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Use of parameters within *Euphausia superba* Grym simulations

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Introduction

The SC-CAMLR last estimated a precautionary harvest rate (gamma) used for management advice in the Area 48 krill fisheries in 2007 (SC-CAMLR, 2007 Annex 4 paras. 2.38-2.39). Subsequently, a range of various methods have been tried, with limited success, to produce both input parameters and stock assessments which can be used for management advice. Following the work plan outlined by SC-CAMLR (2019, Annex 4 paras. 2.60 – 2.64) endorsed by the Commission (CCAMLR, 2019, para. 5.53) the Generalised Yield Model (GYM) software was reimplemented in R as the Grym package, with the intention of updating the previous krill assessment. However, the methods used to estimate some input parameters to the previous assessment were not documented in detail, and there remains considerable ambiguity as to how to compute these inputs, and how these inputs are used within the assessment simulations.

Here we aim to clarify what each parameter within the Grym models are used for, and where possible provide examples as to how they have been calculated.

Methods

We have divided the model parameters into two categories; 1) those calculated based on observed data, 2) those which are decisions on how the model runs (Table 1).

Table 1. Grym parameters required for initial krill simulation. Origin describes if a parameter is 'Calculated' based of observed data, a 'Decision' made to implement the model, or an 'Output' of the model expected to fall within this range.

Parameter group	**Parameter**	**Origin**
Age Classes	First Age Class	Decision
	Last Age Class	Decision
Growth	t0	Calculated
	L∞	Calculated
	k	Calculated
	Start growth period (dd/mm)	Calculated
	End growth period (dd/mm)	Calculated
Weight-at-Length relationship	Weight-length parameter - A (g)	Calculated
	Weight-length parameter - B	Calculated
Maturity	Min length, 50% mature	Calculated
	Max length, 50% mature	Calculated
	Range over which maturity occurs	Calculated
Spawning Season	Start of spawning season (dd/mm)	Calculated
	End of spawning season (dd/mm)	Calculated
Recruitment	Recruitment function	Decision
	Mean proportional recruitment	Calculated
	SD of proportional recruitment	Calculated
	Proportional Recruitment age class	Decision
	Number of surveys in recruitment	Calculated
Selectivity	Min length, 50% Selected	Calculated
	Max length, 50% Selected	Calculated
	Range over which selection occurs	Calculated
Future fishing parameters	B0logSD	Calculated
	Fishing Season (dd/mm)	Decision
	Reasonable upper bound for Annual F	Decision
Model Decisions	Reference Date (dd/mm)	Decision
	Target Escapement	Decision
	Model iterations	Decision
	Model time steps	Decision
	Projection period (years)	Decision
	Monitoring interval (dd/mm)	Decision
Output	Natural Mortality range	Output

For each parameter we outline 1) how the parameter is used within the current implementation of the Grym model, and 2) Examples of how the parameter can be calculated (where appropriate) to be consistent with either the previous implementation of the krill assessment, or the current accepted CCAMLR practices in other fisheries.

When searching through WG-EMM reports, there are no recent examples of many of these parameters being calculated. Whilst many parameters had data reported for them, and changes in the data tracked and linked to environmental effects, the follow-on steps of calculating the parameters used in the assessment were not conducted. This provides limited scope to refer to previous methods used.

Age classes

Model use:

Age classes in the Grym are defined so that the model simulates the age range that we have information on, either from the fishery, or from surveys, or both. As krill are assumed to not live past 7, and as krill below 1 year old are rarely seen, the simulations use the age classes 1-7 years.

A note when referring to ages both in the models and in general discussion, there appears to be a mismatch between the terms age and age+. Within the model, if referring to 2+ year class, or the two years old cohort, it means any krill that are between the ages of 2, up to but not including age 3, conversely krill referred to as two years old are assumed to be exactly two years old in the model. The latter of these is very rarely used within stock assessments as they tend to model year classes not krill of an exact age.

Length-at-Age

Model use:

The growth model is used for calculating the length for each age class at every timestep in the model. This is then used for calculating at specific time steps what proportions of the population: are available to the fishery, are mature, and what weight each individual will be.

Growth consists of five parameters; the first three relating directly to the von Bertalanffy growth model ($L\infty$, k, t_0), and the last two relating to the growth period of krill.

Method:

Upon searching the recent WG-EMM reports, there does not appear to be recent estimates, or an agreed upon method to estimate von Bertalanffy growth parameters.

Whether estimated as continual or punctuated (only growing for part of the year) growth is integral to the Grym simulations, and effort should be focused towards identifying a method that is both reliable and the required data either exists or can be obtained.

Drawing examples from allied fisheries, in the Division 58.5.2 icefish fishery where direct age information is not available, a von Bertalanffy growth model was fitted to the modal length estimates of each cohort identified by the CMIX analysis from survey data between 2010 - 2017 using non-linear least squares with the function *nls*() in R:

$$L_{(t)} = L_{\infty}\left(1 - e^{-k(t-t_0)}\right).$$

Here L_{∞} is the asymptotic mean length, k is the growth rate, and t_0 the hypothetical age at length zero. Ages were assigned to cohorts as proportion of the year since the nominal birthdate of December 1 to the time of survey, and each cohort was weighted by the inverse square of the standard error of the modal length (Maschette et al., 2017).

For calculating the growth period, Thanassekos et al., (2021) estimated the growth period by fitting a loess regression through area averaged, daily Photosynthetically Active Radiation (PAR) satellite data between 2002-2020. The time period for an area where PAR was above 25 was assumed to be the likely growth period for krill in that area.

Weight-at-Length

Model use:

Together with the length-at-age relationship, a weight-at-length relationship is used to determine the average weight of an individual for each age class at each time step. The Grym then scales these weights by the modelled abundance in each age class to determine a total biomass for each age class at each time step. This biomass is then multiplied by the fraction mature (see below) in each age class and averaged over the nominated spawning season to determine the spawning biomass in each year.

Method:

The parameters of the weight-at-length relationship, a and b based on the relationship:

$$W = aL^b$$

where W is the weight (g) and L is the length (mm) of individual krill.

This most recent implementation for fitting this relationship for krill within CCAMLR was Cox et al., (2021) who estimated the parameters using the *nls*() function with parametric bootstrap in R (R Development Core Team 2020) fitting to survey caught krill measurements.

Maturity

Model use:

The maturity ogive is used within the Grym model to determine the proportion of each length class, and in turn age class, that is mature. This determines the overall proportion of individuals in the population which are considered to be part of the spawning stock.

Method:

A Bayesian nonlinear Binomial random effects model was recently used to estimate the width and slope of a ramp-shaped maturity ogive as required by the Grym, details are contained in Maschette et al., (2021, Appendix 3).

Spawning Season

Model use:

The spawning season provides the time period which the model calculates spawning stock biomass over. It also tells the model the spawning period used when estimating virgin spawning stock biomass.

Method:

Spawning season is estimated from observations of gravid females getting ready to spawn through to the presence of spent females being more common in the population (See Kawaguchi, 2016).

Recruitment

Model use:

The Grym estimates both the variability in recruitment and the natural mortality from the fraction of the population that are recruits.

Natural mortality can be estimated from the proportion of the population that are recruits. If natural mortality is low, individuals are live longer, the proportion of the population that is old is larger, and the proportion that are recruits is lower. But as natural mortality increases, lifespans are shortened and the fraction of the population that is old diminishes, and the proportion that are recruits increases. For example, if 60% of the population are recruits then natural mortality must be high (~1 given a 20%SD) and very few would survive 4 years beyond recruitment. Conversely if the proportion of recruits is low then natural mortality must also be low.

Variability in recruitment is estimated from the variability in the proportion of recruits. In a year with stronger recruitment, the recruits will be a greater fraction of the population, and in a year with weaker recruitment, the recruits will be a smaller fraction of the population.

Method:

Proportional Recruitment (PR) is fitted to survey data as outlined by De la Mare (1994a, 1994b) and expanded by Pavez et al., (2021). The PR model expects four parameters to be provided: Mean PR, SD of PR, PR age class, and number of surveys used in estimating PR. Whilst the PR model itself as proposed by Pavez et al., (2021) has been implemented within the setup of the krill simulations, the calculation of the four input parameters for this model have been discussed at length at WG-EMM. Upon reviewing the original by De la Mare (1994a, 1994b) papers, as well as considering the way in which survey and length frequency data is treated in other CCAMLR fisheries we developed the flow chart and notes presented in Appendix 1.

Selectivity

Model use:

The selectivity ogive is used within the Grym model to indicate what proportion of each length class, and in turn age class is available to the fishery. This determines the overall proportion of individuals in the population which are subject to fishing mortality.

Method:

Selectivity was estimated by Krag et al., (2014) using the standard ICES methods to fit a logistic model (Wileman et al., 1996) to catch data:

$$r(l, L50, SR) = \frac{\exp(\frac{\ln(9)}{SR} \times (l - L50))}{1.0 + \exp(\frac{\ln(9)}{SR} \times (l - L50))}$$

Where L50 is the length at which there is 50% retention likelihood for the individual, and SR is the selection range.

Future fishing parameters

The model requires three parameters for estimating future fishing effort: fishing season, Reasonable upper bound for Annual F, and B0logSD.

Model use:

Fishing Season (dd/mm): Period of the year which are subjected to fishing mortality.

Reasonable upper bound for Annual F: The upper bound that the Grym can apply to the annual fishing mortality.

B0logSD: The Grym uses B0logSD to add variability to the calculated B_0 at the beginning of each run. This is to account for the sampling and methodological error in surveys during the forward projections.

Method:

B0logSD: The Grym requires an estimate of the expected measurement error in future surveys. This can be calculated in a number of ways 1) take the CV from the most recent survey, 2) average across the time series of surveys, or 3) estimate the expected CV of future planned surveys.

Model Decisions and Output

The remainder of the parameters are decisions to control aspects of the model:

Reference Date (dd/mm): This is the start day of the year in the model. It dictates at what day the youngest age class enter the model, and what day each age class progresses to the next age class. All other dates are calculated as an increment from this date.

Target Escapement: The target median spawning stock status to be achieved after the projection period. For krill, under the current CCAMLR decision rules this is 75%.

Model iterations: How many projection runs of the model should be conducted.

Model time steps: How many time steps should the year be split into within the model. Typically, this is daily time steps.

Projection period (years): How many years should the model project forward for. Currently for krill this is 20 years.

Monitoring interval (dd/mm): Time of the year in which surveys are done to estimate B0.

Natural Mortality range: Natural mortality is an output from the PR model, it can be compared to the expected range to see if the recruitment parameters R.mean, R.SD, and N.surveys make ecological sense.

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Appendix 1: Proportional recruitment input parameter calculations.

Here we outline the steps to calculate input parameters for the proportional recruitment model from research surveys as outlined within de la Mare (1994a, 1994b).

The steps are mostly simple and have two possible end points (Figure 1).

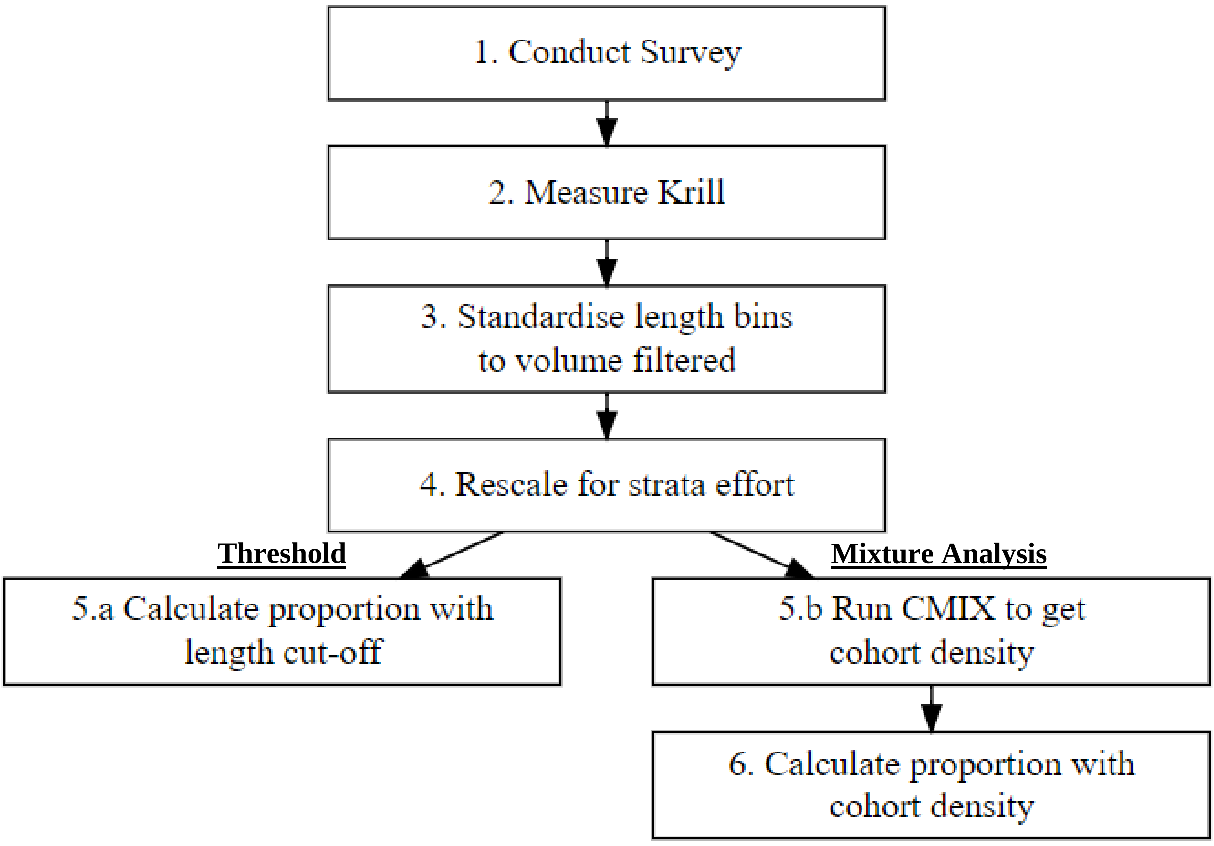

Figure 1: Steps to calculate proportional recruitment model input parameters.

Whichever point you plan to exit the flow chart the first three steps are needed. The first two steps are simple enough, however, have some core assumptions associated with them.

1. Surveys should have adequate hauls to representatively sample the population.
2. Krill should be sampled randomly and in sufficient quantity to ensure measurements are representative of the overall catch.

Once these steps have been done, step 3 of Figure 1 is to convert haul-by-haul counts in each length bin into a density per unit of volume. Typically, this is either per m^3 or per $1000m^3$. Where density of krill d at length l in krill per m^3 was estimated for each haul as:

$$d_l = \frac{N_l C}{Ac}$$

where N_l is the numbers at length l, A is the swept volume of the net for that haul, C is the total catch numbers of the haul, and c is the total count of the sample from the haul.

Mixture Analysis

For the mixture analysis, the CMIX mixture model is fitted to the entire survey to estimate the total density in each age cohort.

As a single mixture model is fitted across all strata, the haul densities are scaled to account for unequal sampling effort in each stratum (step 4). The data is re-scaled so that the mean of the re-scaled data is the same as the stratified mean of the raw data. For each haul in k strata, the density data is re-scaled by the composite sampling fraction following de la Mare & Williams (1996):

$$D_{i,j} = d_{i,j}\,\frac{A_i}{\sum_k A_k} \times \frac{\sum_k n_k}{n_i}$$

where $D_{i,j}$ is the re-scaled density for haul i in stratum j, $d_{i,j}$ is the original density estimate for that haul, and A_i and n_i are the area and the number of hauls in stratum i respectively.

Step 5b involves fitting the mixture model to the rescaled length density distributions in order to calculate cohort densities. These densities can then be used in step 6 to calculate the proportion of recruits in the population (See de la Mare 1994b).

Threshold

The alternative analysis identifies recruits through a simple length threshold.

Individuals of length 36mm or shorter are identified as recruits, and larger individuals are identified as adults. Within each haul, the length densities for lengths at or below 36mm are summed to give the total density $d_{i,j}^{(r)}$ of recruits in haul i and stratum j, and the length densities for lengths greater than 36mm are summed to give the total density $d_{i,j}^{(a)}$ of adults in haul i and stratum j.

Similar to the mixture analysis, threshold calculations need to account for unequal sampling effort in each stratum. Within each stratum these densities are scaled to indices of relative abundance

$$d_{i,j}^{(r)} = d_{i,j}^{(r)}\,\frac{A_i}{\sum_k A_k}$$

$$d_{i,j}^{(a)} = d_{i,j}^{(a)}\,\frac{A_i}{\sum_k A_k}$$

where again A_i are the strata areas.

The mean and variance of these indices are then calculated within each strata, and then summed across strata to give the estimated mean relative abundance $\hat{r}$ of recruits and $\hat{a}$ of adults, and their corresponding variances σ_r^2 and σ_a^2. The proportion of recruits is then calculated as $R = \frac{\hat{r}}{\hat{r}+\hat{a}}$, with variance $\sigma_R^2 = (\hat{r}^2\sigma_a^2 + \hat{a}^2\sigma_r^2)/(\hat{r} + \hat{a})^4$,

The final part of the process is, in situations where you have multiple surveys is to combine the estimates to get an inverse variance weighted mean and variance for use in the proportional recruitment model of the krill simulation fitted in the Grym (de la Mare 1994b, Maschette et al., 2020).

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