# RETROCALCULATED LARVAL ABUNDANCE INDEX OF ATLANTIC BLUEFIN TUNA IN THE WESTERN MEDITERRANEAN SEA, 2001-2020

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*SUMMARY*

*This document presents the update of the bluefin tuna retrocalculated larval abundance indices from the Balearic archipelago (western Mediterranean). The index has been calculated following methods presented in 2020 (SCRS/2020/067) and 2021 (SCRS/2021/033). The abundance index shows an increasing trend with a maximum value in 2020. A previous version of the index (SCRS/P/2019/055) is also provided for comparison.*

*RÉSUMÉ*

*Ce document présente la mise à jour des indices d'abondance rétro calculés des larves de thon rouge de l'archipel des Baléares (Méditerranée occidentale). L'indice a été calculé selon les méthodes présentées en 2020 (SCRS/2020/067) et 2021 (SCRS/2021/033). L'indice d'abondance montre une tendance à la hausse avec une valeur maximale en 2020. Une version précédente de l'indice (SCRS/P/2019/055) est également fournie à titre de comparaison.*

*RESUMEN*

*Este documento presenta la actualización de los índices de abundancia retrocalculada de larvas de atún rojo del archipiélago Balear (Mediterráneo occidental). El índice se ha calculado siguiendo los métodos presentados en 2020 (SCRS/2020/067) y 2021 (SCRS/2021/033). El índice de abundancia muestra una tendencia creciente con un valor máximo en 2020. También se proporciona una versión anterior del índice (SCRS/P/2019/055) para su comparación.*

*KEYWORDS*

*Standardisation of CPUE, Environmental variability,
Balearic Sea, larval index,* Thunnus thynnus

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## 1. Introduction

Here we present the Bluefin tuna (*Thunnus thynnus*) retrocalulated larval abundance index in the Balearic Sea. The index informs about larval abundances just at the hatching time. The index is computed following the methods presented in 2020 (SCRS/2020/067), which is the version  selected for inclusion in the bluefin tuna MSE, also presented in 2021 (SCRS/2021/033), as proxy for the bluefin tuna spawning stock biomass trends in the fisheries assessment of the Bluefin tuna working group of the ICCAT SCRS. This larval index (denoted as "revised version")  includes data from the systematic sampling campaigns from 2001 to 2005,and from 2012 to 2019 (not including data from 2018), with additional data for 2008 and 2011, taking advantage of smaller campaigns of ichthyoplankton surveys conducted those years. Previous version of the index (SCRS/P/2019/055), denoted as "strict update", that was used for previous VPA, is also presented for comparison.

The index is based on survey campaigns developed around the Balearic Sea, a known aggregation area of spawniners and a geographically restricted area with adequate larval habitats at basin scale (Reglero *et al.,* 2018, Diaz-Barroso *et al.,* 2022). The standardisation of the CPUE is resolved with a two stage model combining a binomial and a log-normal submodel, both resolved with general additive models (GAMs). Corrections for unbalanced factors and back-transformation of the errors are resolved with EMMEANS (Searle *et al.*, 1980, Lenth 2020). The larval index shows an increasing trend with maximum value in the last updated year (2020). Nominal catches and percentages of stations with positive presences of bluefin tuna larvae also present a general increase in values with maximums in 2020.

## 2. Material and methods

### 2.1 Data collection

*Biological data*

Atlantic Bluefin tuna larvae were collected during fifteen ichthyoplankton surveys from 2001 to 2020 around the Balearic Islands during summer (**Table 1**) in systematic ichthyoplankton surveys targeting the spawning peak (June-July) of Atlantic Bluefin tuna in the area. Survey design consisted of a regular grid of $10 \times 10$ nautical miles covering the area between 37.858–40.358 N and 0.778–4.918 E, covering an area of 86,351 $Km^2$ (see Supplementary data, **Figure S1**). In order to ensure a better representativity of the sampling in relation to the location of the different water masses within the spawning ground the sampling strategy has been assessed with the use of the Mediterranean Sea Surface Exploration Tool, an open source for exploring surface oceanographic conditions in the Mediterranean Sea (Alvarez-Berastegui 2020).

Fishing operations were conducted at around 2 knots, during 8–10 minutes and covered a linear distance of about 600 m. The volume of water filtered was measured with flowmeters located at the centre of the net. During the period 2001-2005, tows were performed using a bongo net of 60 cm mouth diameter, stepped obliquely to a depth of 70 m (deep oblique), or from 5 m above the bottom at coastal stations, to the surface maintaining the vessel speed at two knots. For the years after 2005 the sampling was conducted using bongo 90 nets fitted with 500 microns meshes towed down to 20 – 30 metres (mixed layer oblique), covering the whole mixed layer depth in this area and season (Torres *et al.*, 2014). The standardisation method includes a correction factor for this difference on sampling gear obtained from experimental fishing (see details in the section 2.2 below).

In all surveys, plankton samples were preserved with 4% formalin buffered with borax. Tuna larvae were identified to the species level and measured in standard length. Once in the laboratory, the number of larvae were counted and standardised at each hauling station, following Álvarez-Berastegui *et al.*, (2018).

*Environmental data*

In-situ environmental data was also retrieved by means of a CTD probe. Collected variables driving larval habitats are: the mean salinity down to the mixed layer depth (SML, psu), temperature down to the mixed layer depth (TML, in ºC), fluorescence down to the mixed layer depth (FML, in $mg/m^3$), oxygen down to the mixed layer depth (OML, ml/l) and depth of the mixed layer (MLD, m). Other variables such as latitude (lat), longitude (lon), day of the year (jd), hour of the day (hournorm), year and month were also checked.

## 2.2 Data processing

*Input data exploration*

In order to assess potential variability of sampling and environmental conditions among years that could affect the standardisation of the catches we explored boxplots of the following variables: volume filtered by nets per year, Tmezcla, Smezcla, Oxygen concentration in the mixed layer depth (OMEZCLA), day of the year (jd) and hour of the fishing operation (hournorm), larval length distributions (see Supplementary material, Figures S2.1, S2.2 and S.2.3).

*Retrocalculation approach: correction for the larvae length decay in numbers*

The abundance of bluefin tuna with different lengths was standardised to larvae at reference length of 2 mm to avoid the exponential decay due to natural mortality and changes on catchability of older larvae (details in Alvarez-Berastegui *et al.,* 2018). In order to maintain the index as much similar to previous versions, the retrocalculation model has not been re-adjusted with new catch distributions from 2017 to 2020, therefore we used the following equation developed for previous versions of the index:

$$N_{2mm} = 109294 \, e^{-0.722 \, L_i} \quad \text{(Eq. 1)}$$

where $N_{2mm}$ is the number of larvae at 2 millimetres and $L_i$ total length of larvae, in mm. In order to avoid extreme effects on the index derived from single very large larvae, larvae avobe 8.5mm are set to a that threshold length in the retrocalculation.

Second, the catch per unit area (CPUA$_{2mm}$, in N larvae_2mm / m$^2$) is obtained using the equation:

$$CPUA2mm = \frac{N2mm}{V_{filt}} \, D_{tow} \quad \text{(Eq. 2)}$$

where $V_{filt}$ is the volume of water filtered by the net (in m$^3$) and $D_{tow}$ is the towing depth (in m), obtaining a CPUA at 2mm.

*Standardisation for changes in fishing methods*

CPUA was standardised for changes in fishing methods in the periods 2001-2005 (Bongo 60 with 333 $\mu$m mesh size) and 2012-2019 (Bongo 90 down to 30 meters and 500 $\mu$m mesh size), following an exponential relationship between B60 deep oblique and B90 mixed layer oblique obtained from experimental hauls on bluefin tuna larvae (details in Alvarez-Berastegui *et al.,* 2018):

$$CPUA_{B90} = 0.58 \, CPUA_{B60} \, e^{0.00115 \, CPUA_{B60}}, R^2 = 0.998 \quad \text{(Eq. 3)}$$

*Larval index standardisation models*

The inter annual variability of the CPUA of larvae at 2 mm was modelled using a two-stage generalised additive modelling (GAM) approach using the 'mgcv' package (Wood 2004, 2006), following a similar approach to that applied for bluefin tuna larval index in the study area (Álvarez-Berastegui *et al.,* 2020, 2021). This method combines a binomial submodel predicting probabilities of larval presence and a log-normal submodel to predict log-transformed positive abundances. Environmental variables were included to improve the standardisation of the larval indices. The explanatory variables considered in the modelling were year, day time (night or day), mean salinity in the mixed layer depth (SMEZCLA) accounting for the spatial distribution of water masses (Balbín *et al.*, 2014) that affect the spawning of bluefin tuna (Alemany *et al.,* 2010, Reglero *et al.,* 2014), the day of the year (jd) accounting for changes on spawning probability along the spawning period, and the residual temperature (tempres) as the residuals of a linear model where temperature was fitted to the day of the year (R$^2$=0.48, p-value $< 2.2e^{-16}$). The residual temperature allowed including inter annual differences of temperature in the models considering the existing significant correlation between the mean temperature in the mixed layer depth and the day of the year (R$^2$=0.70, p-value $< 2.2e^{-16}$). The anomaly of temperature (Tanom) and the anomaly of salinity (SALanom) were computed as the temperature and salinity at the mixed layer after removing the annual mean temperature and salinity, respectively. Binomial and log-normal GAM submodels were fitted following a stepwise forward method, starting from models with only one variable and subsequently adding significant variables (p-value<0.05) by means of restricted maximum likelihood (REML; Wood 2011). REML is more efficient than other available methods like general cross-validation (Marra and Wood, 2011). The degree of smoothness of each particular variable was limited in order to avoid overfitting, i.e. a maximum of 3 knots for single variable relationships and 9 knots for interactions between two variables.

Model performance was assessed by inspection of the Area Under the Curve (AUC) plot and density plot of real positive and negative estimates, for the presence probability (binomial) submodel. For the log-transformed positive abundance submodel, model performance was evaluated through the deviance of the residual versus theoretical quantiles, residuals versus linear predictor, histogram of the residuals and the response versus fitted values.

The index value for each year ($I'_y$) was calculated as follows:

$$I'_y = c'_y \, p'_y \text{ (Eq. 4)}$$

where $c'_y$ is the back-transformed mean CPUA from the lognormal submodel in the year 'y' and $p'_y$ probability of presence of Bluefin tuna larvae estimated from the binomial submodel, both compensated accounting for changes in factors among years by means using estimated marginal means with the 'emmeans' package (Searle *et al.*, 1980, Lenth 2020). The estimation of the standard error (*se'*) was also computed using the compensation for unbalanced factors with 'emmeans'. The upper and lower 95% confidence intervals (*UCI* and *LCI*) for the index were calculated to measure the precision of the mean, using the approximation for non-normal data as proposed by Ingram *et al.*, (2010), according to the following equations:

$$UCI = I'_y \times C \text{ (Eq. 5)}$$

$$LCI = \frac{I'_y}{C} \text{ (Eq. 6)}$$

where $C = e^{\, 2 \, x \, \sqrt{log\,(1 - CV'^2)}}$, *CV'* is the coefficient of variation of the index $I'_y$, computed as the standard error of the index (*se'*) divided by the value of the index ($I'_y$), both compensated for unbalanced factors. All calculations were computed in R software (R Core Team 2021).

*Previous version of the index*

The previous version of the index, denoted as "strict update", used originally for the VPA in previous assessments, has been calculated for comparison. This index was computed with a two-stage log-normal model using GAMs and a bootstrap approach for correcting the unbalanced factors in sampling (following methods described in the SCRS/P/2019/055).

## 3. Results

The proportion of positive stations for Bluefin tuna larvae and the nominal CPUA based on the 2 mm standardised larvae show an increasing trend in the last 20 years (**Table 2**). Following the strict update of the 2021 version of the larval index (Álvarez-Berastegui *et al*., 2020, 2021), the binomial and abundance submodels were conceptualised according to the formulas:

Presence-Absence ~ as.factor (year) + s (SALanom, k=3) + s (jd, k=3) + s (tempres, k=3)
log (CPUA) ~ as.factor (year) + s (lon, lat) + s (SALanom, k=3) + s (tempres, k=3)

Model summaries, diagnostic plots and model partial responses for both components of the modelling approach are shown in Supplementary materials (**Tables S3.1 and S3.2 and Figures S4.1, S4.2, S5.1 and S5.2**). Either in the binomial and abundance submodels, residual temperature showed a positive effect in bluefin tuna, showing that warmer years have a positive effect in the spread of larvae (becoming more widespread and "colonising" most of the study area) as well as in the amount of larvae that is encountered at each station. The models also reveal a preference for the stations with intermediate salinity anomalies which are related to the waterfront present in the area, where the mixing of Atlantic and Mediterranean waters occurs.

The values of the larval index ($I'_y$) as well as the associated dispersion parameters shows an increasing trend since 2010 (**Table 2, Figure 1**).

*Previous version of the index (SCRS/P/2019/055, "strict update").*

Appendix S.6 presents the model used and Larval index values (**Table S6.1**) for this "strict update" index, and comparison figure with the "revised version" is presented in **Figure S6.2.**

### 4. Conclusions

- The levels of larvae abundances in the last year updated, 2020, are above the value from previous years. This pattern is also found in the nominal CPUE. The general trend of the index shows that retrocalculated larval abundances are increasing along the last decade.

- The previous version of the index ("strict update") shows a similar pattern to the revised version which also includes data from 2008 and 2011.

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**Table 1.** Ichthyoplankton survey, fishing and gear characteristics and sampling effort.

| Year | Dates | Gear | Haul type | No. samples | Tow depth |
|------|-------|------|-----------|-------------|-----------|
| 2001 | 16 Jun - 07 Jul | B60 | Deep oblique | 162 | 70 |
| 2002 | 07 Jun - 28 Jun | B60 | Deep oblique | 171 | 70 |
| 2003 | 03 Jul - 29 Jul | B60 | Deep oblique | 198 | 70 |
| 2004 | 18 Jun - 08 Jul | B60 | Deep oblique | 166 | 70 |
| 2005 | 27 Jun - 23 Jul | B60 | Deep oblique | 186 | 70 |
| 2006 | - | - | - | - | - |
| 2007 | - | - | - | - | - |
| 2008 | 29 Jul - 11 Aug | B90 | Mixed layer oblique | 41 | 30 |
| 2009 | - | - | - | - | - |
| 2010 | - | - | - | - | - |
| 2011 | 14 May - 17 Jul | B90 | Mixed layer oblique | 85 | 30 |
| 2012 | 21 Jun - 08 Jul | B90 | Mixed layer oblique | 153 | 30 |
| 2013 | 20 Jun - 10 Jul | B90 | Mixed layer oblique | 124 | 30 |
| 2014 | 13 Jun - 30 Jun | B90 | Mixed layer oblique | 92 | 30 |
| 2015 | 23 Jun - 09 Jul | B90 | Mixed layer oblique | 94 | 30 |
| 2016 | 21 Jun - 07 Jul | B90 | Mixed layer oblique | 95 | 30 |
| 2017 | 26 Jun - 12 Jul | B90 | Mixed layer oblique | 92 | 30 |
| 2018 | - | - | - | - | - |
| 2019 | 19Jun – 29 Jun | B90 | Mixed layer oblique | 108 | 30 |
| 2020 | 25Jun – 05 Jul | B90 | Mixed layer oblique | 91 | 30 |

**Table 2.** Positive stations (%), nominal CPUA and larval index (Index, n larvae at 2 mm/ 10 m$^2$), precision of the index estimated as the coefficient of variation (CV, %) and the 95% lower and upper confidence intervals (LCI and UCI).

| | | | *2020 SCRS & 2021 SCRS* | | | |
|---|---|---|---|---|---|---|
| *Year* | *Positive stations (%)* | *Nominal CPUA* | *Index* | *CV (%)* | *LCI* | *UCI* |
| 2001 | 16,67 | 6,64 | 4,58 | 41,69 | 2,05 | 10,19 |
| 2002 | 10,53 | 4,23 | 9,58 | 48,83 | 3,80 | 24,14 |
| 2003 | 12,12 | 8,19 | 2,67 | 54,00 | 0,97 | 7,35 |
| 2004 | 15,66 | 28,87 | 10,86 | 41,97 | 4,85 | 24,31 |
| 2005 | 20,43 | 8,21 | 2,27 | 39,64 | 1,06 | 4,88 |
| 2006 | - | - | - | - | - | - |
| 2007 | - | - | - | - | - | - |
| 2008 | 19,51 | 0,36 | 1,96 | 78,90 | 0,49 | 7,87 |
| 2009 | - | - | - | - | - | - |
| 2010 | - | - | - | - | - | - |
| 2011 | 31,76 | 39,27 | 9,92 | 39,84 | 4,61 | 21,38 |
| 2012 | 69,28 | 212,99 | 26,57 | 21,55 | 17,35 | 40,69 |
| 2013 | 62,90 | 178,00 | 40,32 | 30,18 | 22,34 | 72,77 |
| 2014 | 52,17 | 85,15 | 20,10 | 29,58 | 11,26 | 35,87 |
| 2015 | 80,85 | 196,26 | 36,61 | 24,25 | 22,70 | 59,04 |
| 2016 | 62,11 | 185,38 | 32,41 | 27,78 | 18,79 | 55,91 |
| 2017 | 84,78 | 521,10 | 73,03 | 24,78 | 44,82 | 118,99 |
| 2018 | - | - | - | - | - | - |
| 2019 | 70,37 | 478,57 | 46,16 | 23,29 | 29,15 | 73,10 |
| 2020 | 89,01 | 533,49 | 107,15 | 23,14 | 67,86 | 169,20 |
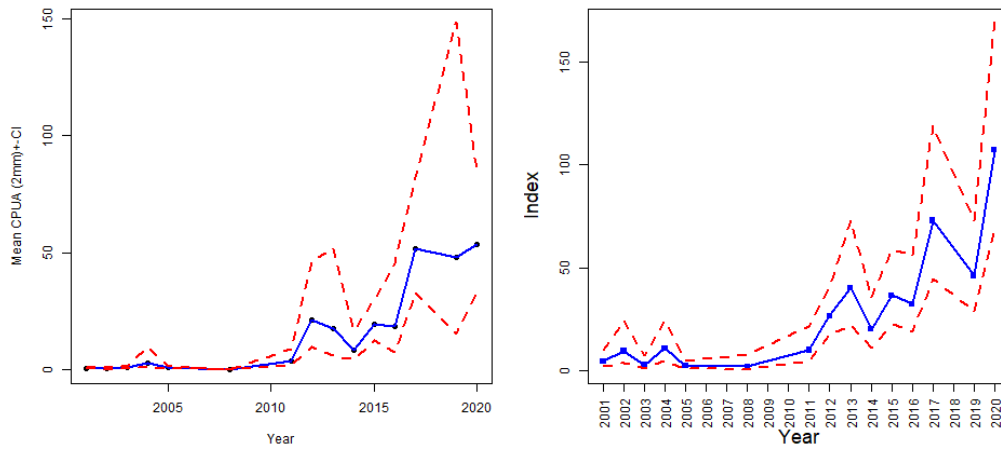
**Figure 1.** Bluefin tuna nominal CPUA (left) and "Revised version" larval index (right) for the period 2001-2020.

# Supplementary data

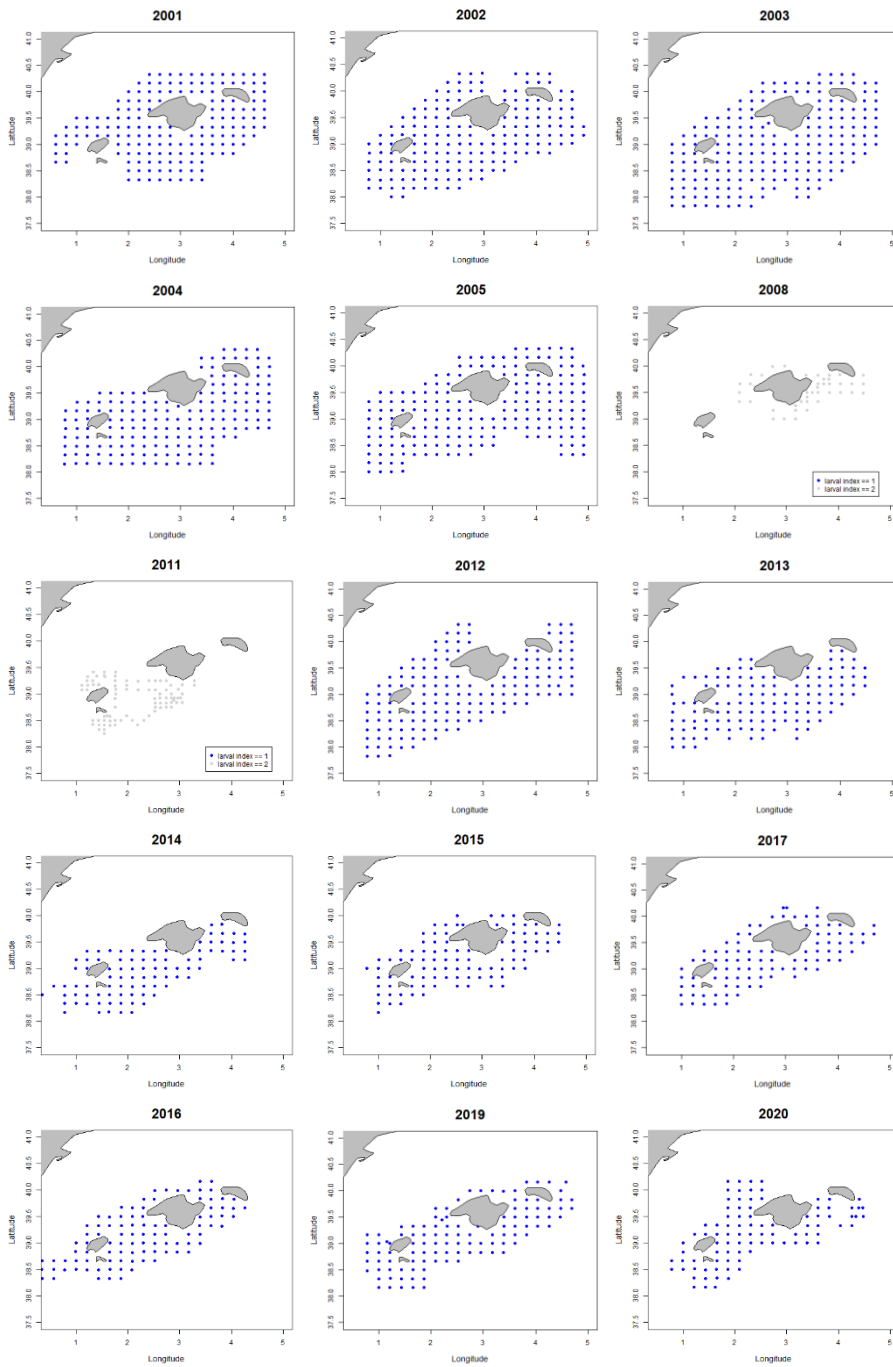## S1. Sampling locations



**Figure S1.** Sampling locations of the ichthyoplankton surveys used in the estimation of the larval index.

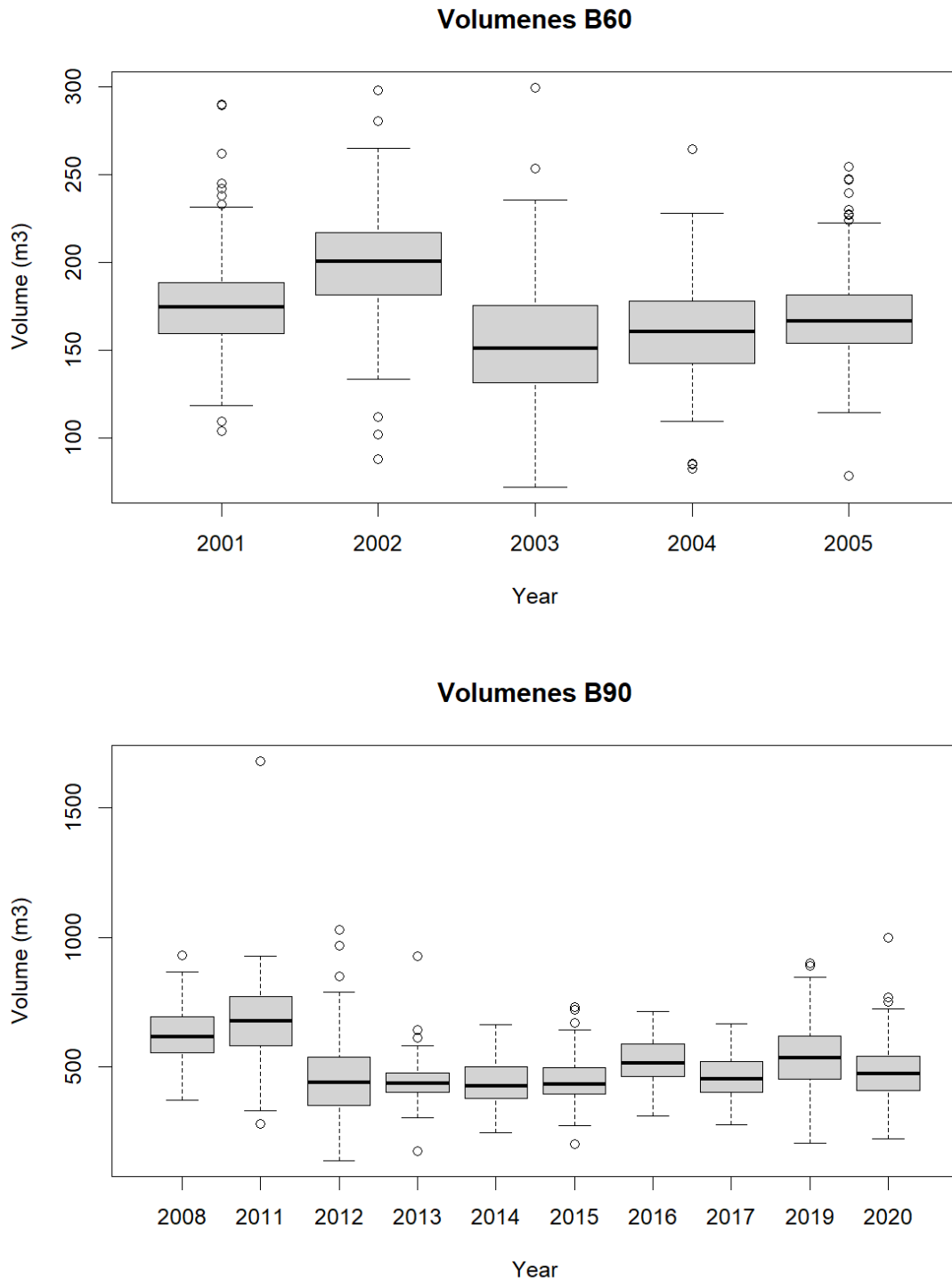**S2. Data exploration for volumes of water filtered and environmental variables**

## Volumenes B60



## Volumenes B90



**Figure S2.1.** Boxplot of the volumes of water filtered per year for the two fishing deployments: bongo-60 with 333 μm and bongo-90 with 500 μm.
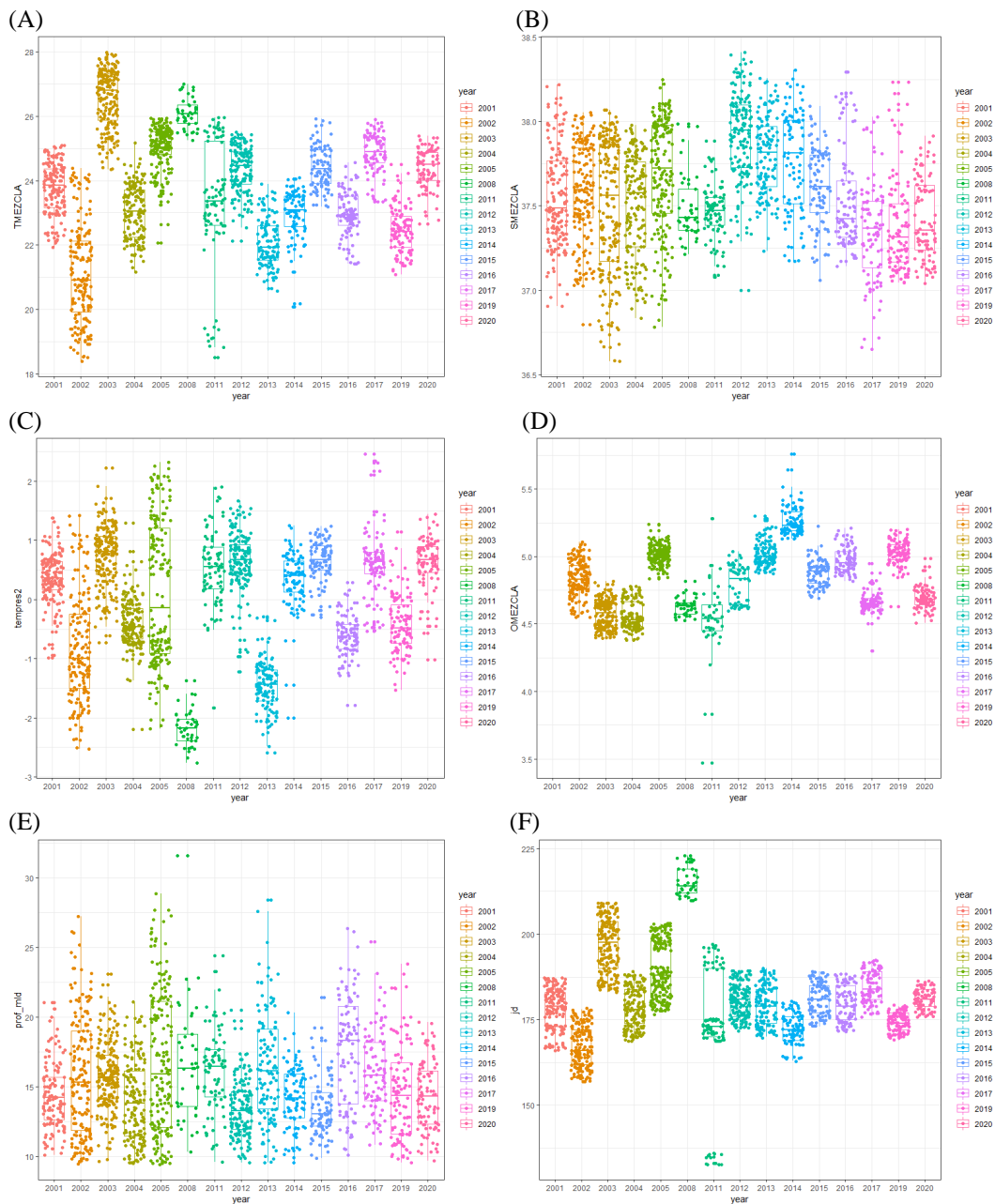
**Figure S2.2.** Boxplot of the environmental variables: (A) Temperature in the mixed layer depth (TMEZCLA); (B) Salinity in the mixed layer depth (SMEZCLA); (C) Residual temperature in the mixed layer depth (restemp2) (extracted the effect of the day of the year using a linear model); (D) Oxygen in the mixed layer depth (OMEZCLA); (E) Mixed layer depth; (F) Day of the year.
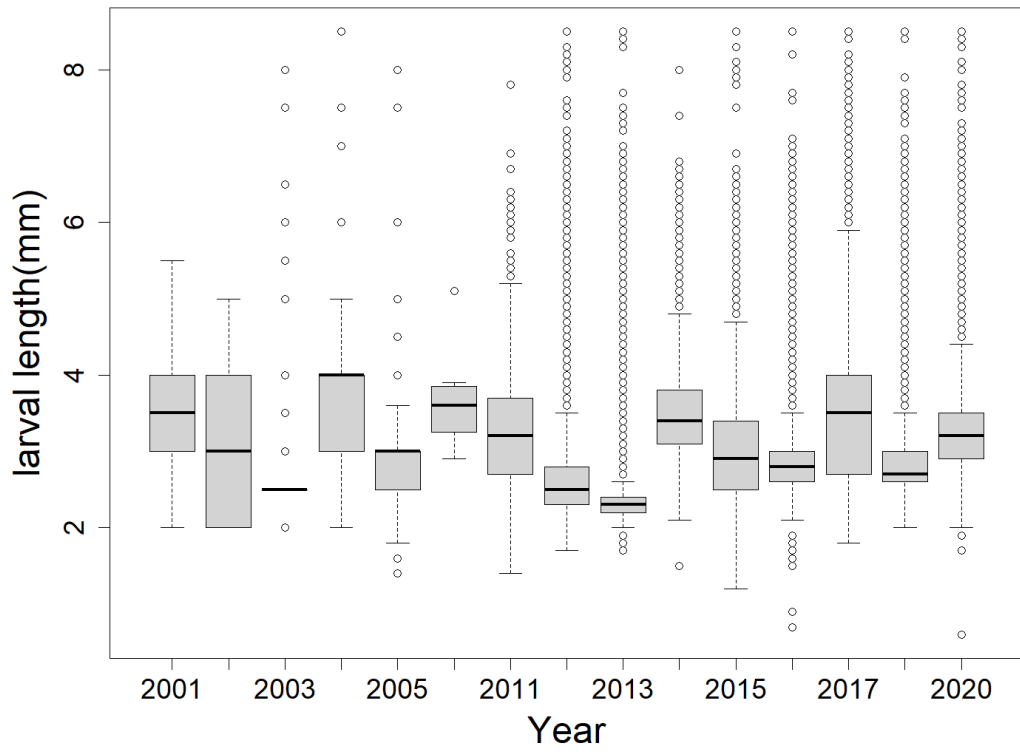
**Figure S2.3.** Boxplot of the larval lengths distributions.

**S3. Summary of the larval index model** ("revised version", SCRS SCRS/2020/067)

**Table S3.1. Summary of the binomial model**

Family: binomial (link function="logit")
Formula: lpres ~ as.factor(year) + s(SALanom, k = 3) + s(jd, k = 3) + s(tempres2, k = 3)

Parametric coefficients:

|  | Estimate | Std. Error | z value | Pr(>|z|) |  |
|---|---|---|---|---|---|
| (Intercept) | -1.9599 | 0.2348 | -8.345 | < 2e-16 | *** |
| as.factor(year)2002 | 1.1142 | 0.3764 | 2.960 | 0.003072 | ** |
| as.factor(year)2003 | -1.2235 | 0.4040 | -3.028 | 0.002460 | ** |
| as.factor(year)2004 | 0.2740 | 0.3188 | 0.860 | 0.389999 | |
| as.factor(year)2005 | -0.3113 | 0.3171 | -0.982 | 0.326164 | |
| as.factor(year)2008 | 1.4157 | 0.8949 | 1.582 | 0.113667 | |
| as.factor(year)2011 | 1.1669 | 0.3466 | 3.367 | 0.000761 | *** |
| as.factor(year)2012 | 2.1480 | 0.2856 | 7.520 | 5.46e-14 | *** |
| as.factor(year)2013 | 2.9730 | 0.3847 | 7.727 | 1.10e-14 | *** |
| as.factor(year)2014 | 2.6411 | 0.3343 | 7.899 | 2.80e-15 | *** |
| as.factor(year)2015 | 2.7068 | 0.3457 | 7.831 | 4.85e-15 | *** |
| as.factor(year)2016 | 2.5935 | 0.3353 | 7.735 | 1.04e-14 | *** |
| as.factor(year)2017 | 2.7529 | 0.3721 | 7.399 | 1.37e-13 | *** |
| as.factor(year)2019 | 3.5063 | 0.3428 | 10.228 | < 2e-16 | *** |
| as.factor(year)2020 | 3.3481 | 0.4040 | 8.288 | < 2e-16 | *** |

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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

|  | edf | Ref.df | Chi.sq | p-value |  |
|---|---|---|---|---|---|
| s(SALanom) | 1.774 | 2 | 21.11 | 6.18e-06 | *** |
| s(jd) | 1.948 | 2 | 75.95 | < 2e-16 | *** |
| s(tempres2) | 1.475 | 2 | 21.13 | 3.56e-06 | *** |

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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.393   Deviance explained =  33%
-REML =  862.5  Scale est. = 1       n = 1858

**Table S3.2. Summary of the abundance model**

Family: gaussian (link function="identity")
Formula: log(BFTab_gs) ~ as.factor(year) + s(lon, lat, k = 9) + s(SALanom,
  k = 3) + s(tempres2, k = 3)

Parametric coefficients:

| | Estimate | Std. Error | t value | Pr(>\|t\|) | |
|---|---|---|---|---|---|
| (Intercept) | 2.947588 | 0.372174 | 7.920 | 8.54e-15 | *** |
| as.factor(year)2002 | -0.016658 | 0.590197 | -0.028 | 0.977490 | |
| as.factor(year)2003 | 0.524429 | 0.552059 | 0.950 | 0.342442 | |
| as.factor(year)2004 | 0.654985 | 0.539431 | 1.214 | 0.225047 | |
| as.factor(year)2005 | -0.446496 | 0.489681 | -0.912 | 0.362161 | |
| as.factor(year)2008 | -1.758931 | 0.838967 | -2.097 | 0.036368 | * |
| as.factor(year)2011 | -0.009653 | 0.530410 | -0.018 | 0.985485 | |
| as.factor(year)2012 | 0.565463 | 0.415549 | 1.361 | 0.173997 | |
| as.factor(year)2013 | 0.795125 | 0.496757 | 1.601 | 0.109878 | |
| as.factor(year)2014 | 0.160337 | 0.463098 | 0.346 | 0.729268 | |
| as.factor(year)2015 | 0.746435 | 0.431796 | 1.729 | 0.084278 | . |
| as.factor(year)2016 | 0.648255 | 0.465965 | 1.391 | 0.164573 | |
| as.factor(year)2017 | 1.428003 | 0.428462 | 3.333 | 0.000902 | *** |
| as.factor(year)2019 | 0.861868 | 0.443981 | 1.941 | 0.052604 | . |
| as.factor(year)2020 | 1.721099 | 0.427927 | 4.022 | 6.35e-05 | *** |

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

| | edf | Ref.df | F | p-value | |
|---|---|---|---|---|---|
| s(lon,lat) | 1.4154 | 8 | 0.488 | 0.06430 | . |
| s(SALanom) | 0.8499 | 2 | 2.724 | 0.01108 | * |
| s(tempres2) | 0.8929 | 2 | 4.155 | 0.00224 | ** |

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.116   Deviance explained = 13.5%
-REML = 1592.1  Scale est. = 3.6561          n = 770

**S4. Partial effects of the environmental variables in the models** ("revised version", SCRS SCRS/2020/067 and SCRS/2021/033)
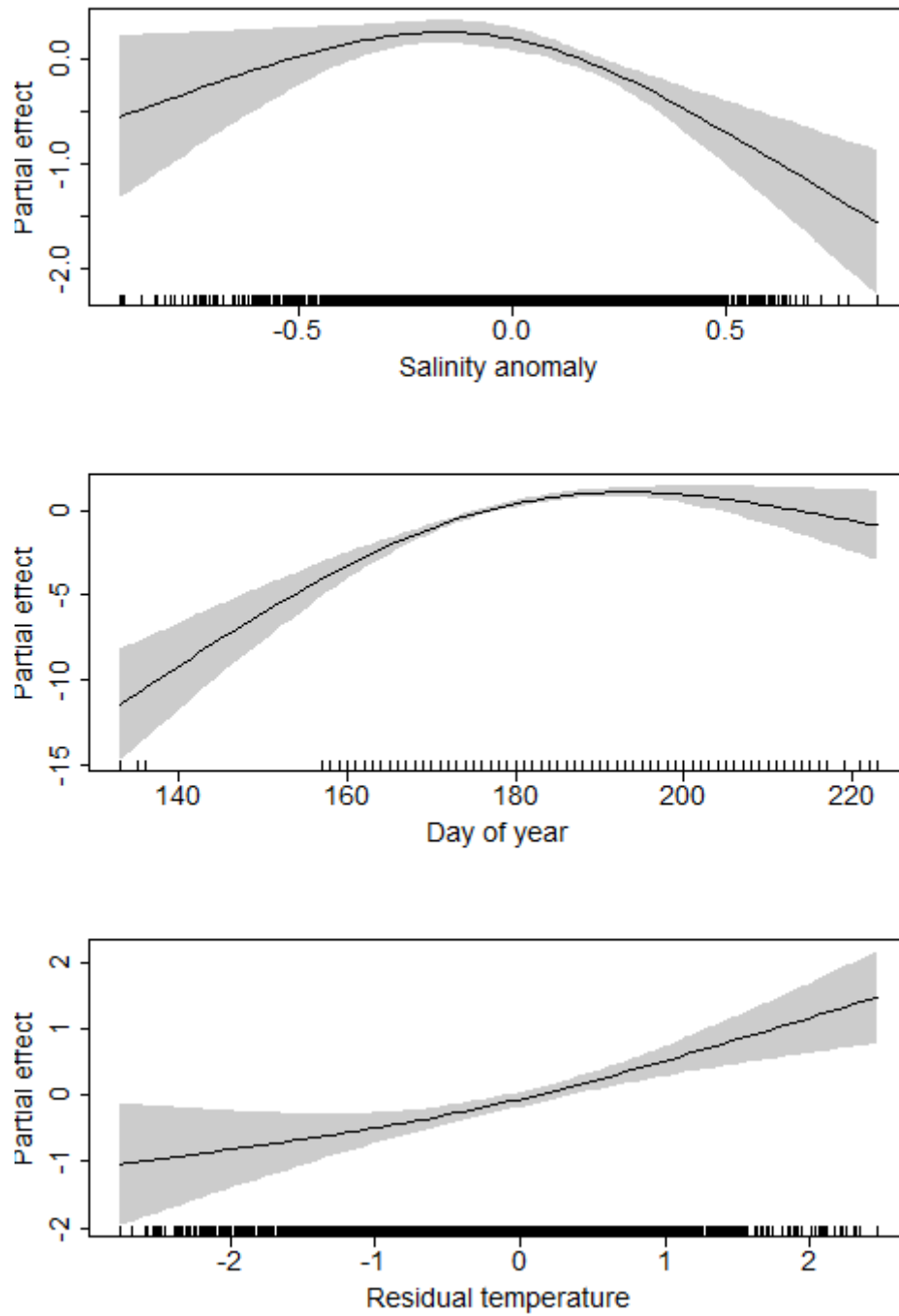


**Figure S4.1.** Partial effects of the significant variables included in the final selected model for bluefin tuna presence-absence.
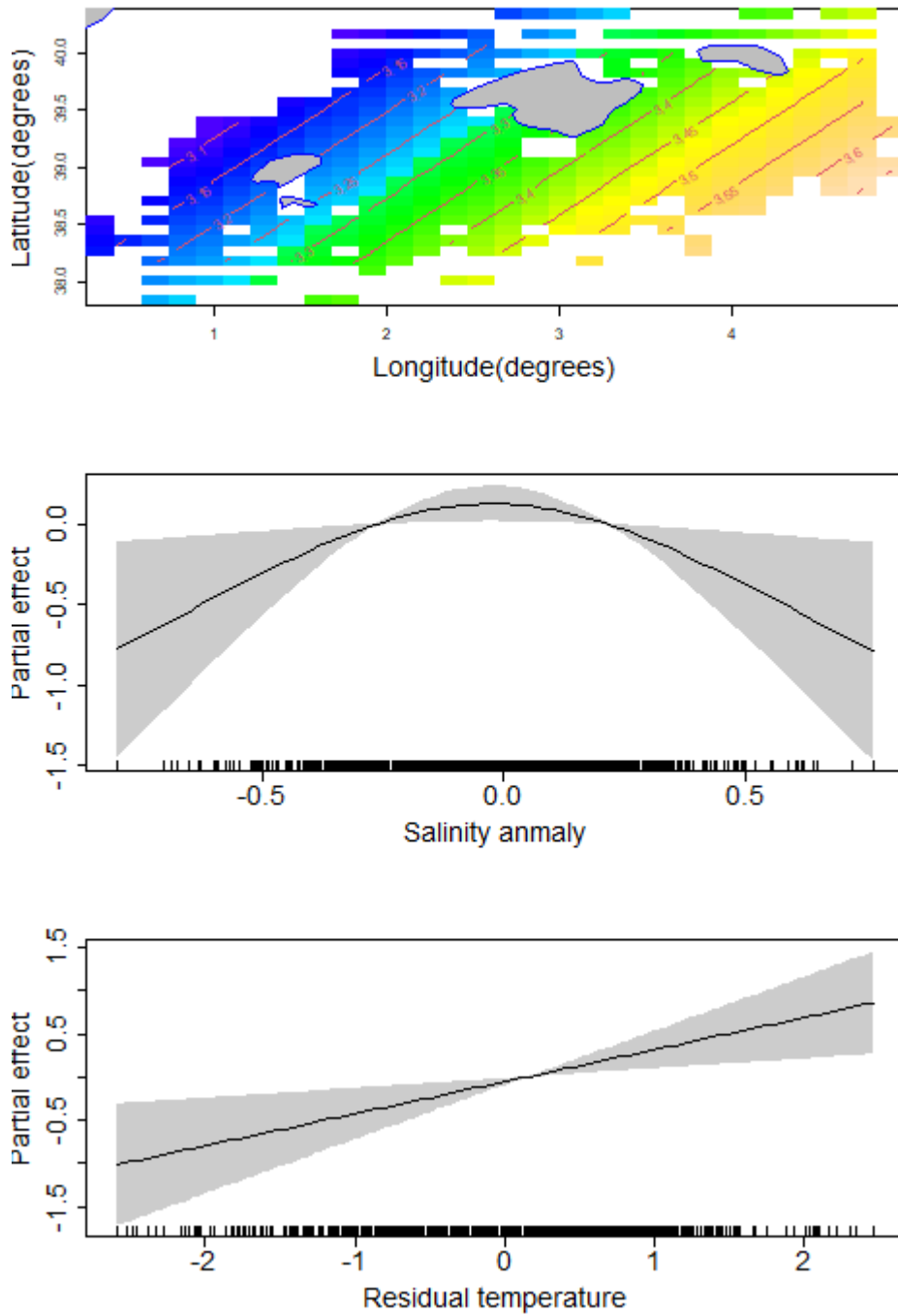
**Figure S4.2.** Partial effects of the significant variables included in the final selected model for Bluefin tuna abundance.

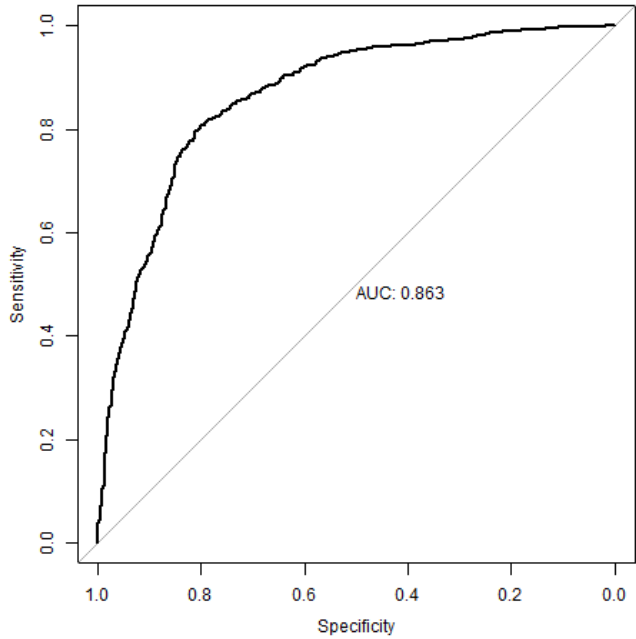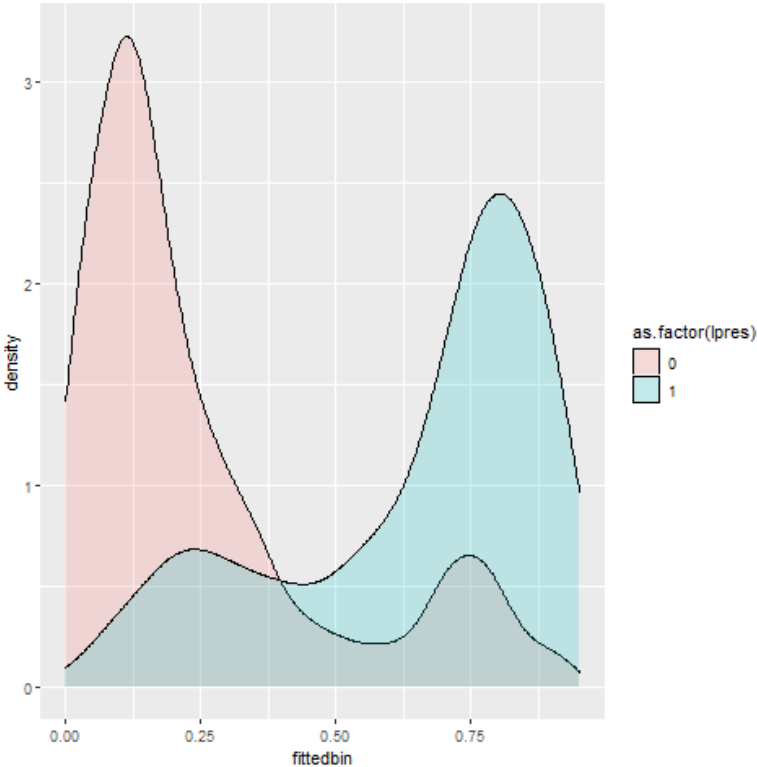**S5. Model performance** ("revised version", SCRS SCRS/2020/067 and SCRS/2021/033)





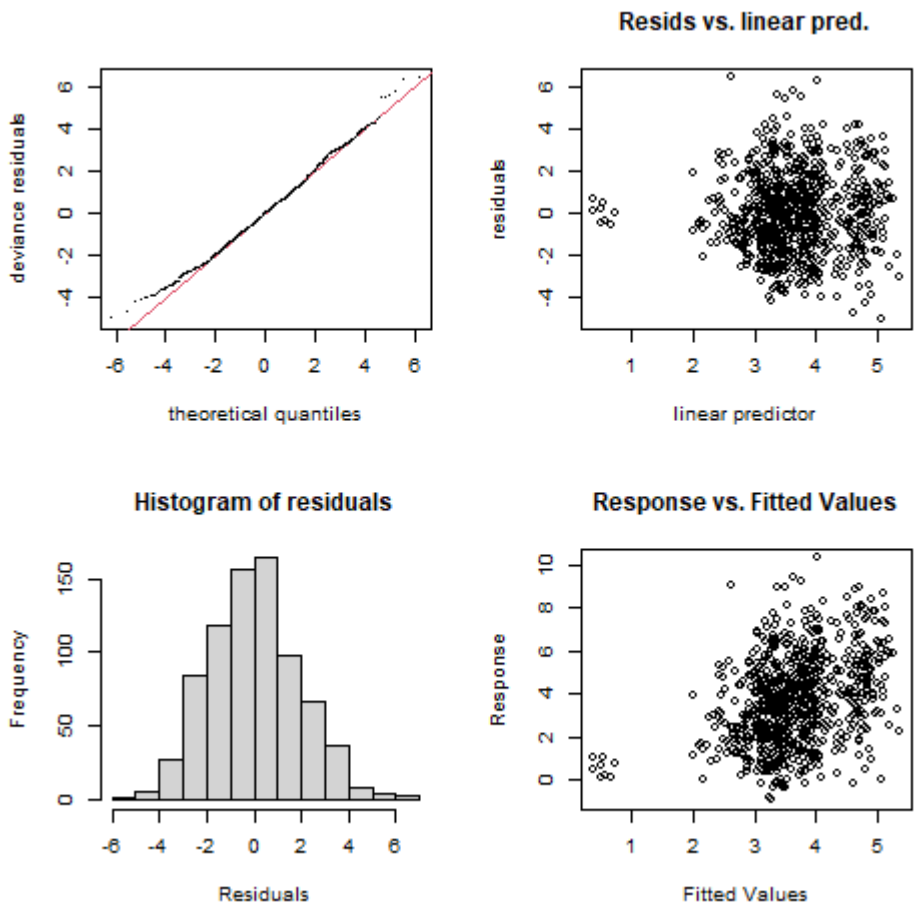**Figure S5.1.** Model performance of the binomial model.

**Figure S5.2.** Model performance of the abundance submodel.

**S6. Details of the previous "strict update" larval index model and comparison with the current "revised version".**

**Summary of the binomial model**

Family: binomial (link function="logit")
Formula: lpres ~ as.factor(year) + s(lat, lon, k = 9) + s(jd, k = 3) + s(SMEZCLA, k = 3) + s(residualtemp, k = 3)

Parametric coefficients:

| | Estimate | Std. Error | z value | Pr(>|z|) | |
|---|---|---|---|---|---|
| (Intercept) | -1.93398 | 0.23496 | -8.231 | < 2e-16 | *** |
| as.factor(year)2002 | 0.80252 | 0.43311 | 1.853 | 0.0639 | . |
| as.factor(year)2003 | -0.85423 | 0.50585 | -1.689 | 0.0913 | . |
| as.factor(year)2004 | 0.17658 | 0.32634 | 0.541 | 0.5884 | |
| as.factor(year)2005 | -0.08292 | 0.36339 | -0.228 | 0.8195 | |
| as.factor(year)2012 | 2.59853 | 0.32383 | 8.024 | 1.02e-15 | *** |
| as.factor(year)2013 | 3.15558 | 0.41474 | 7.609 | 2.77e-14 | *** |
| as.factor(year)2014 | 2.65998 | 0.35974 | 7.394 | 1.42e-13 | *** |
| as.factor(year)2015 | 2.72306 | 0.35309 | 7.712 | 1.24e-14 | *** |
| as.factor(year)2016 | 2.48678 | 0.34464 | 7.216 | 5.37e-13 | *** |
| as.factor(year)2017 | 2.71863 | 0.40325 | 6.742 | 1.56e-11 | *** |
| as.factor(year)2019 | 3.23510 | 0.35155 | 9.202 | < 2e-16 | *** |
| as.factor(year)2020 | 3.22099 | 0.41384 | 7.783 | 7.07e-15 | *** |

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

| | edf | Ref.df | Chi.sq | p-value | |
|---|---|---|---|---|---|
| s(lat,lon) | 6.848 | 7.711 | 10.29 | 0.139483 | |
| s(jd) | 1.969 | 1.999 | 28.75 | 4.81e-07 | *** |
| s(SMEZCLA) | 1.889 | 1.987 | 17.15 | 0.000441 | *** |
| s(residualtemp) | 1.386 | 1.622 | 16.07 | 0.002116 | ** |

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.398   Deviance explained = 33.8%
UBRE = -0.068442  Scale est. = 1            n = 1732

**Summary of the abundance model**

Family: gaussian (link function="identity")
Formula: $\log(BFTab\_gs) \sim$ as.factor(year) + s(lat, lon, k = 9) + s(TMEZCLA, k = 3) + s(SMEZCLA, k = 3) + s(hournorm, bs = "cc", k = 7)

Parametric coefficients:

| | Estimate | Std. Error | t value | Pr(>\|t\|) | |
|---|---|---|---|---|---|
| (Intercept) | 2.8592 | 0.3798 | 7.529 | 1.55e-13 | *** |
| as.factor(year)2002 | 0.4032 | 0.6336 | 0.636 | 0.52478 | |
| as.factor(year)2003 | 0.4945 | 0.7351 | 0.673 | 0.50137 | |
| as.factor(year)2004 | 0.5156 | 0.5509 | 0.936 | 0.34968 | |
| as.factor(year)2005 | -0.4406 | 0.5439 | -0.810 | 0.41816 | |
| as.factor(year)2012 | 0.7039 | 0.4552 | 1.546 | 0.12245 | |
| as.factor(year)2013 | 0.9567 | 0.5131 | 1.865 | 0.06266 | . |
| as.factor(year)2014 | 0.4250 | 0.4931 | 0.862 | 0.38906 | |
| as.factor(year)2015 | 0.8496 | 0.4488 | 1.893 | 0.05876 | . |
| as.factor(year)2016 | 0.6239 | 0.4643 | 1.344 | 0.17944 | |
| as.factor(year)2017 | 1.4320 | 0.4622 | 3.098 | 0.00202 | ** |
| as.factor(year)2019 | 1.1234 | 0.4693 | 2.394 | 0.01693 | * |
| as.factor(year)2020 | 1.7319 | 0.4396 | 3.940 | 8.96e-05 | *** |

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

| | edf | Ref.df | F | p-value | |
|---|---|---|---|---|---|
| s(lat,lon) | 2.725 | 3.294 | 0.366 | 0.8421 | |
| s(TMEZCLA) | 1.846 | 1.975 | 5.821 | 0.0066 | ** |
| s(SMEZCLA) | 1.637 | 1.866 | 1.086 | 0.4016 | |
| s(hournorm) | 2.712 | 5.000 | 0.732 | 0.2428 | |

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.0949   Deviance explained = 12.1%
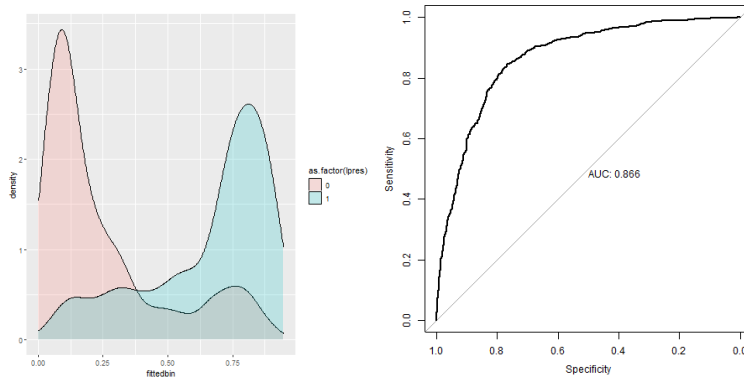GCV = 3.8091  Scale est. = 3.6955  n = 735

**Model performance**
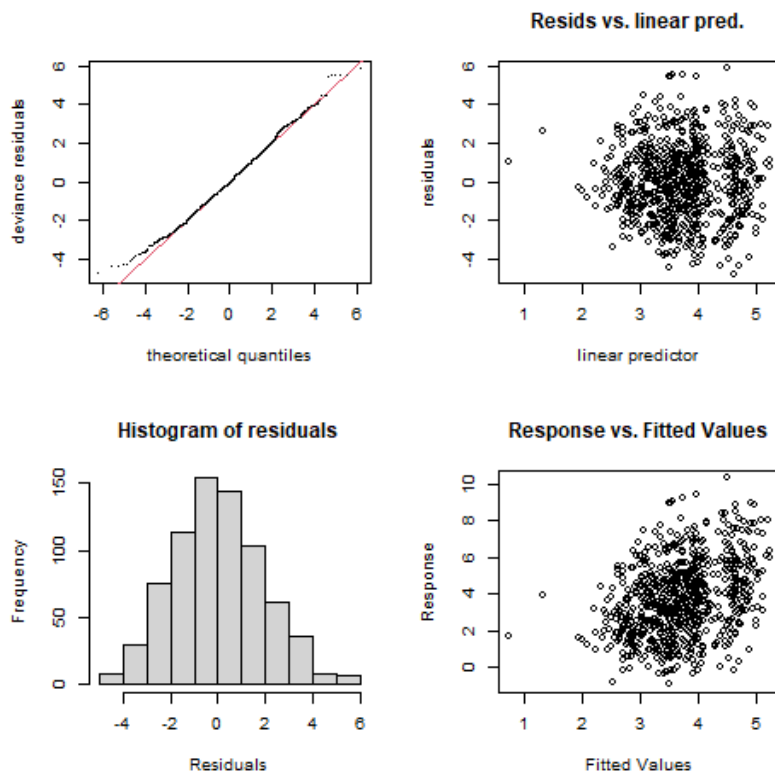


**Figure S6.1.** Model performance of the binomial model.

**Figure S6.2.** Model performance of the abundance submodel.

**Table S6.1.** Index values for the 2019 SCRS version.

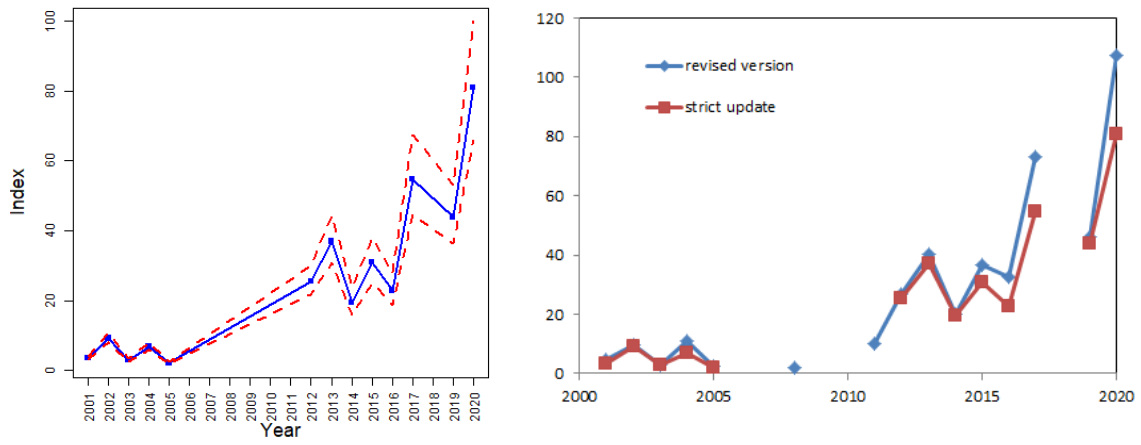| Year | 2019 SCRS | | | |
|---|---|---|---|---|
| | **Index** | **CV (%)** | **LCI** | **UCI** |
| 2001 | 3,54 | 7,86 | 3,03 | 4,14 |
| 2002 | 9,19 | 7,65 | 7,89 | 10,71 |
| 2003 | 2,95 | 7,11 | 2,56 | 3,40 |
| 2004 | 6,76 | 7,76 | 5,79 | 7,89 |
| 2005 | 2,15 | 7,33 | 1,86 | 2,49 |
| 2006 | - | - | - | - |
| 2007 | - | - | - | - |
| 2008 | - | - | - | - |
| 2009 | - | - | - | - |
| 2010 | - | - | - | - |
| 2011 | - | - | - | - |
| 2012 | 25,48 | 8,08 | 21,68 | 29,94 |
| 2013 | 36,92 | 8,98 | 30,86 | 44,16 |
| 2014 | 19,48 | 10,43 | 15,83 | 23,99 |
| 2015 | 30,91 | 10,31 | 25,16 | 37,97 |
| 2016 | 22,81 | 10,26 | 18,58 | 27,99 |
| 2017 | 54,70 | 10,43 | 44,43 | 67,34 |
| 2018 | - | - | - | - |
| 2019 | 43,87 | 9,62 | 36,21 | 53,16 |
| 2020 | 80,99 | 10,48 | 65,71 | 99,83 |

**Figure S6.2.** "Strict update" larval index trend (left) and comparison with the "Revised version" larval index (right).