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A LENGTH-STRUCTURED META-POPULATION STOCK ASSESSMENT MODEL: APPLICATION TO SKIPJACK TUNA IN THE EASTERN PACIFIC OCEAN.

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1. INTRODUCTION

There is growing evidence that fish populations have more spatial structure than is considered in most fisheries stock assessments, and ignoring this spatial structure may bias stock assessment results and management advice (Goethal *et al.* 2011; Cope and Punt 2011; Berger *et al.* 2012). Many species that are considered highly migratory (*e.g.* bigeye, yellowfin, and skipjack tuna) are widely distributed, but have limited movement (Hilborn and Sibert 1988; Schaefer 2009). There may be no genetic difference within an ocean basin due to diffusion or larval dispersal, but for practical purposes sections of the ocean basin can be considered separate populations for assessment and management. These species differ from truly highly migratory species that often make large ontogenetic related movements or seasonal spawning migrations (*e.g.* albacore and bluefin tuna).

Lack of large-scale movement and exchange among sub-populations can result in differences in biological processes, exploitation levels, and stock status among areas (e.g. Montenegro et al. 2009). For

example, growth rates, age at maturity, and recruitment levels may be different in areas of high food availability compared to those with low food availability. Populations in heavily fished areas may be more depleted than those in areas that are only lightly exploited. Most fisheries are assessed and managed based on the assumption of a single stock, and applying the management advice to a group of sub-stocks with different biological processes and depletion levels will result in suboptimal management, since optimal harvest levels will differ among sub-stocks and a single management strategy will not be optimal for all sub-stocks. It is therefore important to consider the population structure when assessing a fishery.

Modeling population structure is not new, and has been used in the assessment of many species (*e.g.* Maunder 1998; Hampton and Fournier 2001; Goethal *et al.* 2011). Unfortunately, there is often not enough information to reliably assess each sub-stock. However, there may be adequate information for some sub-stocks, and borrowing information from the data-rich stocks to use in the data-poor stocks (the Robin Hood approach; Punt *et al.* 2011) might be useful (*e.g.* Jiao *et al.* 2011), or combining information from multiple stocks might increase the total information available (*e.g.* Montenegro *et al.* 2009). Moderate exchange among sub-stocks may require the modeling of movement, which requires additional information (*e.g.* from tagging data; Maunder 1998, 2001; Hampton and Fournier 2001; Goethal *et al.* 2011).

We developed a length-structured stock assessment model that simultaneously models multiple substocks and allows for information to be shared among the sub-stocks. The model is implemented in the integrated analysis framework (Fournier and Archibald 1982; Maunder and Punt submitted), to allow a variety of data sources to be included in the assessment. The model is applied to skipjack tuna in the eastern Pacific Ocean (EPO).

2. METHODS

The basic population dynamics model can be represented in matrix notation:

$$N_t = (\boldsymbol{G}\boldsymbol{\varphi}_{t-1})N_{t-1} + R_t$$

where

 N_t is a column vector of numbers at length at the start of time t;

G is the growth transition matrix where the columns represent the proportion of individuals transitioning to the different length classes from a single length class (*i.e.* they sum to one);

 φ is the survival matrix with the diagonals equal to survival for each length class;

 R_t is a column vector of recruitment for each length class in time t;

The basic model can be converted into a model of independent sub-populations by introducing the superscript z to identify sub-populations (zones):

$$N_t^z = G^z \varphi_{t-1}^z N_{t-1}^z + R_t^z$$

where N_t^{z} is a vector of numbers at length in sub-population z at the start of time t

In most of the equations below, the sub-population index, z, is omitted from the equations unless it is needed for clarity.

2.1. Recruitment

Recruitment variability is comprised of an overall variability that is shared among all sub-populations and a sub-population-specific variability. This allows both global (*e.g.* whole ocean) and local processes to affect recruitment. No stock-recruitment relationship is used because there is no evidence of such a relationship for skipjack, and the lag between spawning and recruitment to the fishery is uncertain. Recruitment variation is assumed to be lognormally distributed and parameterized using median recruitment (i.e. no lognormal bias correction factor).

$$\widetilde{R}_{t}^{z} = \mu_{R}^{z} exp\left(\sigma_{R}^{EP0,z} \varepsilon_{R,t}^{EP0} + \sigma_{R}^{z} \varepsilon_{R,t}^{z}\right)$$

where

 \widetilde{R}_{t}^{z} is the total recruitment in zone z at time t.

 μ_{R}^{z} is the median recruitment in zone z

 $\varepsilon_{R,t}^{EPO}$ is the recruitment deviate in time t common to all areas

 $\sigma_{p}^{EPO,z}$ is the standard deviation of the common deviate for zone z

 $\varepsilon_{R,t}^{z}$ is the recruitment deviate in time t specific to zone z

 σ_{R}^{z} is the standard deviate for deviate specific to zone z

Recruitment is distributed over the length classes using normalized and truncated discrete points from a normal distribution:

$$R_t^{z} = \widetilde{R}_t^{z} f(L)$$

$$f(L) = \frac{exp\left(-\frac{(L - \mu_{Rdist})^2}{2\sigma_{Rdist}^2}\right)}{\sum_l exp\left(-\frac{(L - \mu_{Rdist})^2}{2\sigma_{Rdist}^2}\right)}$$

where μ_{Rdist} and σ_{Rdist} are parameters to estimate.

2.2. Growth

We use Francis' (1995) general model, which is based on Baker et al.'s (1991) length-based

$$\mu_G = -L + \left[L^b e^{-a\Delta t} + c \left(1 - e^{-a\Delta t} \right) \right]^{\frac{1}{b}} \qquad a \neq 0, b \neq 0$$

where *L* is the initial length, $\Delta t = 1$ in the assessment model, and *a*, *c*, λ_1 and λ_2 are variables to make the calculations more convenient.

$$a = \ln\left[\frac{y_2^b - y_1^b}{\lambda_2^b - \lambda_1^b}\right]$$
$$c = \frac{y_2^b \lambda_1^b - y_1^b \lambda_2^b}{\lambda_1^b - y_1^b + y_2^b - \lambda_2^b}$$
$$\lambda_1 = y_1 + g_1$$
$$\lambda_2 = y_2 + g_2$$

The model includes five parameters: y_1 and y_2 are arbitrary fish lengths, small and large respectively, g_1 and g_2 are the mean growth increments for fish of length y_1 and y_2 , respectively, over a given time period (months in the skipjack application); and *b*, which has no biological meaning but describes the curvature in the model. The general growth model reduces to the von Bertalanffy growth model when *b* is set equal to one.

The growth increment is assumed to be normally distributed, with the variance a function of both time and initial length, using Maunder's (2002a) generalized growth variation model (note that the time component is used for modeling growth increments over varying times at liberty when fitting to tag growth increment data).

$$\sigma_{\rho}^{2}(L,\Delta t) = \alpha L^{\beta} \Delta t^{\gamma}$$

To avoid computational problems the variance model is reparameterized:

$$\sigma_g^2(L,\Delta t) = \exp(\alpha' + \beta \ln(L) + \gamma \ln(\Delta t))$$

The growth increment is expected to reduce with increasing initial length and increases with time; therefore, β and γ are expected to be negative and positive, respectively.

The growth increment used in the growth transition matrix is the integral over the lower and upper bounds of the length class. The distribution is truncated at the current length (negative growth is not allowed) and accumulated at the maximum length.

$$\mathbf{G}_{L} \sim \int_{L_{l}}^{L_{l+1}} N\left(\mu_{G}(L,1) + L, \sigma_{g}^{2}(L,1)\right) dL \qquad L < L_{\max}$$
$$\mathbf{G}_{L} \sim 1 - \int_{0}^{L_{l}} N\left(\mu_{G}(L,1) + L, \sigma_{g}^{2}(L,1)\right) dL \qquad L = L_{\max}$$

The growth transition matrix is normalized so the columns sum to one. L_{max} is the length of the lower bound of the maximum length interval in the model.

2.3. Survival

Survival is separated into natural and fishing mortality, with natural mortality occurring after fishing mortality. This is used to fill in the diagonals of the survival matrix used in the population dynamics equation.

$$\varphi_{t,l,l} = \exp\left(-M_{l}\right) \left(1 - \sum_{f} s_{l}^{f} u_{t}^{f}\right)$$
$$u_{t}^{f} = \frac{C_{t}^{f}}{B_{t}^{f}}$$
$$B_{t}^{f} = \sum_{l} N_{t,l} s_{l}^{f} w_{l}$$

where

 B_t^f is the exploitable biomass based on fishery f in time t

 u_t^f is the exploitation rate of fishery f in time t

 M_l is the natural mortality at length l

 s_l^f is the selectivity of length *l* to fishery *f*

2.4. Selectivity

Selectivity is modeled using the double normal. The variance parameter, v, can be set to a large number to

represent asymptotic selectivity.

$$s_{L}^{f} = \begin{cases} \exp\left(-\frac{\left(L-\mu_{s}^{f}\right)^{2}}{2v_{l}^{f}}\right) & \text{if } L \leq \mu_{s}^{f} \\ \\ \exp\left(-\frac{\left(L-\mu_{s}^{f}\right)^{2}}{2v_{r}^{f}}\right) & \text{if } L > \mu_{s}^{f} \end{cases}$$

2.5. Initial conditions

The numbers at length in the population in the first year of the model, N_{inib} are modeled based on an equilibrium exploitation rate and a fixed number (x) of recruitment cohorts with variable recruitment:

$$N_{init} = \sum_{i=0}^{x} (\boldsymbol{G}\boldsymbol{\varphi}_{init})^{i} \left(R_{init} \exp\left(\varepsilon_{init,i} \sqrt{\sigma_{EPO}^{2} + \sigma_{z}^{2}}\right) f(L) \right)$$
$$\boldsymbol{\varphi}_{init,l,l} = \exp\left(-M_{l}\right) \left(1 - \sum_{l} s_{l}^{f} u_{init}^{f}\right)^{\sqrt{1 - \sum_{l} s_{l}^{f} u_{init}^{f}}}$$

where

 R_{init} is the average recruitment used to generate the initial conditions.

 $\varepsilon_{init i}$ is the recruitment deviate for cohort *i*

 u_{init}^{f} is the exploitation rate for fishery f that is used to generate the initial conditions

2.6. Likelihoods

The model is fitted to length-composition data and CPUE¹-based indices of abundance by sub-population. Penalties are added to the likelihood to implement the distributional assumptions about temporal recruitment variation.

2.7. Length-frequency data

The length-frequency data are fitted using the multinomial distribution-based negative log-likelihood, with a small constant added to the predicted proportions to avoid numerical errors:

$$-\ln L(\mathbf{\theta} \mid data) = -\sum_{t,l} n_{t,l} \ln \left[\hat{p}_{t,l} + 0.001 \right]$$
$$\hat{p}_{t,l} = \frac{s_l N_{t,l}}{\sum_l s_l N_{t,l}}$$

2.8. CPUE data

The CPUE is assumed to be lognormally distributed (the log-normal bias correction factor may be needed if the standard deviation differs over time or if it differs between sub-stocks and q is shared):

¹ catch per unit of effort

$$-\ln L(\boldsymbol{\theta} \mid I) = \sum_{t,l} \left\{ \ln \left[\sigma_{I} \right] + \frac{\left(\ln \left[I_{t} \right] - \ln \left[\hat{I}_{t} \right] \right)^{2}}{2\sigma_{I}^{2}} \right\}$$
$$\hat{I}_{t} = qB_{t}$$

The catchability coefficient and standard deviation can be calculated analytically (Maunder and Starr 2003), but only if not using a bias correction factor. Otherwise, a different formula is needed for q and σ is estimated as free parameter; different formulations are needed if σ differs over time.

$$q = \exp\left(\frac{\sum_{t} \ln\left(\frac{I_{t}}{B_{t}}\right)}{n}\right)$$
$$\sigma = \sqrt{\frac{\sum_{t} \left(\ln\left(I_{t}\right) - \ln\left(\hat{I}_{t}\right)\right)^{2}}{n}}$$

2.9. Recruitment temporal variation penalties

Penalties are added to the likelihood function to implement the lognormal temporal variation in recruitment for both the modeled period and the initial conditions.

$$0.5\sum_{i}\varepsilon_{init,i}^{2}+0.5\sum_{t}\left((\varepsilon_{t}^{EPO})^{2}+\sum_{z}(\varepsilon_{t}^{z})^{2}\right)$$

3. APPLICATION

The length-structured meta-population model is applied to skipjack tuna in the eastern Pacific Ocean. The model is implemented using AD Model Builder (Fournier *et al* 2011). The time step is monthly, to approximate continuous recruitment. Six sub-populations are modeled, based on aggregating the yellowfin tuna measurement areas (Table 1 and Figure 1).

Catch is divided into three fisheries for each region (Figure 2). The removals by the floating-object and unassociated fisheries are retained catch, plus some discards resulting from inefficiencies in the fishing process. Catch from other minor fisheries is added to the unassociated fishery. Removals by the discard fisheries are only discards resulting from sorting the catch taken by the floating-object and unassociated fisheries. Discards that result from the process of sorting the catches are treated as separate fisheries, and the catches taken by these fisheries are assumed to be composed only of fish that are less than 60 cm in length.

The estimates from the western Pacific Ocean (Hampton 2000) were used to develop a length-specific natural mortality curve to use in the assessment (Figure 3). Hampton's estimates of high natural mortality for old skipjack may be an artifact of the tagging data, due to older fish moving out of the fishery. Therefore, it is assumed that natural mortality is constant over large sizes. Hampton's estimates of high natural mortality for young skipjack may also be an artifact of the tagging data due to tagging mortality, and a lower natural mortality rate is used here.

The growth parameters were taken from Maunder (2002a). The estimates for north and south were used for the corresponding regions. The growth increments are quarterly, and are therefore divided by three to use in the monthly model. This produces a slight bias compared to fitting a monthly growth model to the

length-increment data. The weight-length relationship of skipjack in the EPO is $W = (5.5293 \text{ x } 10.6)L^{3.336}$, where W = weight in kilograms and L = length in centimeters (Hennemuth, 1959).

The stock assessment model is fitted to CPUE and length-composition data by fishery for each region. Indices of abundance were derived from purse-seine catch and effort data. The CPUE for the purse-seine fisheries was calculated as catch divided by number of days fished. The number of days fished, by set type, was estimated from the number of sets, using a multiple regression of total days fished against number of sets by set type (Maunder and Watters 2001).

4. **RESULTS**

There is insufficient information in the CPUE and length-composition data to produce reliable estimates of skipjack tuna stock size. In all but one region (Region B, off the coast of Ecuador) the estimates of abundance and exploitation rates were unrealistic. The selectivity or growth rates are sufficiently different among stocks that sharing selectivity information from region B for the other regions also produces unrealistic estimates. Therefore, results from the length-structured stock assessment model are presented for region B only.

The stock assessment model for region B is able to fit some of the general patterns in the CPUE data, but the CPUE is highly variable, so the fit is generally poor (Figure 4). On average, the stock assessment model is able to fit the general pattern in the length composition data, but is unable to fit the semi-bimodal pattern in the observed length composition data from the floating-object fishery (Figure 5). The model is not able to predict the highly variable observed mean length (Figure 6), indicating that the fit to individual length compositions is poor.

The model estimates that the floating-object fishery selects larger skipjack than the unassociated fishery (Figure 7). The estimated exploitation rate is highly variable over time, and was higher in the early half of the time period compared to the latter half (Figure 8). Recruitment is highly variable over time, with a large recruitment in 1999 (Figure 9). Consequently, biomass is also highly variable over time, with a spike in biomass in 1999 (Figure 10). There is also a general increase in biomass since 1980.

5. DISCUSSION

The application of the length-structured model to all six regions in the EPO was problematic, and for all but region B the fishing mortality and biomass estimates were unrealistic. Previous age-structured assessment models applied to the whole EPO also were problematic, and under some model structure assumptions also produced unrealistic estimates of biomass and exploitation rates (Maunder 2002b; Maunder and Harley 2005). The model was only fitted to CPUE and length-composition data, which may not be very informative for a highly productive and variable species like skipjack tuna. Traditional stock assessments are dependent on the indices of abundance measuring depletion caused by the fishery to inform abundance estimates. The variability and high productivity of skipjack tuna hides this signal. The proportion of large fish in the length-composition data, in combination with the selectivity curve, also provides information on the exploitation rate, but the short-lived nature of skipjack and small sample size hides this signal. In addition, the shape of the selectivity curve, and particularly if it is dome-shaped or not, is also uncertain.

Integrating the tagging data into the length-structured stock assessment model can potentially improve the results. However, uncertainty in the fishing mortality estimates from the tagging analysis indicate that any improvements may be minor (Maunder 2012). Sharing information among stocks has the potential to improve estimates for the regions that have little information in their data. However, initial analyses suggest that differences in selectivity and/or growth among regions may prevent the sharing of selectivity parameters. The catchability of the CPUE index of relative abundance might be shareable among regions if the CPUE is calculated as the sum of the CPUEs across 1x1 degree squares, for example, in a region. This method has been used for longline CPUE in the western and central Pacific Ocean (Davies *et al.* 2011). In the future, when the post-stratification methodology has been developed, more appropriate areas

will be used for skipjack.

5.1. Extensions

There are several extensions of the modeling framework that may improve the analysis.

5.1.1. Sharing parameters

Parameters can be shared among sub-populations, assuming that the parameters come from a common distribution (*e.g.* normal):

$$\theta^{z} = \mu_{\theta} + \sigma_{\theta} \varepsilon_{\theta}^{z}$$

where the penalty added to the objective function for parameter θ is:

$$0.5\sum_{z}(\varepsilon_{\theta}^{z})^{2}$$

Possible candidate parameters to share among regions include selectivity, catchability, average recruitment, and growth. The average recruitment would have to be parameterized in terms of recruits per habitat area to be meaningful. To share catchability, the CPUE index would have to be calculated by weighting the CPUE by the sum of the 1x1 effects, for example, from the CPUE analysis for each region.

5.1.2. Growth increment data

Francis' (1995) general method, which is based on Baker *et al.*'s (1991) length-based analog of Schnute's (1981) size-at-age model, can be used to estimate growth with mark-recapture data. Francis' model combines a general length-based growth function that predicts the mean growth increment from the length at release and time at liberty, with an error structure that includes both measurement error and individual variability in growth. This model was used by Maunder (2002a) to estimate growth for skipjack tuna in the EPO. The observed growth increment is assumed to be normally distributed, with the variance of the growth increment a function of both time at liberty and length at release, using Maunder's (2002a) generalized growth variation model. To simplify the calculations, it is assumed either that this assumption is an adequate approximation to measurement error in both the length at release and length at recapture, or that measurement error is only in length at recapture A robust version of the normal distribution-based likelihood is used to reduce the influence of outliers that may be due to incorrect recording of lengths or dates:

$$\ell\left(\theta \mid L, L', \Delta t\right) = \frac{1}{\sqrt{2\pi\left(\sigma_m^2 + \sigma_G^2\right)}} \exp\left(-\frac{\left(G_{obs} - \mu_G - \mu_m\right)^2}{2\left(\sigma_m^2 + \sigma_G^2\right)}\right) + 0.01$$

where μ_m and σ_m^2 are the mean and variance of the measurement error, respectively.

5.1.3. Tag-recapture data

The predicted number of recoveries, by tag release group, fishery, and time, can be calculated using the same population dynamics equations as are used to model the total population. The modeling of tag data differs in that recruits are releases. The model can be modified to include tagging-related mortality and reporting rate parameters. The recaptures during each time period for each fishery summed across length at recapture can be fitted using the negative binomial likelihood. The length composition of the recaptures can be fitted using a multinomial.

5.1.4. Movement

The basic model can be converted into a model of interacting sub-populations by introducing the movement transition matrix (ψ) to model movement after growth and survival. Recruitment occurs at the

end of the time period after movement occurs. However, the modeling of the tagged fish becomes more complicated:

$$\widetilde{N}_{t-1}^{z} = G^{z} \varphi_{t-1}^{z} N_{t-1}^{z}$$
$$N_{t}^{z} = R_{t}^{z} + \sum_{i} \psi_{i \to z} \widetilde{N}_{t-1}^{i}$$

where

 N_t^z is a vector of numbers at length in sub-population z at the start of time t;

 $\widetilde{N}_t^{\overline{z}}$ is a vector of numbers at length in time *t* after recruitment, survival, and growth.

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TABLE 1. Regions defined for the stock assessment of skipjack tuna in the EPO. The sampling areas are shown in Figure 1.

TABLA 1. Regiones definidas para la evaluación de la población de atún barrilete en el OPO. En la Figura 1 se ilustran las áreas de muestreo.

Region	Description	Sampling areas
Región	Descripción	Areas de muestreo
А	Inshore north	
	Costera norte	1,2,4,8
В	Inshore central	
	Costera central	5,6
С	Central	7,9
D	Offshore north	
	Alta mar norte	3,10
Е	Offshore south	
	Alta mar sur	11,12
F	Inshore south	
	Costera sur	13

TABLE 2. Parameter definitionsTABLA 2. Definiciones de los parámetros.

	Definition		
Index			
l	Length class		
L	length		
t	Time		
Z.	Sub-population		
f	fishery		
i	Generic index		
Other			
Т	Number of time periods		
L	Number of length classes. This needs to be changed		
EPO	Denotes a variable or parameter common to all sub-populations		
init	Indicates a quantity related to the calculation of the numbers at length in the		
	initial year		
θ	Generic symbol for any parameter		
n	Generic symbol for number of items		
x	Number of cohorts used to generate the initial conditions.		
Variable			
N	Column vector of numbers in each length class		
C	Growth transition matrix where the columns represent the proportion of		
U	individuals transitioning to the different length classes from a single length		

	class (<i>i.e.</i> they sum to one)		
Φ	<i>b</i> survival matrix with the diagonals equal to survival for each length class		
R	column vector of recruitment for each length class		
\widetilde{R}	Total recruitment		
f(L)	Proportion of a recruiting year class assigned to length class with length L		
	Mean growth increment. May need to change to mean length of growth		
μ _G	transition		
σ_g	Standard deviation of growth increment		
S	Selectivity		
и	Exploitation rate		
М	Natural mortality		
В	Vulnerable biomass		
W	Average weight		
p	Observed proportion at length		
\widehat{p}	Predicted proportion at length		
τ	Length composition variance scaling parameter		
I	Observed index of abundance		
I	Predicted index of abundance		
Parameters			
μ_R	Mean recruitment		
σ_R	Standard deviation of the deviation in recruitment		
E _R	Deviation in recruitment		
и	Mean of the normal distribution for distributing recruitment among length		
^{PR} Rdist classes			
U Pdict	Standard deviation of the distribution for distributing recruitment among		
- ABIST	length classes		
В	Shape parameter of the Francis (1995) growth model		
<i>g</i> ₁	Mean growth increment parameter for fish of arbitrary length y_1 of the Francis		
0.	(1995) growth model		
<i>g</i> ₂	Mean growth increment parameter for fish of arbitrary length y_2 of the Francis (1005) except have defined		
	(1995) growth model Decompton of Moundar's (2002) concentized crowth variation model		
a R	Parameter of Maunder's (2002) generalized growth variation model.		
0	Parameter of Maunder's (2002) generalized growth variation model.		
Y	Mean of the double normal selectivity curve		
μ_s	Verieure of the second include horizontal selectivity curve		
Vl	Variance of the ascending limb of the double normal selectivity curve.		
V_r	A variance of the descending filmb of the double normal selectivity curve		
K _{init}	Exploitation rate used to calculate the initial conditions		
u_{init}	Exploitation fate used to calculate the initial conditions		
Einit	Man of the house distribution for some to C		
μ_{θ}	Nean of the hyper distribution for parameter θ		
σ_{θ}	Standard deviation of the hyper distribution for parameter θ		
Ea	Sub-population deviate for parameter θ		

σ_I	Standard deviation for the index of abundance likelihood
q	Catchability coefficient for the index of abundance
μ_m	Mean measurement error for the growth increment data
σ_m	Standard deviation of the measurement error for the growth increment data





FIGURA 1. Extensión espacial de las subpoblaciones (regiones) definidas para la evaluación del atún barrilete en el OPO.

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FIGURE 2a. Monthly catches in purse-seine sets on floating objects, by region. FIGURA 2a. Capturas mensuales en lances cerqueros sobre objetos flotantes, por región.



FIGURE 2b. Monthly catches in purse-seine sets on unassociated tunas, by region. **FIGURA 2b.** Capturas mensuales en lances cerqueros sobre atunes no asociados, por región.



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FIGURE 2c. Monthly discards of small skipjack, by region. **FIGURA 2c.** Descartes mensuales de barriletes pequeños, por región.



FIGURE 3. Rates of monthly natural mortality (M) used for the length-structured assessment of skipjack tuna.

FIGURA 3.1. Tasas de mortalidad natural (*M*) mensual usadas para la evaluación por talla del atún barrilete.



FIGURE 4. Estimated (line) and observed (circles) CPUE for the floating-object (upper panel) and unassociated (lower panel) fisheries in region B.

FIGURA 4. CPUE estimada (línea) y observada (círculos) de las pesquerías sobre objetos flotantes (panel superior) y no asociada (panel inferior) en la región B.



FIGURE 5. Estimated (line) and observed (circles) average length composition for the floating-object (upper panel) and unassociated (lower panel) fisheries in region B.

FIGURA 5. Composición media por talla estimada (línea) y observada (círculos) de las pesquerías sobre objetos flotantes (panel superior) y no asociada (panel inferior) en la región B.



FIGURE 6. Estimated (line) and observed (circles) mean length for the floating-object (upper panel) and unassociated (lower panel) fisheries in region B.

FIGURA 6. Talla media estimada (línea) y observada (círculos) de las pesquerías sobre objetos flotantes (panel superior) y no asociada (panel inferior) en la región B.



FIGURE 7. Selectivity estimated for the floating-object (solid line) and unassociated (dotted line) fisheries, and fixed for the discard fishery (dashed line) in region B.FIGURA 7. Selectividad estimada para las pesquerías sobre objetos flotantes (línea sólida) y no asociada (línea de puntos), y fijada para la pesquería de descarte (línea de trazos) en la región B.



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FIGURE 8. Monthly exploitation rate for region B, estimated using the length-structured stock assessment model.

FIGURA 8. Tasa de explotación mensual correspondiente a la región B, estimada con el modelo de evaluación basado en talla.



FIGURE 9. Monthly recruitment in region B, estimated by the length-structured model. **FIGURA 9.** Reclutamiento mensual en la región B, estimado con el modelo basado en talla.



FIGURE 10. Exploitable biomass for the unassociated fishery in region B, estimated by the length-structured assessment model.

FIGURA 10. Biomasa explotable para la pesquería no asociada en la región B, estimada con el modelo basado en talla.