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## **WG-FSA STANDARD ASSESSMENT METHODS**

Working Group on Fish Stock Assessment

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## WG-FSA STANDARD ASSESSMENT METHODS

### STANDARDISATION OF CPUE TIME SERIES FOR *DISSOSTICHUS ELEGINOIDES*

Standardisation of catch per unit effort for *Dissostichus eleginoides* in Subarea 48.3 has followed an accepted standard methodology since 1995 (SC-CAMLR, 1995). This approach has also been applied to Division 58.5.1 when the data have been available.

The aim of this method is to obtain a standardised time series of catch per unit effort as a relative index of abundance. It is currently used to adjust the assessments arising from the Generalised Yield Model (GYM) according to the method of Kirkwood and Constable (2001).

#### Method

(1) Haul-by-haul catch and effort data (fine-scale data) are extracted by the CCAMLR database manager for all years except for the first season (1985/86), when fishing had been restricted to very shallow depths (mainly less than 300 m). All months are included in the analyses. The data is first set up in the form of an EXCEL spreadsheet with the following variables:

season	month	area	nationality	hooks	bait	depth	depth.class	catch.kg	cpue
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(2) The CPUE in kg/hook is used as the response variable, and nationality, season, month, area (East South Georgia, NW South Georgia, South Georgia, West Shag Rocks and Shag Rocks), depth and bait type are considered as predictor variables. Depth information is also treated as a categorical variable with four levels (0–500 m, 500–1 000 m, 1 000–1 500 m, 1 500 m and above).

(3) Analyses are conducted in Splus; an annotated Splus history file of all steps used during the 2001/02 assessment is provided in Box 1.

(4) GLM analyses are conducted on positive CPUE data only, with an adjustment for zero catches being made afterwards.

(5) To conduct the analysis, a square root transformation is applied and a robust quasi-likelihood form of GLM fitted. Models are first fitted using all listed predictor variables as main effects. Of these, the statistically significant predictors are usually nationality, season and depth class. Thus the model form used is

$$\text{cpue} \sim \text{season} + \text{nationality} + \text{depth.class, family} = \text{robust}(\text{quasi}(\text{link} = \text{sqr}t)).$$

(6) A standardised time series of CPUEs in kg/hook is plotted in Figure 1. The standardisation is with respect to Chilean vessels fishing at depths of 1 000–1 500 m. This time series is adjusted for the presence of hauls with zero catches, by multiplying the standardised CPUEs predicted from the GLMs by the proportions of non-zero catches.

**Box 1:** Documentation for Standardization of *D. eleginoides* CPUEs of Area 48.3 CCAMLR 2002: script from S-plus

```
attach("c:/CCAMLR2002/CPUE483/splus",pos=1)
objects()
#
# READ IN DATA FROM EXCEL FILE (This analysis used the 2002 GLM data TOP to Splus.xls sheet)
TOP483.frame<-read.table(file="clipboard",header=T)
summary(TOP483.frame)
#
# MESSAGE DATA AND FACTORIZE
TOP483.frame<-na.omit(TOP483.frame)
TOP483.frame$season<-factor(TOP483.frame$season)
TOP483.frame$month<-factor(TOP483.frame$month)
TOP483.frame$area<-factor(TOP483.frame$area)
TOP483.frame$bait<-factor(TOP483.frame$bait)
TOP483.frame$nationality<-factor(TOP483.frame$nationality)
TOP483.frame$depth.class<-factor(TOP483.frame$depth.class)
summary(TOP483.frame)
summary(TOP483.frame$month)
summary(TOP483.frame$season)
summary(TOP483.frame$depth.class)
summary(TOP483.frame$nationality)
summary(TOP483.frame$area)
summary(TOP483.frame$bait)
#
# CHECK CROSSOVER IN DATA BY SEASON AND NATIONALITY, AND BY SEASON, NATIONALITY AND
MONTH
#
tapply(TOP483.frame$season,list(TOP483.frame$season,TOP483.frame$nationality),length)
tapply(TOP483.frame$season,list(TOP483.frame$month,TOP483.frame$nationality,TOP483.frame$season),length)
#
# GET RID OF DATA IN MONTH=9 BECAUSE
# THERE WERE FEW HAULS
ttdrop<-(TOP483.frame$month!=9)
table(ttdrop)
TOP483.frame<-TOP483.frame[ttdrop,]
summary(TOP483.frame)
#
# ALLOW FOR GINORMOUS OBJECT SIZE WHEN FITTING MODELS WITH INTERACTIONS.
#
options(object.size=6000000)
#
Fit a model with season, nationality, area, depthclass only, since bait and month are not significant
#
GLM483.No2 <- glm(cpue ~ season + nationality + area + depth.class,family = robust(link =
sqrt)),subset=season!=1986&area!="Wshag", na.action=na.omit, data = TOP483.frame,maxit = 100)
anova(GLM483.No2, test="Chi")
#
Fit a model with season, nationality, depthclass only, since area is not significant (this is similar to 2001)
#
GLM483.No3 <- glm(cpue ~ season + nationality + depth.class,family = robust(link =
sqrt)),subset=season!=1986&area!="Wshag", na.action=na.omit, data = TOP483.frame,maxit = 100)
anova(GLM483.No3, test="Chi")
```

**Box 1. cont.**

```
#
make some diagnostic plots
#
graphsheat()
par(mfrow=c(2,2))
plot(GLM483.No3,se=T, ask=T)
plot.gam(GLM483.No3,se=T, ask=T)

#NOW SET UP PREDICT DATA FRAME AND PREDICT STANDARDIZED CPUES AND SES
GLM483.predict.frame <- data.frame(season=c(1987:1989,1991:2002),
nationality=rep("CHL",15),depth.class=rep("1000_1500",15))
GLM.TOP.483.pred.rev<-predict.gam(GLM483.No3, newdata=GLM483.predict.frame,
type="response",se.fit=T)
GLM483.predict.frame
GLM.TOP.483.pred.rev
#
standard.No3<-GLM.TOP.483.pred.rev
standard.No3$hi <- GLM.TOP.483.pred.rev$fit+2*GLM.TOP.483.pred.rev$se.fit
standard.No3$lo <- GLM.TOP.483.pred.rev$fit-2*GLM.TOP.483.pred.rev$se.fit
standard.No3<-as.data.frame(standard.No3)
standard.No3$x <- c(1987:1989, 1991:2002)
standard.No3
#
This is now ready to plot
```

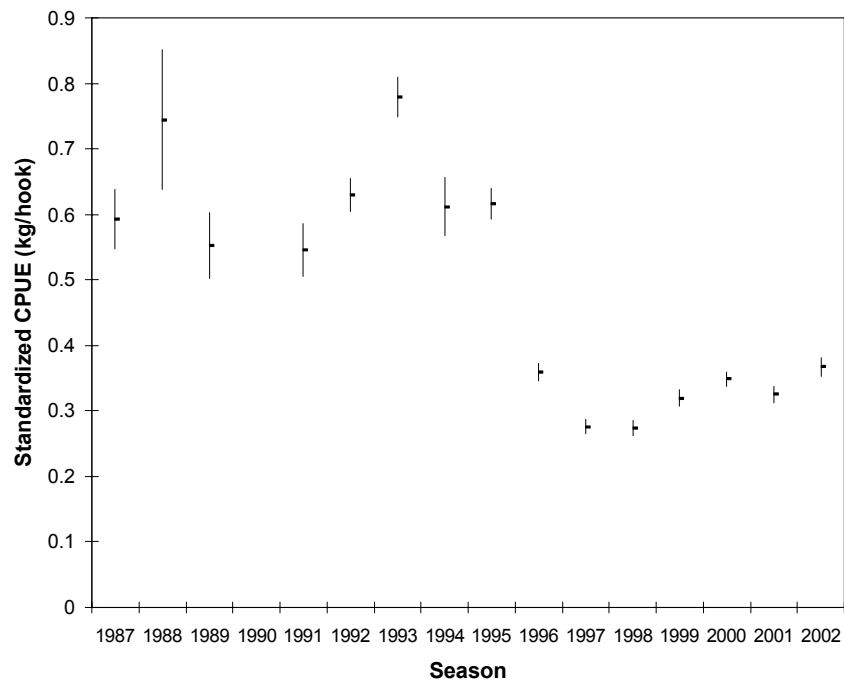


Figure 1: Standardised CPUEs and 95% confidence intervals in kg/hook for Subarea 48.3.

## ESTIMATING LONG-TERM ANNUAL YIELD USING ESTIMATES OF ABUNDANCE OF RECRUITS AND THE GYM

The method adopted by CCAMLR for assessing yield in *D. eleginoides* currently evaluates the long-term annual yield using estimates of abundance of recruits and the GYM (Constable and de la Mare, 1996) in order to apply the decision rules underpinning the precautionary approach of CCAMLR (CCAMLR, 2000).

### General Description

The GYM is a Monte Carlo simulation tool that allows for these assessments to integrate across uncertainties in the population parameters (see Constable et al., 2000 for a description of its origins and development). A simple population model, which includes estimates of recruitment and its variability, is run hundreds of times with values for growth, mortality and abundance drawn at random from suitable statistical distributions, to allow natural variability in the population as well as uncertainty in the parameter estimates to be incorporated. Thus, the simulation model is used to calculate a distribution of possible population sizes both in the absence of fishing and under various harvest scenarios.

Each of the many simulations starts with a biomass and stock structure of toothfish drawn from the recruitment function. In each simulation year, the biomass is recalculated by adding an amount for annual growth and deducting an amount corresponding to natural mortality. Similarly, the biomass of each year's recruits is added and the constant annual catch is deducted. Variability in the simulated population biomass in each year arises because the recruitment varies from one year to the next. Annual recruitment is applied according to known estimates of recruitment for a given year or, in the absence of such estimates, drawn from a log-normal statistical distribution derived from the time series of recruitments.

The long-term annual yield is selected, which gives a statistical distribution of the outcomes of all simulations that meet the criteria described below.

The first criterion requires determination of the catch which leads to a 10% probability of the spawning biomass dropping below 20% of its pre-exploitation median level over a 35-year harvesting period. Applying this criterion requires the examination of the statistical distribution of the lowest population size (in terms of spawning biomass) in any year over the 35 years of each simulation, collected over hundreds of simulation replicates. The probability of attaining a lowest spawning biomass less than or 20% of the pre-exploitation biomass is estimated from the relative frequency of this event over the set of replicates. This is done for a range of catch values. The required *Catch 1* is that which has this relative frequency at 10%.

The second criterion also leads to a catch, which is determined by the statistical distribution of spawning biomass at the end of the 35-year period in each simulation. The selected *Catch 2* is that which results in this distribution having a median that is 50% of the median prior to exploitation.

The values of *Catch 1* and *Catch 2* will usually be different, and so the third part of the decision rule chooses the lower value of the two.



The current model structure of the GYM and use of the simulation software are described in Constable et al. (2002).

### Estimating Recruitment

This method is based on estimates of recruitment of age 4 fish to the population. For years with unknown recruitment (from a time series), a recruitment function is used. In the current application, a log-normal recruitment function is used, although a bootstrap function from a vector of recruitments could also be used.

### Estimating Parameters for the Log-normal Recruitment Function

Estimates of mean recruitment,  $\bar{R}$ , and its CV are used to estimate the parameters for the log-normal function, which are entered into the GYM as parameters in the  $\log_e$  domain.

These parameters are determined as

$$\sigma = \sqrt{\ln(1 + CV^2)}$$

$$\mu = \ln(\bar{R}) - \frac{\sigma^2}{2}$$

$$SE = \frac{\sigma}{\sqrt{n}}$$

where  $n$  is the number of recruitment estimates used to estimate these parameters.

### Using a Time Series of Recruitments

For assessments in Subarea 48.3 and Division 58.5.2, the densities at age from surveys are input into the model in order to ensure that the time-series of recruitments is consistent with the estimate of natural mortality being applied in a trial. In this case, the abundance of each age class in a survey is estimated using a method (mixture analysis) for assessing the abundance of individual cohorts from a length-density distribution derived from the survey (de la Mare, 1994).

Densities of each length class at a survey station are estimated by estimating the abundance of the length class in the catch and converting this to density using the surveyed swept area at that station. If the survey is stratified then the observed densities of each length class from each stratum,  $D_{o,s}$ , are combined into a single dataset prior to the mixture analysis by weighting each observed density ( $D \cdot \text{km}^{-2}$ ) from a stratum by the sampling density within that stratum relative to the sampling density overall, such that the weighted observation,  $D'_{o,s}$ , is given by

$$D'_{o,s} = D_{o,s} \frac{\sum_s n_s \frac{A_s}{n_s}}{\sum_s A_s} \quad (1)$$

where  $o$  and  $s$  are the observation and stratum respectively,  $n_s$  is the number of observations taken in a given stratum,  $A_s$  is the corresponding area of the stratum, and  $S$  is the number of strata.

A mixture of normal distributions is fitted to this length-density distribution using the method of de la Mare (1994) and software (CMIX) (see de la Mare et al., 2002). The estimated density of a given year class is taken to be the area under a designated component of the mixture distribution. The standard error of this estimate of this density is also estimated. The abundance and standard error of the year class is then calculated as the product of the density and the area of the survey.

The fitting of mixture components is guided by the assessment of length at age. The expected length at age at the time of the survey is derived from a von Bertalanffy growth function (note that the time of the survey is relative to the birthday of the fish in the von Bertalanffy function). If the length at age function is reliable and there is an estimate of the coefficient of variation of length at age then these parameters could be used directly in the estimation of densities of fish in each mixture component (age class) by fixing these input parameters in the CMIX software.

The time series of recruitment of *D. eleginoides* is estimated from survey data using the method first established by WG-FSA in 1995 (SC-CAMLR, 1995). This adjusts the numbers in each age class observed for the cohort to the numbers at age 4, using the natural mortality rate adopted for the area.

When the abundance of a cohort has been estimated from more than one survey, the mean abundance is determined using an inverse variance weighting of each observation, such that an estimate of recruitment strength in a given year ( $R_y$ ) for a cohort at age 4 is given by

$$R_y = e \frac{\sum_o \left[ (\ln(\bar{A}_o) - M[a_r - (a_o + t_o)]) \left( \frac{\bar{A}_o}{\sigma_o} \right)^2 \right]}{\sum_o \left( \frac{\bar{A}_o}{\sigma} \right)^2} \quad (2)$$

where  $o$  is a given observation from a survey,  $\bar{A}_o$  is the estimated mean abundance and  $\sigma$  is its standard error,  $a_r$  is the designated age of recruitment (age 4 in this case),  $a_o$  is the age class of the observed cohort and  $t_o$  is the time of the survey as a fraction of the year from the reference starting day in the year.

These can be calculated manually or left to the procedure in the GYM. It is recommended to use the survey data in the GYM.

## Input Parameters

The parameters used in this assessment of *D. eleginoides* are provided in a series of tables (Tables 1 to 4). Most biological, fishery and simulation parameters are included in Table 1.

Recruitment data and parameters are provided in Tables 2 and 3.

A number of checks need to be made prior to running the GYM:

- (i) the projection period (currently set at 35 years) needs to reflect the expected longevity of an age class in the population;
- (ii) the start date of the projection year has been specified;
- (ii) functions of within-year dates (natural mortality, fishing mortality) have as their first date the same date as the start date of the projection;
- (iii) the origin of the von Bertalanffy growth curve needs to be altered to coincide with the beginning of the projection year rather than the birthday;
- (iv) the number of increments in the year provides an adequate approximation of the fishing season and other within-year functions i.e. if there are too few increments then selectivity and vulnerability functions (age-based and intra-year functions) may become biased;
- (v) output files are appropriately specified to be saved;
- (vi) sufficient trials are given for the desired precision of results; and
- (vii) if the median pre-exploitation spawning biomass is being determined using Monte Carlo methods then sufficient samples are being derived for the desired precision.

Table 1: Input parameters for generalised yield model to assess the long-term annual yield of *D. eleginoides*. Parameters are an example for a trawl fishery in Division 58.5.2.

Category	Parameter	Values
Age structure	Recruitment age	4 years
	Plus class accumulation	35 years
	Oldest age in initial structure	55 years
Recruitment		See Table 3
Natural mortality	Mean annual M	0.13-0.2
von Bertalanffy growth	$t_0$	-2.46 <sup>1</sup> years
	$L_\infty$	2465 mm
	$K$	0.029 year <sup>-1</sup>
Weight at age	Weight-length parameter – A (kg)	2.59E-09 kg
	Weight-length parameter – B	(mm <sup>B</sup> ) 3.2064
Maturity	$L_{m50}$	930 mm
	Range: 0 to full maturity	780–1080 mm
Spawning season		1 Jul–1 Jul
Simulation characteristics	Number of runs in simulation	1001
	Depletion level	0.2
	Seed for random number generator	-24189
Characteristics of a trial	Years to remove initial age structure	1
	Observations to use in median SB <sub>0</sub>	1001
	Year prior to projection	1985
	Reference start date in year	01/12
	Increments in year	24
	Vector of known catches	See Table 2
	Years to project stock in simulation	35
	Reasonable upper bound for annual F	5.0
Tolerance for finding F in each year	0.000001	
Fishing mortality		See Table 3

<sup>1</sup> Adjusted from estimated parameter of  $t_0 = -2.56$  years to start of fishing season on 1 December.

Table 2: Cohort strengths from surveys. Observed and expected data are from the mixture analyses, the closeness of which indicates the quality of the fit. Data are an example for recruitment surveys in Division 58.5.2.

Survey Year	Time	Area (km <sup>2</sup> )	Observed	Expected		Density (n.km <sup>-2</sup> )					
						Age 3	Age 4	Age 5	Age 6	Age 7	Age 8
1990	0.58	97 106	107.2	108.1	Mean	8.080	33.508	20.208	0.827	25.226	0.000
					SE	5.897	13.552	11.251	11.505	14.082	0.000
1992	0.25	70 271	51.7	51.8	Mean	14.117	13.200	14.501	3.430	0.019	2.117
					SE	5.156	7.036	7.845	4.473	5.449	3.342
1993	0.85	71 555	97.4	114.7	Mean	13.567	38.259	8.191	16.961	3.066	20.884
					SE	8.804	18.172	13.483	12.606	30.294	16.333
1999	0.41	85 428	366.2	357.9	Mean	17.741	16.206	138.11	56.785	60.897	40.323
					SE	7.862	13.323	42.657	55.348	50.870	38.189
2000	0.55	41 144	185.0	179.5	Mean	28.124	21.969	47.817	59.121	7.565	10.989
					SE	5.298	7.996	14.885	20.578	15.142	11.383
2001	0.56	85 169	247.5	252.4	Mean	19.542	34.018	38.172	45.538	32.165	16.738
					SE	7.798	12.849	20.534	30.762	42.367	41.086
2002	0.56	85 910	208.5	204.8	Mean	18.590	29.333	59.400	20.726	53.199	
					SE	6.722	11.475	21.202	21.993	17.117	

Table 3: Time series of recruitments (millions of fish) for *Dissostichus eleginoides*. Parameters are an example from surveys in Division 58.5.2. Estimates are based on a mean natural mortality of 0.165 year<sup>-1</sup>.

Year at Age 4 Birthday	WG-FSA (2000)	Revised Time Series based on New Growth Parameters	Revised Estimates following 2002 Survey
1986		4.321	4.321
1987	1.550	0.120	0.120
1988	1.590	2.586	2.586
1989	3.649	3.790	3.790
1990	1.956	1.118	1.118
1991	1.793	0.667	0.667
1992	4.575	1.447	1.447
1993	2.435	0.825	0.825
1994	2.944	7.205	7.205
1995	5.674	9.226	9.226
1996	9.548	7.295	7.295
1997	21.557	15.043	15.043
1998	3.440	3.487	6.532
1999	1.059	2.291	2.332
2000	0.241	1.465	1.931
2001	0.152	1.632	2.236
2002			1.625
Mean	4.144	3.907	4.018
CV	1.297	1.021	0.975

Table 4: Catch histories and fishing vulnerabilities (selectivities) for *Dissostichus eleginoides*. Parameters are an example for a trawl fishery in Division 58.5.2. In this case the catch series has since been modified at WG-FSA 2002.

Season	Catch (Reported and IUU) (tonnes)	Size / Age (Vulnerability)	Size/Age Units
1995/96	17 094	550 (0), 790 (1)	mm
1996/97	1 866	(0), 6.0 (0.0), 7.0 (1), 7.9 (1), 8.0 (0)	years
1997/98	3 913	0.0 (0), 6.0 (0.0), 10.0 (1), 10.0 (1), 12.0 (0)	years
1998/99	3 628	0.0 (0), 5.5 (0.0), 6.0 (1), 13.0 (1), 15.0 (0)	years
1999/2000	4 385	0.0 (0), 4.0 (0.0), 8.0 (1), 14.0 (1), 15.0 (0)	years
2000/01	4 644	0.0 (0), 4.0 (0.0), 8.0 (1), 14.0 (1), 15.0 (0)	years
2001/02	TAC 2 815 t + illegal catch of 3 000 t = 5 815 t	0.0 (0), 4.0 (0.0), 8.0 (1), 14.0 (1), 15.0 (0)	years

#### Adjustments for Standardised CPUE Time Series

The assessment can be adjusted using a time series of catch per unit effort (see standard method description) according to the method of Kirkwood and Constable (2001). It can be undertaken using the GYM user interface or through the use of the Excel spreadsheet ‘GYM CPUE Master.XLS’.

If the spreadsheet is to be used then the macro needs to be checked to be sure that the sorting function is operating correctly.

This assessment requires the time series array of Year, CPUE. Note that the Year needs to coincide with the year in the GYM outputs.

The CPUE is compared to the average vulnerable biomass in the corresponding year of each trial in the GYM. The average vulnerable biomass is the weighted biomass derived from the vulnerability function combined with the specified fishing season.

#### Results and Outputs

If recruitment data from surveys was used then the time series of recruitments and its mean and CV for the average rate of natural mortality can be obtained from either the log file or the specially generated file with the summary recruitment calculations (\*.RSV file).

The log file should be examined to ensure that all parameters were input correctly.

Diagnostic information can be obtained mostly from the general population outputs provided in ASCII files or through by using the GYM user interface.

Results are normally presented in a manner illustrating the catch levels associated with the CCAMLR decision rules. The lower catch level is then applied (as per the third part of the rules). These results are displayed in a table similar to Table 5.

Potential outputs based on the general population outputs are illustrated in Figure 2.

Table 5: Results from 2002 assessments of yield according to the CCAMLR decision rules for *Dissostichus eleginoides* in Division 58.5.2 using the GYM.

Lowest catch giving 0.1 probability of depletion to 20%	Catch giving median escapement of 50%
...	...

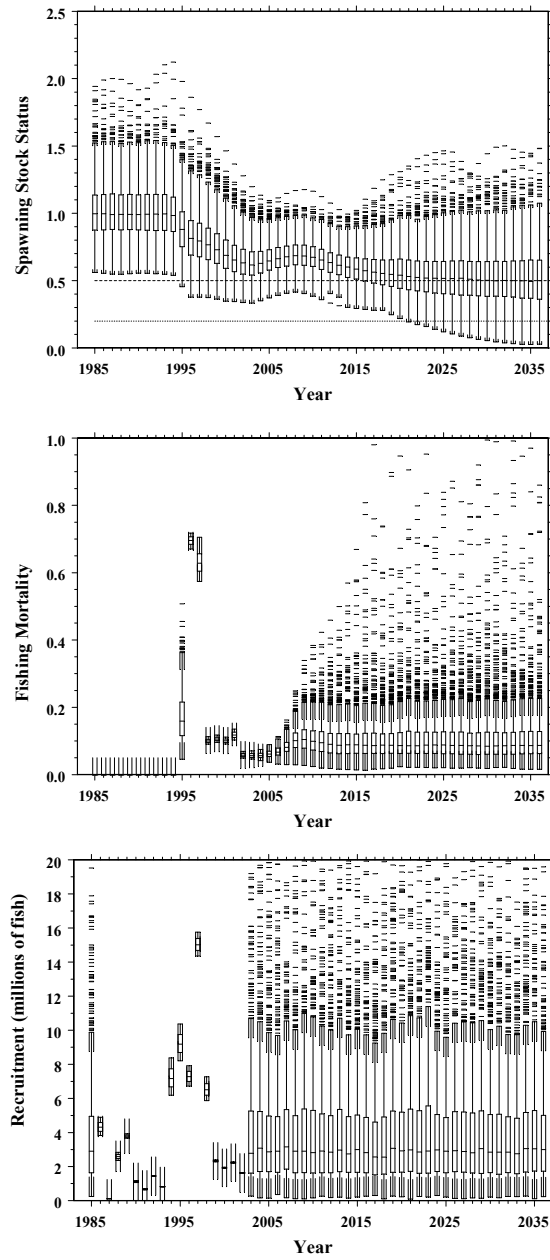


Figure 2: Box and whisker plots showing the distribution of spawning stock status, fishing mortality and recruitment of *Dissostichus eleginoides* for each year in 1001 GYM simulation trials to determine long-term annual yield for the Heard Island Plateau in Division 58.5.2.



## ESTIMATING LONG-TERM ANNUAL YIELD AS $\gamma \cdot B_0$ USING THE GYM

WG-FSA, October 2002

The method adopted by CCAMLR for assessing long-term annual yield as a proportion ( $\gamma$ ) of a biomass estimate prior to exploitation ( $B_0$ ) was developed as the Krill Yield Model (Butterworth et al., 1991, 1994), based on the method of Beddington and Cooke (1983), in order to apply the decision rules underpinning the precautionary approach of CCAMLR (CCAMLR, 2000). This approach has been incorporated into the GYM, the description of which is provided above.

This method description characterises the main elements of the estimation of  $\gamma$  that differs from the description for *D. eleginoides*.

- (i) This procedure works with relative rather than absolute stock sizes. Consequently, the only recruitment parameters required are to do with recruitment variability (CV) which is input to the model in the  $\log_e$  domain where

$$\sigma = \sqrt{\ln(1 + CV^2)}$$

- (ii) The estimate of  $\gamma$  is dependent also on the coefficient of variation from the survey of pre-exploitation biomass,  $B_0$ .
- (iii) No catch history is used in this assessment. Only the fishing vulnerability functions are required.

The list of input parameters is given in Table 6.

Table 6: Input parameters for generalised yield model for an assessment of  $\gamma$ .

Category	Parameter
Age structure	Recruitment age Plus class accumulation Oldest age in initial structure
Recruitment	Minimum – Maximum CV
Natural mortality	Mean annual M
von Bertalanffy growth	$t_0$ $L_\infty$ $K$
Weight at age	Weight-length parameter – A (kg) Weight-length parameter – B
Maturity	$L_{m50}$ Range: 0 to full maturity
Spawning season	
Biomass ( $B_0$ ) survey	Coefficient of variation
Simulation characteristics	Number of runs in simulation Depletion Level Seed for random number generator
Characteristics of a trial	Years to remove initial age structure Observations to use in median $SB_0$ Year prior to projection Reference start date in year Increments in year Vector of known catches Years to project stock in simulation Reasonable upper bound for annual F Tolerance for finding F in each year
Fishing mortality	Selectivity function – age or size

ESTIMATING ANNUAL YIELD FOR *CHAMPSOCEPHALUS GUNNARI* USING ESTIMATES OF ABUNDANCE AND A METHOD OF SHORT-TERM PROJECTION

The method adopted by CCAMLR for assessing yield in *Champsoccephalus gunnari* was published in de la Mare et al. (1998). This method was developed as an interim step to enable higher catches in seasons when strong year classes are present, a situation not possible under the usual decision rules of the precautionary approach developed by CCAMLR. A new criterion was developed to assess a catch level such that fishing should, without any substantial risk, not reduce the spawning stock biomass to below 75% of the level that would occur in the absence of fishing. Thus, the approach uses the criterion

*to calculate the fishing mortality which would result in a probability of no more than 0.05 that the spawning stock after fishing would be less than 75% of the level that would have occurred in the absence of any fishing.*

The estimation of fishing mortality is achieved by using the bootstrap one-sided lower 95% confidence bound on the trawl survey estimate as the current stock biomass. The application of the criterion with respect to this estimate of abundance is illustrated in Figure 3.

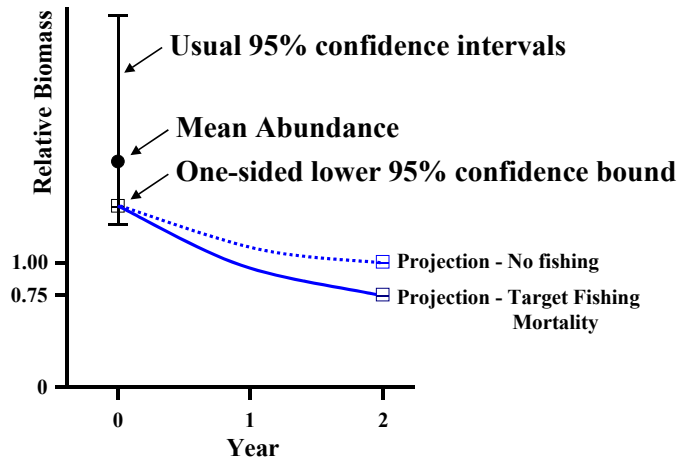


Figure 3: Illustration of the decision rule adopted by CCAMLR in 1997 for determining yield in the subsequent year for *Champsoccephalus gunnari* based on a survey in the current year.

The numbers of fish in the cohorts are calculated using the following formula:

$$\tilde{N}_a = \frac{\hat{N}_a}{\sum_i \hat{N}_i} \cdot \tilde{B} \quad (3)$$

where  $\tilde{N}_a$  is the number of fish of age  $a$ , given the current age structure and a population biomass at the lower 95% confidence bound  $\tilde{B}$ ,  $\hat{N}_a$  is the estimated abundance of fish aged  $a$  in the current population and  $\bar{w}$  is the average weight of a fish in the current population. The average weight is given by:

$$\bar{w} = \frac{w_a \hat{N}_a}{\sum_i \hat{N}_i} \quad (4)$$

where  $w_a$  is the average weight of fish of age  $a$ , calculated from the growth curve and weight-length relationship.

The fishing mortality is found numerically by solving the usual fisheries differential equations with an initial age structure derived from equation (1).

The numbers at age satisfies the equation:

$$\frac{dN_a}{dt} = -(M + F) N_a \quad (5)$$

where  $N_a$  is the number of fish in age class  $a$ ,  $M \text{ year}^{-1}$  and  $F \text{ year}^{-1}$  give the annual rates of natural and fishing mortalities respectively.

The biomass  $B_{a,y}$  in each age class in each year satisfies the equation:

$$\frac{dB_a}{dt} = w(a+t) \frac{dN_a}{dt} + N_a \frac{d w(a+t)}{dt} \quad (6)$$

where  $w(a+t)$  is a growth function which gives the average weight of fish at age during the year at time,  $t$ .

The yield,  $Y$ , from each age class satisfies the equation:

$$\frac{dY_a}{dt} = F B_a \quad (7)$$

The yield from each class taken over one year is calculated by simultaneous numerical integration of equations (5), (6) and (7) using an adaptive Runge-Kutta procedure (Press et al., 1992). The total yield is the sum of the yields from all age classes.

The assessment is currently undertaken using a routine developed with the *Mathcad* software, although it is recommended to develop this in S-plus.

## Input Parameters

A summary of the biological parameters used in this assessment is provided in (Table 7).

The age structure is derived using a method (mixture analysis) for assessing the abundance of individual cohorts from a length-density distribution derived from the survey (de la Mare, 1994).

Table 7: Parameters for the short-term assessment of yield for *Champscephalus gunnari*.

Category	Parameter
Survey details	Survey date
Mean length at age at time of survey	Age 2 Age 3 Age 4 etc.
Age structure (density n.km <sup>2</sup> )	Age 2 Age 3 Age 4 etc.
Biological parameters:	Birthday
von Bertalanffy growth	$t_0$ $L_\infty$ $K$
Weight at age	Weight-length parameter A Weight-length parameter B
Natural mortality	Mean annual M
Fishery parameters	Season Catch between survey and season
Selectivity	Age fully selected Age first selected

### Assessment of Biomass

The one-sided lower 95% confidence bound is determined using a bootstrap procedure written in *S-plus 2000* statistical software. A general script is provided in Box 2. If required, observed densities from each stratum,  $D_{o,s}$ , are combined into a single dataset prior to the bootstrap procedure by weighting each observed biomass density (kg.km<sup>-2</sup>) from a stratum by the sampling density within that stratum relative to the sampling density overall, such that the weighted observation,  $D'_{o,s}$ , is given by

$$D'_{o,s} = D_{o,s} \frac{\sum_s n_s A_s}{n_s \sum_s A_s} \quad (8)$$

where  $o$  and  $s$  are the observation and stratum respectively,  $n_s$  is the number of observations taken in a given stratum,  $A_s$  is the corresponding area of the stratum, and  $S$  is the number of strata.

**Box 2:** General S-plus script for use in bootstrap procedure for estimating confidence intervals in biomass estimate

```
ResultsFromBootstrap<-function(dframe,AreaSt,NamesSt,MassToTonne,Brep,TraceInBoot=F,Boots=F)
{
# par for the function are the next:
# dframe - the data frame contain Raw Data as in A. Constable script
#
# columns - one column per stratum"
# rows - one row for each haul (number of hauls differ between strata, hence some"
# values for a stratum will be NA when the number of hauls is less than in "
# other strata)"
#
# AreaSt is a vector with area of each simple stratum
# NamesSt is a vector of name to combine from a set of simple stratum
# MassToTonnes is a constant to obtain results in tonnes, for example = 0.001 if observations are in kg.
# Brep is a constant, number of the replicates in bootstrap
# TraceInBoot if T then during bootstrap there will be printing the number of current replicates in bootstrap
# (each 100)
# Boots if T then the main output will contain standard output from bootstrap including set of replicates

# in dframe names of the columns should contains the names of the Stratum combined and reweighted
# dim of Vector AreaSt = number of columns in dfame = numbers of Stratum in calculations
#

ncolumn<-ncol(dframe)
nrows<-nrow(dframe)
if (ncolumn!=length(AreaSt)){
  stop("Error! number of columns do not = length of Area")
}
dframe1<-rbind(dframe,AreaSt) #they are very small frames
n<-length(NamesSt) # number of combined stratum
SumArea<-sum(dframe1[nrows+1,NamesSt]) # Area of the Subdivision

SumN<-0
WeightedHauls<-c()
for (i in 1:n)
{
  N1<-NamesSt[i]
  CurrentSt<-as.matrix(na.omit(dframe[,N1] ))

  Number<-length(CurrentSt)
  SumN<-SumN+Number # add to summarize total number of stations
  WeightedHauls<-c(WeightedHauls,CurrentSt/Number*dframe1[nrows+1,N1]/SumArea)
}
WeightedHauls<-WeightedHauls*SumN
#
S1<-mean(WeightedHauls)*SumArea*MassToTonne
S2<-sqrt(var(WeightedHauls)/length(WeightedHauls))*SumArea*MassToTonne

btstrap<-bootstrap(WeightedHauls,mean,Brep,sampler=samp.boot.mc,trace=TraceInBoot)
S3<-limits.emp(btstrap,prob=c(0.025))*SumArea*MassToTonne
S4<-limits.emp(btstrap,prob=c(0.975))*SumArea*MassToTonne
S5<-limits.emp(btstrap,prob=c(0.05))*SumArea*MassToTonne
```

**Box 2 cont.**

```
# ----- Results from bootstrap -----  
if (!Boots)  
list(WeightedHauls=WeightedHauls,SumArea=SumArea,Summary=as.vector(c(S1,S2,S3,S4,S5)))  
# WeightedHauls contains the sample reweighed by the density of obs. in diff. stratum  
# SumArea containd the area of the combined stratum  
# Summary is a vector contained: mean, SE, LowerCL, UpperCL,OneSided95LowBound  
  
# if Boots=T it is possible to obtain full results from standard output of bootstrap  
else  
  btstrap # here it is possible to obtain full set of replicated
```

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**SCALING HAUL DENSITIES IN ORDER TO POOL ALL HAUL  
DENSITIES INTO A SINGLE CALCULATION WHEN SAMPLING  
INTENSITY VARIES BETWEEN STRATA IN A SURVEY**

(see de la Mare and Williams, 1996 [WG-FSA-96/38]).

This appendix elaborates the formula for scaling haul densities in order to pool all haul densities into a single calculation. This scaling formula is required when sampling intensity varies between strata in a survey (see de la Mare and Williams, 1996 [WG-FSA-96/38]).

Because the sampling intensities in each strata are different, the data have to be re-scaled so that mean of the re-scaled data is the same as the stratified mean of the raw data. It is easily shown that for  $k$  strata this is achieved by re-scaling the density data in each haul by the composite sampling fraction according to the following expression:

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

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.

The proof of this equation is as follows:

Mean density in a stratum:

$$\hat{d}_i = \frac{\sum_j d_{i,j}}{n_i}$$

Number of fish in a stratum:

$$F_i = \hat{d}_i \cdot A_i$$

Average Density in the survey area:

$$\frac{\sum_i \hat{d}_i \cdot A_i}{\sum_k A_k} = \frac{\sum_i \sum_j D_{i,j}}{\sum_k n_k}$$

Expand the mean densities for a stratum to the observed haul densities and isolate re-scaled densities:

$$\sum_i \sum_j D_{i,j} = \frac{\sum_k n_k}{\sum_k A_k} \cdot \sum_i \left( A_i \cdot \frac{\sum_j d_{i,j}}{n_i} \right)$$

Solve for individual re-scaled density (the above formula is a simple rearrangement of this one):

$$D_{i,j} = \frac{\sum_k n_k}{\sum_k A_k} \cdot \left( A_i \cdot \frac{d_{i,j}}{n_i} \right)$$