

Modelling spatio-temporal patterns of fish community size structure across the northern Mediterranean Sea: an analysis combining MEDITS survey data, environmental and anthropogenic drivers

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Supplementary material

Table S1. – List of the 23 species included in the analysis for the calculation of community indicators.

Mediterranean code	Latin name	Mediterranean code	Latin name
ASPICUC	<i>Chelidonichthys cuculus</i>	PAGEBOG	<i>Pagellus bogaraveo</i>
CITHMAC	<i>Citharus linguatula</i>	PAGEERY	<i>Pagellus erythrinus</i>
EUTRGUR	<i>Eutrigla gurnardus</i>	PHYIBLE	<i>Phycis blennoides</i>
GALUMEL	<i>Galeus melastomus</i>	RAJACLA	<i>Raja clavata</i>
HELIDAC	<i>Helicolenus dactylopterus</i>	SCYOCAN	<i>Scyliorhinus canicula</i>
LEPMBOS	<i>Lepidorhombus boscii</i>	SOLEVUL	<i>Solea vulgaris</i>
LOPHBUD	<i>Lophius budegassa</i>	SPICFLE	<i>Spicara flexuosa</i>
LOPHPIS	<i>Lophius piscatorius</i>	SPICSMA	<i>Spicara smaris</i>
MERLMER	<i>Merluccius merluccius</i>	TRIPLAS	<i>Trigloporus lastoviza</i>
MULLBAR	<i>Mullus barbatus</i>	TRISCAP	<i>Trisopterus m. capelanus</i>
MULLSUR	<i>Mullus surmuletus</i>	ZEUSFAB	<i>Zeus faber</i>
PAGEACA	<i>Pagellus acarne</i>		

Adequacy of data to the analysis

According to Kaiser-Meyer-Olkin test, the available data were considered relatively adequate to the analysis (Table S2). Globally, GSAs 2, 17 and 22+23 showed the lowest KMO-Criterion, indicating widespread variance that could be scarcely interpreted as common variability. For all the GSAs the Bartlett test returned a $p < 0.05$, thus we always rejected the null hypothesis that the correlation matrix was equal to the identity matrix. The results of the tests carried out ensure the validity of the hypothesis of the PCA allowing to perform the analysis on the available data.

Table S2. – Kaiser-Meyer-Olkin test: Measure of sampling Adequacy (MSA) by GSA. In bold the KMO-Criterion values < 0.5 .

Kaiser-Meyer-Olkin	LFI	Measure of sampling Adequacy (MSA) Evenses.index	LSI	MML	MW	Typical_Length	KMO-Criterion
GSA 1	0.76	0.22	0.69	0.80	0.43	0.59	0.60
GSA 2	0.40	0.44	0.43	0.33	0.59	0.19	0.41
GSA 5	0.66	0.70	0.75	0.60	0.72	0.68	0.68
GSA 6	0.70	0.69	0.55	0.28	0.60	0.70	0.63
GSA 7	0.50	0.53	0.27	0.52	0.62	0.57	0.53
GSA 8	0.61	0.16	0.57	0.36	0.62	0.77	0.56
GSA 9	0.51	0.56	0.79	0.41	0.78	0.57	0.57
GSA 10	0.60	0.55	0.61	0.56	0.49	0.57	0.57
GSA 11	0.55	0.84	0.46	0.44	0.52	0.59	0.56
GSA 15	0.68	0.74	0.79	0.56	0.72	0.76	0.72
GSA 16	0.60	0.57	0.74	0.63	0.56	0.65	0.63
GSA 17	0.45	0.31	0.45	0.41	0.53	0.47	0.44
GSA 18	0.40	0.82	0.77	0.76	0.82	0.70	0.74
GSA 19	0.81	0.90	0.64	0.62	0.51	0.68	0.69
GSA 20	0.56	0.75	0.54	0.60	0.62	0.58	0.60
GSA 22+23	0.36	0.17	0.33	0.33	0.21	0.35	0.30
GSA 25	0.57	0.69	0.54	0.91	0.62	0.61	0.64

Average lifespan by species

Table S3. – Lifespan by species used to estimate the average lifespan of the fish community considered.

Species	Latin name	Lifespan	Reference
ASPICUC	<i>Chelidonichthys cuculus</i>	7	Papaconstantinou 1983
CITHMAC	<i>Citharus linguatula</i>	6	Papacostantinou and Vassilopoulou 1994
EUTRGUR	<i>Eutrigla gurnardus</i>	9	Boudaya et al. 2008
GALUMEL	<i>Galeus melastomus</i>	15	http://www.marinetraining.eu/content/determination-age-and-growth-galeus-melastomus-rafinesque-1810-deep-water-shark-using
HELIDAC	<i>Helicolenus dactylopterus</i>	10	Romanelli et al. 1997
LEPMBOS	<i>Lepidorhombus boscii</i>	9	Landa and Fontenla 2016
LOPHBUD	<i>Lophius budegassa</i>	21	Landa et al. 2001
LOPHPIS	<i>Lophius piscatorius</i>	24	Landa et al. 2001
MERLMER	<i>Merluccius merluccius</i>	20	Muus et al. 1999
MULLBAR	<i>Mullus barbatus</i>	10	max age observed in GSAs 10, 18 and 19
MULLSUR	<i>Mullus surmuletus</i>	10	Arslan and Ismen 2013
PAGEACA	<i>Pagellus acarne</i>	12	Velasco et al. 2011
PAGEBOG	<i>Pagellus bogaraveo</i>	15	Muus and Dahlstrom 1966
PAGEERY	<i>Pagellus erythrinus</i>	12	Livadas 1989
PHYIBLE	<i>Phycis blennoides</i>	14	Casas and Piñeiro 2000
RAJACLA	<i>Raja clavata</i>	12	Ryland and Ajayi 1984
SCYOCAN	<i>Scyliorhinus canicula</i>	12	Ivory et al. 2005
SOLEVUL	<i>Solea vulgaris</i>	15	Tmax Taylor on GSA10 and 18 DCF growth parameters
SPICFLE	<i>Spicara flexuosa</i>	5	Mytilineou and Papaconstantinou 1991
SPICSMA	<i>Spicara smaris</i>	5	Soykan et al. 2010
TRIPLAS	<i>Trigloporus lastoviza</i>	4	El-serafy et al. 2015
TRISCAP	<i>Trisopterus m. capelanus</i>	6	Šantić et al. 2015
ZEUSFAB	<i>Zeus faber</i>	12	Maigret and Ly 1986

Temperature preference by species

This section reports a table containing the available information of the temperature preference for the species under consideration. The mean temperature of the catch is obtained from Cheung et al. (2013), where available. For selected species, information from the online source Aquamaps (Kaschner et al. 2019; <http://www.aquamaps.org>) or from other sources was gathered.

The species with preference temperature higher than or equal to 17°C were considered thermophile.

Table S4. – Mean temperature of the catch, as found in Cheung et al. (2013), related to the species under investigation. For deep-water species (indicated by *), SST is not considered a reliable indicator of temperature preference.

Species	MTC	Aquamaps	Other
ASPICUC	-		
CITHMAC	22		
EUTRGUR	11		
GALUMEL*	17	9-20; mean: 10.4	13.9-14.16; Ragonese <i>et al.</i> 2009
HELIDAC*	22		
LEPMBOS	14		
LOPHBUD*	25		
LOPHPIS*	14		
MERLMER	18		
MULLBAR	17	17 – 20	
MULLSUR	19		
PAGEACA	19		
PAGEBOG	18		
PAGEERY	18	12.2-21; mean: 17.2	
PHYIBLE	16		
RAJACLA	17		
SCYOCAN	17		
SOLEVUL	16		
SPICFLE	-		
SPICSMA	-	11.8-17.8; mean: 14.4	
TRIPLAS	18		
TRISCAP	15		
ZEUSFAB	23		

Normality of residuals in DFA

The Shapiro-Wilk test detected deviations from normal distributions in the residuals of the DFA best fits for TyL and MML; this was investigated by scale finite mixture model. This analysis indicated that for TyL the 90% of residuals are represented by a normal distribution with mean -0.17 and standard deviation 0.69, while the second normal component (10% of residuals) is characterized by mean of 1.72 and standard deviation 0.77. For MML the residuals are divided in 96% due to a normal distribution with mean -0.13 and standard deviation 0.81 and another normal distribution (4% of residuals) with mean -1.82 and standard deviation 0.41 (Fig. S1).

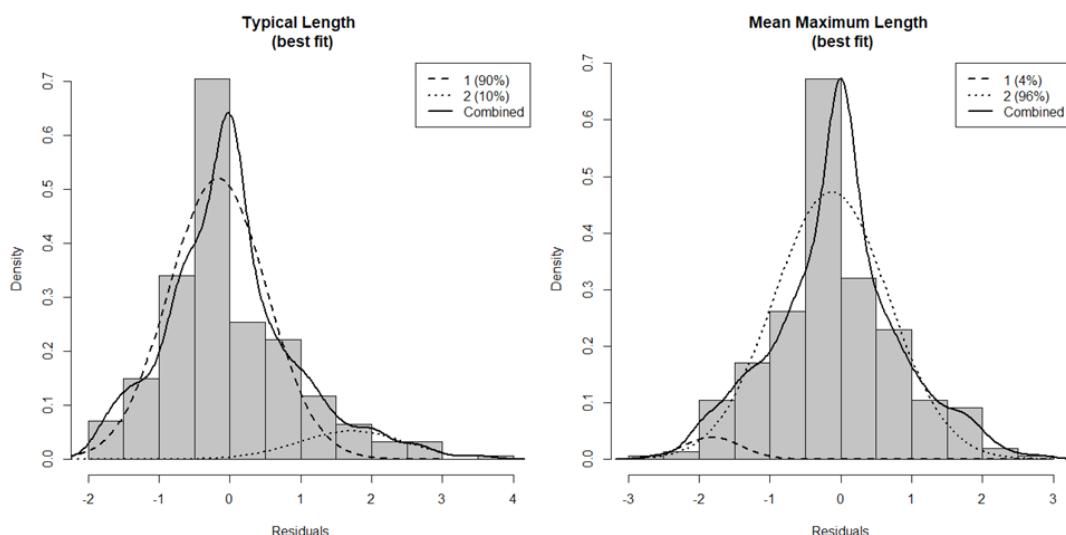


Fig. S1 – Residuals histograms of the best DFA fit for TyL and MML broken down by normal mixed distributions through scale mixture model.

Correlations among the indicators by GSAs

Before carrying out the PCA, the hypotheses needed to apply any factor analysis were verified. The correlations among the six indicators for each GSAs were statistically tested using Pearson's coefficient and the results are reported in Table S4.

Table S5. – Correlations (Pearson) among the indicators by GSAs. In bold the significant correlations ($P < 0.05$) are reported.

	Indicator	LFI	Evenness	LSI45	MML	MW	TyL
GSA1	LFI	1					
	Evenness	0.31	1				
	LSI45	0.98	0.35	1			
	MML	0.85	0.34	0.9	1		
	MW	0.65	0.34	0.56	0.47	1	
GSA2	TyL	0.98	0.25	0.95	0.82	0.74	1
	LFI	1	Evenness	LSI45	MML	MW	TyL
	Evenness	-0.37	1				
	LSI45	0.88	-0.51	1			
	MML	0.54	-0.16	0.77	1		
GSA5	MW	-0.53	0.71	-0.75	-0.54	1	
	TyL	0.03	0.42	-0.1	-0.25	0.44	1
	LFI	1	Evenness	LSI45	MML	MW	TyL
	Evenness	0.71	1				
	LSI45	0.61	0.76	1			
GSA6	MML	0.38	0.72	0.93	1		
	MW	0.9	0.8	0.72	0.54	1	
	TyL	0.95	0.76	0.74	0.54	0.97	1
	LFI	1	Evenness	LSI45	MML	MW	TyL
	Evenness	0.53	1				
GSA7	LSI45	0.87	0.34	1			
	MML	0.12	-0.24	0.4	1		
	MW	0.67	0.94	0.43	-0.14	1	
	TyL	0.87	0.81	0.76	0.11	0.9	1
	LFI	1	Evenness	LSI45	MML	MW	TyL
GSA8	Evenness	0.21	1				
	LSI45	-0.17	-0.03	1			
	MML	-0.34	-0.07	0.34	1		
	MW	0.47	0.89	-0.13	-0.3	1	
	TyL	0.91	0.48	-0.32	-0.36	0.7	1
GSA9	LFI	1	Evenness	LSI45	MML	MW	TyL
	Evenness	-0.12	1				
	LSI45	0.98	0.01	1			
	MML	0.37	0.36	0.5	1		
	MW	0.73	0.35	0.74	0.43	1	
GSA10	TyL	0.97	-0.03	0.94	0.31	0.83	1
	LFI	1	Evenness	LSI45	MML	MW	TyL
	Evenness	0.04	1				
	LSI45	0.75	-0.2	1			
	MML	0.44	-0.38	0.84	1		
GSA11	MW	0.34	0.72	0	-0.2	1	
	TyL	0.85	0.29	0.56	0.29	0.69	1
	LFI	1	Evenness	LSI45	MML	MW	TyL
	Evenness	0.64	1				
	LSI45	0.2	0.11	1			
	MML	-0.14	0.05	0.83	1		
	MW	0.45	0.64	0.11	0.14	1	
	TyL	0.91	0.71	0.38	0.12	0.67	1

Table S5 (Cont.). – Correlations (Pearson) among the indicators by GSAs. In bold the significant correlations ($P<0.05$) are reported.

	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA15	Evenness	0.94	1			
	LSI45	0.97	0.89	1		
	MML	0.61	0.62	0.73	1	
	MW	0.9	0.89	0.86	0.5	
	TyL	0.98	0.93	0.97	0.66	0.95
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA16	Evenness	0.02	1			
	LSI45	0.93	-0.15	1		
	MML	0.47	0.09	0.57	1	
	MW	0.46	0.8	0.29	0.35	1
	TyL	0.92	0.32	0.81	0.53	0.74
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA17	Evenness	0.33	1			
	LSI45	-0.09	0.56	1		
	MML	-0.4	0.26	0.9	1	
	MW	0.75	0.23	-0.28	-0.51	1
	TyL	0.89	0.54	0.09	-0.22	0.86
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA18	Evenness	0.03	1			
	LSI45	0.26	0.79	1		
	MML	0.01	0.81	0.9	1	
	MW	0.34	0.86	0.76	0.71	1
	TyL	0.67	0.69	0.76	0.6	0.87
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA19	Evenness	0.71	1			
	LSI45	0.87	0.68	1		
	MML	0.53	0.62	0.8	1	
	MW	0.5	0.66	0.35	0.35	1
	TyL	0.93	0.82	0.87	0.63	0.69
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA20	Evenness	-0.03	1			
	LSI45	0.12	0.54	1		
	MML	-0.33	0.59	0.67	1	
	MW	0.45	0.54	0.21	0.16	1
	TyL	0.79	0.29	0.15	-0.16	0.78
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA22+23	Evenness	-0.34	1			
	LSI45	0.88	-0.08	1		
	MML	0.5	0.34	0.6	1	
	MW	-0.09	0.78	0.05	0.71	1
	TyL	0.94	-0.15	0.9	0.7	0.2
	LFI	Evenness	LSI45	MML	MW	TyL
	1	1	1	1	1	1
GSA25	Evenness	0.78	1			
	LSI45	0.97	0.65	1		
	MML	0.91	0.9	0.85	1	
	MW	0.8	0.89	0.74	0.97	1
	TyL	0.95	0.89	0.88	0.97	0.93

Time series

Figure S2 shows the trend of the TyL for each GSA; Figure S3 the MML by GSA. Figure S4 reports the biomass indices (summing up the different GSAs) by species related to the GSAs where an increasing trend was found in the Typical length (Fig. S2), namely in GSAs 1, 10, 11, 15, 16, 25, 6, 7, 8 and 9. This Figure highlights the species responsible of the trend in the TyL, focusing on the areas where a stronger relationship between the indicator and the biomass (which the definition of Typical length is based on) was found. Figure S5 shows the abundance (density) indices by species, summing up the GSAs where a decreasing trend in the MML was observed (Fig. S3). Figure 5S has the aim to highlight the species responsible of the trend in the MML, focusing on the areas where a stronger relationship between the indicator and the density (which the definition of MML is based on) was found.

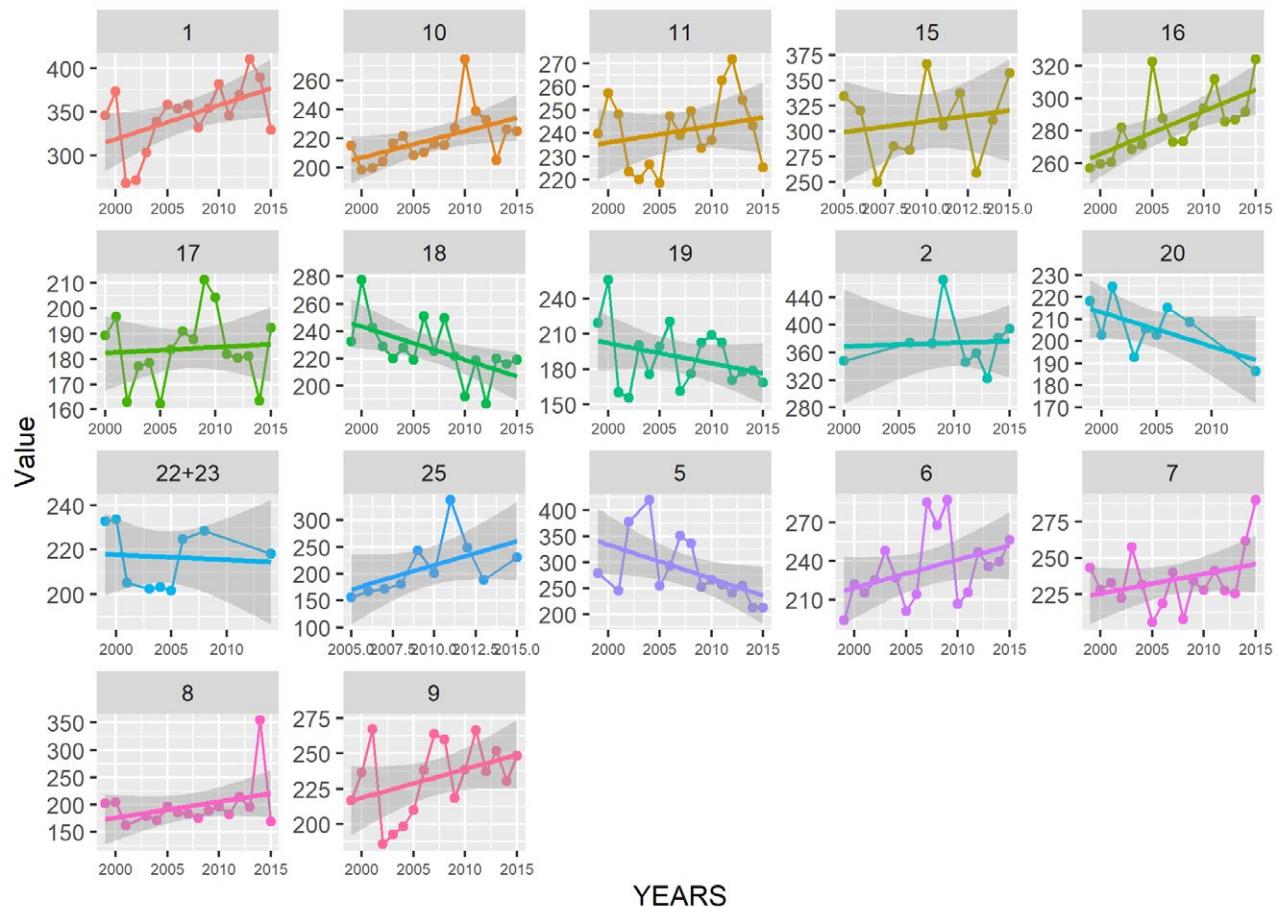


Fig. S2. – TyL time series by GSA.

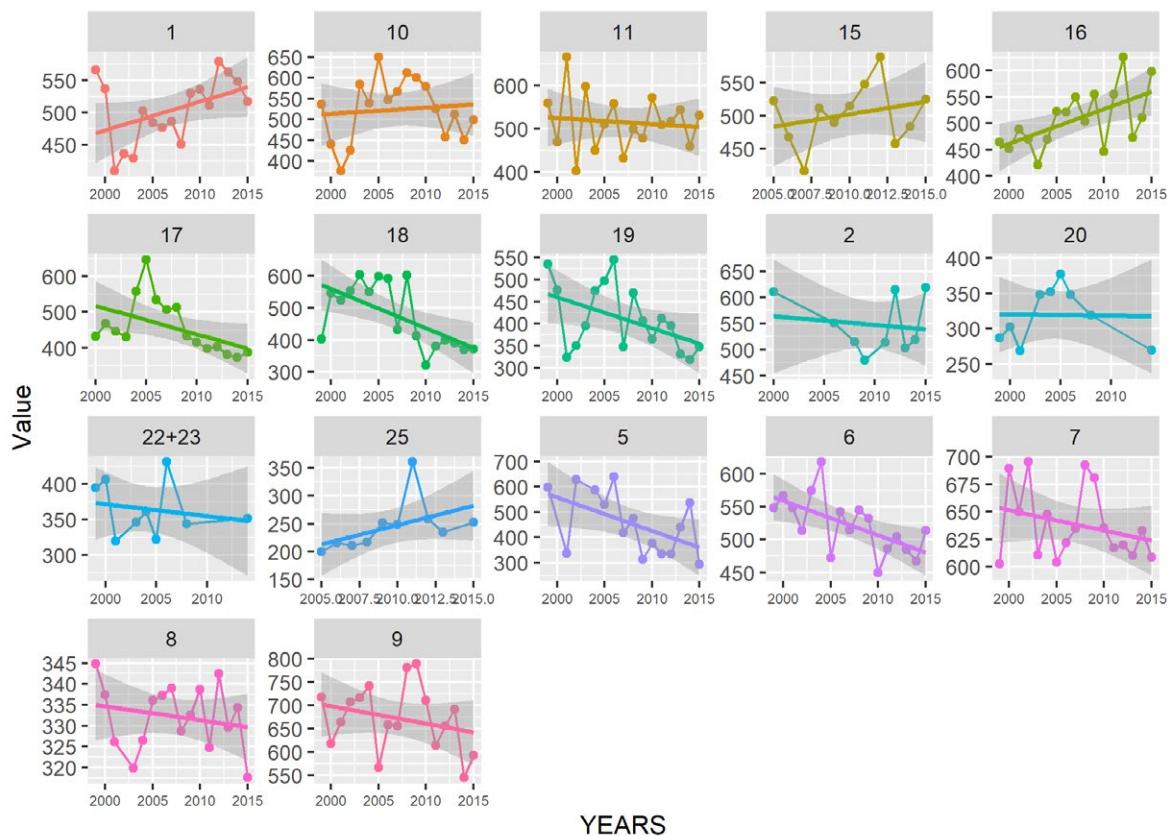
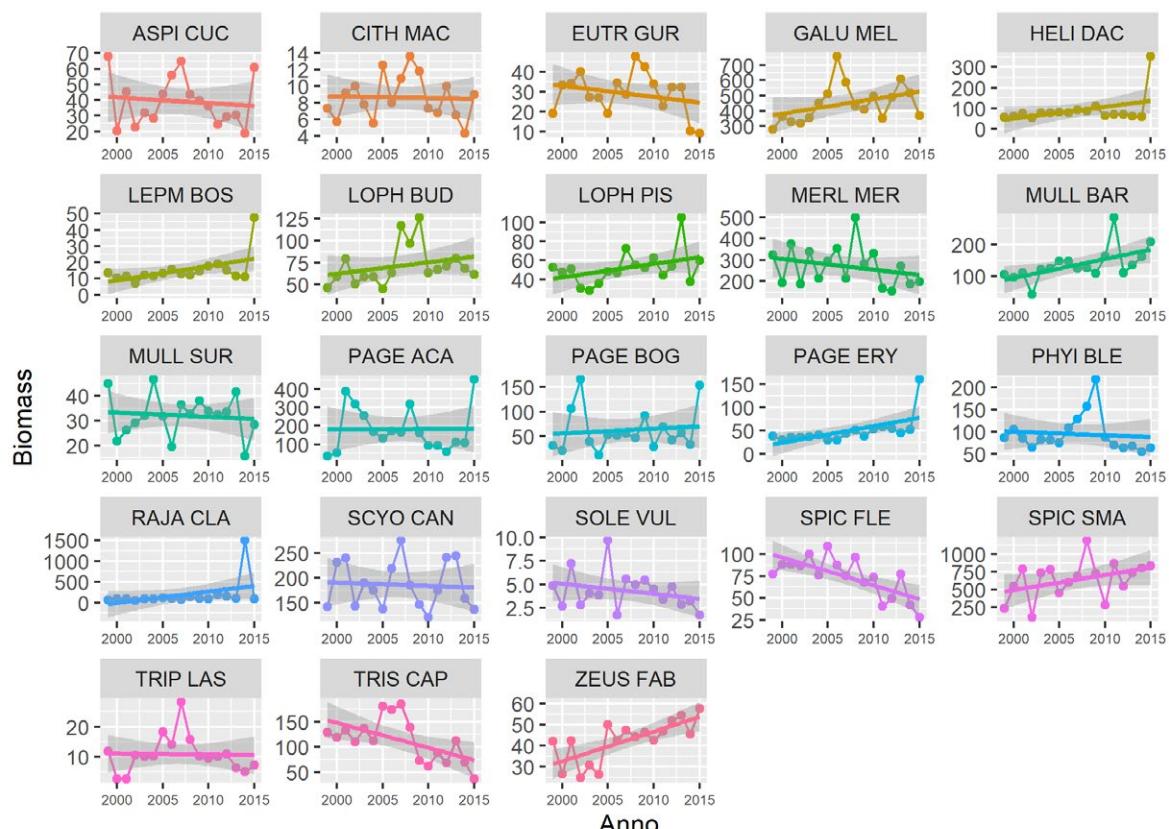


Fig. S3. – MML time series by GSA.

Fig. S4. – Trend in biomass (kg km⁻²) by species. The index is related to GSAs 1, 7, 8, 9, 10, 11, 15, 16 and 25.

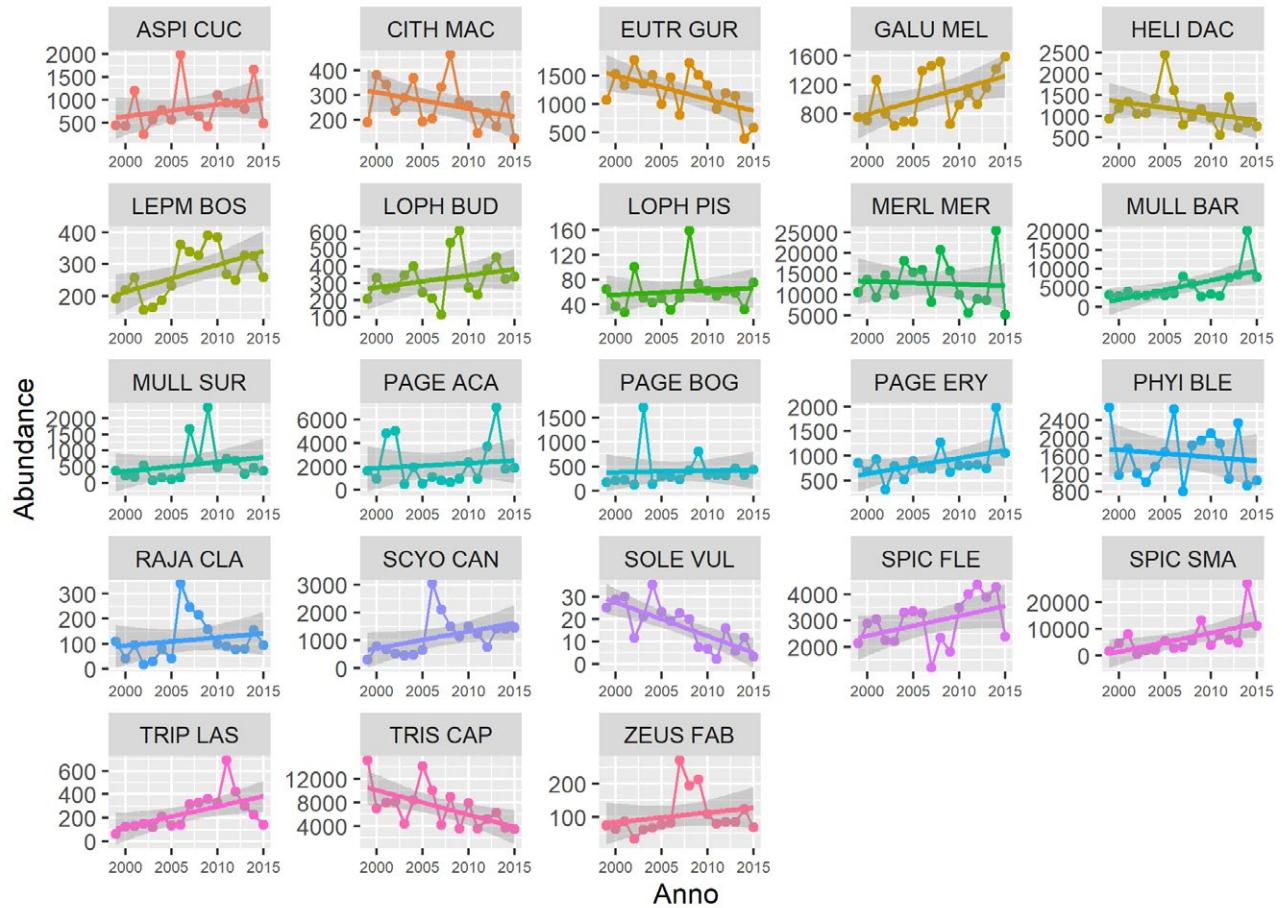


Fig. S5. – Trend in abundance ($N \text{ km}^{-2}$) by species. The index is related to GSAs 5, 6, 7, 8, 9, 11, 17, 18, 19.

Trends by GSA/species

In this section the trends of biomass and abundance indices per species and GSA are reported.

Table S6. – Trends of Biomass (kg km^{-2}) by GSA/species across the time series (1999-2015) represented. Species not considered in determinate areas are indicated as NA.

Species/GSA	1	10	11	15	16	17	18	19	20	22+23	25	5	6	7	8	9
<i>C. cuculus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>C. linguatula</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>E. gunnardus</i>	NA	NA	NA	NA	NA	NA	NA									
<i>G. melastomus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>H. dactylopterus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>L. bocki</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>L. budegassa</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>L. piscatorius</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>M. merluccius</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>M. barbatus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>M. surmuletus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>P. acarne</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>P. bogaraveo</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>P. erythrinus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>P. blennoides</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>R. clavata</i>	NA	NA	NA	NA	NA	NA	NA									
<i>S. canicula</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>S. vulgaris</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>S. flexuosa</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>S. smeris</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>T. lastoviza</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>T. m. capelanus</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
<i>Z. faber</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—

Table S7. – Trends of Abundance ($N \text{ km}^{-2}$) by GSA/species across the time series (1999-2015) represented. Species not considered in determinate areas are indicated as NA.

Species/GSA	1	10	11	15	16	17	18	19	20	22+23	25	5	6	7	8	9
<i>C. cuculus</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>C. linguatula</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>E. gunnardus</i>	NA	NA	NA	NA	NA	NA	NA									
<i>G. melastomus</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>H. dactylopterus</i>	—	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>L. boscii</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>L. buddegassa</i>	—	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>L. piscatorius</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>M. merluccius</i>	—	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>M. barbatus</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>M. surmuletus</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>P. acarne</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>P. bogaraveo</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>P. erythrinus</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>P. blennoides</i>	—	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>R. clavata</i>	NA	NA	NA	NA	NA	NA	NA									
<i>S. canicula</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>S. vulgaris</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>S. flexuosa</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>S. smaris</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>T. lastoviza</i>	—	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>T. m. capelanus</i>	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑
<i>Z. faber</i>	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—

Model fits by DFA

Table S8. – Best models fitted by DFA for TyL and MML. The characteristics of the best models are described: the observation error covariance matrix R ; the list of covariates included (none, one, two or up to three) and the Akaike Information Criteria corrected for small sample size (AICc), used to identify the best model for each of the indicators TyL and MML. The best model for both indicators, shown in bold font, has matrix diagonal and equal and no covariates.

Obs. error cov. matrix (R)	Covariates included	AICc TyL	AICc MML
diagonal and equal	None	690	675
diagonal and equal	<i>NAO</i>	706	701
diagonal and equal	<i>MedAnomaly</i>	721	-
diagonal and equal	<i>Fleet capacity</i>	728	714
diagonal and equal	<i>SST</i>	730	716
diagonal and equal	<i>NAO-MedAnomaly</i>	734	736
diagonal and equal	<i>Fleet_cap-SST</i>	743	737
diagonal and equal	<i>Fleet capacity -NAO</i>	744	743
diagonal and equal	<i>NAO-SST</i>	746	743
diagonal and equal	<i>Fleet capacity -MedAnomaly</i>	748	746
diagonal and equal	<i>NAO-SST- Fleet capacity</i>	763	766
diagonal and equal	<i>NAO-MedAnomaly- Fleet capacity</i>	770	-
equalvarcov	<i>MedAnomaly</i>	-	709
equalvarcov	<i>NAO-MedAnomaly- Fleet capacity</i>	-	783

The number of common trends detected (M) is equal to 1 in all models selected.

Fitting of best model selected by DFA

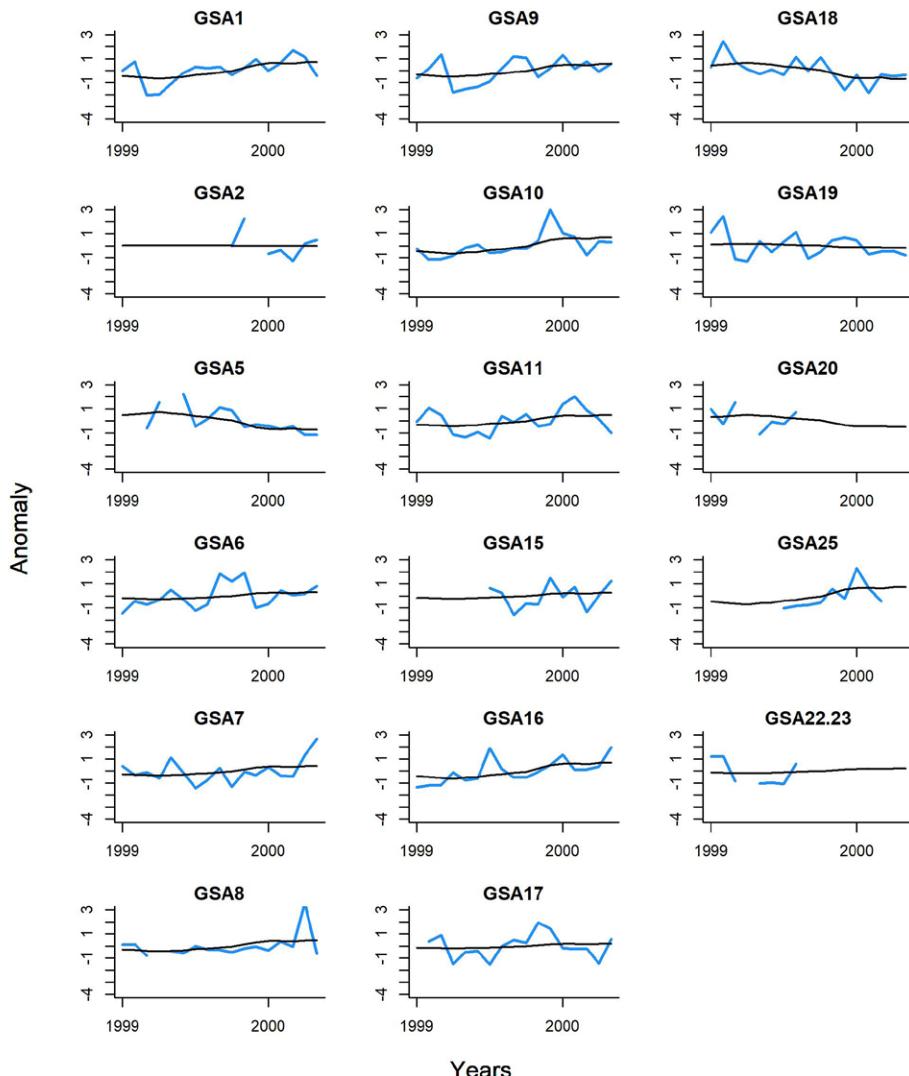


Fig. S6. – Fitting of the best model selected by DFA for TyL. The blue lines represent TyL time series for each GSA. The smoothed black line represents the common trend for TyL.

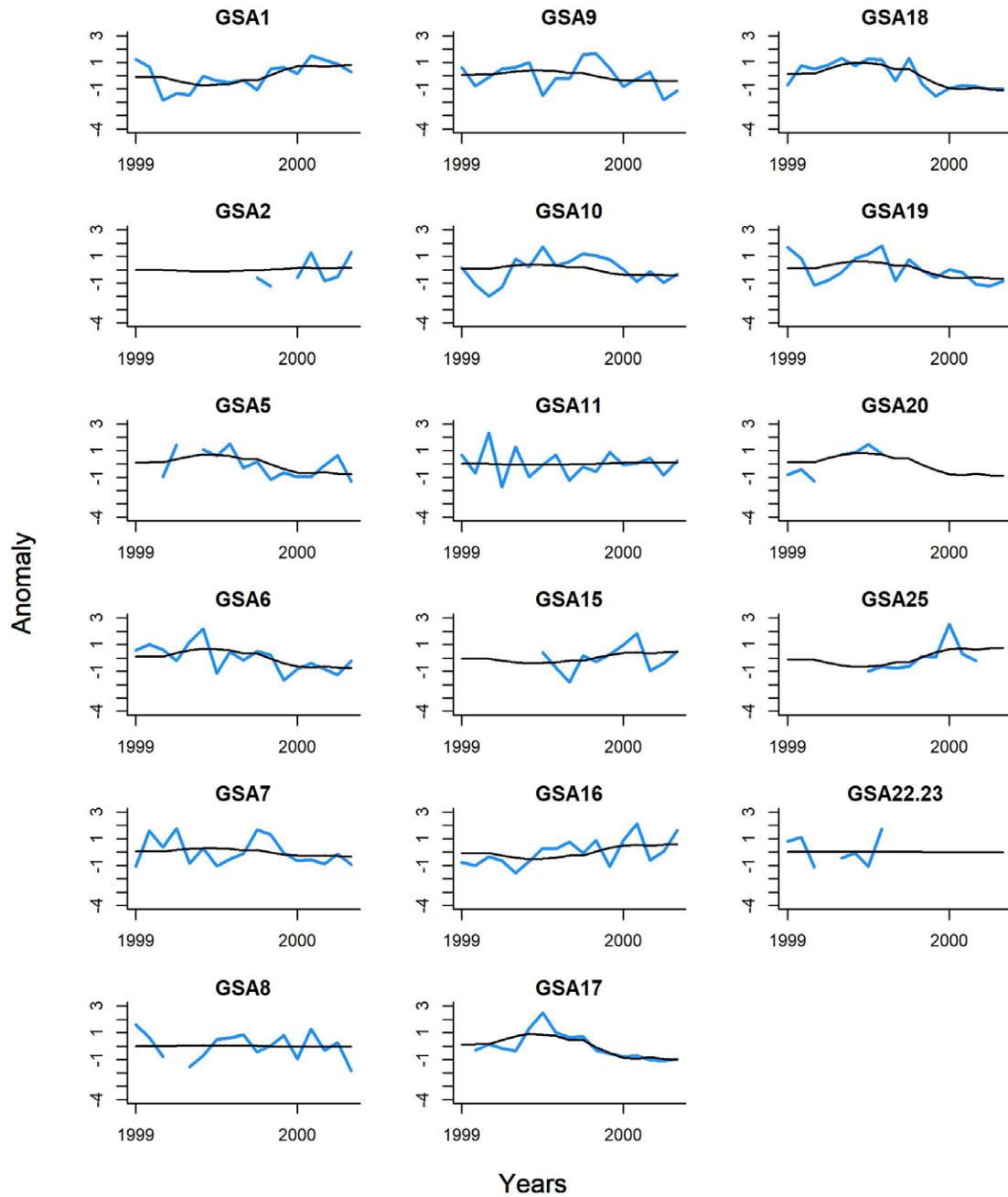


Fig. S7. – Fitting of the best model selected by DFA for MML. The blue lines represent MML time series for each GSA. The smoothed black line represents the common trend for MML.

Covariates and correlations with trends

Table S9. – Correlations between covariates. The significant ($p < 0.05$) correlations are indicated in bold.

	Fleet capacity	MedAnomaly	NAO	SST
Fleet capacity	1	-0.88	-0.25	-0.69
MedAnomaly	-0.88	1	0.20	0.91
NAO	-0.25	0.20	1	0.06
SST	-0.69	0.91	0.06	1

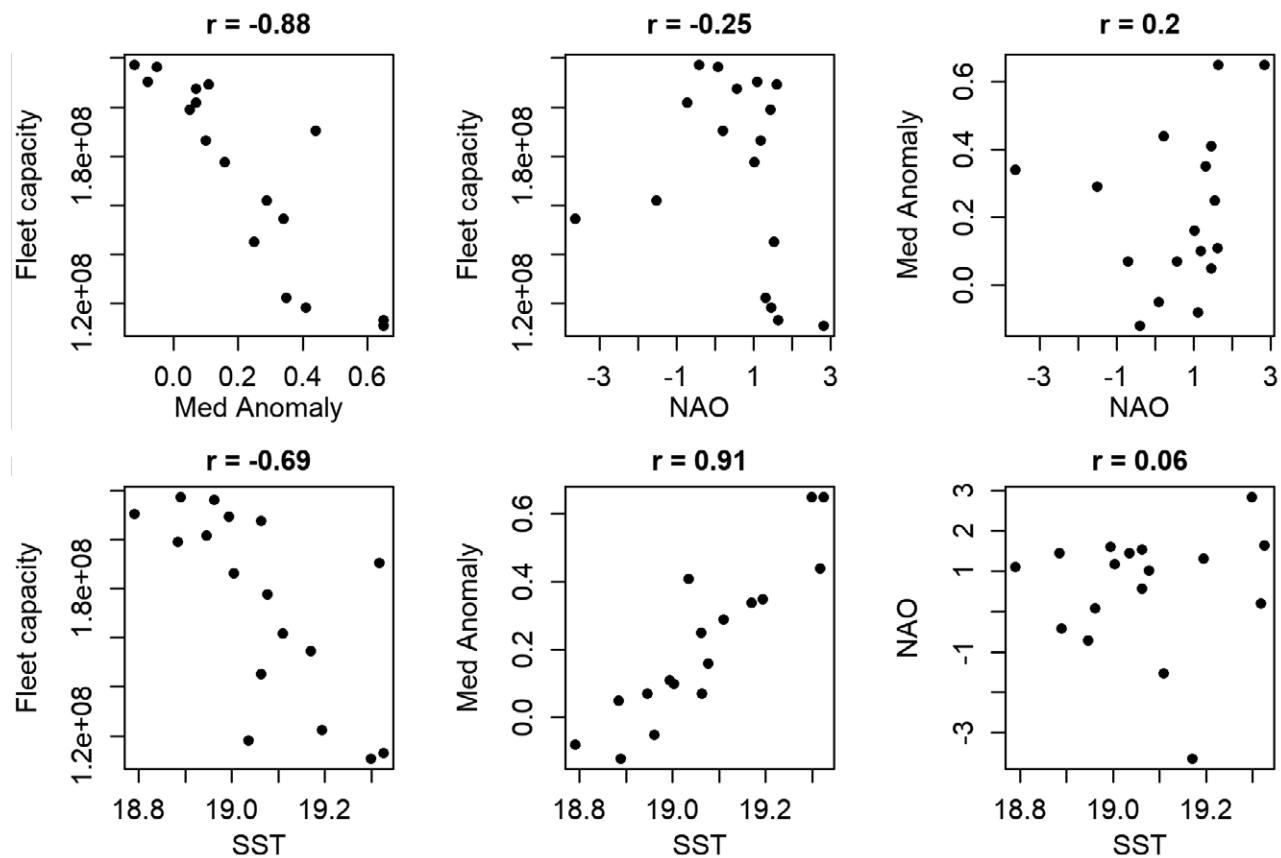


Fig. S8. – Correlation between the four covariates used in the analysis: Fleet capacity (GT×Kw×N of vessels), NAO, Med Anomaly and SST ($^{\circ}\text{C}$). Correlation values are reported for each plot.

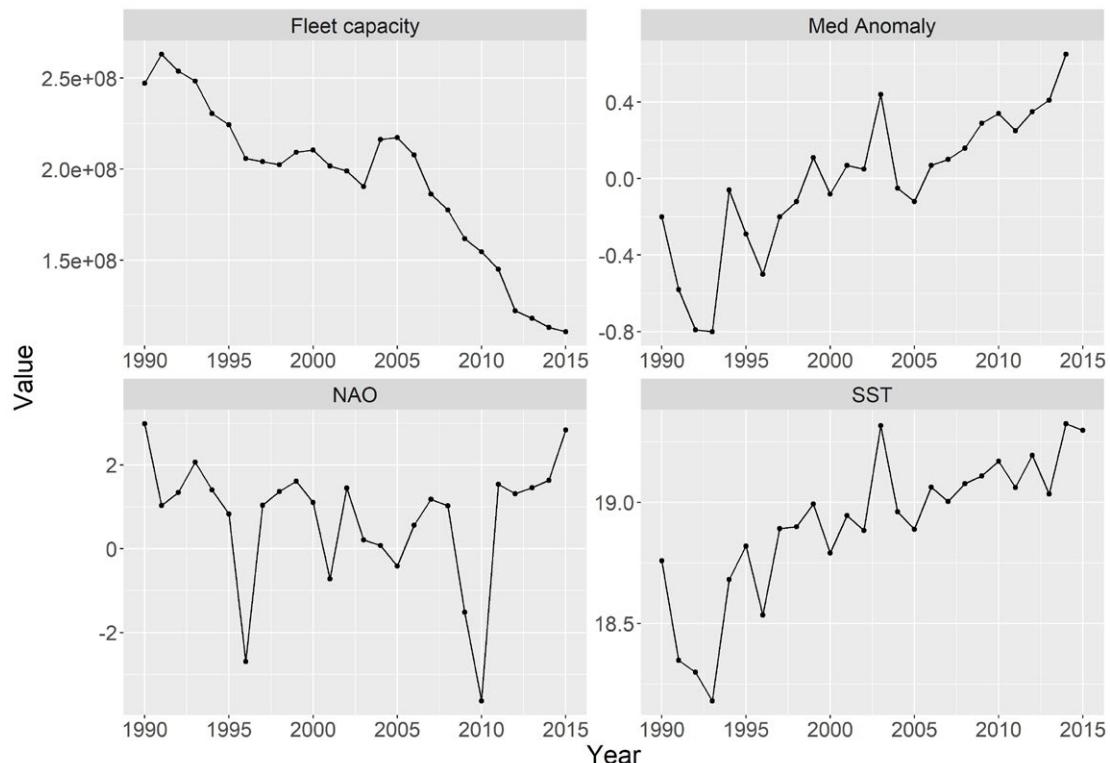


Fig. S9. – Temporal patterns of the four covariates used in the analysis: Fleet capacity (GT×Kw×number of vessels), NAO, Med Anomaly and SST ($^{\circ}\text{C}$).

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