 1758	x	x ^{1,3,4}	x	x	x	x	x	x	x	x	x	x	x	-	

Chapter 12

Appendix B



Annex 2. Temporal series of fishing effort measures in number of vessels, kilowatt per day at sea (kw*days at sea) and gross tonnage per days at sea (GT*days at sea) for each GSA and species. Effort measures used to calculate trends in fishing effort for each GSA and strata are marked with (*). References are listed below the table.

GSA	Species	Effort measure	Years	Reference
GSA 1	<i>M. barbatus</i>	Number of vessels	2005-2007	SAC GFCM 2008a
	<i>M. barbatus</i>	kw*days at sea (*), GT*days at sea	2009-2013	STECF 2015a
	<i>P. longirostris</i>	kw*days at sea (*)	2003-2015	STECF 2016b
GSA 5	<i>A. antennatus</i>	Number of vessels (*)	2011	SAC GFCM 2012a
	<i>A. antennatus</i>	Number of vessels (*)	1998-2009	SAC GFCM 2010a
	<i>A. antennatus</i>	Number of vessels (*)	1999-2010	SAC GFCM 2011a
	<i>M. barbatus</i>	Number of vessels	2000-2009	SAC GFCM 2010b
	<i>M. barbatus</i>	kw*days at sea, GT*days at sea	2009-2012	STECF 2013b
	<i>M. surmuletus</i>	Number of vessels	2000-2009	SAC GFCM 2010c
	<i>M. surmuletus</i>	Number of vessels (*)	2000-2010	SAC GFCM 2011b
	<i>N. norvegicus</i>	Number of vessels (*)	2002-2009	SAC GFCM 2010d
	<i>N. norvegicus</i>	kw*days at sea, GT*days at sea	2009-2013	STECF 2015a
	<i>P. longirostris</i>	kw*days at sea, GT*days at sea	2009-2012	STECF 2013a
GSA 6	<i>A. antennatus</i>	Number of vessels	1996-2006	SAC GFCM 2007
	<i>A. antennatus</i>	kw*days at sea, GT*days at sea	2009-2014	STECF 2015b
	<i>M. barbatus</i>	Number of vessels (*)	1999-2010	SAC GFCM 2011c
	<i>M. barbatus</i>	Number of vessels, kw*days at sea, GT*days at sea	2009-2012	STECF 2013b
	<i>M. surmuletus</i>	Number of vessels (*)	1998-2009	SAC GFCM 2010e
	<i>N. norvegicus</i>	Number of vessels (*), kw*days at sea, GT*days at sea	2004-2015	STECF 2016b
	<i>P. longirostris</i>	Number of vessels	2001-2010	SAC GFCM 2011d
	<i>P. longirostris</i>	Number of vessels	2001-2011	SAC GFCM 2012b
	<i>P. longirostris</i>	Number of vessels	2001-2012	SAC GFCM 2013
	<i>P. longirostris</i>	Number of vessels, kw*days at sea, GT*days at sea	2009-2012	STECF 2013a
	<i>M. barbatus</i>	Number of vessels	2002-2013	STECF 2014a
	<i>M. barbatus</i>	Days at sea, kw*days at sea, GT*days at sea	2004-2006	STECF 2008a
	<i>M. barbatus</i>	Number of vessels	2004-2008	SAC GFCM 2009a
GSA 7	<i>M. barbatus</i>	Number of vessels	2004-2009	SAC GFCM 2010f
	<i>M. barbatus</i>	Number of vessels (*)	2004-2011	SAC GFCM 2012c
	<i>M. surmuletus</i>	Number of vessels	2004-2010	SAC GFCM 2011e
GSA 9	<i>A. foliacea</i>	kw*days at sea	2004-2012	STECF 2013a
	<i>A. foliacea</i>	kw*days at sea (*)	2004-2014	STECF 2015b
	<i>N. norvegicus</i>	kw*days at sea	2004-2013	STECF 2014a
	<i>N. norvegicus</i>	Number of vessels, kw*days at sea, GT*days at sea	2004-2015	STECF 2016b
	<i>P. longirostris</i>	kw*days at sea (*)	2002-2015	STECF 2016b
	<i>P. longirostris</i>	kw*days at sea	2004-2013	STECF 2015a
	<i>P. longirostris</i>	Number of vessels	2006-2008	SAC GFCM 2009b
GSA 10	<i>A. foliacea</i>	kw*days at sea	2004-2014	STECF 2015b
	<i>P. longirostris</i>	kw*days at sea (*)	2002-2015	STECF 2016b
	<i>P. longirostris</i>	kw*days at sea	2004-2012	STECF 2013a
GSA 11	<i>A. foliacea</i>	Number of vessels, kw*days at sea (*), GT*days at sea	2004-2014	STECF 2015b
	<i>M. surmuletus</i>	GT*days at sea (*)	2004-2012	STECF 2013b
	<i>N. norvegicus</i>	Number of vessels, kw*days at sea, GT*days at sea	2004-2015	STECF 2016b
	<i>P. longirostris</i>	kw*days at sea (*)	2002-2015	STECF 2016b
GSA 15-16	<i>A. foliacea</i>	GT*days at sea	2004-2008	SAC GFCM 2009c
GSA 16	<i>P. longirostris</i>	Number of vessels	2006-2007	SAC GFCM 2008b
GSA 17	<i>M. barbatus</i>	kw*days at sea (*), GT*days at sea	2004-2012	STECF 2013b
	<i>N. norvegicus</i>	kW*days at sea (*)	2002-2015	STECF 2016b
GSA 17-18	<i>M. barbatus</i>	kw*days at sea, GT*days at sea	2004-2014	STECF 2016a
	<i>N. norvegicus</i>	kw*days at sea, GT*days at sea	2006-2014	STECF 2016a
GSA 18	<i>A. foliacea</i>	kw*days at sea (*), GT*days at sea	2002-2014	STECF 2016a
	<i>M. barbatus</i>	kw*days at sea (*)	2004-2013	STECF 2015a
	<i>P. longirostris</i>	kw*days at sea, GT*days at sea (*)	2007-2014	STECF 2016a
GSA 22-23	<i>P. longirostris</i>	Days at sea, kw*days at sea, GT*days at sea	2003-2006	STECF 2008a

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