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LENGTH-BASED ASSESSMENT FOR MACKEREL ICEFISH (*CHAMPSOCEPHALUS GUNNARI*) AT SOUTH GEORGIA

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Abstract

The current CCAMLR assessment method for mackerel icefish (*Champsocephalus gunnari*) in Subarea 48.3 employs the CCAMLR mixture analysis program (CMIX) and generalised yield model (GYM) packages, which derives population numbers-at-age and projects these numbers forward under the given harvest control rule to set a two-year total allowable catch (TAC). One issue is the accurate identification of age cohorts from the survey data. In this paper a length-based approach is described that removes the problem of cohort determination. A bootstrap technique (consistent with the current CCAMLR approach) is used to estimate the length distribution of the population from the survey data which, in conjunction with the bootstrapped survey biomass data, yields an estimate of the population numbers-at-length. A comparison of this method and the existing age-based CMIX/GYM methodology showed very good agreement in calculated yields for 2006, 2007 and 2009, and some differences for 2008 which were explained by an unusual length distribution from which it was difficult to reliably estimate age composition in CMIX. Using the 2009 survey data and the new methodology, a TAC was calculated according to the CCAMLR decision rules of 1 577 and 933 tonnes for the 2009/10 and 2010/11 fishing seasons respectively. The respective estimates using the existing CMIX/GYM methodology were 1 590 and 968 tonnes respectively.

Résumé

La méthode employée actuellement par la CCAMLR pour l'évaluation du poisson des glaces (*Champsocephalus gunnari*) dans la sous-zone 48.3 repose sur le programme d'analyse mixte de la CCAMLR (CMIX) et sur des progiciels de modèles de rendement généralisé (GYM), qui, dans une population, dérivent le nombre selon l'âge et le projette en fonction de la règle de contrôle de l'exploitation, pour fixer une capture totale admissible (TAC) sur deux ans. L'une des difficultés réside dans l'identification précise des cohortes d'âges à partir des données des campagnes d'évaluation. Ce document décrit une approche reposant sur la longueur qui élimine le problème de la détermination de la cohorte. Une technique de bootstrap (conforme à l'approche actuelle de la CCAMLR) est utilisée pour estimer la distribution de longueurs de la population à partir des données des campagnes d'évaluation qui, avec les données de biomasse des campagnes d'évaluation ayant été soumises à la procédure de bootstrap, produit une estimation du nombre d'individus par âge dans la population. Une comparaison de cette méthode et de la méthode existante de CMIX/GYM fondée sur l'âge met en évidence une très bonne concordance en ce qui concerne les rendements calculés pour 2006, 2007 et 2009, mais quelques differences pour 2008. Celles-ci s'expliquent par une distribution de longueurs inhabituelle qui ne permettait pas d'estimer facilement et de manière fiable la composition en âge dans le CMIX. Au moyen des données de la campagne d'évaluation de 2009 et de la nouvelle méthodologie, le TAC calculé selon les règles de décision de la CCAMLR est de 1 577 tonnes pour la saison de pêche 2009/10 et de 933 tonnes pour celle de 2010/11. Par le biais de la méthode de CMIX/GYM, les estimations étaient de 1 590 et 968 tonnes respectivement.

Резюме

Принятый в настоящее время в АНТКОМ метод оценки щуковидной белокровки (*Champsocephalus gunnari*) в Подрайоне 48.3 использует пакеты программы АНТКОМ по композиционному анализу (CMIX) и обобщенной модели вылова (GY-модель), что позволяет получить численность популяции по возрастам и экстраполировать эту численность на будущее в рамках определенного правила контроля вылова в целях установления общего допустимого вылова (ОДУ) на два года. Одной из проблем является точная идентификация возрастных когорт по съемочным данным. В данном документе описывается метод на основе длин, который снимает проблему определения когорт. Для оценки распределения длин по съемочным данным используется метод бутстрап (соответствующий применяемому в АНТКОМ подходу), что в сочетании со съемочными данными о биомассе, полученными методом бутстрап, дает оценку численности популяции по длинам. Сравнение этого метода с существующими методами CMIX/GYM, основанными на возрасте, продемонстрировало очень хорошее совпадение рассчитанных уловов в 2006, 2007 и 2009 гг., и некоторые различия в 2008 г., объясняющиеся необычным распределением длин, из-за которого было трудно дать надежную оценку возрастного состава по CMIX. С использованием данных съемки 2009 г. и новой методологии, и в соответствии с правилами АНТКОМ о принятии решений был рассчитан ОДУ в размере 1 577 и 933 т соответственно на промысловые сезоны 2009/10 и 2010/11 гг. Соответствующие оценки, полученные на основе метода CMIX/GYM, составили соответственно 1 590 и 968 т.

Resumen

El método de evaluación actual de la CCRVMA para el draco rayado (*Champsocephalus gunnari*) en la Subárea 48.3 utiliza el programa de análisis de mezcla (CMIX) y el modelo de rendimiento generalizado (GYM), que deriva la abundancia de las clases de edad de las poblaciones y proyecta esta abundancia ateniéndose al criterio de control de la captura dado para sentar un límite de la captura total permisible (TAC) para dos años de pesca. Uno de los problemas a enfrentar es la identificación correcta de las clases de edad a partir de los datos de prospección. Este estudio describe un enfoque basado en la talla que soluciona el problema de la identificación de las cohortes. Se utiliza una técnica de bootstrap (concordante con el enfoque actual de la CCRVMA) para estimar la distribución de tallas de la población estudiada de los datos de la prospección que, conjuntamente con los datos de la biomasa de dicha prospección también tratados con la técnica bootstrap, rinden una estimación de la abundancia de las clases de talla de la población. La comparación de este método con la metodología CMIX/GYM existente en base a la edad demostró una muy buena concordancia de los rendimientos calculados para 2006, 2007 y 2009, y algunas diferencias para 2008 que fueron atribuidas a la distribución inusual de tallas que dificultó la estimación fiable de la composición por edades con el CMIX. Utilizando los datos de prospección de 2009 y la nueva metodología, se calculó un TAC de acuerdo con los criterios de decisión de la CCRVMA de 1 577 y 933 toneladas para las temporadas de pesca de 2009/10 y 2010/11 respectivamente. Las estimaciones correspondientes obtenidas con la metodología CMIX/GYM existente fueron de 1 590 y 968 toneladas respectivamente.

Keywords: mackerel icefish, length-based assessment, CCAMLR

Introduction

In order to determine the catch levels that satisfy a given harvest control rule (HCR), the population is projected forwarded in time in order to assess what the sustainable catch over that time would be. Population models that project forward on the basis of the age of individuals require that the population can be separated into known-age cohorts. CCAMLR currently uses an age-based assessment of mackerel icefish (*Champsocephalus gunnari*) at South Georgia which requires the clear identification of cohorts from the fisheries research surveys. This is problematic for several reasons, including differential recruitment dates (birthdays) for the sub-populations at Shag Rocks and South Georgia and some uncertainty in the growth dynamics. The CCAMLR mixture analysis (CMIX) program (de la Mare, 1994) has previously been used with the haul-level survey density-at-length and the growth curve to estimate an appropriate density-at-age for the population. A bootstrap procedure is then employed to obtain an estimate of the total biomass in the population. The one-sided lower 95-percentile of this bootstrapped biomass, along with the CMIX-derived population density-at-age, is used to define numbers-at-age in the population. Assuming a closed population (i.e. with no recruitment) the generalised yield model (GYM) package (Constable and de la Mare, 1996) is then used to project the population forward for two years under a fixed harvest rate. The target harvest rate is that which ensures that the exploited biomass is equal to 75% of the unexploited biomass (after two years). From this target harvest rate a two-year total allowable catch (TAC) is obtained.

Given that this process depends on distinguishing age-based cohorts and the difficulties of doing so, as outlined above, the aim of this analysis is to explore the management procedure for this resource using a fully length-based assessment. Length-based models are extremely useful when growth data are scarce (Chen et al., 2003; Zheng et al., 1995) or when a population is difficult to age directly. They are also useful when there are issues separating cohorts that have different birthdays: in an age-structured modelling sense this requires the 'tracking' or separation of these cohorts through time. In a length-based setting this is not required as the growth dynamics are (usually) invariant to such a temporal structure in the recruitment of the population sub-levels – animals of a given length grow from one length class to a subsequent length class (given the time frame) irrespective of when they were born.

Under such an assessment the HCR applied would be the same but the process by which the size of the initial population is estimated, and the population model that is used to estimate the target harvest rate (and resultant two-year TAC), will be in a length- not an age-structured paradigm. In such a length-based assessment, numbers-at-length are derived directly from the survey data and projected forward using a length-based model to find a suitable exploitation rate under the HCR. This approach has been presented previously (Hillary et al., 2009), and is updated here to include the results from a research survey conducted in 2009. In order to examine the performance of the length-based assessment approach, the results from age-based assessments (using the procedure described above) are given alongside results from the length-based method.

Methods

Population abundance-at-length

The process of estimating the current population abundance-at-length was broken down into three steps:

1. Use a bootstrap procedure on the haul-level survey data to estimate the length frequency of the current population.

2. Use a bootstrap procedure on the stratified biomass density (kg/km^2) data in combination with the stratum area information to estimate the total biomass of icefish in the population.

3. Use the length-frequency and biomass information (along with the weight-at-length relationship) to estimate the total numbers of icefish-at-length (for a given length partition).

Length frequency in the population

The current CCAMLR approach uses the CMIX package to generate the population density-at-age given the haul-level survey data and an assumed growth curve. Initially, a stratified bootstrap approach was explored: given the stratified survey density data $I_{l,m,n}$ by length bin l, region m, and haul n, for each length bin the data were bootstrapped across hauls but within regions to obtain mean and variance estimates for the survey density by length bin and region. A population length frequency was then derived by taking a weighted mean of the regional density estimates per length bin, with the weighting being a multiplication of the inverse variance of the estimate and the relative area covered by the region, akin to the weighting defined in de la Mare (1996). However, given the sparseness or missing nature of the data for many length bins in certain regions, this approach was not considered viable. Given these data availability issues, an alternative unstratified bootstrap procedure was used. This used survey data that were pre-weighted according to the approach detailed in de la Mare (1996) and is the same procedure applied to the survey data before CMIX is run: given the regional area A_m, and the number of hauls in that region M_m, the raw survey data were transformed as follows:

$$\tilde{I}_{l,m,n} = I_{l,m,n} \frac{A_m}{\sum_i A_i} \frac{\sum_i M_i}{M_m}. \tag{1}$$

These re-weighted data were then bootstrapped across all regions and hauls to obtain the mean population density-at-length $\tilde{I}_l$, which was then normalised to obtain the population length frequency:

$$p_l = \frac{\tilde{I}_l}{\sum_i \tilde{I}_i}. \tag{2}$$

In Figure 1 the stratified and aggregated density-at-length from the 2009 survey can be seen and in Figure 2, also for 2009, the aggregated density-at-length (mean and standard error) as derived from the re-weighted survey data using the non-stratified bootstrapping approach.

Generating the estimate of total icefish biomass

In line with the CCAMLR assessment method, haul-level biomass density data were re-weighted according to the de la Mare (1996) approach and a bootstrap sample taken across all strata to estimate the distribution of biomass. Previous work by Hillary et al. (2009) has shown there to be insufficient data to perform a stratum-stratified bootstrap. The lower one-sided 95%ile was taken from the resultant bootstrap distribution to represent the total population biomass B (adjusted for the extra pelagic component of the population).

Combining biomass and length frequency to estimate icefish numbers-at-length

Table 1: Parameter values for the yearly weight-at-length relationship (length in mm, weight in kg) used in the analyses.

Year	*a*	*b*
2006	6e-10	3.004
2007	6e-10	3.400
2008	5.47e-10	3.420
2009	5.47e-10	3.420

Given the population length-frequency p_l, and population biomass B, the estimated numbers-at-length in the population can be constructed. Using the standard allometric weight-at-length relationship $w_l = al^b$ with a and b values given in Table 1, the total numbers of icefish in the population N, can be calculated as follows:

$$N = \frac{B}{\sum_{l=1}^{P} p_l w_l \psi_l} \tag{3}$$

where ψ_l is the selectivity-at-length of the survey gear (assumed to be one across all lengths) and w_l is the weight-at-length. The total numbers-at-length in the population is simply $N_l = Np_l$. To be clear about the sources of uncertainty present, and how they are dealt with in estimating the initial abundance-at-length, it is assumed that the uncertainty in the length-density data has been dealt with in the bootstrap estimation of the initial population length frequency, with the uncertainty in the survey biomass being dealt with via the bootstrap procedure and the use of the lower one-sided 95%ile. From this point on *only* these point estimates are used in the assessment process.

Population projection model

A population projection model is required to calculate catch limits using the HCR. The current method used by CCAMLR uses the GYM package, but this requires an estimate of the age structure of the population. The length-based approach suggested here employs a population dynamics model that works using length, not age. With length-based models, animals make transitions between elements of the length-partition instead of moving from one age-class to the next. The basic premise is that, for a given time increment τ, there exists a (length) transition matrix Γ_{ij}, which defines the probability of an animal in length partition element i moving to element j in time τ. The length-transition matrix can be calculated given a growth curve in a number of ways (Punt et al., 1997; Hillary, 2010). The method proposed in Hillary (2010) is used here. The method works as follows: assume that the expected length of an animal-at-time $t + \tau$ is calculable from the length at time t given the growth increment function $G(\circ)$, derived from the growth curve:

$$\hat{l}_{t+\tau} = G(l_t, \tau, \theta) \tag{4}$$

so that in the case of a von Bertalanffy growth curve (as is used for icefish in Subarea 48.3)

$$G(l_t, \tau, \theta) = (L_\infty - l_t)(1 - \exp[-k\tau]) \tag{5}$$

where $\theta = (k, L_\infty)$ and k and L_∞ are the growth rate and asymptotic length parameters respectively.

For the given length partition $\lambda = \lambda_1, \ldots, \lambda_P$ the (i,j)-th transition matrix element is defined to be the relative overlap (intersection) of the image (under growth) of element λ_i with element λ_j. This can be expressed mathematically as follows:

$$\Gamma_{ij} = \frac{\mu[G(l_t, \tau, \theta) \cap \lambda_j]}{\mu[G(l_t, \tau, \theta)]}. \tag{6}$$

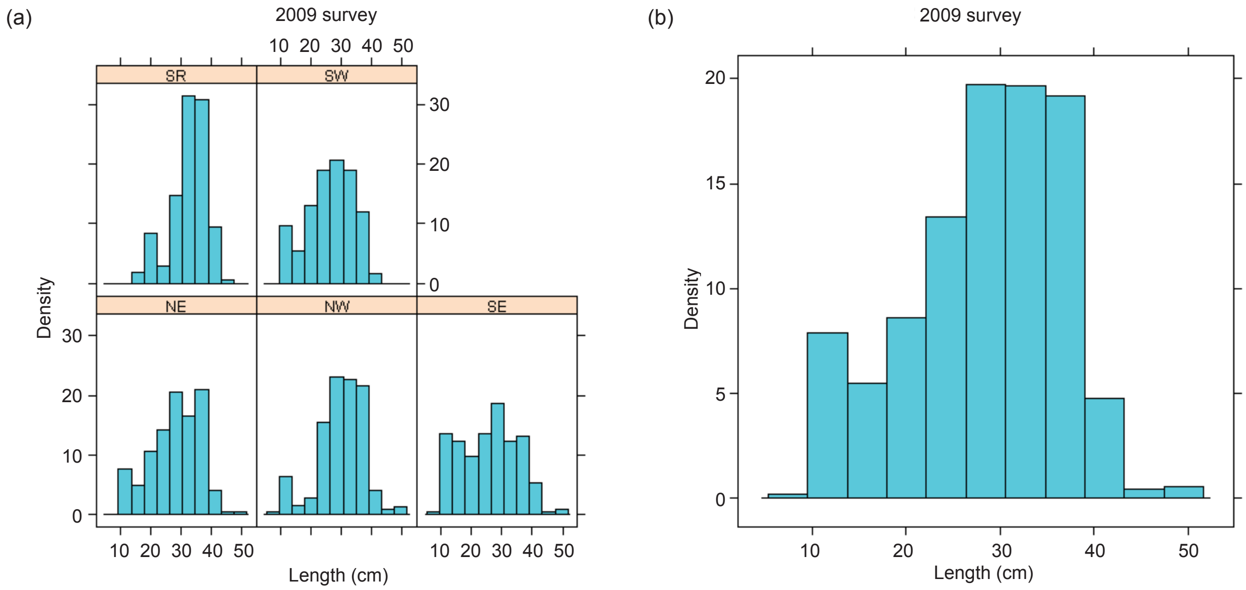

Figure 1: Raw icefish density-at-length from the 2009 survey: (a) stratum-stratified (left) and (b) stratum-aggregated (right).

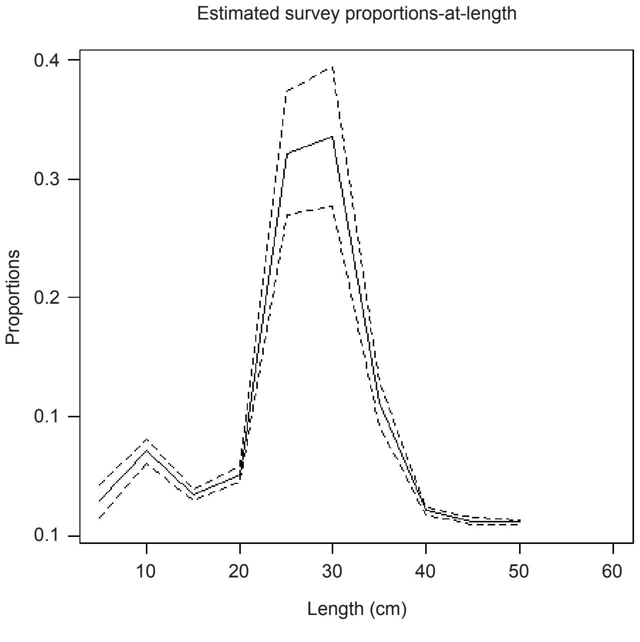

Figure 2: Bootstrapped estimate of proportional population length frequency for 2009 using the unstratified bootstrap procedure. Mean and standard error bounds are shown. No data were collected for 50–60 cm length bin.

In equation (6) the function $\mu[\circ]$ denotes Lebesgue measure which, assuming continuous length elements, translates naturally to the size of the interval in question. This formulation is very generic, allowing for any kind of distribution of length to be assumed within the length partition elements. To make the concept easier to understand in a real-world sense, consider two elements of the icefish length partition: λ_1 = [5,10) and λ_2 = [10,15). For icefish in Subarea 48.3 k = 0.17 and L_∞ = 55.7 cm (SC-CAMLR, 2008) so with τ = 1, a 1-year time-horizon, $G(\lambda_1,\circ)$ = [12.926,17.145), $G(\lambda_1,\circ) \bigcap \lambda_3$ = [12.926,15) and so from equation (6) the (1,2)-th element of the transition matrix is given by Γ_{12} = (15 – 12.926) / (17.145 – 12.926) = 0.492. This calculation is done for all the possible pairs of length partition elements (of which there are P times P) to generate the transition matrix Γ. Note also that no error distribution was required for the random individual variations in the growth increment – something essential to the most common method as detailed in Punt et al. (1997) – only the growth parameters themselves are required. If such a distribution is known, the details of how to incorporate this information into the estimation of Γ can be found in Hillary (2010). For *C. gunnari* in Subarea 48.3, growth parameters were estimated from length-at-age data, not mark-recapture data, therefore this error distribution cannot be easily derived; as a result, only the growth parameters were used to estimate a single growth transition matrix.

Over a time frame defined by the population dynamics, for a given natural mortality level M_τ, and harvest rate ξ_τ, the population dynamics in a length-based sense are simply expressed:

$$N_{t+\tau,l} = \sum_{j=1}^{P} N_{t,j} e^{-M_{t,j}} \left(1-\xi_{t,j}\right)\Gamma_{jl}. \qquad (7)$$

The catch biomass removed from the population, C, and the harvest rate are related as follows:

$$\xi_t = \frac{C}{\sum_{l=1}^{P} N_{t,l} w_l \chi_l} \qquad (8)$$

where χ_l is the commercial selectivity ogive. The final step in defining the icefish population model is to fully explain the temporal structure of the projection employed by the HCR:

1. The estimated numbers-at-length are assumed to be the total closed population abundance (i.e. there is no future recruitment or migration) – the survey marks the start of the first ‘year’.

2. Any TAC remaining from the previous year is assumed to be taken immediately from the population.

3. The model advances the population (accounting for growth and natural mortality) to when the next fishing period begins – assumed to be 0.9 of the first ‘year’.

4. At this point the TAC is immediately removed from the population and the model advances the dynamics (now including this exploitation rate) to the end of the first ‘year’.

5. Steps 3 and 4 are then repeated to give the population abundance at the end of the second ‘year’.

To calculate the consecutive two-year TAC, a numerical root-finding algorithm is used to estimate the fixed harvest rate that ensures that the biomass at the end of the two-year population projection is equal to 75% of that expected in the absence of fishing. The whole procedure uses the FLR (Fisheries Libraries in R) (Kell et al., 2007) framework and the code (and required packages) maybe obtained from the author on request.

Data

For data and parameters (for growth and weight-at-length) pre-2009, the information was derived from the survey data and taken from the Working Group on Fish Stock Assessment (WG-FSA) reports respectively. Biomass and length-density data for 2009 were obtained directly from the survey (Belchier et al., 2009), applying a correction factor to account for the semi-pelagic component of the stock. We assume that 3 573 tonnes of the 2009 TAC was taken after the survey, with an assumed fraction of 0.9 of the season remaining.

Results

There were no systematic differences between results from the proposed length-based method and the current CCAMLR method from 2006 to 2009 (Table 2). The estimated TACs for 2010 and 2011 were 1 577 and 933 tonnes respectively, using the proposed length-based method and 1 590 and 968 tonnes using the CCAMLR age-based assessment method. The differences were greatest in the projections performed in 2008 and there was much closer agreement in other years, especially in 2009.

Table 2: Comparison estimates of two-year TACs (tonnes) obtained using the current CCAMLR method (CMIX/GYM) and the proposed method (length-based), for sequential assessment years.

	Assessment year:	2006	2007	2008	2009
	Year of TAC:	2007, 2008	2008, 2009	2009, 2010	2010, 2011
Assessment method:	CMIX/GYM	4337, 2885	2462, 1569	3834, 2631	1590, 968
	Length-based	4438, 3381	2338, 1443	3019, 1778	1577, 933

Discussion

This paper proposes a new length-based assessment method for *C. gunnari* in Subarea 48.3. The philosophy behind the new method is very similar to that of the current method; with bootstrapping procedures used to estimate the standing stock size (at-length) and a simple projection method used to estimate the two-year TAC given the HCR used for this stock. The main reason for moving to a length-based framework was to avoid the issues with the identification of known-age cohorts from the surveys. The length-based approach is not affected by differential recruitment dates which can complicate the interpretation of survey data/growth-curve derived estimates of population density-at-age.

To fully explore the potential utility of the proposed method as a new assessment procedure for this stock, a three-year comparison between the proposed method and the CMIX/GYM procedure was performed for the years 2006 to 2009. For each year, the same input parameters were assumed (growth, *M*, selectivity, weight-at-length, population biomass) for both methodologies. There was no clear trend in the observed differences between the two methods but they did not always agree very closely in all years. The main cause of the differences was the estimated length–age structure of the initial population derived from the surveys. Given the closed nature of both population models (no recruitment) and the fact that they both employ the same growth curve, any differences in initial population structure will be transmitted through the whole projection and resultant TAC calculation. A length partition from 5 to 60 cm in 5 cm bins was employed in these analyses and discrete ages (especially at the younger ages) can span multiple length classes; as a result, given the differences between using the CMIX package and a simpler bootstrap-at-length, one can obtain different biomass distributions at length–age using the two different procedures. Clearly, there are also differences to be expected when using either the GYM or the length-based population model but it appears to be the estimation of the initial population length–age structure that is the main driver.

The comparison between the two approaches in 2009 showed close agreement in terms of the estimated TACs. This is because the decomposition of the population into ages and lengths (via the different methods) gave similar distributions of numbers across the different age or length classes (i.e. the length distribution can be mapped directly onto the age distribution using the growth curve). Both methods show that the population was dominated by older/larger classes, with 3+ and 4+ animals accounting for around 80% of the total.

In 2008 the population consisted of mostly 2+ animals with considerable uncertainty in the age structure generated by CMIX (SC-CAMLR, 2008). This uncertainty was largely a consequence of the difficulty in assigning age classes to fish collected from regions with different recruitment dates (North, 2005). This likely contributed to the divergence in the age structure of the population in the GYM runs and the length structure of the population used in the length-based assessment model. With a potentially younger input population one would expect to see the same numbers undergo more growth and yield a higher TAC level, which is what seemed to occur (GYM-derived TACs larger than the length-based assessment-derived values).

Conclusion

It is clear is that when similar assumptions (about the initial structure of the population by either age or length) are made, the length- and age-based assessment methods yield comparable answers. Importantly, the proposed length-based method potentially avoids the cohort identification problem. It is also simple to run in an open-source platform-independent package, making the evaluation of the approach in a management strategy context much simpler than for the CMIX/GYM method, therefore it is suggested that future assessments of *C. gunnari* in Subarea 48.3 could be undertaken using the length-based approach detailed in this paper.

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Табл. 1: Значения параметров для годового соотношения веса и длины (длина в мм, вес в кг), использовавшиеся в исследованиях.

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