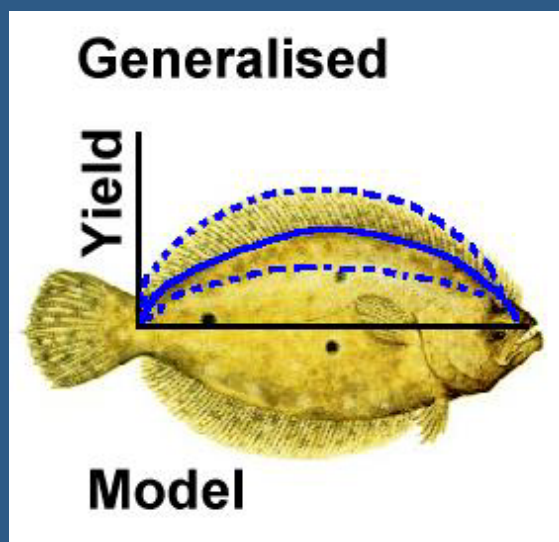# Generalised Yield Model (GYM)

Specifications
Parts 4 & 5

Version 5.01b

DEVELOPMENT & ACKNOWLEDGEMENTS

The GYM has been developed following input and advice from members of the Scientific Committee of CCAMLR and its working groups as well as from staff of the Australian Antarctic Division. Many thanks to all who have provided assistance.

VERSION INFORMATION

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User's Manual and Specifications

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GYM: a flexible tool for combining functions of recruitment, natural mortality, growth, maturity and fishing mortality to analyse and explore population scenarios based on historical and future harvest strategies.

Generalised Yield Model

User's Manual & Specifications

Australian Antarctic Division

CONTENTS

GLOSSARY OF TERMS

It is important to make note of the specific terminology used within the *GYM User's Manual and Specifications*. To facilitate its use, we have attempted to formulate consistent terminology for GYM based on the standard stock assessment and programming language.

Scenario	The folder that groups all of the input/output forms.
Test	The use of a catch, gamma or F value to run a set of simulation trials (example 1, 001).
Trial	The use of a single set of parameters following a setup routine that is then projected over the years of the trial which might include a pre-exploitation period, a period with a catch and/or recruitment history and a projection period.
Year	The projection of the stock over one split-year.
Increment	The time step within one year (it is possible to have as many as 365 time steps in one year).
Parameters	All the simulation and biological data needed to create the input files required by GYMxxx.exe.
Batch	A batch is a set of scenarios. Within a batch, each scenario is independent of the others. This is simply a convenience for running a number of scenarios without the need for user interaction.
Pointer	The visual graphic for the mouse position on the screen.

Part 4

SPECIFICATIONS FOR THE GENERALISED YIELD MODEL

PART 4
SPECIFICATIONS FOR THE GENERALISED YIELD MODEL

4.1   Introduction

The Generalised Yield Model (GYM) was first developed in 1995 (Constable & de la Mare 1996) as a generalised form of the Krill Yield Model (Butterworth et al 992, 1994) which was based on the method for evaluating yield by developed by Beddington & Cooke (1983). The first version incorporated options for assessing long-term annual yield according to catches set by a proportion of an estimate of pre-exploitation biomass (as in krill), a specified catch in the units of biomass and relative to the recruitment parameters (as in toothfish) or according to a constant fishing mortality (F). It also included the capacity to evaluate yield per recruit. The capability to incorporate other features has mostly evolved for use in assessments of long-term annual yield of Patagonian toothfish.

GYM Version 5.01b differs from earlier versions in 2 ways:

    i)   improved storage of output, population characteristics and presentation,

    ii)   new features to allow specifying the starting biomass and/or age structure of the population obtained from surveys during a year.

In addition, S-plus scripts have been developed to help with diagnostics. The GYM User's Manual, Specifications and Examples are also vastly improved.

These features now provide the flexibility to undertake a wide range of assessments on stocks, not just specific to CCAMLR. In CCAMLR, the latest version of GYM can be used on

    i)   Antarctic krill, for which a survey of abundance is used to undertake a precautionary assessment,

    ii)   Patagonian toothfish, for which recruitment surveys are used as the foundation for long-term assessments, and

    iii)   Mackerel icefish, for which surveys of biomass and age structure are used to undertake short term assessments.

These specifications for the Generalised Yield Model Version 5.01b detail the population model used in the projection program, the algorithm for evaluating yields and the requirements for inputting parameters into the model. It also details how different parts of the model can be manipulated to explore alternative functions.

The structure of the specifications begins with the formulation for projecting the stock over one year. The order of the remainder of the specifications is governed by the derivation of parameters used in the annual projection followed by details of how to control various kinds of scenarios.

Finally, some examples are presented to show how the GYM can be validated by the user. The input and output files for these examples are available.

4.2   The Population Model

The model is a cohort model, with the annual advance of each cohort (in numbers and biomass) being calculated by numerical integration over a one year period.   The model is initialised by setting up the number of fish in each age class at the start of the simulation period. The starting year is nominated in order to ensure that known information on recruitment, catch histories and other parameters can be correctly aligned in the projections if required.

Each age class is projected through one year by numerical integration of the basic population differential equations.   Catch and spawning stock is calculated for each age class during the projection. At the completion of a projection over a single year, the numbers surviving to the end of the period in each age class are assigned to the next highest age class and the lowest age class is assigned from a recruitment function (see *GYM Specification Example G01*; Figure GS1).   The process is repeated until the required time span is modelled, to produce a single realisation (trial) of a stock trajectory (Figure GS1).
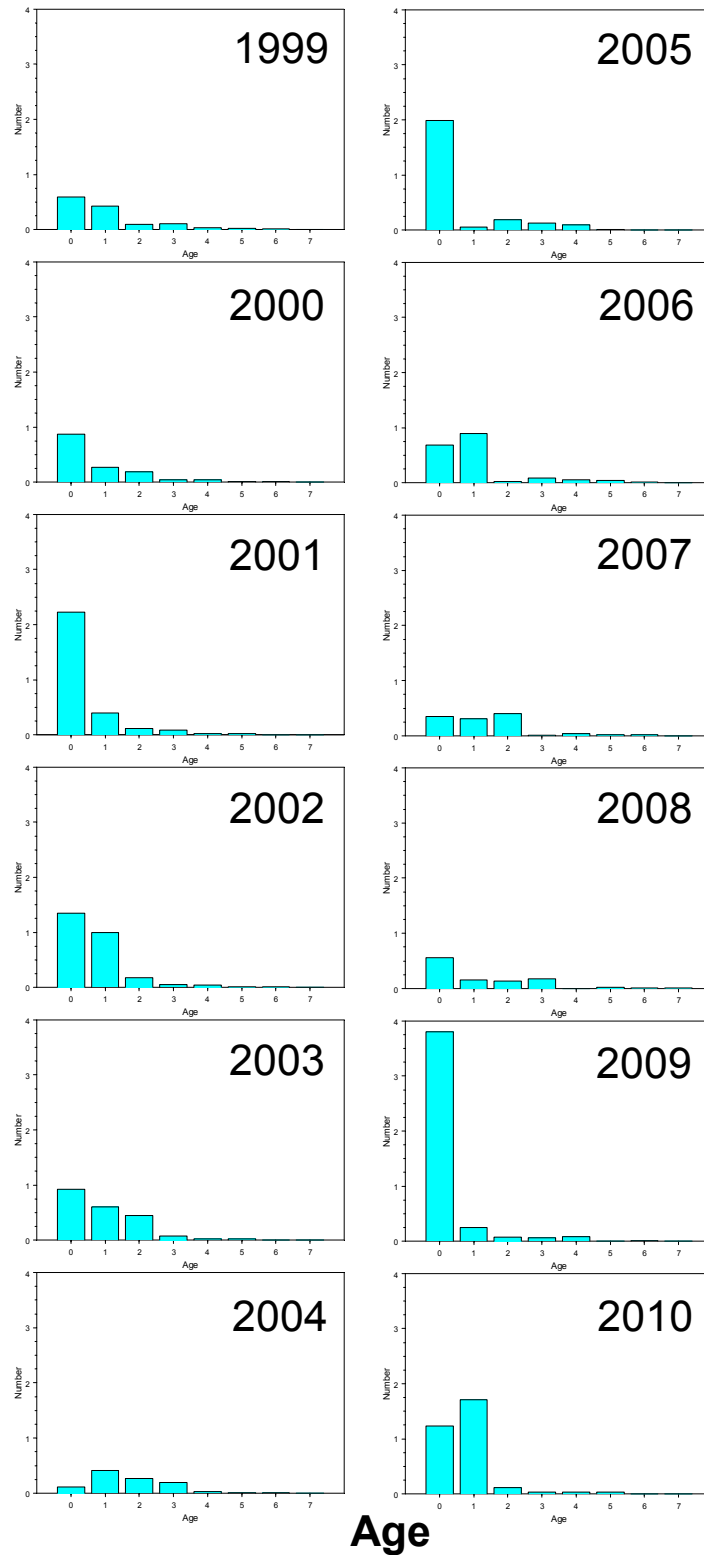
Figure GS1: Age structure of a population over 12 years from the initial year nominated as 1999. These are derived from the outputs from *GYM Specification Example G02* (M = 0.8, Ages 0-7 with no plus class).

4.3 Stock projection over one year

The core of the model surrounds the projection of the population over one year. The primary inputs for a year are the numbers in each age class and the catch rate, specified as a catch or as a fishing mortality rate. The other inputs include the coefficients for each of the differential equations below. The primary outputs are the numbers at age at the end of the year advanced to the next age and the catch (in numbers and biomass) taken during the year.

4.3.1 Projection using Differential Equations

The model is based on the usual differential equations which describe the rates of change in numbers and biomass in each age class and the accumulation of catch over one year.

The number in each age class satisfies the differential equation:

$$\frac{dN_{a,y}}{dt} = -\left(\mathrm{m}(a,t,y)M_y + \mathrm{f}(a,t,y)F_y \right) N_{a,y} \tag{1}$$

where $N_{a,y}$ is the number of fish in age class *a*, at time of year *t*, in year *y*. The terms $\mathrm{m}(a,t,y)M_y$ and $\mathrm{f}(a,t,y)F_y$ give the rates of natural mortality and fishing mortality respectively which apply to age class *a* at time of year, *t*, in year, *y*. These are illustrated in *GYM Specification Examples G02* (natural mortality) and *G03* (natural and fishing mortalities plus illustration of how the coefficients might be used to generate intra-annual and age-specific mortality functions).

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

$$\frac{dB_{a,y}}{dt} = \mathrm{w}(\tau)\frac{dN_{a,y}}{dt} + N_{a,y}\frac{d\,\mathrm{w}(\tau)}{dt} \tag{2}$$

where $\mathrm{w}(\tau)$ is a growth function which gives the average weight of fish of total age τ, where $\tau = a + t$, for fish of age *a* at time of year *t*. The growth function covers the entire lifespan of a cohort.

The yield from each age class satisfies the equation:

$$\frac{dY_{a,y}}{dt} = \mathrm{f}(a,t,y)F_y B_{a,y} \tag{3}$$

Numerical integration over one year

The yield from each class taken over one year is calculated by simultaneous numerical integration of equations (1), (2) and (3) using an adaptive Runge-Kutta procedure (Press *et al.*, 1992). The total yield is the sum of the yields from all age-classes.

Look-up Tables

In order to speed computation, the time dependent functions for natural mortality [$\mathrm{m}(\tau)$], weight at age [$\mathrm{w}(\tau)$], fishing mortality [$\mathrm{f}(a,t)$] and maturity [$\theta(a,t)$] (below) are calculated as vectors of discrete numeric values prior to numerical integration. This is done to avoid the estimation of the parameters at each time step or during the integration.

The discrete points are calculated at a series of fixed points with a constant interval. The interval can be selected to be sufficiently small to adequately approximate the required functional forms. The values of the functions at any instant are calculated by linear interpolation between the nearest points included in the vectors of discrete values. Thus, the functions are replaced by piecewise continuous linear approximations. In the case of functions which have fixed transition points (corners), the corners may be cut by the linear interpolation.

These vectors are stored in Lookup Tables. As discussed below, the lookup tables will be updated for each trial and for each known fishing year as required depending on how the different parameters change over time during a trial and how uncertainty in the parameters is evaluated between trials.

The lookup tables can be printed to a file during the setup phase of the program (see *GYM Specification Example G04*). However, these outputs only apply to the forward projection functions and will not include the length-based components of fishing selectivity or maturity as these may be varied between trials. The updates of these length-based components at the beginning of each trial and during a trial can be logged during the course of the simulations. The application of different functions during a trial, such as during the known fishing period, will need to be checked by examining the outputs on stock and cohort status for the relevant years (*GYM Specification Example G04* presents the workings for this process). Figure GS2 illustrates the lookup tables used in a trial (as calculated in *GYM Specification Example G04*).
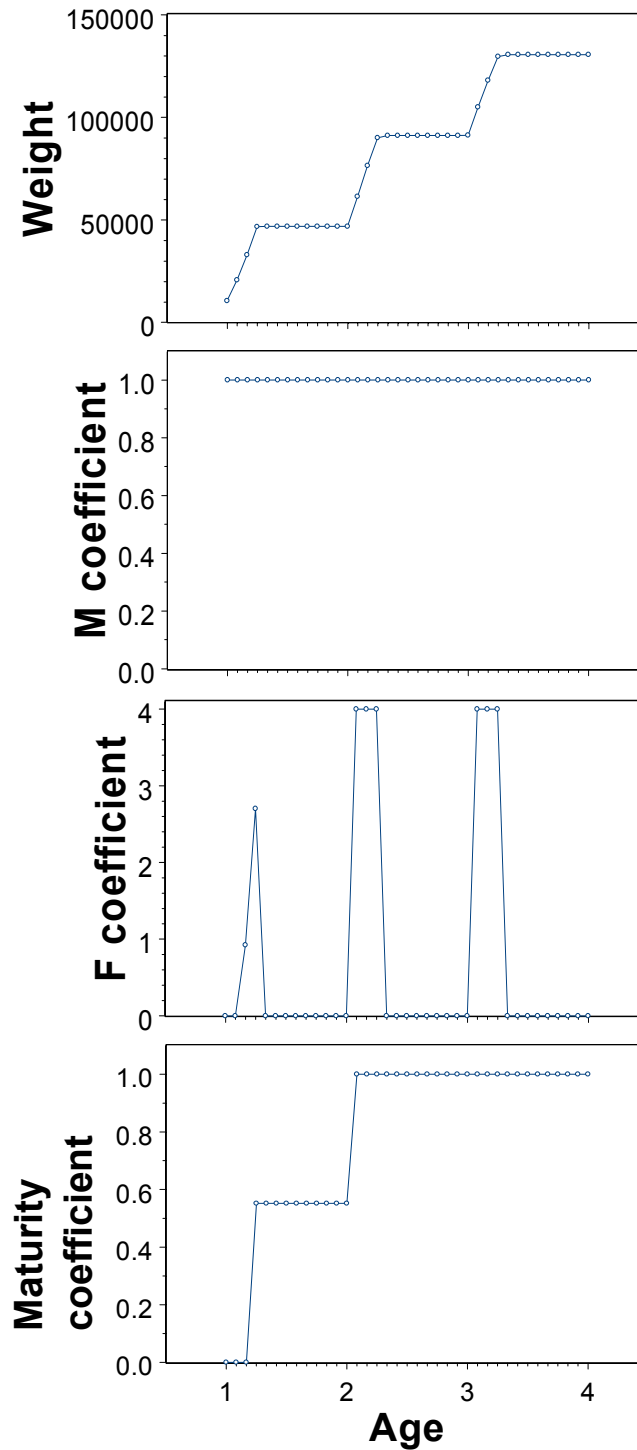
Figure GS2: Illustration of lookup tables, based on a krill assessment for the South Atlantic with 12 increments per year, the growth and fishing seasons restricted to summer (first 3 increments in each year). Derived from the outputs from *GYM Specification Example G04*. Plots restricted to Agest 1-4 for Year 2003 in Trial 1.

Interpolation within increments during the integration

During the integration, the adaptive Runge Kutta may seek values between increment values in the lookup table. As described above, a choice has been made to allow linear interpolation between

increment values in the lookup tables. This means that the results from the GYM may be slightly different from other yield calculations that expect constant values within an increment and a knife-edge change from one increment to another.   Such differences will be most evident if there is only one or a few increments in a year.

Extracting a specified catch in a year

If Catch>0 then F is solved using Newtons method encapsulated in ZBRENT (Press *et al*., 1992), which resolves the function FINDF (minimising the difference between the specified catch and the catch determined from a nominated F in the Runge-Kutta above), returning the mean annual fishing mortality that gives the designated catch.

Sometimes the stock may be sufficiently low that the catch may require a very large fishing mortality in order for the catch to be removed or, in fact, cannot be removed. In such cases, a maximum F is required to keep the simulation going. This maximum combined with a tolerance in the solution of F will influence the accuracy of the solution and the resulting catches observed in the output.

4.3.2 Recruitment

The age structure of the population is determined, in the first instance, through the addition of recruits at a given recruitment age. For some populations, observations of Age 0 fish will not be possible; in such cases, the first fully-observed age class may be some years older, say at Age 4. This reference age is used as the age at which the recruitment functions apply.

For a trial simulation, estimates of recruitment may or may not be available for a given year. When available, these estimates can be used in a trial. When they are not available, recruitment for that year will be drawn as required from a recruitment function nominated by the user.

Known Estimates of Recruitment

Estimates of recruitment for given years can be entered in two ways.

Vector of recruitments

The vector of recruitments is based on estimates, $\widehat{R}_y$, with their associated coefficients of variation, $CV_{\hat{R}_y}$, for given years. The values used in a trial, R_y, will be drawn from a log-normal distribution where

$$R_y = \widehat{R}_y . \exp(\eta - \frac{\sigma_{\hat{R}_y}^2}{2}) \tag{4}$$

where η is drawn randomly from $N(0; \sigma_{\hat{R}_y}^2)$, which is a normal distribution with zero mean and variance $\sigma_{\hat{R}_y}^2$ which is estimated from the CV by

$$\sigma_{\hat{R}_y}^2 = \sqrt{\ln(1 + CV_{\hat{R}_y}{}^2)} \tag{5}$$

Estimated Numbers at Age from Surveys

Most instances for known recruitments will arise from estimates of abundance of different age classes from one or a number of surveys. In order to convert these to estimates of abundance for a recruitment age in a given year, the estimates from the survey will need to be projected backwards or forwards in time to the required recruitment age. This is done by using an estimate of natural mortality to adjust the numbers at age to the appropriate recruitment age. For example, the abundance of age 2 fish from a survey could be adjusted to numbers of recruits at age 4 by removing the numbers that would have died over two years of natural mortality. Thus, such projections will depend upon the estimate of natural mortality.

Given the potential for natural mortality to be varied in these simulations between trials, years and periods within years, then a better method than estimating recruitments from surveys prior to the running of the GYM is to provide the survey information as input data and for these calculations to be made following the determination of natural mortality for a given trial. This will ensure that the time-series of recruitments in a trial is consistent with the estimates of natural mortality being applied in that trial.

The input data and calculations are based on the results arising from a method (mixture analysis) for assessing the abundance of individual cohorts from a length-density distribution derived from a survey described by de la Mare (1994) and included in the software (CMIX) (see de la Mare et al. 2002). The outputs of this analysis are:

  i) Estimates of numerical density of each age class in a survey/observation ($D_{o,a}$)

  ii) Standard errors of the density estimates ($\sigma_{D_{o,a}}$)

  iii) Estimate of total survey area (sA_o)

  iv) Observed mean density of fish for the survey area ($\bar{D}_o$)

  v) Estimated mean density of fish for the survey area ($\bar{D}'_o$)

The estimated mean density arises from the sum of the densities estimated for each age class from the estimation procedure, while the observed mean density arises from the mean density of fish observed in the surveys. The numerical abundance at age in a survey, $N_{o,a}$, and its standard error, $\sigma_{N_{o,a}}$, are estimated by

$$N_{o,a} = c_o D_{o,a}$$

$$\sigma_{N_{o,a}} = c_o \sigma_{D_{o,a}} \tag{6}$$

$$where \quad c_o = sA_o \frac{\bar{D}_o}{\bar{D}'_o}$$

If different procedures are used to give numerical abundances then the estimates of density could be equivalent to total abundance of each age class while the survey area and observed and estimated mean densities would all equal 1.0.

A time series of recruitments can be estimated from a number of surveys such that multiple observations of a cohort can be combined using an inverse variance weighting of each observation following projection to the recruitment age (SC-CAMLR, 1995, Report of the Working Group on Fish Stock Assessment), such that an estimate of recruitment strength in a given year (R_y) for a cohort of a given age is given by

$$R_y = e^{\dfrac{\sum\limits_{o}\left[\left(\ln(\bar{N}_o) - M\left[a_r - (a_o + t_o)\right]\right)\left(\dfrac{\bar{N}_o}{\sigma_{\bar{N}_o}}\right)^2\right]}{\sum\limits_{o}\left(\dfrac{\bar{N}_o}{\sigma_{\bar{N}_o}}\right)^2}} \tag{7}$$

where o is a given observation from a survey, $\bar{N}_o$ is the estimated abundance and $\sigma_{\bar{N}_o}$ is its standard error, a_r is the designated age of recruitment, 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.

Recruitment Functions for when recruitment is unknown

There are currently three functions for determining recruitment in years when no estimates are available:

1. numbers of recruits are drawn randomly with replacement from a vector of recruitment estimates;

2. numbers of recruits are independently and identically distributed according to a lognormal distribution, with a possibility of recruitment being dependent on the status of the spawning biomass below a specified level; and

3. proportions of recruits are independently and identically distributed according to a beta distribution, with a possibility of recruitment being dependent on the status of the spawning biomass below a specified level (de la Mare, 1994).

Bootstrap from a vector of recruits

In this case, recruitment for each year is determined using a bootstrap procedure where the numbers of recruits are drawn randomly with replacement from a vector of recruitment estimates. This routine can also use the CV of each estimate in finding the value to be used in a given year if using the CVs is set to True. This assumes log-normally distributed residuals.

Log-normal recruitment function

In the lognormal case, recruitment (R_y) is drawn each year at random from a log-normal distribution based on a specified mean, $\bar{R}$, and coefficient of variation, $CV_{\bar{R}}$, such that

$$R_y = \bar{R}.\exp(\eta - \frac{\sigma_R^2}{2}) \tag{8}$$

where η is drawn randomly from $N(0;\sigma_R^2)$, which is a normal distribution with zero mean and variance σ_R^2, which is estimated from $CV_{\bar{R}}$ by

$$\sigma_{\bar{R}}^2 = \ln(1 + CV_{\bar{R}}^2) \tag{9}$$

These parameters can be adjusted to give a mean recruitment of 1.0 and variation greater than or equal to zero.

Uncertainty

Parameters of the log-normal recruitment function can be varied between trials in two ways, taking account of uncertainty in these estimates.

The first method is by specifying a range in the coefficient of variation for situations when recruitment variability is not well estimated. A value for the coefficient of variation for a trial is then randomly drawn from a uniform distribution between the minimum and maximum values of the CV.

Alternatively, when the mean recruitment and its CV are estimated, uncertainty in the estimates of recruitment can be incorporated in the $\log_e$ domain where the parameters for the log-normal function are determined from both equation (9) and

$$\mu_{\bar{R}} = \ln(\bar{R}) - \frac{\sigma_{\bar{R}}^{2}}{2}$$

$$SE = \frac{\sigma_{\bar{R}}}{\sqrt{n}}$$

(10)

Values for μ in a trial are then drawn randomly from $N(\mu_{\bar{R}}; SE)$, which is a normal distribution with mean $\mu_{\bar{R}}$ and variance *SE.*

Proportional recruitment function

For a number of populations, the abundance of recruits may be difficult to determine. However, the proportion of the population comprising newly recruited individuals might be readily estimated. de la Mare (1994) presents a method for modelling krill recruitment, such that the proportion of recruits are independently and identically distributed according to a beta distribution.

This method assumes that recruitment is independent of stock size over the range of interest, the recruitment is a random variable with constant mean and variance (estimated above as $\bar{R}$ and $CV_{\bar{R}}$), that is the recruitments over a series of years are independent, identically distributed random variables. If we can only estimate the proportion of recruits over time rather than the actual number of recruits then we need a method to convert the parameters we can estimate, the mean and variance in the proportion of recruits, into random numbers of recruits, which in simulations will reproduce the observed mean and variance in the proportion of recruits.

Summary extracts of the development of this approach are provided here but the full derivation should be consulted in de la Mare (1994).

The proportion of recruits, $p_R(t)$, is the ratio of numbers in age class *t*, to the numbers in that age class and above, that is:

$$p_R(t) = \frac{A_t}{\sum_{i=t}^{n} A_i}$$

(11)

where A_i is the number of animals in age class *i*, and *n* is the age of the oldest age class present in non-negligible numbers in the population. This can also be written:

$$p_R(t) = \frac{A_t}{A_t + \sum\limits_{i=t+1}^{n} A_i}$$

(12)

where A_t is the number of recruits in the population.

For a given year, random proportions of recruits need to be drawn from a distribution with mean proportion equal to the observed mean, $\overline{p}_R(t)$, and the variance, $V\left[p_R(t)^*\right]$, calculated according to equation (21) below. Since the proportion of recruits is bounded 0 - 1, a beta distribution would be appropriate for generating these random values.

Estimating recruitments from the mean proportional recruitment and its variance

The following steps are undertaken to generate a series of random recruitments for the observed mean proportion and its variance.

1. Estimating natural mortality from mean proportional recruitment

For a given mean proportional recruitment, the natural mortality rate must be such that the population declines to negligible levels by the nth age class (see equation (12)). In an unexploited population which is on average in equilibrium, the proportion of recruits is a function of S, the survival rate from one age class to the next, which is given by:

$$S = e^{-M}$$

(13)

If M is assumed independent of age up to age n, and infinite thereafter, then in an equilibrium population $p_R(t)$ is:

$$\tilde{p}_R(t) = \frac{1}{\sum\limits_{i=t}^{n} S^{i-t}}$$

(14)

S can be found as the root of the function:

$$f\left[S, \tilde{p}_R(t)\right] = \frac{1 - S^{n+1}}{1 - S} - \frac{1}{\tilde{p}_R(t)}$$

(15)

which is solved using Newton's method, using:

$$f'\left[S, \tilde{p}_R(t)\right] = \frac{1 - S^{n+1}}{(1-S)^2} - \frac{(n+1)S^n}{1 - S}$$

(16)

A starting guess for the iteration should be S → 1.

For the krill example developed by de la Mare (1994), simulation tests showed that the value of survivorship calculated using the average value $\overline{p}_R(t)$ from net haul surveys as the value for estimating survivorship was slightly too high (because $\overline{p}_R(t)$ is a random variable). A less biased average value for the simulated $p_R(t)$ is obtained when the value for S is calculated using $\overline{p}_R(t) + V(p_R(t))$ in place of $\tilde{p}_R(t)$ in equations (15) and (16). *This adjustment is used in the current version of the GYM.*

Note that this formulation does not provide for age-specific variation in mortality. Thus, age-specific variation in M should not be included in the input parameters at this stage.

2. Correcting the variance in $p_R(t)$ for the effects of variability in the population size

Although we can use the average value of $p_R(t)$ for generating random values of recruitment, we are not able to use directly the observed variance estimate of $p_R(t)$ from independent samples to generate the random values. This is because the variance of $p_R(t)$ includes a component of variation due to the cumulative effects of variability in recruitment in every age class. If we put:

$$T = \sum_{i=t+1}^{n} S^{i-t}$$
(17)

then equation (14) can be written as:

$$\tilde{p}_R(t) = \frac{1}{1+T}$$
(18)

from which it follows that:

$$\left(\frac{\tilde{p}_R(t)}{1 - \tilde{p}_R(t)} \right) \overline{A}_t T = \overline{A}_t$$
(19)

where $\overline{A}_t$ is the average number of recruits to be produced by the model. If $\tilde{p}_R(t)$ is replaced by a random observation with the appropriate properties, it follows that the random recruitment A_t is given by:

$$A_t = \left(\frac{p_R(t)}{1 - p_R(t)} \right) \overline{A}_t T$$
(20)

Clearly, even though $p_R(t)$ can only take values in the range 0 - 1, A_t can have a large positive value as $p_R(t) \to 1$.

The variance needed in generating random $p_R(t)$ values by means of equation (20) is that which would apply when there is no variation in the total population older than the recruiting age class. This variance is determined using the delta method approximation for the variance of a function of random variables (de la Mare 1994) which gives:

$$V\left[p_R(t)^*\right] = \frac{V\left[p_R(t)\right]T^2}{T^2 + \sum_{i=1}^{n} S^{2i}} \qquad (21)$$

3. Estimating the parameters of the Beta Distribution

A beta random variable has a probability density between 0 and 1. The parameters of the beta distribution, *a* and *b*, are derived from the mean proportion, $\overline{p}_R(t)$, and its adjusted variance, $V\left[p_R(t)^*\right]$. For the beta distribution of proportional recruitment the parameters are estimated by

$$a = \frac{1 - \overline{p}_R(t)}{k^2} - \overline{p}_R(t)$$

$$where \quad k = \frac{\sqrt{V\left[p_R(t)^*\right]}}{\overline{p}_R(t)} \qquad (22)$$

$$b = a\left(\frac{1}{\overline{p}_R(t)} - 1\right)$$

4. Drawing a random recruitment and correcting for the bias in the mean number of recruits

Because the number of recruits given by equation (20) has a random variable in the denominator, the mean of the distribution of recruitments will be biased. The delta method and subsequent simulation tests were used by de la Mare (1994) to determine a bias correction factor, *B*, in equation (20) such that recruitment in a year is estimated as

$$A_t = \left(\frac{p_R(t)}{1 - p_R(t)} - B\right)\overline{A}_t T \qquad (23)$$

where

$$B = V\left[p_R(t)^*\right]\left(\frac{1}{\left(1 - \overline{p}_R(t)\right)^3}\right)\overline{p}_R(t) \qquad (24)$$

and $p_R(t)$ is drawn from the beta distribution.

Notes for use of the GYM: If recruitment is estimated to be less than zero in this procedure then the random variate is redrawn. The number of such events in a test are printed to the log file and the summary results file. They should occur only rarely.

de la Mare (1994) noted that this still appears to be slightly biased, and further tinkering could reduce the bias further. However, bias correction is not necessary if the population model is used in a way which involves scaling results to the mean unexploited population size, and the model is run for *n* years without exploitation prior to calculating the mean unexploited population size. By that time the slight bias in recruitment will have worked its way through all the age classes.

He also noted that simulation trials showed that this method satisfactorily converted the observed parameters on proportional recruitment into numerical recruitments with the required properties.

Since the original formulation of equation (24), the krill model was modified and equation (24) was revised to be

$$B = V\left[p_R(t)^* \right] \left(\frac{1}{\left(1 - \bar{p}_R(t)\right)^2} + \frac{\bar{p}_R(t)}{\left(1 - \bar{p}_R(t)\right)^3} \right) \bar{p}_R(t) \tag{25}$$

In addition, the use of the random recruitments in the initial population structure means that there is no need to project the population for a number of years until the initial population size is estimated.

Accounting for uncertainty in the estimates of the proportional recruitment distribution

Uncertainty in the estimates of the mean and variance of proportional recruitment is incorporated into the simulations by drawing these from appropriate statistical distributions at the beginning of each trial and then recalculating the parameters above.

The variance of proportional recruitment, $V\left[p_R(t) \right]$, can be approximated by a χ^2 distribution with N-1 degrees of freedom, where N is the number of observations used in estimating the proportional recruitment distribution parameters. Thus, prior to starting each trial, a new $V\left[p_R(t) \right]$ is generated by:

$$V\left[p_R(t) \right] = \frac{\Gamma\left(N-1, 2(N-1)\right) V_{obs}\left(p_R(t)\right)}{N-1} \tag{26}$$

where $\Gamma(x,y)$ denotes a random deviate from a gamma distribution with mean x and variance y. If this is chosen first, the value for the average value of $p_R(t)$ for that trial can be drawn from a normal distribution:

$$\bar{p}_R(t) = N\left[\bar{p}_R(t)_{(obs)}, V\left[p_R(t) \right] \right] \tag{27}$$

where $N[\mu, \sigma^2]$ denotes a random deviate from a normal distribution with mean μ and variance σ^2. Given that the distribution of $p_R(t)$ is bounded 0 - 1 and reasonably bell shaped, the sampling distribution of $\bar{p}_R(t)$ should approach a normal distribution for a relatively small sample size. It is unlikely that random values of $\bar{p}_R(t)$ will fall outside the range 0 - 1, and it should not introduce much bias if these are rare, and the normal distribution truncated at the feasible range.

The model for recruitment variability provided by de la Mare (1994) is expected to result in a family of recruitment distributions which is consistent with the data used in estimating the observed mean and variance in proportional recruitment. This family of distributions will converge on the true recruitment function as the number of observations, $N \to \infty$, provided of course the assumption holds that $p_R(t)$ has a beta distribution.

Input parameters and important steps in the application of this method

The parameters required for input are:

i)   mean recruitment at age ($\overline{A}_t$)

ii)   Mean proportional recruitment

iii)   Standard deviation of proportional recruitment

iv)   Age class in which the recruits enter

v)   Number of observations of proportional recruitment

Important steps in the configuration of a trial:

i)   This method can only be applied correctly if the age structure has no plus class. It is important to have enough age classes so that the last age class will have negligible fish in it and that the natural mortality rate is plausible.

ii)   take note of the number of 'fixes' that arise, which result from the random proportional recruitment is outside the range of 0 to 1. If this is a substantial number relative to the number of trials then the results may not be reliable.

Recruitment Time Series in Projections

A time series of recruitments in a projection is built as a combination of the known time-series (either as the vector of recruitments or from surveys) and, in years when the recruitment is not known, the recruitment functions (log-normal, bootstrap from a vector, proportional recruitment). The recruitment functions are the sole means for projecting into the future.

Currently, the known recruitment period is modelled as part of the known catch period, irrespective of whether the recruitment series is longer or shorter than the catch period. In order to achieve this successfully, zero catches should either be placed in years when no catch was taken but recruitment is estimated directly or such years will be filled automatically.

During the forward projection, recruitment is set at the beginning of the year and can be based on the status of the spawning stock in the previous year – the stock-recruitment relationship.

Stock-Recruitment Relationship

A simple stock-recruitment function can be applied during the time series for both the log-normal and proportional recruitment functions. This is applied after the recruitment has been determined from the appropriate function, R, and then, based on the status of the spawning stock in the previous year (B_s, see below), is adjusted such that the adjusted recruitment is

$$R^*(R, B_s, B_{crit}) = \begin{vmatrix} R\dfrac{B_s}{B_{crit}} & ;if(B_s < B_{crit}) \\ R & ;if(B_s \geq B_{crit}) \end{vmatrix} \tag{28}$$

where B_{crit} is the critical status of the spawning stock, say 0.2 of the median pre-exploitation spawning biomass, $\hat{S}_0$ (see below), below which the recruitment is adjusted proportionally.

Example time series of recruitments

Examples:

1. Surveys (with and without uncertainty)

2. Bootstrap Vector (with and without uncertainty)

3. Log-normal (with and without uncertainty)

4. Proportional recruitment (with and without uncertainty)

5. Effect of stock recruitment relationship

Yield per Recruit

Yield per recruit is a special case built into the GYM. It requires that the mean recruitment is equal to 1.0. Projections are only for one year. This could be set up by constraining the relevant parameters or the function selected and the parameters will be constrained automatically.

Examples:

i)   Yield per recruit function selected

ii)   Yield per recruit undertaken by constraining relevant parameters

4.3.3 Size at Age

Size at age is currently modelled using a length at age function combined with a length to weight conversion.

Two methods can be used to generate a length at age vector

1. von Bertalanffy growth curve

2. user-defined array of age and length

The conversion from length, *L*, to weight, *W*, follows the usual formulation of

$$W = aL^b \tag{29}$$

where *a* and *b* are input parameters.

Curently, there are no provisions for incorporating uncertainties in the growth and length parameters. Sensitivity to incorrect estimates or variability in growth need to be done using different simulation tests.

von Bertalanffy growth functions

The von Bertalanffy growth function is specified in a single formulation, which provides for all annual growth occurring within a fraction of the year based on the method for Antarctic krill specified by Rosenberg *et al.* (1986), such that the length, *L*, for fish age *a* at time, *t,* during the year is

$$L(a,t) = \begin{vmatrix} L_\infty \left(1-e^{-K(a-t_0)}\right) & ; if\ t < g_0 \\ L_\infty \left(1-e^{-K\left(a+\frac{t-g_0}{g_1-g_0}-t_0\right)}\right) & ; if\ g_0 \le t \le g_1 \\ L_\infty \left(1-e^{-K(a+1-t_0)}\right) & ; if\ t > g_1 \end{vmatrix} \tag{30}$$

where L_∞ is the asymptotic length, *K* is the growth rate, t_0 is the appropriate time adjustment for having a length at age 0, g_0 is the fraction of the year prior to the growth period and g_1 is the fraction of the year including the initial period without growing plus the growth period.

Note: the application of this formula in the GYM is in the determination of the lookup tables. In that respect, t *in the formula is determined as the (increment/number of increments in the year).*

Examples:

   i)   von Bertalanffy growth curve with growth over the whole year

   ii)   the same von Bertalanffy growth curve but with growth only during a fraction of the year

The length at age relationship needs to be standardised to the nominated first day of the year, which may not be the first of January or the date referenced by t_0 in a von Bertalanffy function. The reference date for t_0 can be input into the set of parameters and the value of t_0 will be adjusted, t_0' , so that the fish length at time 0 will coincide correctly with the first day of the year such that

$$t_0' = t_0 - \left(f_{start} - f_{vB}\right) \tag{31}$$

where f_{start} is the fraction of the year from 1 January to the start date of a projection year and f_{vB} is the fraction of the year from 1 January to the reference date for t_0.

Length at age vector

In the user-defined array, the age can be input with fractions of the year. In this way, the pattern of growth within a year can be described even though it may not be a smooth function. The program does not need to have every value of length at age for each increment in a year. It assumes linear growth occurs between two consecutive points and will automatically interpolate between these to determine the appropriate values for the increments in each year in the life of the fish. If no growth over a period is to occur then two consecutive points of age (at the boundaries of the period in which no growth occurs) should have the same length.

Examples:

   i)   user defined length at age vector with interpolation showing the potential for including

          negative growth

4.3.4 Natural Mortality

M is the average rate of natural mortality over the life of a cohort and $\mathrm{m}(\tau)$ is a function which gives the ratio between the natural mortality rate for fish of total age $\tau = a + t$ to the average value over the lifetime of a cohort. This requires that:

$$\frac{\int_0^T \mathrm{m}(\tau)\,d\tau}{T} = 1 \tag{32}$$

Partitioning the natural mortality into an overall average level, which can be modified by relative patterns against age and time of year, is a convenient method for incorporating Monte-Carlo integration over the effects of uncertainty in natural mortality rates into the assessments. This is because only the average value needs to be modified for each trial/projection. The ability to specify a relative pattern allows sensitivity analyses on age-specific and seasonal effects on natural mortality to be readily investigated.

Coefficients are entered as age-specific mortality and as a function for the time of the year. In the latter case, it is assumed that all ages have the same time-specific variation in natural mortality through the year.

> *Uncertainty*

Uncertainty in the annual average rate of natural mortality can be incorporated by drawing a value at random from a uniform distribution over specified ranges at the beginning of each trial.

M will automatically vary each trial with use of the proportional recruitment function. *It is not recommended that age-specific variation in mortality rate be applied at this stage when the proportional recruitment function is being used. This is in the process of being incorporated.*

Random variation around the mean annual natural mortality rate, $\bar{M}$, can be included for each year in a trial according to a log-normal distribution if the coefficient of variation, $CV_{\bar{M}}$, is greater than 0. An additional feature (since 1997) is to allow for stochastic high mortality events as described by Agnew *et al.* (1998). This is achieved by nominating the proportion by which the mean annual natural mortality will be increased (a multiplier - m_{high}) and the probability of this occurring in a given year, m_{high}. Thus, random variation between years can follow a log-normal function such that

$$M_y = \bar{M} . \exp\left(\eta - \frac{\sigma_M^2}{2}\right) \begin{vmatrix} m_{high} & U(0,1) \le p_{m_{high}} \\ 1 & U(0,1) > p_{m_{high}} \end{vmatrix} \quad ; \eta \text{ from } N(0, \sigma_M^2) \tag{33}$$

where η is drawn randomly from $N(0; \sigma_M^2)$, which is a normal distribution with zero mean and variance σ_M^2, which is estimated from $CV_{\bar{M}}$ as for equation (9).

The application of interannual variation in M is an important consideration in the development of the initial age structure (see below). The inclusion of annual variation in *M* does not affect the age-specific or season-specific variation in *M*. There is no provision for uncertainty in the seasonal and age-specific trends in natural mortality. Thus, the lookup tables generated in the Setup routine are not altered during the simulation trials.

4.3.5 Harvest Strategy

Fishing Mortality

F_y in equation (1) is the average fishing mortality over all age classes in year y and $\mathrm{f}(a,t)$ is a function which gives the relative distribution of the fishing mortality of age class *a* and at the time of year *t*. This is partitioned to facilitate the numerical solution for fishing mortality in each year so that only the single parameter F_y needs to be evaluated.

The age and season specific multipliers allow for a number of different effects to be combined, including the effects of age and size specific selectivity, and the effects of the seasonality in fishing. Specifically, $\mathrm{f}(a,t)$ is derived from three functions: a size-selectivity function, s(*a,t*) (the usual modification to *F* arising from gear selectivity, which is re-expressed as an age selection function, which depends on *t* because of growth during the year), an age-selectivity function, $\alpha(a)$ (allows for a fishery that targets specific age classes due to, for example, geographic or depth stratification of the stock according to age), and variation in fishing effort through the year, $\varepsilon(t)$ (e.g. open and closed seasons or relative fishing effort at different times based on the number of vessels). Thus:

$$\mathrm{f}(a,t) = \mathrm{s}(a,t)\alpha(a)\varepsilon(t) \tag{34}$$

The size-selectivity function currently used in the computer program for the model is based on length as described in Butterworth *et al*. (1994) where:

$$\mathrm{s}(a,t) = \begin{cases} 0 & ; \quad \lambda(a+t) < l_1 \\ \left(\lambda(a+t) - l_1\right)/\left(l_2 - l_1\right) & ; \quad l_1 \leq \lambda(a,t) \leq l_2 \\ 1 & ; \quad \lambda(a,t) > l_2 \end{cases} \tag{35}$$

where $\lambda(\tau)$ is a function (growth curve) which gives the mean length of fish at age $\tau = a + t$, l_1 and l_2 are constants which specify the range over which selection changes from 0 to 1. However, alternative functional forms can be readily incorporated in the program.

The program input parameters, l_1 and l_2 are specified from their midpoint and range, that is:

$$\begin{aligned} l_1 &= l_{\mathrm{m}} - \frac{l_{\mathrm{r}}}{2} \\ l_2 &= l_{\mathrm{m}} + \frac{l_{\mathrm{r}}}{2} \end{aligned} \tag{36}$$

where l_{m} and l_{r} are the midpoint and range of l_1 and l_2 respectively.

Notes for use of the GYM:

1. *the first date in the vector of relative fishing effort should correspond to the reference start (birth) date of the year.*

2. *each level of effort should have a specified period with a first date and a last date, except for the last period which only requires a first date followed by the end of data date given by -1.*

3. *the program determines the level of fishing effort in each increment of the year according to the dates given above. If the boundary dates fall in the middle of a program increment then the fishing effort given for that increment is the average effort across the increment.*

4. *the values in the lookup tables generated during the setup phase of the program are solely related to the age-based function for the future projection period. The length-based function has provision for variation from one trial to another and can be varied from one year to another in the catch series. Consequently, the lookup tables for the Runge-Kutta are completed for fishing mortality after these parameters are established prior to each year of the catch series and prior to the future projection.*

5. *The fishing selectivity and vulnerability for the forward projection are entered first followed by the details for the catch series.*

Known catch history

In each year of a catch history, the weight of catch taken along with all of the parameters detailed above can be varied. It is possible to retain the same parameters from one year to the next without inputting all the data. Similarly, years when the catch was zero do not need to be entered.

In the first year and subsequent consecutive years of the known fishery, it is possible not to specify fishing vulnerability and use that specified for the forward projection as the default. However, it is advisable to include the selectivity and vulnerability details in the first year of a catch history in order to avoid inadvertent errors in the application of the forward projection parameters early in the catch history.

The length of the period "Known catch history" is determined by combining the years in which catches have been taken with the years of known recruitments. This may result in a number of years in which no catches are taken. This procedure is undertaken within the GYM.

Mixed-gear fisheries

A new version is currently being developed that will provide for mixed gear fisheries. The structure of this can be observed in the user interface form.

Uncertainties in fishing vulnerability

Uncertainties in fishing vulnerability can only be included as a length based function. The sizes at which 50% of fish are recruited to the fishery, l_m, can be used to allow for such uncertainty by drawing these at random from uniform distributions, each with a specified range. This can occur for each year of the catch history as well as just prior to the forward projection (as described above).

Forward Projection: Harvest Strategy to be Evaluated

The forward projection extends from the current time to the end of the projection period shown in Fig. 1. In a single test, the model can project the stock forward under three different options: (i) a constant catch set as a specified proportion (γ) of an estimate of the pre-exploitation stock (B_0); (ii) a constant specified catch; or (iii) a constant fishing mortality, for example $F_{0.1}$.

These are described in more detail under Types of Tests considered in the General characteristics of Tests/Scenarios.

4.4   Characteristics of a Trial

4.4.1 Initial Population Structure

General Age Structure

The age structure of the population can have a recruitment age greater than or equal to 0 and a plus class if required. Recruitment occurs in the first age class identified.

The Last Age Class is the last age or plus class to be used in the projections. A plus class is initiated by having the oldest age greater than the last age.

Initial Age Structure

The initial age structure for a trial can be determined in three ways:

i)   Deterministic age structure

ii)   Age structure drawn from random recruitments

iii)   Nominated age-structure

The age structure can then be scaled to an initial biomass if required.

Deterministic age structure

A deterministic age structure maintains comparability with the original krill yield model outlined by Butterworth *et al*. (1994). Each successive age class is the product of the median value of the specified recruitment function, $\hat{R}$ (in the case of Butterworth *et al*. 1994, this was equal to 1.0 at age 0) and the survivorship, $e^{-\ddot{M}_r^a}$, from recruitment age, *r*, to the current age, *a*, (detailed further below) such that the number at age *a* is:

$$N_a = \hat{R}e^{-\ddot{M}_r^a} \tag{37}$$

In order to remove the influence of the initial deterministic age structure on the estimation of stock status in the early years of a trial, it is recommended that this age structure be projected for a number of years prior to the first nominated year of the trial. The number of years is recommended to be equivalent to at least one generation, i.e. the number of age classes in the stock, with recruitment varying from year to year as specified in the recruitment function.

Note that the stock should be projected for at least one year prior to the trial projection in order to estimate the biomass prior to any exploitation if the initial biomass is not set (see below).

Age structure drawn from random recruitments

An age structure drawn from random recruitments as specified by the recruitment functions above introduces recruitment variability into the formulation of the initial age structure, eliminating the need to project the stock forward one generation. In this formulation, each age class is assigned a different number of recruits, *R*, at recruitment age. The numbers at age are determined using equation (37) by replacing $\hat{R}$ with *R*.

Note that the stock should be projected for at least one year prior to the trial projection in order to estimate the biomass prior to any exploitation.

Handling a Plus Class

A plus class is a sum to infinity of numbers at each age greater than or equal to the last age-class in the simulated stock. In a deterministic case with no variation in the annual mortality rate, the plus class would be determined as

$$N_{a^+} = \frac{\hat{R}e^{-\bar{M}\left(a^+ - a_r\right)}}{1 - e^{-M}} \qquad (38)$$

where a^+ is the age at which the plus class accumulates and a_r is the age of recruitment.

However, variation in recruitment and/or the annual rate of natural mortality can lead to this formulation being biased, which will be particularly important if the plus class is a non-trivial proportion of the stock. The bias can be reduced by including a large number of ages in which interannual variability in recruitment and mortality can be applied. This is achieved by increasing the Oldest Age of fish, a_o, in the Plus Class, a^+, to which such variability applies until the bias is reduced satisfactorily, such that the plus class is

$$N_{a^+} = \sum_{c=a^+}^{a_o} Re^{-\breve{M}_r^c} + \frac{\hat{R}e^{-\bar{M}\left(a_o - a^+ + 1\right)}}{1 - e^{-M}} \qquad (39)$$

The bias can be checked by examining whether the median spawning stock escapement (see below) departs appreciably from 1 for a test in which there is no catch. i.e. the stock should remain stable (note that a departure from 1.0 can also be observed because of stochastic variability if the number of replicate trials is insufficient to account for variability in some of the input parameters - see below).

Note that the consequence of adding more years in the plus class is to slow down the computation of median pre-exploitation spawning biomass

Handling variability in Natural Mortality in the initial age structure

Interannual variability in natural mortality requires that mortality for a given year is applied consistently across all age classes that are extant in that year. This can be visualised in the following table showing an example of years in which cohorts are extant relative to the other cohorts in a simulation:

					Age				
Year	**0**	**1**	**2** **r**	**3**	**4**	**5**	**6**	**7**	**8** **o**
2000									X
2001								X	X
2002							X	X	X
2003						X	X	X	X
2004					X	X	X	X	X
2005				X	X	X	X	X	X
2006			X	X	X	X	X	X	X
2007									
2008									

Consequently, the vector of $\ddot{M}_r^a$ is constructed for each age class, *a*, as

$$\ddot{M}_r^a = \begin{vmatrix} \sum_{c=r}^{a} M_{y=(o-1-c)} \int_0^1 \mathrm{m}(c,\tau)\,d\tau & ; a > r \\ 0 & ; a = r \end{vmatrix} \tag{40}$$

where *o* is the oldest age class and the vector of M_y is drawn according to the variability functions above. Similarly, fishing mortality can be added to this calculation such that the total mortality, $\ddot{Z}_r^a$, replaces $\ddot{M}_r^a$ in the equations above and

$$\ddot{Z}_r^a = \begin{vmatrix} \sum_{c=r}^{a} M_{y=(o-1-c)} \int_0^1 \mathrm{m}(c,\tau)\,d\tau + \sum_{c=r}^{a} F_{y=(o-1-c)} \int_0^1 f(c,\tau)\,d\tau & ; a > r \\ 0 & ; a = r \end{vmatrix} \tag{41}$$

Nominated Age Structure

The initial age structure can be provided in place of using either of the above options. In this case, the numbers at age are drawn from a log-normal distribution given the respective mean and standard errors provided for each age.

Scaling the Age Structure to an Initial Total Biomass

An option to initiate each trial from a specified total biomass is available (including all fish from the age at recruitment to the plus class). Uncertainty can be incorporated such that a total biomass is sampled from a log-normal distribution with a specified mean and CV at the beginning of each trial. This is then applied in the nominated year.

A number of features have been included to take account of

i)   the initial total biomass estimate being obtained at a time during the year rather than on the reference start date of the year,

ii) the total biomass estimate for a given date in the simulations is the average biomass over the increment in which it falls, and

iii) the age structure may or may not be estimated during that survey.

These three points are accounted for in the following two formulations.

Known age structure

In the case of a known age structure estimated at the same time as the biomass survey, the initial age structure at the beginning of the year is determined by first ensuring that the known age structure scales appropriately to the estimate of biomass and then projecting the age structure back to the beginning of the year.

Thus, at the time of the survey, numbers at age, N_a^*, are drawn from a log-normal distribution based on a specified mean, $\overline{N}_a$, and coefficient of variation, $CV_{\overline{N}_a}$, such that

$$N_a^* = \overline{N}_a . \exp(\eta - \frac{\sigma_{\overline{N}_a}^2}{2})$$
$$\text{where } \sigma_{\overline{N}_a}^2 = \sqrt{\ln(1 + CV_{\overline{N}_a}{}^2)}$$

(42)

where η is drawn randomly from $N(0; \sigma_{\overline{N}_a}^2)$, and the total biomass, B^*, is also drawn from a log-normal distribution based on a specified mean, $\overline{B}$, and coefficient of variation, $CV_{\overline{B}}$, such that

$$B^* = \overline{B} . \exp(\eta - \frac{\sigma_{\overline{B}}^2}{2})$$
$$\text{where } \sigma_{\overline{B}}^2 = \sqrt{\ln(1 + CV_{\overline{B}}{}^2)}$$

(43)

where η is drawn randomly from $N(0; \sigma_{\overline{B}}^2)$.

The numbers at age are then re-scaled to the estimate of biomass, B^*, keeping the relative proportions in tact. This rescaling takes account of the biomass being the average biomass in an increment. However, it is undertaken only approximately, recognising that the average biomass is a result of both change in the individual weight of a fish and the change in numbers of fish. Thus, the approximation for an appropriately scaled age class, N_a', is

$$N'_a = N^*_a s_{B^*} s_{i^*}(a) s_{y^*}(a)$$

$$\text{where} \quad s_{B^*} = \frac{B^*}{\sum_i \left[N^*_i \left(\frac{W(i,t_1) - W(i,t_0)}{2} \right) \right]}$$

$$s_{i^*}(a) = \frac{2}{\left(1 + e^{-(M(a,t_0) + F(a,t_0))} \right)} \tag{44}$$

$$s_{y^*}(a) = \frac{1}{e^{-\left(\bar{M} \int_0^{t_0 - 1} m(a,\tau)d\tau + \bar{F} \int_0^{t_0 - 1} f(a,\tau)d\tau \right)}}$$

where s_{B^*} is the factor to scale the age structure to the estimate of biomass, where the average weight of fish in the increment is determined from the average of *W* at the beginning, t_0, and end, t_1, of the increment in which the survey was taken. $s_{i^*}(a)$ is the factor to give the number of fish in cohort, *a*, at the beginning of the increment rather than at the average point. $s_{y^*}(a)$ is the factor to project the cohort back to the beginning of the year.

Note that biases in these approximations can be reduced by increasing the number of increments in the year.

Unknown age structure

In the case of an unknown age structure, the initial age structure at the beginning of the year is determined is first established using the deterministic or random methods above followed by scaling to the estimate of biomass taken during the year. The scaling requires projecting the age structure forward to the time of the survey, determining the scaling factor and then applying that to the original age structure. Thus, the appropriately scaled age class, N'_a, is

$$N'_a = N_a \frac{B^*}{\sum_i \left[N_i e^{-\left(\bar{M} \int_0^{t_0 - 1} m(a,\tau)d\tau + \bar{F} \int_0^{t_0 - 1} f(a,\tau)d\tau \right)} \left(\frac{W(i,t_0) + e^{-(M(a,t_0) + F(a,t_0))} W(i,t_1)}{2} \right) \right]} \tag{45}$$

where the symbols are as described above for the known age structure.

4.4.2 Estimating Spawning Stock Status

The tests in the GYM are based on the status of the spawning stock. The status is governed by estimating the spawning stock in each year and relating that to a specified level, either as a median pre-exploitation biomass or as the spawning biomass at the beginning of the projections.

Spawning Stock Biomass

The spawning stock is specified in terms of its biomass. The biomass of each age class, *a*, at time *t* during the year is determined during the projection from equation (2). The proportion of each age class that is able to spawn at time *t* during the year is determined from three functions:

1. $g(l,t)$, the proportion of fish of length *l* being mature at time of year *t*;

2. $h(a,t)$, the proportion of fish of age *a* being mature; and

3. $p(t)$, the proportion of the mature stock spawning at t (spawning seasonality).

Thus, the proportion of an age class spawning is given by:

$$\theta(a,t) = g(l,t)\,h(a,t)\,p(t) \tag{46}$$

This formulation allows for considerable flexibility in taking account of age and size specific maturity. $g(l,t)=1$ if maturity is purely age dependent. Similarly, $h(a,t)=1$ if maturity is purely size dependent. The size-specific maturity function used in this model is based on length as described in Butterworth *et al*. (1994) where:

$$g(l,t) = \begin{cases} 0 & ; & l < m_1 \\ (l-m_1)/(m_2-m_1) & ; & m_1 \le l \le m_2 \\ 1 & ; & l > m_2 \end{cases} \tag{47}$$

where: $l = \lambda(\tau)$, the mean length of fish at age $\tau = a + t$, m_1 and m_2 are constants which specify the range over which selection changes from 0 to 1 (in the GYM, input parameters, m_1 and m_2 are specified from their midpoint m_m and range m_r).

The spawning stock at time t during the year is given by:

$$S(t) = \sum_a \theta(a,t).B_a(t) \tag{48}$$

The mean spawning biomass over a spawning period is calculated as:

$$\overline{S} = \frac{\displaystyle\int_{t_s}^{t_e} S(t).dt}{t_e - t_s} \tag{49}$$

where t_s and t_e are the respective start and end times of the spawning season within the year. This is the estimate used in determining spawning stock status.

Note that the spawning dates are converted by the program to the first and last increments in the year when spawning occurs. If either date falls mid way through an increment then spawning is considered to occur throughout the increment. If the first date is on the borderline between two increments then it is considered to be the start of the second increment. If the last date is on a borderline then it is considered to be at the end of the first increment in the pair.

The number of increments in a year may be sufficiently few that setting these two dates to different points of the year may be operationally the same as having them on the same day.

Better resolution of the spawning season can be obtained by increasing the number of increments in a year.

Uncertainty in the Maturity Function

Uncertainties in the maturity function are incorporated in the same way as for the fishing vulnerability. The length at which 50% of fish are mature, m_m, are taken into account by drawing these at random from uniform distributions, each with a specified range. This occurs at the beginning of each trial.

Reference level for estimating spawning stock status

The reference level for estimating the status of the spawning stock during the trials can be determined in two ways:

    i)   the spawning stock biomass in Year 0 of the projection, S_0 ;

    ii)   estimate of the median pre-exploitation spawning biomass

In the first case, the stock is projected over Year 0 to give the estimate of S_0 during the spawning season in that year.

Estimating Median Pre-exploitation Spawning Biomass

Two methods are available for determining the median pre-exploitation spawning biomass at Time 0: (i) based on the deterministic initial age-structure, and (ii) Monte Carlo sampling of random initial age structures.

The approximation for the median pre-exploitation spawning biomass based on the deterministic initial age structure is derived from Butterworth *et al.* (1994). This initial age structure is then projected one year to numerically solve equation (49), with $F_y = 0$, to determine the approximate median unexploited spawning biomass, $\widetilde{S}_0$. This formulation can contribute to a bias in the median spawning biomass (Constable & de la Mare, 1998).

The Monte Carlo method for estimating the median pre-exploitation spawning biomass, $\hat{S}_0$, allows S_0 to be estimated from multiple applications of the random method used to set up the initial age structure. This option has the advantage over $\widetilde{S}_0$ of being unbiased, but requires more computation, and is subject to sampling variability. Consequently, it is important to nominate a large number of replicate observations for estimating the pre-exploitation median spawning biomass in this case.

Note that the stock-recruitment relationship is not applied when the median pre-exploitation spawning biomass is being estimated.

4.4.3 Managing Time during a Test

Time 0 of the projection

Time 0 of the projection does not have to coincide with the beginning of the calendar year. It can begin on any date nominated. For example, the fishing year may be best described as beginning on 1 December of one year and ending on 30 November in the following year. The projection year is best undertaken in alignment with the fishing year rather than the calendar year.

In this context, the user needs to input the reference start date in the year (day/month e.g. 01/12) as well as the reference year, say 1982, as the elements for describing Time 0. Thus, the starting date of the projections will be 01/12/1982. Each subsequent year in this example will therefore be

Projection Year	Start Date	End Date
0	01/12/**1982**	30/11/1983
1	01/12/**1983**	30/11/1984
2	01/12/**1984**	30/11/1985
3	01/12/**1985**	30/11/1986
4	01/12/**1986**	…

Years in Input and Output

Convention normally has a split-year quoted by the second year. For ease of programming, the reference to a split year is the year corresponding to the start date rather than the end date (see bold years in table above). Thus, years referred to in the catch history and in the recruitment series need to correspond to the start date of the split year rather than the printed convention of the year corresponding to the end date.

There is no need to make such an alteration to the input of survey data for estimating recruitment because the dates of the survey will be handled appropriately within the GYM.

Timing of different functions to the reference start date in the year

A number of functions will require being started at the reference start date rather than at the beginning of the calendar year. Care will be needed in characterising the functions in this way, such as intra-annual variation in natural mortality, fishing mortality and maturity. The first date of these functions will need to correspond to the reference date of the projection year. Similarly, recruitment occurs at the beginning of the year.

Also, the length at age relationship needs to be standardised to the nominated first day of the year, which may not be the first of January or the date referenced by t_0 in a von Bertalanffy function. Some thought will need to be given as to the timing of growth in the function as it can affect the outcome when abundance in biomass is being determined. This is particularly pertinent with respect to estimates of biomass from set dates in the year but with variation in survey times between years, such as in the case of estimating gamma for the krill fishery based on an estimate of biomass at a given time (see GYM Manual for further explanation).

Years prior to the projection

An option is available to run the simulation prior to the catch series or a projection time-series with fishing. This could be necessary for two reasons:

    i)   to remove the effects of the initial age structure, and

    ii)   to provide for estimating the total biomass and/or spawning biomass in the year prior to

             fishing.

For this reason, it has been termed "Years to remove initial age structure". If there of these options is required then this will be equal to 1 or greater. Year 0 in the table above will correspond to the final year in this projection.

On the other hand, if there is no need for such estimation, i.e. the starting biomass is specified and fishing must start immediately, then this would be set to zero. In this case, Year 0 would be the first year of fishing.

Normally, this would be set to the year prior to or at the beginning of the recruitment series or the catch series or in a suitable reference year such as when the biomass has been estimated.

Periods in a Trial

The trial can be effectively divided into two main periods, excluding the period prior to the projections. The first period comprises the catch and recruitment series up to the present followed by the second period projecting into the future. The former case comprises all the years that would encompass the combined catch and recruitment series. The latter case comprises the number of years nominated in the Characteristics of a Trial.

Increments in a Year

Each year comprises a number of increments. This can be set to the number of days in the year, 365, or lesser numbers of increments. Accuracy during the year will be potentially reduced with lower numbers of increments. Thus, care will be needed in defining the number of increments relative to the characteristics of the functions incorporated into the trials.

4.4.4 Monitoring

Monitoring can be undertaken for individual cohorts or for the whole population. Monitoring at specific survey times, such as in the total biomass in Year 0, gives the status for the increment in which the survey time falls in a given year. This is the average status in that increment.

The spawning biomass is monitored as described in equation (49).

The vulnerable biomass during a year is monitored as the average over a period specified in a manner similar to spawning biomass.

4.5 Assessing harvest strategies

4.5.1 Types of harvest limits - γB_0, Catch, *F*

The GYM was designed as a tool to evaluate three types of methods for setting harvest limits into the future. If there is a desire to examine the condition of the stock during a known catch period then the output files will need to be used in the evaluation.

The Generalised Yield Model can be used to evaluate the consequences to the stock of three types of scenarios: (i) a constant catch set as a specified proportion (γ) of an estimate of the pre-exploitation stock (B_0); (ii) a constant specified catch; or (iii) a constant fishing mortality, for example $F_{0.1}$.

This method for setting a catch limit is based on the work of Beddington & Cooke (1983) and later elaborated in the krill yield model of Butterworth *et al*. (1992, 1994). It does not require estimates of mean recruitment, but does need an estimate of the pre-exploitation biomass, B_0 (see Butterworth *et al*., 1992 for discussion). Uncertainty in the estimate is incorporated into the simulation by using the coefficient of variation in the survey estimate of biomass, κ. The value of gamma results in the calculation of the constant yield where yield for the single projection trial is

$$Y = \gamma B_0 \exp\left(\varepsilon - \frac{\sigma_S^2}{2}\right) \quad ; \quad \varepsilon \text{ from } N(0;\sigma_S^2) \tag{50}$$

where $N(0;\sigma_S^2)$ is a normal distribution with mean 0 and variance $\sigma_S^2 = \ln\left(1+\kappa^2\right)$.

The second option allows projection of the stock under a constant catch specified by total weight. In this case, estimates of parameters for mean recruitment must reflect actual levels of recruitment.

The third option allows the performance of the stock to be examined under a given fishing mortality.

A special case is to nominate fishing mortalities to be analysed as for a yield per recruit analysis. The yield per recruit analysis requires that a fixed fishing mortality is used in the setting up the initial population structure.

4.5.2 CCAMLR Decision Rules

The application of the CCAMLR decision rules requires multiple stochastic realisations of stock trajectories (trials) in order to produce statistical distributions of stock abundance for a given test level, and to allow for Monte Carlo integration of uncertainty in key demographic parameters. Monte Carlo integration is carried out by drawing key demographic parameters for each stock trajectory at random from appropriate statistical distributions described above. A single realisation consists of three parts: (1) setting basic demographic parameters; (2) setting up the initial population age structure; and (3) projecting the stock over a period of known catches followed by the required projection period in which the test value is applied.

The two estimates required by CCAMLR for the evaluation of a test value (long term annual yield specified as γB_0, or Catch, or a long-term annual F) a long term annual yield are: (i) the probability of depletion at any time during the projection period, where the spawning biomass falls below a specified proportion, p_{dep} (e.g. 0.2) of the pre-exploitation median level; and (ii) the overall escapement, E, of spawning biomass, given by the ratio of the median spawning biomass at the end of the specified period to the median pre-exploitation spawning biomass.

These estimates are obtained by undertaking a large number of projection trials (e.g. 1001). For each trial, the program records the spawning stock biomass during the projection. The performance measures require the lowest spawning biomass during the projection period and the spawning biomass at the end of the projection period to be converted to ratios of these values to the median pre-exploitation biomass determined before the trial is undertaken. The median pre-exploitation biomass is determined for each trial because the demographic parameters will alter between trials when uncertainty in these is present (see above).

Depletion probability

The probability of depletion can be estimated using two methods based on the two different formulations of the median pre-exploitation spawning biomass described above. The first is that arising from the use of the deterministic formulation, $\widetilde{S}_0$, so that the estimated probability of depletion is calculated from the proportion of runs where:

$$S_{\min} < p_{dep} \widetilde{S}_0 \tag{51}$$

The second option based on the Monte Carlo method uses $\hat{S}_0$ in place of $\widetilde{S}_0$ in estimating the probability of depletion, that is:

$$S_{\min} < p_{dep} \hat{S}_0 \tag{52}$$

These two options should give similar results when there is no Monte Carlo integration over uncertainty in demographic parameters. For cases where Monte Carlo integration is included, it would be expected that the second option would be less biased, particularly if the range of uncertainty in the parameters is large.

It is recommended that only the Monte Carlo method be used.

Median escapement of spawning biomass

The recommended formulation for estimating the median escapement of the spawning biomass is

$$\hat{E} = \text{median}\left(\frac{S'_E}{\hat{S}_0} \right) \tag{53}$$

where S' is the spawning biomass at the end of the projection and $\hat{S}_0$ is the median pre-exploitation spawning biomass derived using the Monte Carlo method prior to each trial.

The method used in the original krill yield model (Butterworth *et al.* 1994) based on the deterministic method needs to be corrected by dividing by the estimate for when there is no yield from the stock, that is:

$$\widetilde{E} = \frac{\text{median}\left(\dfrac{S'_E}{\widetilde{S}_0} \right)}{\text{median}_{Y=0}\left(\dfrac{S'_E}{\widetilde{S}_0} \right)} \tag{54}$$

Note that a departure from 1.0 in the median escapement can be observed when there is no yield because of stochastic variability if the number of replicate trials is insufficient to account for variability in some of the input parameters. Thus, a preliminary assessment with yield set to zero is recommended for investigating whether the population is stable and to determine how many trials may be needed to ensure an appropriate level of precision for estimates of median escapement.

4.5.3 Alternative assessments

Alternative assessments can be formulated based on depletion probabilities and escapement. For example, an assessment of the stock trajectory based on an initial starting point can be evaluated in a similar way but using the initial spawning biomass rather than the median pre-exploitation spawning biomass. Similarly, the output files could be used to examine stock status at different times using total, spawning or vulnerable biomass (or numbers).

If a stock-recruitment relationship is not important in these scenarios then the maturity function could be used to mimic the total biomass or the vulnerable biomass to undertake a similar assessment using those assessment parameters instead of spawning stock status.

4.6   Run Time

The efficiency of the Generalised Yield Model can be governed by a number of parameters. The user is encouraged to run sensitivity trials on these parameters to determine the minimum required to obtain estimates of the yield with the appropriate level of precision. The parameters to examine are

Parameter	Sensitivity
Trials	Primarily effects the precision on median spawning stock status at any time and probabilities of depletion below a critical level
Increments in Year	Greater number of increments will give better approximation to length, maturity, mortality functions. Lower numbers of increments can help speed up the program.
Years in future projection	The number of years needs to be at least a full generation to be confident that the yield being tested has been fully applied to the population
Upper Bound for F	This is set to stop the program from attempting to take fish when the catch is greater than the available stock. If set too low then the program may stop sooner than necessary, resulting in potentially incorrect stock trajectories. Keeping it low in early tests can help speed up the finding of the yield that satisfies decision rules.
Tolerance for finding F	Large tolerance will potentially result in poor resolution of the catches in the catch series and larger variation than desired in the estimates of catch in the future projections. Large tolerances could be used early to help find the yield that satisfies the decision rules.
Seed for random number generator	The random number generator can be seeded with a specified value to ensure consistency between tests. This can be reset to the same value for each test in a scenario if desired.

4.7 Guide to Parameter Input Table

This is an example of a parameter table for an assessment of Patagonian toothfish

Table GY1: Parameters input to the GY model for evaluation of precautionary yield of *Dissostichus eleginoides* in SubArea 58.5.2

Category	Parameter	*D. eleginoides*
Age composition	Recruitment age in simulation Number of age classes Plus class present – years in plus class in initial age structure	4 56 21
Characteristics of Year	Reference Start Date in year Resolution - Number of increments per year	01/11 360
Natural mortality	Mean annual *M*	0.12-0.20
Fishing selectivity	Age selectivity function: Age (Selectivity)	0. (0.) , 3. (0.), 3.5 (0.07), 4.5 (0.311), 5.5 (0.699), 6.5 (1.0), 7.5 (1.038), 8.5 (0.849), 9.5 (0.579), 10.5 (0.341), 11.5 (0.179), 12.5 (0.085), 13.5 (0.037), 14.5 (0.015), 15. (0.)
Fishing Season Determination of F	Effort by season Reasonable upper bound for annual fishing mortality Tolerance (error) for determining fishing mortality in each year	Uniform effort over whole year 5 1E-05
Length at Age	von Bertalanffy - time 0 von Bertalanffy - L_∞ von Bertalanffy - *K*	0 170.8 cm 0.088
Weight-length $(W = aL^b)$	*a* *b*	2.5E-05 2.8
Maturity	Maturity at age function : Age (Proportion Mature)	0. (0.), 1.39 (0.0002), 2.32 (0.0009), 3.10 (0.0027), 4.13 (0.0096), 4.82 (0.0213), 5.76 (0.0564), 6.56 (0.117), 7.67 (0.270), 8.45 (0.418), 9.49 (0.617), 10.70 (0.792), 11.59 (0.871), 12.58 (0.924), 14.07 (0.964), 16.08 (0.985), 18.90 (0.995), 21.48 (1.0)
Spawning Season	Date when spawning begins Date when spawning ends	1 July 1 July (knife edge)
Recruitment	Mean of $\log_e$ (Recruits) Standard error of the mean of $\log_e$ (Recruits) Standard deviation of $\log_e$ (Recruits)	14.585 0.159 0.422
Simulation Characteristics	Type of Tests Number of trials in simulation for each test (catch) Formulation of initial age structure - Deterministic or Random Years to project stock to remove effects of initial age structure Year 0 of projection Estimate of median pre-exploitation spawning biomass prior to trial Vector of real catches to project over known catch period (tonnes) Number of years to project stock following known catch period Seed for random numbers Reset set in each trial	Catch 1001 Random 1 1996 Random method – 1001 observations Run 1: 12061 Run 2: 20261 35 -24189 TRUE
Decision rules	Reference point for depletion	$0.2.SB_0median$

4.8 Running GYM with a user-interface

A user interface has been developed for the GYM. It provides an easy to use directory structure for managing scenarios and using diagnostic tools. Its use is fully described in the manual (Constable *et al*, 2003) and available with the software.

4.9 Running GYM without the interface

4.9.1 Operation & DOS Command Line

The command line to drive the GYM from a DOS prompt is

<div align="center">

..\> **GYMxxx**

</div>

where

      GYMxxx is the GYM version being used e.g. GYM500

4.10 Input Files

Four input files are required:

1. GYDEF.SIM   Main input file with simulation details

2. *<ROOT Filename>*.BIO   Biological parameters with recruitment model

3. *<ROOT Filename>*.REC   Recruitment survey data if available

4. *<ROOT Filename>*.FSH   Fisheries data

5. *<ROOT Filename>*.STR   Initial population structure

The main input file specifies the *ROOT Filename* for which the output files will be named. The input files are named separately but commonly sharing the ROOT Filename is helpful.

The scenario provided here as an example is for the long-lived species with an estimate of initial biomass and population structure as used in example LL03 below.

4.10.1   Simulation parameters – GYDEF.SIM

File lines are separated by dotted lines. Page references are given in parentheses ( ) and equation/parameter references are given in square brackets [ ]. Explanation lines equivalent to Empty lines are indicated as 'Ex' in the description

Description	File Lines		
Ex : Title	simulation file:GYDEF.sim for scenario 'Long-lived 03'		
Empty Line			
Empty Line	**		
Empty Line			
Ex	FILES		
Empty Line			
Input Biological parameters	Biological Parameters for Input	LL02.bio	
Input results from recruitment surveys (87)	File – survey details for recruits	LL02.rec	
Input characteristics of the fishery – historical and future (98)	File – fishery details	LL02.fsh	
Input initial population structure (100)	File – initial population structure	LL03.str	
Root name that will be given to all output files with the relevant extension then added	Root Name for Output files	LL03	
Empty Line			
Ex	GENERAL OUTPUT DETAILS		
Empty Line			
Ex: Type of information printed to log files	Run Time Log Files		
Lookup table printed to *.LUK file (83, 127)	Lookup tables generated in setup	TRUE	
Specify whether the GYM is run only to generate lookup tables (used mainly by the interface)	Run only for lookup tables	FALSE	
Mirror inputs and outputs in the *.LOG file (124)	Input/Output from setup	FALSE	
Print parameters updated in each trial to the *.LOG file	Updated Parameters in each trial	FALSE	
Print percentile tables from each test (mostly not used any more) (127)	Percentile tables at end of each tests	FALSE	
Empty Line			
Ex	Output files - Population Status		
See (129)	General - incl SSB status	TRUE	

Description	File Lines	
See (130)	Specified Survey times	FALSE
See (131)	At all increments	FALSE
Empty Line		
Ex	Output files - Cohort Status	
See (132)	General - incl SSB status	FALSE
See (133)	Specified Survey times	FALSE
See (134)	All increments in each year	FALSE
Empty Line		
Ex	EVALUATION OF YIELD	
Empty Line		
Choose evaluation of gamma (G), catch (C) or fishing mortality (F) (108)	Type of evaluation	F
Empty Line		
Ex	Vector of Gammas,Catches or Fishing Mortalities	
Ex	(Add values below this line and leave single blank line at end)	
Vector of values to be evaluated (separated by a space	0. 0.04 0.05	
Empty Line		
Option to have the special case of yield per recruit undertaken (indicate True if required, False if not) (95)	Do yield per recruit analysis	FALSE
Empty Line		
Ex	SIMULATION CHARACTERISTICS	
Empty Line		
The number of trials in a test – will affect precision of outcome (111)	Number of trials in simulation	1001
Depletion level is a proportion of median (initial) spawning biomass (109) [p_{dep} in (52)]	Depletion Level for Test	0.8
See (111)	Seed for random number generator	-24189
See (111)	Reset seed to this value for each test	TRUE
Empty Line		
Ex	CHARACTERISTICS OF A TRIAL	
Empty Line		
See (107)	Years to remove initial age structure	1
Empty Line		
See (106,110)	Estimate median SB0 before each trial	FALSE
See (106,110)	Estimate med SB0 (deterministic/random)	R
See (106)	Observations to use in median SB0	1001
Empty Line		

Description	File Lines
See (106)	Year 0 of projection 2002
See (106)	Reference Start Date in year 01/01
See (108,111)	Increments in year 12
Empty Line	
See (107, 111)	Years to project stock in simulation 30
Empty Line	
Ex	STOCK PARAMETERS
Empty Line	
See (100)	Last age-class in stock 30
See (85) –it is recommended to leave this set to True	Coefficient values ramp between incs TRUE
Empty Line	
Ex – monitoring of stock at specified dates (130)	GENERAL MONITORING OF STOCK
Format statement for reading in the array of year and date within year for monitoring	(I4,2X,I2,X,I2)
Year, Date (dd/mm)	2002 01/03
End of array line	-1 0
Flag to monitor every year in projection from Year 0 (T) or only years specified for monitoring above (F)	Monitor all Years in projection TRUE
Empty Line	
Ex – specify period over which the average fishable biomass is estimated (126) Used, e.g., for adjustments based on a time series such as CPUE	MONITORING OF FISHABLE BIOMASS DURING YEAR
As for spawning biomass but using fishable biomass [t_s in (49)]	Start of Monitoring Period (dd/mm) 01/03
As for spawning biomass but using fishable biomass [t_e in (49)]	End of Monitoring Period (dd/mm) 01/04
Empty Line	
Ex	ESTIMATING B0 IN GAMMA CALCULATIONS
Empty Line	
See (108)	Estimate B0 (log-normal) FALSE
See (108)	CV of B0 estimate 0.0
Used to adjust the B0	Coverage of survey 1.0

Description	File Lines	
estimate if survey area was greater than or less than the area to which assessment applies. See (108)		
Empty Line		
End of file line	End of File	-100

4.10.2 Biological parameters - <ROOT Filename>.BIO

File lines are separated by dotted lines. Page references are given in parentheses ( ) and equation/parameter references are given in square brackets [ ]. Explanation lines equivalent to Empty lines are indicated as 'Ex' in the description

Description	File Lines	
Ex : Title	biological file: for scenario 'Long-lived 03'	
Empty Line		
Empty Line	**	
Empty Line		
Ex :	AGE STRUCTURE	
Empty Line		
Age of recruitment (86)	First age-class in stock	2
Last age class to be monitored in projections – the plus class (100)	Last age-class in stock	30
Oldest age used in the formulation of the plus class (101) [(38) ,(39)]	Oldest age in last class	60
Empty Line		
Ex :	RECRUITMENT	
Empty Line		
See (88)	Recruitment Function	L
See (87)	Use recruitment surveys to est recs	FALSE
See (86)	Use recruitments in time series	FALSE
Empty Line		
Ex :	Parameters for recruitment	
Ex :	Recruitment from log-normal distribution (Recruitment Function = L)	
See (88) [(8)]	Mean recruitment	1000000.0
A CV range can be used to incorporate uncertainty. See	Min Coefficient of Variation	1.0

Description	File Lines
(88,89)[(8),(9)]	
A CV range can be used to incorporate uncertainty. See (88,89)[(8),(9)]	Max Coefficient of Variation 1.0
See Uncertainty (89) [(10)]	Number of replicates 1
See Uncertainty (11)	Use Standard Error of mean False
Stock-recruitment relationship. See (94) [(28)]	x.SB0 for recruitment depletion - x = 0.5
Empty Line	
Ex : See (86), [(4),(5)]	Vector of Recruitments (Recruitment Function = V) with YEAR,ESTIMATE,CV
	(I4,2X,G14.6,2X,G14.6)
	-1 0.0 0.0
Ex : See (88)	Use Recruitment SEs in bootstrap FALSE
Empty Line	
Ex : Proportional recruitment function (89)	Parameters for recruitment related to M (Recruitment Function = B)
Observed mean (89) [(11)]	est. proportion of stock as recruits 0.0
Observed SD (89) [(11)]	SD of recruitment proportion 0.0
t in [(11)]	age class that recruits 1st enter 1
	data points used to estimate proportion 1
Empty Line	
Ex : see (97)	NATURAL MORTALITY
Empty Line	
Ex :	Mean Annual M
A range of estimates of M can be used to incorporate uncertainty (97)	Min Mean Annual M 0.15
	Max Mean Annual M 0.15
See [(33)]	SD of M between years within runs 0.0
See (97)	Alter Mean Annual M by Multiplier FALSE
P_{mhigh} See [(33)]	Probability of M being multiplied 0.0
m_{high} See [(33)]	Amount Mean M to be multiplied by 1.0
Empty Line	
Ex : m(a) in [(32)] (97)	Natural Mortality coefficient with age
	(F7.3,2X,G14.6)
	0.0 1.0
	-1.0 0.0
Empty Line	
Ex : m(t) in [(32)] (97)	Natural Mortality with time of year (date coefficient)
	(I2,1X,I2,G14.6)

Description	File Lines
	01/01 1.0
	-1 0.0
Empty Line	
Ex : See (95)	LENGTH AT AGE
Empty Line	
Choose von Bertalnffy (VB) or Length at Age input (LAA)	Type of Growth Curve to Generate VB
Ex :	********************************
Ex : See (96)	If von Bertalanffy (type = VB)
Equation [(30)]	time 0 0.0
Equation [(30)]	Linf 100.0
Equation [(30)]	k 0.06
Date in the year for the point of origin of the growth curve – f_{start} in [(31)]	Ref date for growth curve (dd/mm) 01/01
Equation [(30)] Date to estimate g_o to g_1	Date - start growth period (dd/mm) 01/01
Equation [(30)] Date to estimate g_1	Date - end growth period (dd/mm) 31/12
Ex :	********************************
Ex : See (96)	If length at age to be input (type = LAA)
	(F7.3,2X,G14.6)
	-1.0 0.0
Empty Line	
Ex : See 95	WEIGHT AT AGE
Empty Line	
a in [(29)]	Weight-length parameter - A 0.000025
B in [(29)]	Weight-length parameter - B 2.8
Empty Line	
Ex : See (104)	MATURITY
Empty Line	
Ex : Uncertainty incorporated as per (105)	Maturity (length based - if only age-based then make these = 0)
M_m in equation [(47)]	Min length, 50% are mature 50.0
	Max length, 50% are mature 50.0
M_r in equation [(47)]	Range over which maturity occurs 20.0
Empty Line	
Ex : h(a,t) in [(46)]	Maturity function by age (if only length based then all=1)
	(F7.3,2X,G14.6)
	0.0 1.0
	-1.0 1.0
Empty Line	
Ex : See (104)	SPAWNING SEASON

Description	File Lines
Empty Line	
t_s in [(49)]	First Day of Spawning Season (dd/mm) 01/07
t_e in [(49)]	Last Day of Spawning Season (dd/mm) 01/07
Empty Line	
Ex :	**
End of file line	End of File -100

4.10.3   Recruitment survey data - <ROOT Filename>.REC

File lines are separated by dotted lines. Page references are given in parentheses ( ) and equation/parameter references are given in square brackets [ ]. Explanation lines equivalent to Empty lines are indicated as 'Ex' in the description

Description	File Lines
Ex : Title Purpose described at (87)	HIMI Recruitments – dates relative to 1 December
Empty Line	
First age class in population age structure	Age for estimating recruitment 0
Empty Line	
The numbers of the surveys should be consecutive with an empty line between each set of survey information	Survey 1
Year of survey	Year 2001
	Dummy year 1
t_0 in Equation [(7)]	Time of year (relative to 1 Dec) 0.0
sA_0 in Equation [(6)]	Area of survey (km2) 1.0
Dbar in Equation [(6)]	Total Observed Density 1.0
Dbar prime in Equation [(6)]	Total Expected Density 1.0
Ex : a, $N_{a,0}$ and sigma of N in Equation [(6)]	Age Density SE
	(I3,2X,G14.6,2X,G14.6)
	-1 0.0 0.0
Empty Line	
Next survey would start here. If not, then End of file line	End of File -1

4.10.4 Fisheries data and parameters - <ROOT Filename>.FSH

File lines are separated by dotted lines. Page references are given in parentheses ( ) and equation/parameter references are given in square brackets [ ]. Explanation lines equivalent to Empty lines are indicated as 'Ex' in the description

Descr iption	File Lines
Ex : General details for fishery file provided in (98)	2001 WGFSA – Fishery information – Long-lived 02 – trawl fishery from present
Ex :	*****(first selectivity below is Year zero and gives the selectivity for forward projection)*****
Empty Line	
Ex :	GENERAL
Run time (111)	Reasonable upper bound for Annual F 5.0
Run time (111)	Tolerance for finding F in each year 0.00001
Empty Line	
Empty Line	
First line for fishery details. Fisheries should be numbered consecutively (at present only models for one fishery).	FISHERY (Longline) 1
Empty Line	
	Year (0=forward projection details) 0
	Account for uncertainty FALSE
Empty Line	
Ex : s(a,t) in (98)[(34)]	Fishing Selectivity by length (0 if by age)
L_m used to estimate range in [(35)]	Min length, 50% recruited 40.0
Uncertainty incorporated by making this value differ (99)	Max length, 50% recruited 40.0
L_r used to estimate range in [(35)]	Range over which recruitment occurs 10.0
Empty Line	
Ex : a(a) in (98)[(34)]	Fishing Selectivity with age (1 if by length)
	(F7.3,2X,G14.6)
	0.0 1.0
	-1.0 0.0
Empty Line	
Ex : E(t) in (98)[(34)]	Relative fishing effort in each inc. of year (day/month coefficient)
	(I2,1X,I2,G14.6)
	01/01 1.0

Descr iption	File Lines
	-1 0.0
Empty Line	
Each year of the known fishing history is added in chronological order (although not necessarily every year) with this header line. When no more years to add then include this line but with a -1 as the year	Year of fishery 2003
Then insert the catch in the biomass units of the weight-length relationship	Catch (kg) 0.
Then nominate whether to use the vulnerability parameters from the previous year in the time series (this would be the forward projection year if this year is the first in the series).	Selectivity to vary from last one FALSE
Empty Line	
	Year of fishery 2004
	Catch (kg) 10.
If vulnerability is varied from the previous year (T) then enter all the vulnerability information as for the projection details	Selectivity to vary from last one TRUE
Empty Line	
	Fishing Selectivity by length (0 if by age)
	Min length, 50% recruited 40.0
	Max length, 50% recruited 40.0
	Range over which recruitment occurs 10.0
Empty Line	
	Fishing Selectivity with age (1 if by length)
	(F7.3,2X,G14.6)
	0.0 1.0
	-1.0 0.0
Empty Line	
	Relative fishing effort in each inc. of year (day/month coefficient)
	(I2,1X,I2,G14.6)
	01/01 1.0
	-1 0.0
Empty Line	
Each year of the known catch history would be	Year of fishery -1

Descr iption	File Lines
added here	
Empty Line	
End of fishery	FISHERY -1
End of file line	

4.10.5 Initial Population Characteristics - <ROOT Filename>.STR

File lines are separated by dotted lines. Page references are given in parentheses ( ) and equation/parameter references are given in square brackets [ ]. Explanation lines equivalent to Empty lines are indicated as 'Ex' in the description

Description	File Lines
Ex : Details are found in (100)	Long-lived 02 - Initial population structure for each trial
Empty Line	
Empty Line	***
Empty Line	
See (100)	Age structure from random recs TRUE
See (102)	Known age structure FALSE
Empty Line	
Ex : See (103)	Biomass to scale with CV
	(G14.6,2X,G14.6)
Bbar, CV in [(43)]	1500000.0 0.3
Empty Line	
Ex : See (103)	Age Structure (each line = age,abundance,stand.err.)
	(last line with age = -1)
	(I2,2X,G14.6,2X,G14.6)
	-1 0.0 0.0
Empty Line	
Ex :	Date of age structure and/or biomass
	(dd,mm)
	01/03
Empty Line	
End of file line	End of File -100

4.11 Outputs

Output Files are generated according to the selections in the GYDEF.SIM file under **General Output Details.**

Relevant Data Inputs

```
GENERAL OUTPUT DETAILS

Run Time Log Files
 Lookup tables generated in setup        True
 Input/Output from setup                 True
 Updated Parameters in each trial        False
 Percentile tables at end of each tests False

Output files - Population Status
 General - incl SSB status               True
 Specified Survey times                  True
 For CPUE integration                    True

Output files - Cohort Status
 General - incl SSB status               True
 Specified Survey times                  True
 All increments in each year             True


MONITORING OF STOCK
(I4,2X,I2,X,I2)
1985  01/12
-1    0
Monitor all Years in projection         True
```

Notes

The general output details are used to specify the types of results to be entered into the files, particularly the Run-Time Log. These outputs are chosen using T (true) or F (false). Yes or No can be used in the place of these logicals but are converted to logicals in the input code.

The monitoring of the stock specifies the date in each year when the stock is to be monitored. This first date must be greater than or equal to the first day of Year 0 identified above.

4.11.1   Results of the tests

The results of the tests in terms of CCAMLR decision rules are given in GYDEF.SUM. This file will need to be renamed if it is to be retained.

Example
```
      2001 WGFSA HIMI TOP


**************************************************************

FILES

Biological Parameters for Input       01DESAF1.bio
File - survey details for recruits    01DESAF1.rec
File - fishery details                01DESAF1.FSH
Root Name for Output files            01DESAF1

RESULTS OF TESTS
Test           ,Escapement      ,Depletion
 2815000.0     , 0.56046522     ,  0.0000000      ,
```

4.11.2   Diagnostics

Log File

Correct data input can be checked in the LOG file. Also, errors that cause the program to crash will be written into the LOG file if they were trapped.

Logtime Temp File

The LOGTIME.TMP file is a temporary file generated by the graphic user interface and used by it to track and display progress information.

Summary of outputs in each of the Population and Cohort file types

Characteristic (as in file)	Population				Cohort		
	General	Survey	All incs	Time 0	General	Survey	All incs
Test	X	X	X	X	X	X	X
Trial	X	X	X	X	X	X	X
Year	X	X	X		X	X	X
Inc/Incs		X				X	X
Total bms	t=0	t=s	t	t=s			
Total N	t=0	t=s	t				
Spawn bms	$\overline{S}$	t=s	t	$\overline{S}$			
Spawn N	$\overline{S}$	t=s	t				
Vuln. bms	$\overline{F}$	t=s	t				
Vuln. N	$\overline{F}$	t=s	t				
F	Annual		t		Annual		
Catch	$\sum t$		t				
Recruitment	t=0						
M	Annual				Annual		t
SSB status	$\overline{S}$						
SB0 median				$\overline{S}$			
SB0 CV				$\overline{S}$			
TB0 estimate				t=s			
Age					X	X	X
Cohort bms					t=0	t=s	t
Cohort N					t=0	t=s	t
Spawn bms					$\overline{S}$	t=s	
Vuln bms					$\overline{F}$	t=s	
Catch					$\sum t$		t
Length						t=s	t
F						t=s	t
Vulnerability						t=s	t
Maturity						t=s	t
Vuln. x E							t

where X=categorical variable, t = status at beginning of increment or rate through increment or catch taken through increment, s = increment in which survey occurs, Annual = annual rate, $\overline{S}$ = derived from average spawning biomass over spawning season, $\overline{F}$ = derived from average vulnerable (fishable) biomass over nominated period to monitor,

4.11.3   Look-up Tables

LUK -an output file for printing the lookup tables for the coefficients. This is useful for checking the input parameters were correctly used to generate the coefficients. It is also required for graphical presentations in the GYM Interface.

Example

```
LOOKUP TABLES OF COEFFICIENTS
Age classes                              35
Increments in year                       24
        AGE,         LENGTH,          WEIGHT,  SPAWN AT AGE,       M AT AGE,       F AT AGE
(6(G14.8,1X))
 0.0000000     , 169.72696     ,0.36540362E-01, 1.0000000     , 1.0000000     , 0.0000000
0.41666667E-01, 172.49874     ,0.38488428E-01, 1.0000000     , 1.0000000     , 0.0000000
0.83333333E-01, 175.26717     ,0.40504317E-01, 1.0000000     , 1.0000000     , 0.0000000
0.12500000    , 178.03226     ,0.42589137E-01, 1.0000000     , 1.0000000     , 0.0000000
0.16666667    , 180.79401     ,0.44743988E-01, 1.0000000     , 1.0000000     , 0.0000000
0.20833333    , 183.55243     ,0.46969968E-01, 1.0000000     , 1.0000000     , 0.0000000
etc.
```

4.11.4   Percentile tables

Percentile tables are now obsolete. However, if they are chosen to be printed then they will appear in the PCT file.

This file was useful for validating the model and for monitoring the stock. It has been superseded by the Population Status files below.

Note that the main outputs required for assessing the effects of fishing on the stock according to the 2 main decision rules of CCAMLR are found in the output file designated at run time.

4.11.5 Population Status

The population status files are used to monitor the stock over each year in a run. These files will always begin in Year 0 which is the year prior to the first year in the recruitment/catch history or, in the absence of that history, prior to the first year of the future projection period. In the case where the number of years to project the stock prior to the history or future projection is 0 then the values for Year 0 will be recorded as 0, i.e. there were no observations at that time. These would need to be deleted in order to produce appropriate graphics.

Status of the stock in Year 0 in each trial – ROOTname.T0

The status of the stock in Year 0 – prior to exploitation

Test	The test of yield – either γB_0, Catch, F (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
SB0 median	The estimate of the median pre-exploitation spawning biomass for the trial
SB0 CV	The coefficient of variation for the vector of pre-exploitation spawning biomasses used to estimate the median. This variability can indicate the degree to which uncertainty in the input parameters will influence the spawning stock
SB0	Average spawning stock biomass during the spawning season in Year 0
TB0	The total biomass at the time of the survey in Year 0
TB0 estimate	An estimate of total biomass arising from the input CV for the survey.

Example

```
Test          ,Trial,SB0 median     ,SB0 CV          ,SB0           ,TB0            ,TB0 estimate  ,
 2815000.0    ,    1, 53484657.     ,0.24398224      , 56814937.    , 91577819.     , 91577819.
 2815000.0    ,    2, 96365344.     ,0.21350878      , 67664187.    , 99088176.     , 99088176.
 2815000.0    ,    3, 45486856.     ,0.20902495      , 49313955.    , 71554706.     , 71554706.
 2815000.0    ,    4,0.11174549E+09,0.21120483       ,0.11476499E+09,0.19898486E+09,0.19898486E+09
 2815000.0    ,    5,0.10082318E+09,0.21316133       , 86266533.    ,0.14779639E+09,0.14779639E+09
 2815000.0    ,    6, 74239252.     ,0.21415955      , 71612816.    ,0.12327316E+09,0.12327316E+09
 2815000.0    ,    7, 63631700.     ,0.22375013      , 72459943.    ,0.15499242E+09,0.15499242E+09
```
etc.

General - incl SSB status – ROOTname.PG

General characteristics of the population

Test	The test of yield – either γB_0, Catch, F (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
Year	The first year of the split year – can be used to relate this information to other files in a database
Total Biomass	Total biomass in the first increment (0) of the year
Total Number	Total number in the first increment (0) of the year
Spawn Biomass	Average spawning stock biomass during the spawning season in the Year
Spawn Number	Average spawning stock number during the spawning season in the Year
Vulnrbl BMS	Average vulnerable biomass of fish during specified period for monitoring fishable biomass
Vulnrbl Number	Average vulnerable number of fish during specified period for monitoring fishable biomass
F	Average rate of annual fishing mortality for the given year and trial
Catch	Catch for the year
Recruitment	Recruitment for the year
M	Average rate of annual natural mortality for the given year and trial
SSB Status	Status of the spawning biomass relative to the pre-exploitation status (median or SB0) for the trial

Example

Note, in this example, the lines are wrapped around

```
Test            ,Trial,Year ,Total biomass ,Total Number   ,Spawn Biomass ,Spawn Number   ,Vulnrbl BMS    ,Vulnrbl Number,F
,Catch           ,Recruitment    ,M              ,SSB Status

 2815000.0      ,    1, 1985, 86143278.    , 14064680.     , 56814937.    , 3309280.9     , 28447575.     , 7867565.0    ,
0.0000000      , 0.0000000     , 1048020.7    ,0.18911762     , 1.0622661
 2815000.0      ,    1, 1986, 85844286.    , 15743170.     , 55704875.    , 3170176.3     , 26539406.     , 7639911.1    ,
0.0000000      , 0.0000000     , 4708025.4    ,0.18911762     , 1.0415113
 2815000.0      ,    1, 1987, 82586741.    , 13141793.     , 54236708.    , 2987387.8     , 26403762.     , 7466050.7    ,
0.0000000      , 0.0000000     , 127686.85    ,0.18911762     , 1.0140611
```
etc.

Specified Survey times – ROOTname.PS

The data are derived for the specified survey date in each year.

All results are for the survey increment in each year.

Test	The test of yield – either γB_0, Catch, *F* (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
Year	The first year of the split year – can be used to relate this information to other files in a database
Inc	Increment in year as a fraction of the whole year – time refers to the start of the increment.
Total Biomass	Total biomass
Total Number	Total number
Spawn Biomass	Spawning stock biomass – taken from the maturity function
Spawn Number	Spawning stock number – taken from the maturity function
Vulnrbl BMS	Vulnerable biomass – taken from vulnerability/effort
Vulnrbl Number	Vulnerable number – taken from vulnerability/effort

Example

```
Test         ,Trial,Year , Inc  ,Total biomass ,Total Number  ,Spawn Biomass ,Spawn Number  ,Vulnrbl BMS   ,Vulnrbl
Number,

 2815000.0   ,    1, 1985,0.0000, 91577819.    , 16142007.    , 57152628.    , 3368802.0    , 32533695.    , 8774122.4
 2815000.0   ,    1, 1986,0.0000, 91050055.    , 18068589.    , 56384293.    , 3265445.2    , 29456599.    , 8305922.8
 2815000.0   ,    1, 1987,0.0000, 87858037.    , 15082862.    , 55179765.    , 3110365.1    , 28352390.    , 8253574.5
 2815000.0   ,    1, 1988,0.0000, 86031306.    , 15243230.    , 53561778.    , 2934140.7    , 29099318.    , 7945940.9
etc.
```

In each increment – ROOTname.PI

The data are derived as for survey times but for each increment in each year

Test	The test of yield – either γB_0, Catch, *F* (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
Year	The first year of the split year – can be used to relate this information to other files in a database
Inc	Increment in year as a fraction of the whole year – time refers to the start of the increment.
Total Biomass	Total biomass
Total Number	Total number
Spawn Biomass	Spawning stock biomass – taken from the maturity function
Spawn Number	Spawning stock number – taken from the maturity function
Vulnrbl BMS	Vulnerable biomass – taken from vulnerability/effort
Vulnrbl Number	Vulnerable number – taken from vulnerability/effort
F x effort	Fishing mortality for that increment
Catch	Catch taken during that increment
M	Natural mortality rate in that increment

Example

Note, in this example, the lines are wrapped around

```
Test            ,Trial,Year , Inc  ,Total biomass ,Total Number  ,Spawn biomass ,Spawn Number  ,Vulnrbl BMS   ,Vulnrbl
Number,F x effort   ,Catch        ,M

 0.0000000     ,    1, 1999,.00000, 36016.554    , 3.8875147     , 26458.664     ,0.31131061     , 0.0000000     , 0.0000000
, 0.0000000    , 0.0000000    ,0.33003788E-01
 0.0000000     ,    1, 1999,.04167, 39932.115    , 3.7616431     , 31444.972     ,0.37258755     , 0.0000000     , 0.0000000
, 0.0000000    , 0.0000000    ,0.33003788E-01
 0.0000000     ,    1, 1999,.08333, 44823.412    , 3.6394919     , 34991.870     ,0.39546457     , 34991.870     ,0.39546457
, 0.0000000    , 0.0000000    ,0.33003788E-01
etc.
```

4.11.6   Cohort Status

The Cohort Status files are similar to the population files, but for each age class.

General - incl SSB status – ROOTname.CG

As for Population General but note the addition of the Age class for each line.

Test	The test of yield – either γB_0, Catch, *F* (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
Year	The first year of the split year – can be used to relate this information to other files in a database
Age	Age class
Cohort Biomass	Cohort biomass in the first increment (0) of the year
Cohort Number	Cohort number in the first increment (0) of the year
Spawn Biomass	Average spawning stock biomass during the spawning season in the Year
Vulnrbl BMS	Average vulnerable biomass of fish during specified period for monitoring fishable biomass
Catch	Catch for the year

Example

```
Test          ,Trial,Year ,Age,Cohort biomass,Cohort Number ,Spawn Biomass ,Vulnerable bms,Catch

 2815000.0    ,    1, 1985  4, 768399.36    , 913093.66    , 0.0000000    , 94790.409    , 0.0000000
 2815000.0    ,    1, 1985  5, 2881341.7    , 2331792.8    , 0.0000000    , 1040811.3    , 0.0000000
 2815000.0    ,    1, 1985  6, 1875107.9    , 1086823.0    , 0.0000000    , 1124559.1    , 0.0000000
 2815000.0    ,    1, 1985  7, 6923699.1    , 2990342.0    , 0.0000000    , 5806824.9    , 0.0000000
 2815000.0    ,    1, 1985  8, 3455909.7    , 1148549.8    , 0.0000000    , 3308088.8    , 0.0000000
```
etc.

Specified Survey times – ROOTname.CS

As for Population Survey monitoring but with age class added.

All results are for the survey increment in each year.

Test	The test of yield – either γB_0, Catch, *F* (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
Year	The first year of the split year – can be used to relate this information to other files in a database
Inc	Increment in year as a fraction of the whole year – time refers to the start of the increment.
Age	Age class
Cohort Biomass	Cohort biomass
Cohort Number	Cohort number
F	F for the cohort in the increment
Vlnrblty	Vulnerability coefficient
Maturity	Maturity coefficient

Example

```
Test          ,Trial,Year , Day  ,Age,Cohort biomass,Cohort Number ,Length        ,F             ,Vlnrblty      ,Maturity

 2815000.0    ,    1, 1985,0.0000,  4, 705589.51     , 1048020.7     , 421.11623     , 0.0000000     , 0.0000000     ,
0.0000000
 2815000.0    ,    1, 1985,0.0000,  5, 2732966.0     , 2676359.9     , 479.53765     , 0.0000000     ,0.25000000     ,
0.0000000
 2815000.0    ,    1, 1985,0.0000,  6, 1823258.7     , 1247393.4     , 536.28919     , 0.0000000     ,0.50000000     ,
0.0000000
etc.
```

All increments in each year – ROOTname.CI

The status of each age class in each increment in each year of every trial. This file needs to be used with caution. A single test with Ages 4-35 running for the known catch and recruitment history (1985 to 2003) with 11 trials took up 28 MB of space. The data are derived as for survey times but for each increment in each year

Test	The test of yield – either γB_0, Catch, F (the example below is catch)
Trial	The number of the respective trial – can be used to relate this information to other files in a database
Year	The first year of the split year – can be used to relate this information to other files in a database
Inc	Increment in year as a fraction of the whole year – time refers to the start of the increment.
Age	Age class
Cohort Biomass	Cohort biomass
Cohort Number	Cohort number
Length	Length of fish at age in the increment
Maturity	Maturity of fish at age in the increment
M	Natural mortality rate applied in that increment
F	Fishing mortality rate applied in that increment
Vulnrblty	Age-specific x Length-specific Vulnerability
Vulnrblty x effort	Vulnerability x fishing effort in the increment
Catch in Inc	Catch taken during that increment

Example

Note, in this example, the lines are wrapped around

```
Test          ,Trial,Year , Inc ,Age,Cohort biomass,Cohort Number ,Length          ,Maturity      ,M              ,F
,Vlnrblty      ,Vln x effort  ,Catch in Inc

 0.0000000    ,    1, 1999,0.0000,  0, 0.0000000    , 3.0588099    , 0.0000000    , 0.0000000    ,0.33003788E-01,
0.0000000    , 0.0000000    , 0.0000000    , 0.0000000
etc.
```

4.12 PROGRAM STRUCTURE

The structure of the Generalised Yield Model Version 5.00 is illustrated in Figures GS3-GS6.

These figures are ordered to start at the central point of the program, the projection of the population over one year, and progress to the upper layers of the program. This is done to mirror the progression through the specifications.

Figure GS3: Schematic showing the steps involved in projecting a population over one year. Program routines are shown in ***bold italics***. Numbers are given for reference in the text.
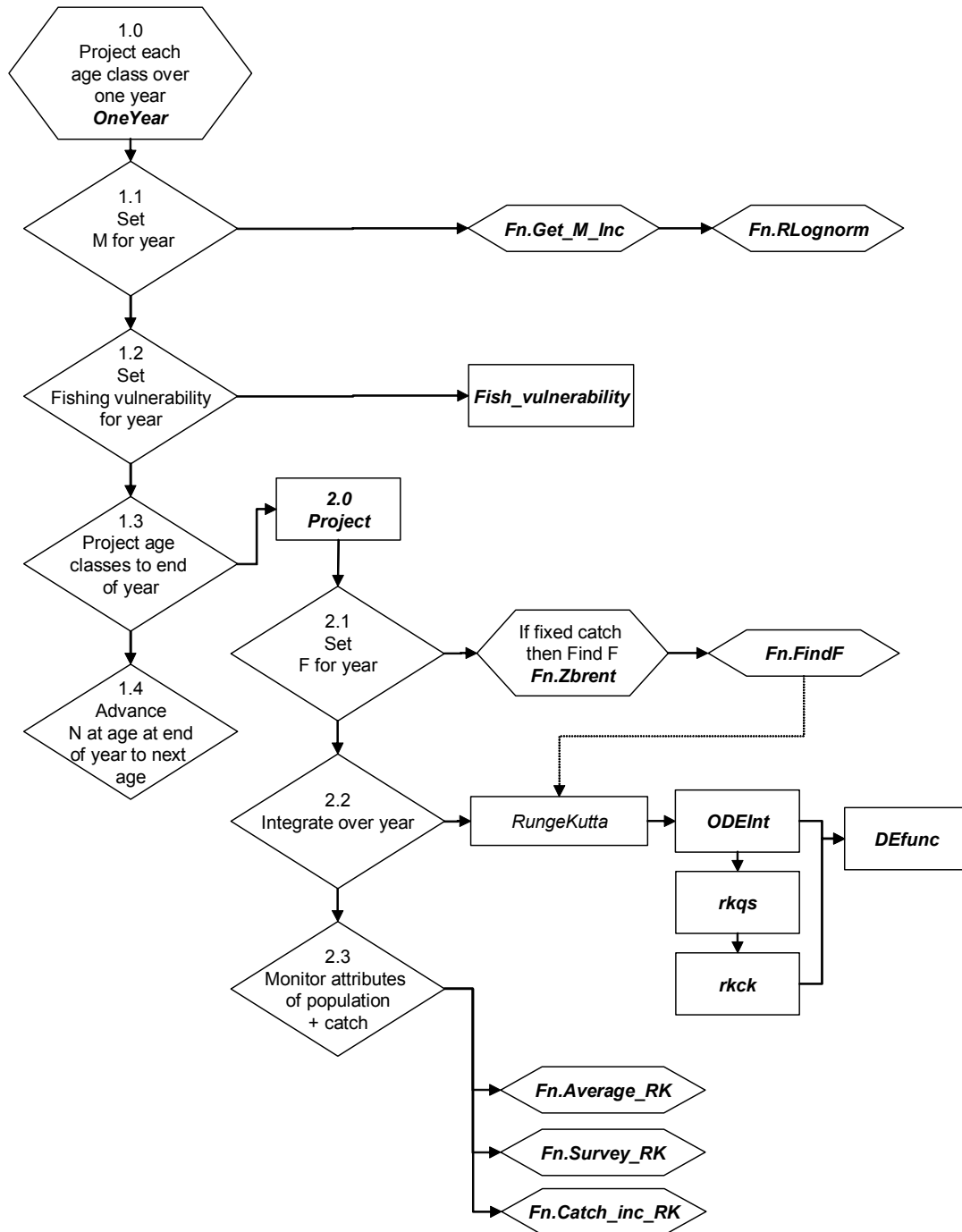
Figure GS4: Schematic showing the steps involved in undertaking a test of a harvest scenario. Program routines are shown in ***bold italics***. Numbers are given for reference in the text.
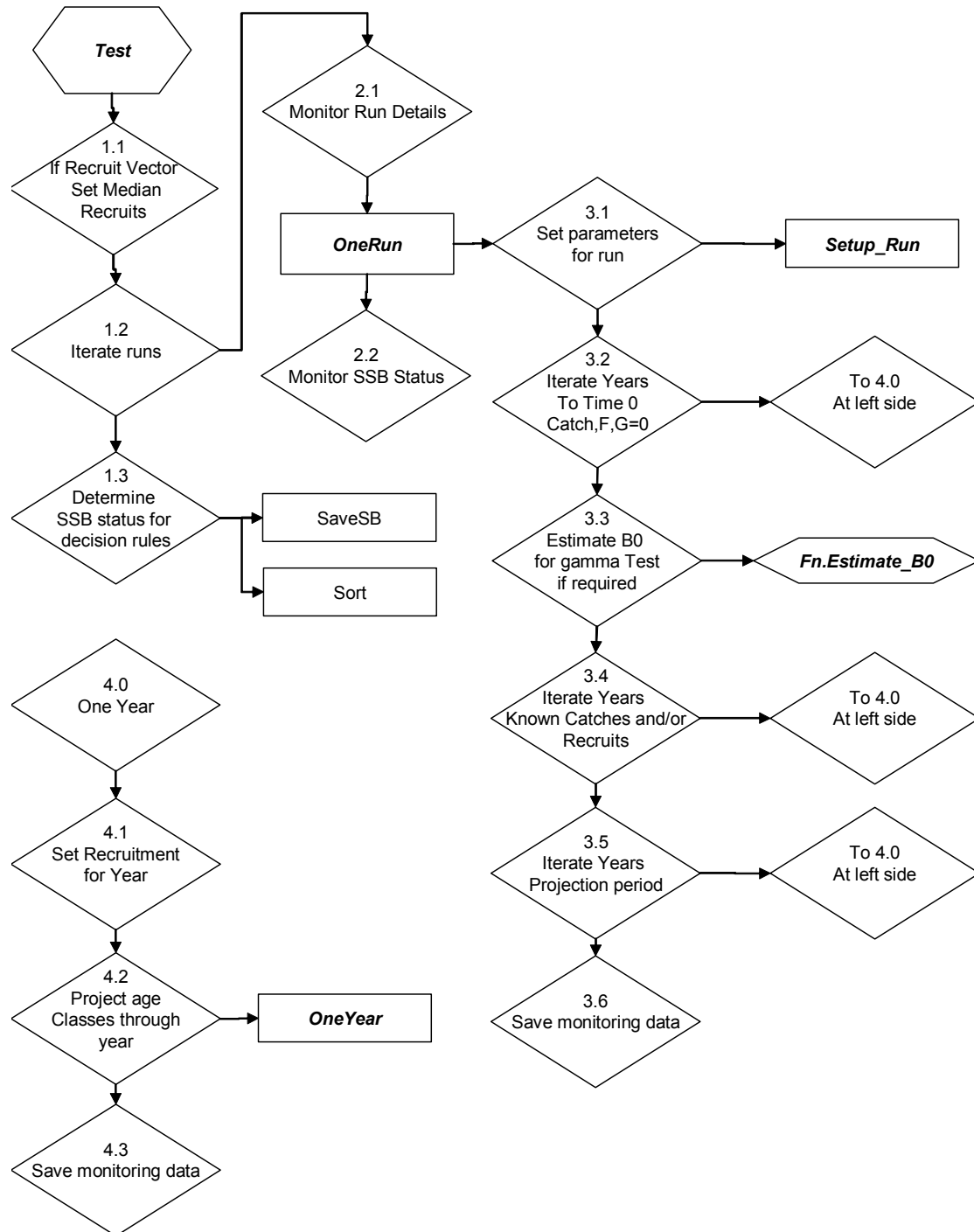
Figure GS5: Schematic showing the steps involved in setting up a test [***Setup_Run***] indicated in Figure GS4. Program routines are shown in ***bold italics***. Numbers are given for reference in the text.
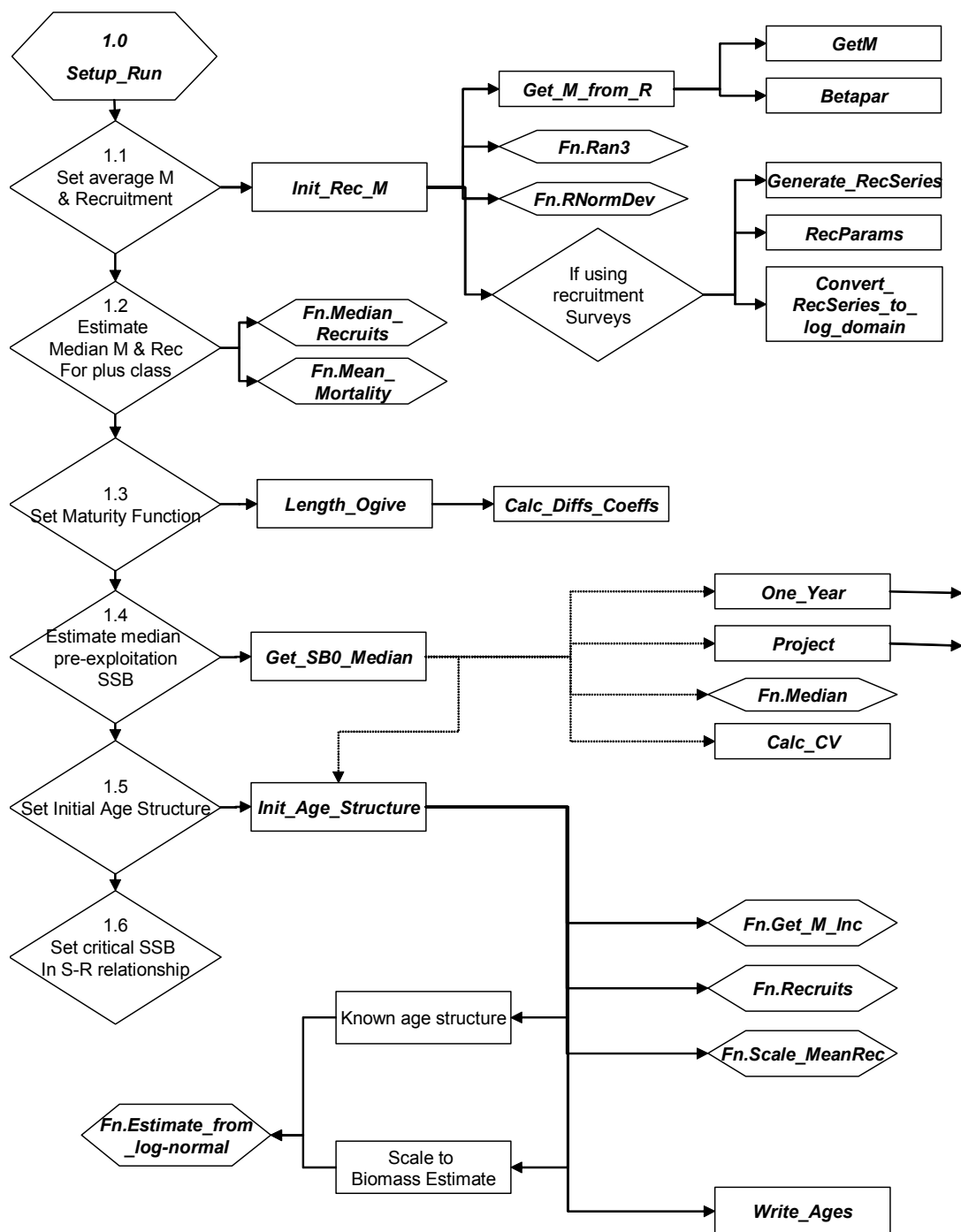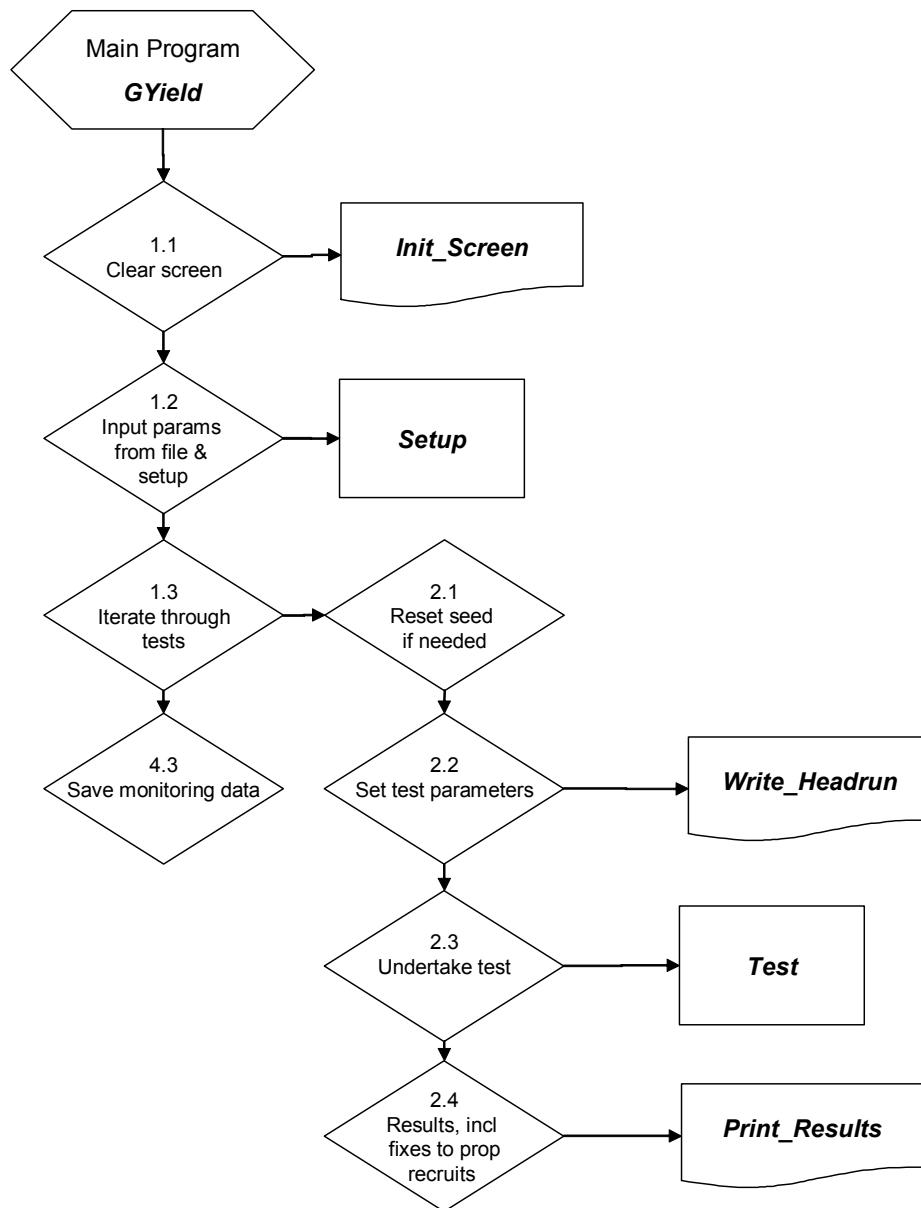
Figure GS6: Schematic showing the steps involved in undertaking all specified tests. Program routines are shown in **bold italics**. Numbers are given for reference in the text.

Part 5

WORKED EXAMPLES OF THE
GENERALISED YIELD MODEL

PART 5
Validating the GYM

The following examples illustrate how to validate the operation of the GYM. These files are provided with the software. These workings of the Generalised Yield Model use Version GYM500. The contents of the files may vary as a result of different random number sequences used by different computers. Nevertheless, the calculations show the means by which the different aspects of the program can be validated.

5.1   Basic Operation Examples

GYM Specification Example G01

Description: Illustration of a cohort advancing from one age class to the next over years with new recruits added at age 0 each year.

Base File rootname: G01
Base File Details:
     Ages in population: 0-7 (no plus class)
     Weight at age function   all ages = 1
     Annual Natural Mortality rate   0
     Recruitment function   log-normal with mode at 1.0
     Increments (time steps) per year   12
Variation: None

Results observed in file: G01.CG
Results example output:

This table is only part of the G01.CG file. Note that the cohort is identified in this example in bold but that there is no identifier in the output table. The records can be sorted into cohorts by generating a new column, 'Cohort', in the table and copying a formula into each record of the column where

Cohort = Year-Age

Year	Age	Cohort Number
1999	0	**0.59639**
1999	1	0.943785
1999	2	0.491751
1999	3	1.135944
1999	4	0.688199
1999	5	1.173503
1999	6	1.373555
1999	7	0.271859
2000	0	0.874111
2000	1	**0.59639**
2000	2	0.943785
2000	3	0.491751
2000	4	1.135944
2000	5	0.688199
2000	6	1.173503
2000	7	1.373555
2001	0	2.227403
2001	1	0.874111
2001	2	**0.59639**
2001	3	0.943785
2001	4	0.491751
2001	5	1.135944
2001	6	0.688199
2001	7	1.173503

GYM Specification Example G02

Description: Effects of annual natural mortality rate during the year and between years.

Base File rootname: G02

Base File Details: G01

Variation:
Annual Natural Mortality rate   M=0.8
Annual Fishing Mortality rate   F=0.0

Results observed in file: G02.PG   indicates the mortality rate each year
Results example output:

Year	Total Number	M
1999	1.284648	0.8
2000	1.450888	0.8
2001	2.877046	0.8
2002	2.635682	0.8
2003	2.10595	0.8
2004	1.056519	0.8
2005	2.467218	0.8
2006	1.793559	0.8
2007	1.153582	0.8

Note that this is only an extract from the file.

Results observed in file: G02.CG   indicates the progression from one year to next in which the mortality rate can be estimated and validated

Results example output:

Year	Age	Cohort Number	*Cohort*	*Estimated M*
1999	6	1.13E-02	*1993*	*0.80*
2000	7	5.08E-03	*1993*	
1999	5	2.15E-02	*1994*	*0.80*
2000	6	9.66E-03	*1994*	
1999	4	2.81E-02	*1995*	*0.80*
2000	5	1.26E-02	*1995*	
1999	3	0.10305	*1996*	*0.80*
2000	4	4.63E-02	*1996*	
1999	2	9.93E-02	*1997*	*0.80*
2000	3	4.46E-02	*1997*	
1999	1	0.42407	*1998*	*0.80*
2000	2	0.190547	*1998*	
1999	0	0.59639	*1999*	*0.80*
2000	1	0.267975	*1999*	

This is only a partial extract of the file for the first two years of the projection, giving the first 3 columns of the table above. Cohort *was estimated as described for Example G01.* Estimated M *was estimated as* ($-\ln(N_{Year+1,Age+1}/N_{Year,Age})$) *to check that the annual natural*

mortality rate was as expected. The table is sorted by Cohort then by Year before M is estimated. Age Class 7 from 1999 is ignored as it has disappeared in 2000.

Results observed in file: G02.CI indicates the numbers at age at the beginning of each increment (time step) in the year and the mortality rate applied to that age over the course of that increment.

Results example output:

Year	Inc	Age	Cohort Number	M Per Inc	Annual
1999	0	0	0.59639	3.33E-02	
1999	0.0417	0	0.576838	3.33E-02	
1999	0.0833	0	0.559127	3.33E-02	
1999	0.125	0	0.541416	3.33E-02	
1999	0.1667	0	0.523705	3.33E-02	
1999	0.2083	0	0.505994	3.33E-02	
1999	0.25	0	0.488283	3.33E-02	
1999	0.2917	0	0.475393	3.33E-02	
1999	0.3333	0	0.462503	3.33E-02	
1999	0.375	0	0.449613	3.33E-02	
1999	0.4167	0	0.436724	3.33E-02	
1999	0.4583	0	0.423834	3.33E-02	
1999	0.5	0	0.410944	3.33E-02	
1999	0.5417	0	0.398054	3.33E-02	
1999	0.5833	0	0.385164	3.33E-02	
1999	0.625	0	0.372275	3.33E-02	
1999	0.6667	0	0.359385	3.33E-02	
1999	0.7083	0	0.346495	3.33E-02	
1999	0.75	0	0.333605	3.33E-02	
1999	0.7917	0	0.320715	3.33E-02	
1999	0.8333	0	0.307826	3.33E-02	
1999	0.875	0	0.296357	3.33E-02	
1999	0.9167	0	0.286896	3.33E-02	
1999	0.9583	0	0.277436	3.33E-02	
1999	1	0	0.267975	3.33E-02	**0.80**

This table is only part of the G02.CI file. The records for one year were sorted by age to extract this subset of the table that shows the progression through the year of the Age 0 cohort. Note that the table shows a mortality rate for the increment '1.0000' This is not used as the beginning of that increment is the end of the year with that increment being the first of the following year. The annual rate of mortality is checked by summing M for all records except that increment '1.0000'. This check is shown in bold adjacent to the last record.

GYM Specification Example G03

Description: Effects of adding fishing mortality.

Base File rootname: G03

Base File Details: G01

Variation:
    Annual Natural Mortality rate   M=0.8
    Annual Fishing Mortality rate   F=0.1

Results observed in file: G03.PG   indicates the mortality rates each year and the catch arising from fishing mortality

Results example output:

Year	Total Number	F	Catch	M
1999	1.284648	0	0	0.8
2000	1.450888	0.1	9.57E-02	0.8
2001	2.815225	0.1	0.185627	0.8
2002	2.487881	0.1	0.164043	0.8
2003	1.933456	0.1	0.127486	0.8
2004	0.896963	0.1	5.91E-02	0.8
2005	2.357493	0.1	0.155445	0.8
2006	1.64416	0.1	0.10841	0.8
2007	1.016649	0.1	6.70E-02	0.8

Tthere is no fishing mortality in the first year because this is the year prior to exploitation. This is only an extract from the file.

Results observed in file: G03.CG   indicates the progression from one year to next in which the mortality rate can be estimated and validated

Results example output:

Year	Age	Cohort Number	*Cohort*	*Estimated Z*
1999	7	1.01E-03	*1992*	
1999	6	1.13E-02	*1993*	*0.80*
2000	7	5.08E-03	*1993*	
1999	5	2.15E-02	*1994*	*0.80*
2000	6	9.66E-03	*1994*	*0.90*
2001	7	3.93E-03	*1994*	
1999	4	2.81E-02	*1995*	*0.80*
2000	5	1.26E-02	*1995*	*0.90*
2001	6	5.12E-03	*1995*	
1999	3	0.10305	*1996*	*0.80*
2000	4	4.63E-02	*1996*	*0.90*
2001	5	1.88E-02	*1996*	
1999	2	9.93E-02	*1997*	*0.80*
2000	3	4.46E-02	*1997*	*0.90*
2001	4	1.81E-02	*1997*	

1999	1	0.42407	*1998*	*0.800001*
2000	2	0.190547	*1998*	*0.9*
2001	3	7.75E-02	*1998*	
1999	0	0.59639	*1999*	*0.800001*
2000	1	0.267975	*1999*	*0.9*
2001	2	0.10895	*1999*	
2000	0	0.874111	*2000*	*0.9*
2001	1	0.355387	*2000*	
2001	0	2.227403	*2001*	

This is only a partial extract of the file for the first two years of the projection, giving the first 3 columns of the table above. The remaining columns were estimated as for Example G02. Estimated Z is the total mortality expected from Z=(M+F). Note that the total mortality in 1999 was equal to natural mortality because of the absence of fishing in that year (as described above). Age 7 in 1999 and Age 0 in 2001 do not have estimates of Z.

Results observed in file: G03.CI indicates the numbers at age at the beginning of each increment (time step) in the year and the mortality rate applied to that age over the course of that increment.

The application of mortality per increment and by age enables the mortality rates to vary during the year and with age through intra-annual and age-specific functions for natural and fishing mortalities. These are specified by varying the coefficients of *M* and *F* (discussed below).

Results example output:

Year	Inc	Age	Cohort Number	M	F	*Annual M*	*Annual F*
2000	0	0	0.874111	3.33E-02	4.17E-03		
2000	0.0417	0	0.841939	3.33E-02	4.17E-03		
2000	0.0833	0	0.813149	3.33E-02	4.17E-03		
2000	0.125	0	0.78436	3.33E-02	4.17E-03		
2000	0.1667	0	0.755571	3.33E-02	4.17E-03		
2000	0.2083	0	0.726781	3.33E-02	4.17E-03		
2000	0.25	0	0.697992	3.33E-02	4.17E-03		
2000	0.2917	0	0.675897	3.33E-02	4.17E-03		
2000	0.3333	0	0.653803	3.33E-02	4.17E-03		
2000	0.375	0	0.631709	3.33E-02	4.17E-03		
2000	0.4167	0	0.609614	3.33E-02	4.17E-03		
2000	0.4583	0	0.58752	3.33E-02	4.17E-03		
2000	0.5	0	0.565425	3.33E-02	4.17E-03		
2000	0.5417	0	0.543331	3.33E-02	4.17E-03		
2000	0.5833	0	0.521237	3.33E-02	4.17E-03		
2000	0.625	0	0.499142	3.33E-02	4.17E-03		
2000	0.6667	0	0.479972	3.33E-02	4.17E-03		
2000	0.7083	0	0.462108	3.33E-02	4.17E-03		
2000	0.75	0	0.44522	3.33E-02	4.17E-03		
2000	0.7917	0	0.428784	3.33E-02	4.17E-03		
2000	0.8333	0	0.41295	3.33E-02	4.17E-03		

2000	0.875	0	0.397739	3.33E-02	4.17E-03		
2000	0.9167	0	0.383094	3.33E-02	4.17E-03		
2000	0.9583	0	0.368993	3.33E-02	4.17E-03		
2000	1	0	0.355387	3.33E-02	4.17E-03	*0.80*	*0.10*

This table is only part of the G03.CI file. The records for one year were sorted by age to extract this subset of the table that shows the progression through the year of the Age 0 cohort. Note that the table shows a mortality rate for the increment '1.0000' This is not used as the beginning of that increment is the end of the year with that increment being the first of the following year. The annual rate of mortality is checked by summing M for all records except that increment '1.0000'. This check is shown in bold adjacent to the last record.

GYM Specification Example G04

Description: Illustration of lookup tables, based on the krill assessment for Area 48.

Base File rootname: 00ES48
Base File Details: As for krill
Variation:
    Increments in year   12
    Number of increments in which growth occurs   3 (i.e. summer)

Results observed in file: G04.LUK
Results example output:

Age Class	Increment	Age	Length	Weight	Maturity at Age	M at age	F at age
1	0	1	22.03221	10694.84	1	1	0
1	1	1.083333	27.43225	20643.55	1	1	4
1	2	1.166667	32.08011	33014.73	1	1	4
1	3	1.25	36.08057	46969.94	1	1	4
1	4	1.333333	36.08057	46969.94	1	1	0
1	5	1.416667	36.08057	46969.94	1	1	0
1	6	1.5	36.08057	46969.94	1	1	0
1	7	1.583333	36.08057	46969.94	1	1	0
1	8	1.666667	36.08057	46969.94	1	1	0
1	9	1.75	36.08057	46969.94	1	1	0
1	10	1.833333	36.08057	46969.94	1	1	0
1	11	1.916667	36.08057	46969.94	1	1	0
2	0	2	36.08057	46969.94	1	1	0
2	1	2.083333	39.52379	61741.27	1	1	4
2	2	2.166667	42.48739	76697.33	1	1	4
2	3	2.25	45.03819	91357.21	1	1	4
2	4	2.333333	45.03819	91357.21	1	1	0
2	5	2.416667	45.03819	91357.21	1	1	0
2	6	2.5	45.03819	91357.21	1	1	0
2	7	2.583333	45.03819	91357.21	1	1	0
2	8	2.666667	45.03819	91357.21	1	1	0
2	9	2.75	45.03819	91357.21	1	1	0
2	10	2.833333	45.03819	91357.21	1	1	0
2	11	2.916667	45.03819	91357.21	1	1	0
3	0	3	45.03819	91357.21	1	1	0
3	1	3.083333	47.23369	105379.4	1	1	4
3	2	3.166667	49.12337	118539.8	1	1	4

3	*3*	3.25	50.74983	130708.5	1	1	4
3	*4*	3.333333	50.74983	130708.5	1	1	0
3	*5*	3.416667	50.74983	130708.5	1	1	0
3	*6*	3.5	50.74983	130708.5	1	1	0
3	*7*	3.583333	50.74983	130708.5	1	1	0
3	*8*	3.666667	50.74983	130708.5	1	1	0
3	*9*	3.75	50.74983	130708.5	1	1	0
3	*10*	3.833333	50.74983	130708.5	1	1	0
3	*11*	3.916667	50.74983	130708.5	1	1	0
4	*0*	4	50.74983	130708.5	1	1	0

This table is only part of the G04.LUK file for Ages 1.0 to 4.0. The columns on 'Age Class' and 'Increment' have been added to illustrate how the values apply during the year and for each Age Class. Note that the age specific functions for maturity, M and F do not include the length based functions.

Results observed in file: G04.CI (using information from G04.PG)
Results example output:

Time	Length	Weight	M coeff	F coeff	Maturity coeff
1	22.03221	10694.84	1	0	0
1.0833	27.43225	20753.2	1	0	0
1.1667	32.08011	33084.96	1	0.924495	0
1.25	36.08057	45133.16	1	2.702473	0.551713
1.3333	36.08057	46970.76	1	0	0.551713
1.4167	36.08057	46970.82	1	0	0.551713
1.5	36.08057	46970.87	1	0	0.551713
1.5833	36.08057	46970.94	1	0	0.551713
1.6667	36.08057	46971.01	1	0	0.551713
1.75	36.08057	46971.07	1	0	0.551713
1.8333	36.08057	46971.15	1	0	0.551713
1.9167	36.08057	46971.24	1	0	0.551713
2	36.08057	46969.94	1	0	0.551713
2.0833	39.52379	61554.4	1	4	1
2.1667	42.48739	76594.83	1	4	1
2.25	45.03819	88490.18	1	4	1
2.3333	45.03819	91333.5	1	0	1
2.4167	45.03819	91331.9	1	0	1
2.5	45.03819	91330.17	1	0	1
2.5833	45.03819	91328.49	1	0	1
2.6667	45.03819	91326.75	1	0	1
2.75	45.03819	91324.79	1	0	1
2.8333	45.03819	91322.54	1	0	1
2.9167	45.03819	91319.97	1	0	1
3	45.03819	91357.21	1	0	1
3.0833	47.23369	105109.3	1	4	1
3.1667	49.12337	118321.2	1	4	1
3.25	50.74983	130225.4	1	4	1
3.3333	50.74983	130720.1	1	0	1
3.4167	50.74983	130720.9	1	0	1
3.5	50.74983	130721.8	1	0	1
3.5833	50.74983	130722.6	1	0	1

3.6667	50.74983	130723.4	1	0	1
3.75	50.74983	130724.4	1	0	1
3.8333	50.74983	130725.5	1	0	1
3.9167	50.74983	130726.8	1	0	1
4	50.74983	130708.5	1	0	1

This table is derived from the G04.CI file to show the method for determining the lookup table used in a trial and in a given year. Steps to obtain this part of the table are:

i) *extract the rows for Trial 1 and Year 2003.*
ii) *Add a column of Time = Age+Inc*
iii) *Delete values for Inc=1.0*
iv) *Sort by Time*
v) *Length at Age is present in Length*
vi) *Weight at Age is Cohort Biomass divided by Cohort Number*
vii) *M coefficient at age is the value for M in the table divided by [M read from G04.PG for Trial 1, Year 2003 divided by Number of Increments (Incs=12 in this example)]*
viii) *F coefficient at age is present in VlnxEffort (note fishing season is set to be contained within one quarter of a year: summer)*
ix) *Maturity at age is present in Maturity*
x) *Only rows for Time (age) from 1 to 4 are copied into the table above for illustration.*

5.2   Long-Lived Species Examples

The following examples step through the checking for the example long-lived species

GYM Specification Example LL01

Description: Long-lived species

Base File rootname: LL01
Base File Details: Long-lived species

Base input parameters

AGE STRUCTURE	First age-class in stock	2
	Last age-class in stock	30
	Oldest age in last class	60
RECRUITMENT	Recruitment Function	L
	Use recruitment surveys to est recs	False
	Use recruitments in time series	False
	Mean recruitment	1000000.0
	Min Coefficient of Variation	1.0
	Max Coefficient of Variation	1.0

	Use Standard Error of Mean	False
	Number of replicates	1
	x.SB0 for recruitment depletion - x =	0
NATURAL MORTALITY	Mean Annual M	0.15
	SD of M between years within runs	0.0
	Alter Mean Annual M by Multiplier	False
	Probability of M being multiplied	0.0
	Amount Mean M to be multiplied by	1.0
	Natural Mortality coefficient with age	0(1)
	Natural Mortality with time of year (date coefficient)	01/01(1)
LENGTH AT AGE	Growth Curve Type	VB
	time 0	0.0
	Linf	100.0
	k	0.06
WEIGHT AT AGE	Weight-length parameter - A	0.000025
	Weight-length parameter - B	2.8
MATURITY	Maturity Type	L
	Length, 50% are mature	50.0
	Range over which maturity occurs	20.0
SPAWNING SEASON	First Day of Spawning Season (dd/mm)	01/07
	Last Day of Spawning Season (dd/mm)	01/07
EVALUATION OF YIELD	Type of evaluation	F
	Vector of Gammas, Catches or Fishing Mortalities	0. 0.1 0.2 0.3 0.4 0.5
	Do yield per recruit analysis	False
SIMULATION	Number of runs in simulation	1001

CHARACTERISTICS		
	Depletion Level for Test	0.2
	Seed for random number generator	-24189
	Reset seed to this value for each test	True
CHARACTERISTICS OF A TRIAL	Init. pop. structure with random recs	True
	Years to remove initial age structure	1
	Estimate median SB0 before each run	True
	Estimate med SB0 (deterministic/random)	R
	Observations to use in median SB0	1001
	Year 0 of projection	2002
	Reference Start Date in year	01/01
	Increments in year	12
	Years to project stock in simulation	30
	Reasonable upper bound for Annual F	5.0
	Tolerance for finding F in each year	0.00001
GENERAL MONITORING OF STOCK		2002 01/03
	Monitor all Years in projection	True
	Start date for monitoring (dd/mm)	01/03
	End date for monitoring (dd/mm)	01/04
	Number of replicates	1
ESTIMATING B0 IN GAMMA CALCULATIONS	Estimate B0 (log-normal)	False
	CV of B0 estimate	0.0
	Coverage of survey	1.0
FISHERIES		
FISHERY	Longline	
	Include fishery in Projection	True
	Tolerance for resolving catches (propn)	0.01

Account for uncertainty	False
Initial year	
Catch by proportion	True
Catch	100
Fishing Selectivity with age	0(1)
Relative fishing effort in each inc. of year (day/month coefficient)	01/01(1)

INITIAL POPULATION STRUCTURE

Age structure from random recs	True
Known age structure	False
Biomass & CV to scale	0/0

Based on the table above of input parameters, the following checks were undertaken.

AGE STRUCTURE

First age-class in stock	2
Last age-class in stock	30
Oldest age in last class	60

Check:

i)   In Excel, Open File: LL01.CG

ii)   Extract numbers at age for 2002 in Trial 1 from Test 0

iii) Plotted in 'LL01.age.structure.2002'

iv)   Check that age 30 appears like a plus class.
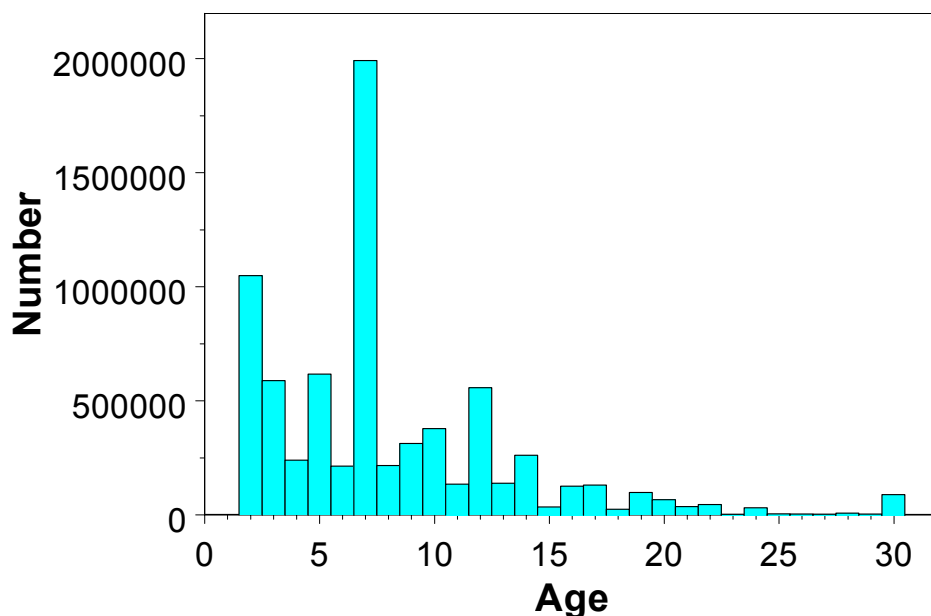
Figure GLL01: Age structure of the long-lived species with mean recruitment at Age 2 of 1 million fish. Note the plus class at Age 30. Drawn from file LL01.CG

RECRUITMENT

Recruitment Function	L
Use recruitment surveys to est recs	False
Use recruitments in time series	False
Mean recruitment	1000000.0
Min Coefficient of Variation	1.0
Max Coefficient of Variation	1.0
Use Standard Error of Mean	False
Number of replicates	1
x.SB0 for recruitment depletion - x =	0.2

Check:

i)   In a text editor or in the GYM post-processing analysis, open File: LL01.PG and extract the test F=0 and save to file.

ii)   The recruitment function for a natural population can be observed by plotting all values of recruitment against the spawning biomass from the previous year. Given the changes in parameters between trials, the median spawning biomass may vary from one trial to another. The stock-recruitment relationship in the GYM is governed by the median spawning biomass prior to the projections (if the median is not estimated then it will be the spawning biomass in the year just prior to projections). Thus, the stock-recruitment relationship is best plotted against the SSB status (which is the spawning biomass for a year relative to the median pre-exploitation spawning biomass for the trial). This plot can be compared to a raw plot of the recruitment vs spawning biomass.

iii)   To create the plot file, add a column to place the recruitment from the following year into the year of the spawning biomass. Note that in Excel a global copy of the formula would need to exclude the last year of a trial from copying the

recruitment for the first year of the next trial. In this example, the formula used was (=if(Year=2032,"NA",Recruitment in next year) i.e. if Year is the last year of the trial then write to the cell a value for a missing value, otherwise right the value of recruitment for the following year.

iv)   Saved file as LL01 – F=0 SSB and recs.xls

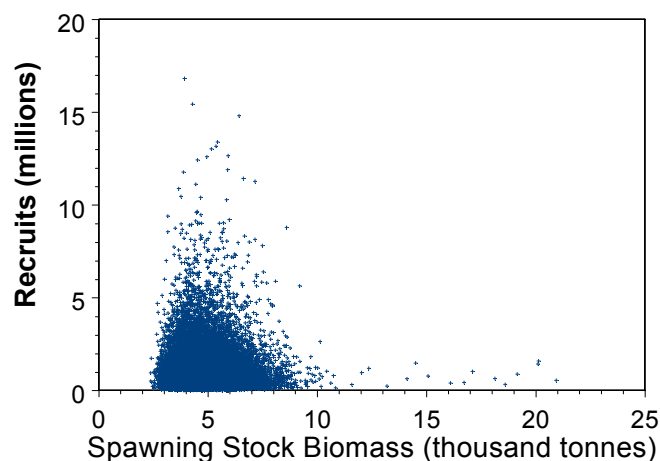v)   Plotted in 'LL01.SSB.status.recruits' and 'LL01.Stock.rec'

Figure GLL02: Relationship between spawning stock biomass and recruitment for 1001 trials of 30 years for F=0. Drawn from file LL01.PG
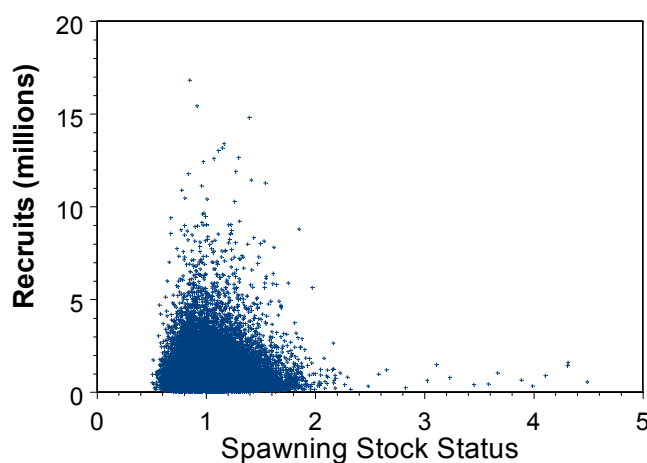
Figure GLL03: Relationship between spawning stock status relative to the median pre-exploitation spawning biomass and recruitment for 1001 trials of 30 years for F=0.

No reduction in recruitment will have occurred because the spawning stock status did not decline below 0.2. Thus, the recruitment parameters can be estimated from all the observations in the test F=0. The summary parameters were estimated from the file above to be

Mean Recruitment   999499

Coefficient of Variation   0.988

The distribution as a box plot is shown below.
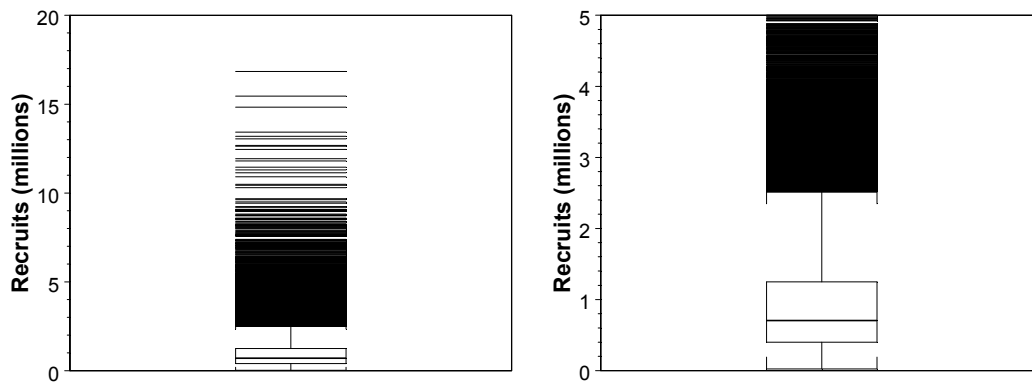
Figure GLL04: Box plot showing the log-normal distribution of recruitments in the trials for F=0 (Mean = 1 million fish, CV = 1.0). Left panel shows the entire distribution while the right panel shows the distribution up to 5 million fish.

NATURAL MORTALITY

Mean Annual M	0.15
SD of M between years within runs	0.0
Alter Mean Annual M by Multiplier	False
Probability of M being multiplied	0.0
Amount Mean M to be multiplied by	1.0
Natural Mortality coefficient with age	0(1)
Natural Mortality with time of year (date coefficient)	01/01(1)

Check:

i)   In Excel, Open File: LL01.CG

ii)   Extract Trial 1 from Test 0

iii)   add Cohort (Year-age)

iv)   sort by Cohort, Age

v)   Extract Year 2000 cohort

vi)   Plot age 2 to 29 (noting that age 30 is a plus class)

vii)   Plotted in 'LL01.mortality'
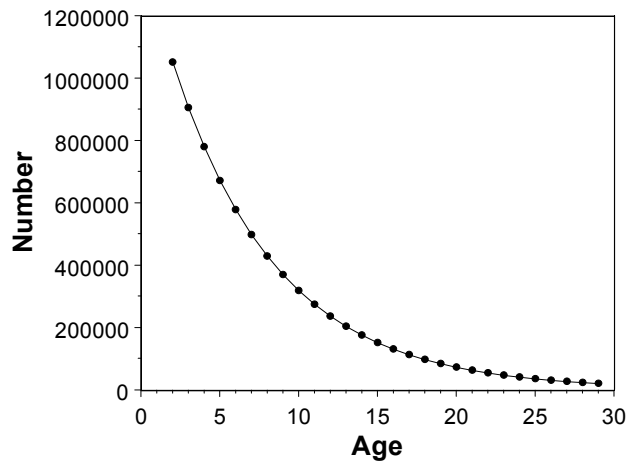
Figure GLL05: Natural mortality for a cohort with initial recruitment marginally greater than the mean recruitment. Drawn from file LL01.CG

LENGTH AT AGE

Growth Curve Type	VB
time 0	0.0
Linf	100.0
k	0.06

Check:

i)   In Excel, Open File: LL01.LUK (the lookup table)

ii)   Plot Length vs Age

iii)   Plotted in 'LL01.length'
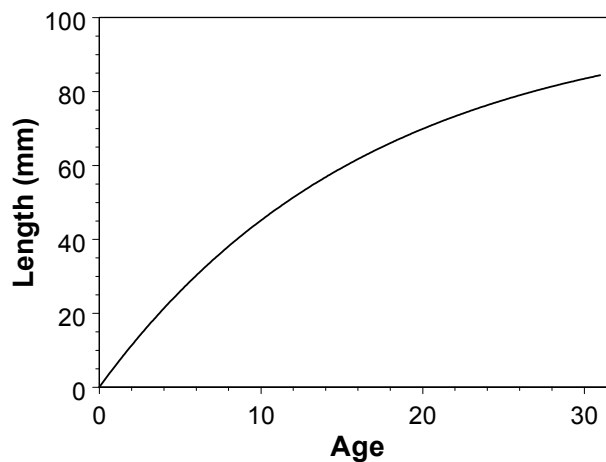
Figure GLL06: Length (mm) at age for the long-lived species. Drawn from file LL01.LUK

WEIGHT AT AGE

Weight-length parameter - A   0.000025

Weight-length parameter - B   2.8

Check:

i)   In Excel, Open File: LL01.LUK (the lookup table)

ii)   Plot Weight vs Age

iii)   Plotted in 'LL01.weight'
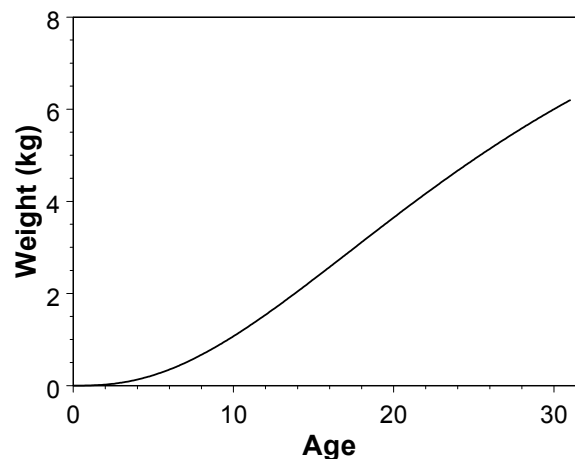
Figure GLL07: Weight (kg) at age for the long-lived species. Drawn from file LL01.LUK

MATURITY

Maturity Type   L

Length, 50% are mature   50.0

Range over which maturity occurs   20.0

Check:

i)   Use the extract of the file LL01.CG above in the examination of age structure using total biomass and spawning biomass at age for 2002 in Trial 1 from Test 0

ii)   Estimate maturity by dividing Spawning biomass by Cohort biomass. Note that this is only approximate as the cohort biomass is estimated at the survey time and the spawning biomass is estimated at the time for spawning. A more accurate calculation is by using the *.CI file.

iii)   Plot Maturity vs Age

iv)   Plotted in 'LL01. maturity'
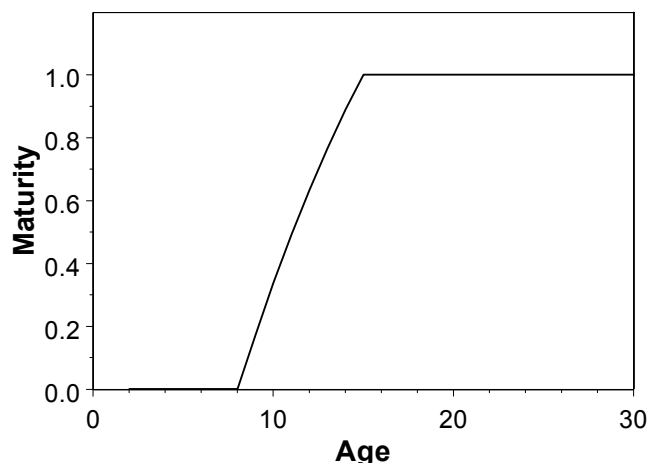
Figure GLL08: Approximate maturity function by age according to the relationship of total biomass and spawning biomass for each cohort at the time of spawning. Drawn from file LL01.CG. Compare the results to length at age in order to check the maturity at length relationship.

SPAWNING SEASON

First Day of Spawning Season (dd/mm)	01/07
Last Day of Spawning Season (dd/mm)	01/07

EVALUATION OF YIELD

Type of evaluation	F
Vector of Gammas, Catches or Fishing Mortalities	0. 0.05 0.075 0.1 0.125 0.15 0.2 0.3
Do yield per recruit analysis	False

SIMULATION CHARACTERISTICS

Number of runs in simulation	1001
Depletion Level for Test	0.2
Seed for random number generator	-24189
Reset seed to this value for each test	True

Check:

i)   The effect of uncertainties in the recruitment function, maturity and natural mortality can be observed in the variation in the estimates of the median pre-exploitation spawning biomass.

ii)   In Excel, Open File: LL01.PG

iii)   Extract all Trials from Test F=0

iv)   Sort by Year and extract only 2002 (the year prior to the projections)

v)   Estimate the median pre-exploitation spawning biomass by dividing the spawning biomass by the SSB status.

vi)   Plot a frequency histogram or box plot of the results.

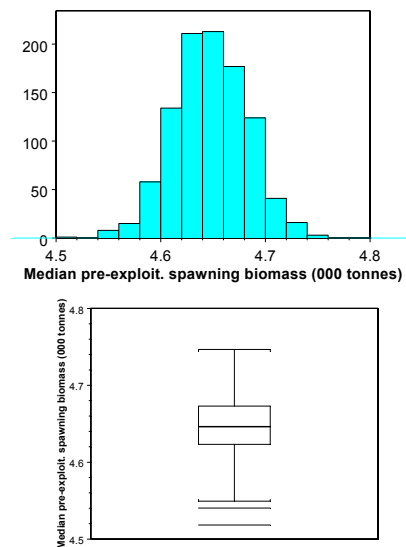vii)   Plotted in 'LL01.median.pre.SSB.hist' and 'LL01.median.pre.SSB.box'

Figure GLL09: Histogram and box plot showing the distribution of estimates of median pre-exploitation spawning biomass (thousand tonnes).

CHARACTERISTICS OF A TRIAL

Init. pop. structure with random recs	True
Years to remove initial age structure	1
Estimate median SB0 before each run	True
Estimate med SB0 (deterministic/random)	R
Observations to use in median SB0	1001
Year 0 of projection	2002
Reference Start Date in year	01/01
Increments in year	12
Years to project stock in simulation	30
Reasonable upper bound for Annual F	5.0
Tolerance for finding F in each year	0.00001

GENERAL MONITORING OF STOCK

	2002 01/03
Monitor all Years in projection	True
Start date for monitoring (dd/mm)	01/03
End date for monitoring (dd/mm)	01/04
Number of replicates	1

ESTIMATING B0 IN GAMMA CALCULATIONS

Estimate B0 (log-normal)	False
CV of B0 estimate	0.0
Coverage of survey	1.0

FISHERIES

FISHERY - Longline

Include fishery in Projection	True
Tolerance for resolving catches (propn)	0.01
Account for uncertainty	False
Initial year	
Catch by proportion	True
Catch	100
Fishing Selectivity with age	0(1)
Relative fishing effort in each inc. of year (day/month coefficient)	01/01(1)

Check:

v)   Use the extract of the file LL01.CG above in the examination of age structure using total biomass and spawning biomass at age for 2002 in Trial 1 from Test 0

vi)   Estimate vulnerability by dividing Vulnerable biomass by Cohort biomass. Note that this is only approximate as the cohort biomass is estimated at the survey time and the vulnerable biomass is estimated at the time for estimating vulnerable biomass. A more accurate calculation is by using the *.CI file.

vii)   Plot Vulnerability vs Age

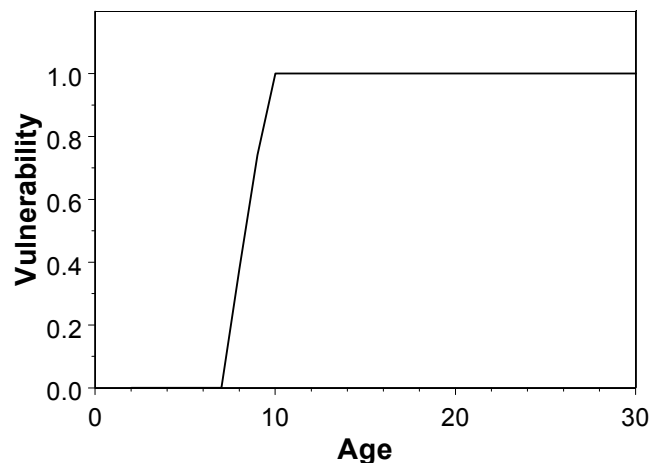viii)   Plotted in 'LL01.vulnerability'

Figure GLL10: Approximate maturity function by age according to the relationship of total biomass and spawning biomass for each cohort at the time of spawning. Drawn from file LL01.CG. Compare the results to length at age in order to check the maturity at length relationship.

INITIAL POPULATION STRUCTURE

Age structure from random recs	True
Known age structure	False
Biomass & CV to scale	0/0

5.3 Projections based on starting biomass compared to general projections

The following projections have been undertaken:
i) random projections according to the above requirements (LL01)
ii) projections from a fixed estimate of total biomass (1500 tonnes) but with unknown age structure (LL02)
iii) projections from an estimate of total biomass (1500 tonnes) with a CV of 0.3 and an unknown age structure (LL03)

The first set of projections aims to determine the fishing mortality according to CCAMLR decision rules for a 35 year projection period (will be filled out in the final version).

The second and third projections consider the period the fishing mortality required to facilitate recovery with a low probability of further depletion (say 0.1 probability of being depleted below 0.8 of the spawning biomass at the time of the survey).

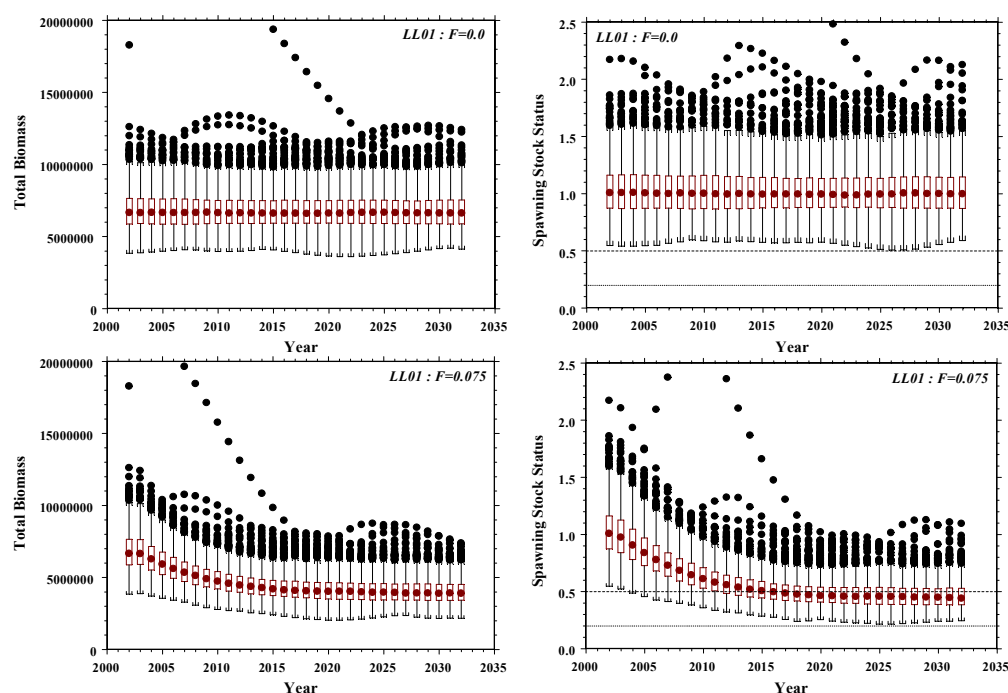The below figures illustrate the text that will be developed over the next couple of days.

Figure GLL11: Box plots (1001 trials) of Total Biomass (left) and Spawning Biomass Status (right) over 35 years for the basic projections above – LL01. Dashed lines correspond with the escapement (0.5 of median pre-exploitation SSB) and depletion (0.2 of median pre-exploitation SSB) rules of CCAMLR.
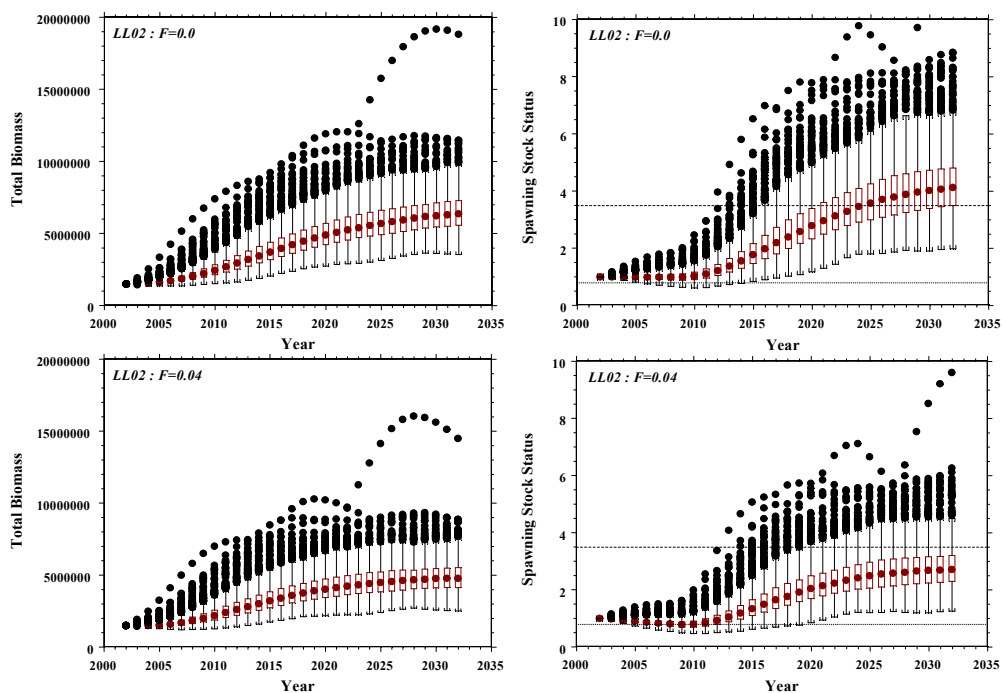
Figure GLL12: Box plots (1001 trials) of Total Biomass (left) and Spawning Biomass Status (right) over 35 years for the fixed initial biomass of 1500 tonnes – LL02. Top panels for F=0.0. Bottom panels for F=0.04. Dashed lines correspond with notional level of recovery (3.5 of initial spawning biomass) and thresholds for further decline (0.8 of initial spawning biomass)
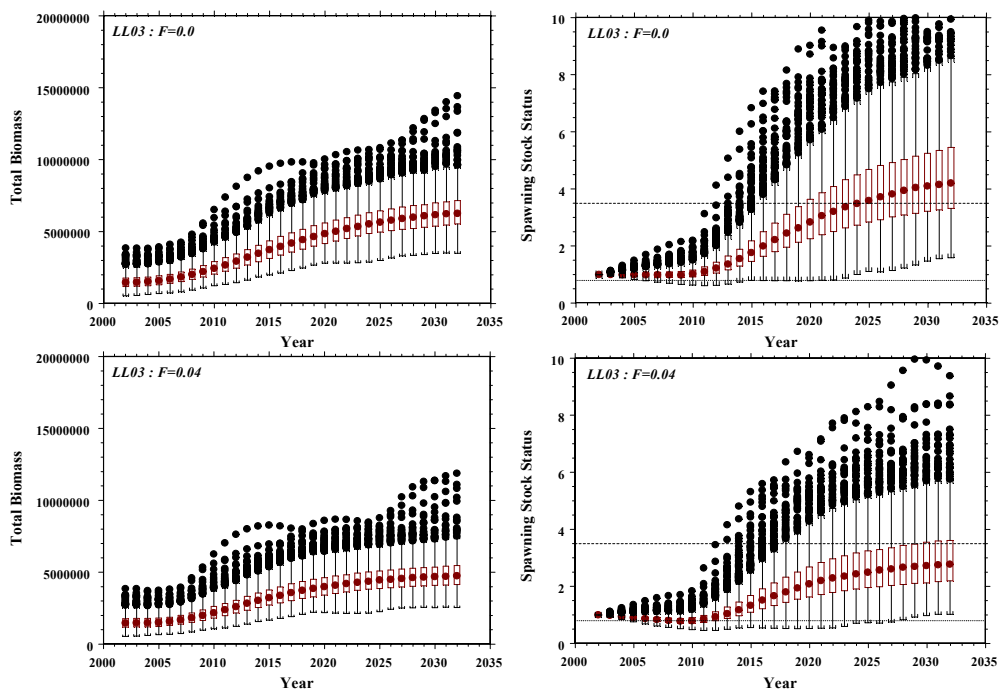

Figure GLL13: Box plots (1001 trials) of Total Biomass (left) and Spawning Biomass Status (right) over 35 years for the estimate of initial biomass of 1500 tonnes with a CV =0.3– LL03. Top panels for F=0.0. Bottom panels for F=0.04. Dashed lines correspond with notional level of recovery (3.5 of initial spawning biomass) and thresholds for further decline (0.8 of initial spawning biomass)

Note: If using a general projection estimating the median pre-exploitation spawning biomass and switching to a specific projection and monitoring status relative to a starting biomass then need to check the following:
   i)   The median pre-exploitation spawning biomass is NOT to be estimated – this is important so that the estimates of status are with respect to the starting biomass
   ii)   the level at which recruitment is considered to be affected. It will need to be set in reference to the starting biomass that comprises the spawning stock rather than expecting it to be set relative to the pre-exploitation median
   iii)   the level considered to be depleted will need to be set relative to the estimate of the initial biomass that comprises the spawning stock.

Points to note:
i) the biomass in the *.PG may not be the same as the starting biomass

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