Technical Description of the Stock Synthesis II Assessment Program

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CONTENTS

INTRODUCTION

This stock assessment model provides a statistical framework for calibration of a population dynamics model using a diversity of fishery and survey data. Such models were first developed in the 1980s (Fournier and Archibald, 1982; Methot, 1989). The Stock Synthesis model (Methot, 2000) was developed in 2 versions. One was an age-length structured model that was developed for assessment of west coast sablefish (Methot and Hightower, 1988) and the other was an age and geographic area model developed for Pacific whiting (Hollowed, Methot and Dorn, 1988). Both versions of synthesis were used for most west coast groundfish and many Alaska groundfish stock assessments during the 1990s. The model documented in this report represents a conversion of synthesis from code written in FORTRAN to code written in C++ with ADMB (Otter Research Ltd., 2000). This conversion provides an opportunity to combine the two previous of synthesis while taking advantage of the advanced features of ADMB and the many lessons learned over the past 15 years with such models.

Stock Synthesis 2 (SS2) is designed to deal with both age and size structure and with multiple stock sub-areas. Thus it is most similar to A-SCALA (Maunders and Watters, 2003); Multifan (Fournier et al, 1990); Multifan-CL (Fournier, Hampton and Siebert, 1998); Stock Synthesis (Methot 2000) and CASAL (Bull, et al, 2004) in basic structure and intent. A general feature of such models is that they tend to cast the goodness-of-fit to the model in terms of quantities that retain the characteristics of the raw data. For example, age composition data that is affected by ageing imprecision is incorporated by building a sub-model of the ageing imprecision process, rather than to pre-process the ageing data in an attempt to remove the effect of ageing imprecision. By building all relevant processes into the model and estimating goodness-of-fit in terms of the original data, we are more confident that the final estimates of model precision will include the relevant sources of variance.

The overall SS2 model is subdivided into three sub-models. First is the population dynamics sub-model. Here the basic abundance, mortality and growth functions operate to create a synthetic representation of the true population. Second is the observation sub-model. This contains the processes and filters designed to derive expected values for the various types of data. For example, survey catchability relates population abundance to the units in which survey CPUE is measured; an ageing imprecision matrix transforms the estimated sampled numbers-at-age into an estimate of the proportions recorded in each otolith ring count. Third is the statistical sub-model that quantifies the magnitude of difference between the various types of data and their expected values and employs an algorithm to search for the set of parameters that maximizes the goodness-of-fit. An additional model layer is the estimation of management quantities, such as a short-term forecast of the catch level that would implement a specified fishing mortality policy. By integrating this management layer into the overall model, the variance of the estimated parameters can be propagated to the management quantities, thus facilitating a description of the risk of various possible management scenarios.

The complexity of the population sub-model should be considered relative to the complexity of the data and observation sub-model. For example, if only biomass-based CPUE data are available, it is simplest to cast the population sub-model as a simple biomass-dynamics model such as the delay-difference model (reference). However, with integrated analysis it is possible to build a more complex, age-structured population sub-model that collapses to the simple biomass level in the observation sub-model. If the various mortality, growth and selectivity parameters necessary in the more complex model are fixed at levels that mimic the inherent assumptions of the simple biomass dynamics model, then both models produce identical results. The advantage of the more complex internal model is that it is primed for a richer array of sensitivity testing and immediate incorporation of more detailed data as these data become available.

The model to be presented here is primarily designed for a particular, although not overly restrictive, set of circumstances and data. The target species are groundfish that are harvested by multiple distinct fleets and for which there commonly are fishery-independent surveys to provide a time series of relative abundance. Some age and length composition data are available from both the fishery and survey, but they are intermittent, often based on small sample sizes, and the age data are influenced by a substantial degree of ageing imprecision. Tagging data are not available for these species and analysis of tagging data has not been built into the observation sub-model.

The dynamics of fishing mortality and growth have been incorporated in a way that captures the effect of size-selective fisheries and surveys on the size and age of fish that are harvested and sampled, and the effect of size-selective fishery harvest on the size composition and mean growth characteristics of the fish that survive the fishery each time period. There are three basic levels of complexity in modeling of size in age-structured models: (1) age-selectivity only; (2) size-selectivity influence on observations; and (3) size-selectivity influence on survivorship. Many integrated analysis models model the dynamics on an age-basis only. Some of these allow inclusion of length data, but only at the level of the observation sub-model (such as Coleraine and the age-only version of synthesis). In such models, a fishery that has low selectivity for 3 year old fish is assumed to capture the same size range of 3 year olds as a fishery that has high selectivity for 3 year olds. There is no size-selectivity in such age-structured models even though they can estimate an expected value for the size composition captured by the fishery. A more complex approach is to build the size composition into the population and to allow for size-selectivity in the characteristics of the fisheries. Now a fishery with delayed size-selectivity will capture larger 3 year olds and have low overall selectivity for 3 year olds compared to a fishery with higher selectivity for small fish. Such models, such as MultiFAN, SCALA, Synthesis, model the effect on size-selectivity on the observed samples, but do not feedback to influence the size-specific survival. There are several approaches to capturing the dynamics of size-specific survival. One is to model the population as simply a size-structured population and to use a transition matrix to update the size-composition into the future (reference). Another is to adjust the moments of the distribution of population size-at-age in response to the size-selective removals (Parma et al). Here, a third approach is used.

The stage-one and stage-two models described above treat a cohort as a collection of homogeneous fish whose size-at-age is characterized by a mean and a variance. Thus,

in each year the same size-at-age distribution is recreated, irrespective of the degree of size-specific fishing mortality. But even these models often partition the cohort into males and females and, because the genders often have different growth characteristics, they will experience different effects of size-specific mortality. The stage-three model described here extends the computational aspects of genders to multiple growth morphs within each gender. Each growth morph has unique growth characteristics and its numbers-at-age are tracked. Thus growth morphs are differentially affected by size-selective mortality. Fish within each morph are not differentially affected by size-selectivity, but the gross effect of size-selectivity is captured between morphs. Of course, we have no data to identify fish to morph like we do to gender. So expected values are summed across morphs within gender in order to match our data. The operational assumption is that it is more accurate to model a cohort as a collection of faster and slower growing morphs than as a single morph.

The structure of SS2 allows for building of stage-one, stage-two and stage-three age-length models. Selectivity can be cast as age-specific only to create a stage-one model. A stage-two model would define just one morph per gender and cast selectivity as size-specific. Finally, a stage-three model would cast selectivity as size-specific and subdivide each gender into multiple, 5 is usually sufficient, morphs to capture the major effect of size-specific survivorship.

POPULATION MODEL

Basic Dynamics

Numbers at age in the model are tracked within each growth morph g. Each morph is associated with a gender γ. The simplest model will contain one morph that represents combined genders. A common configuration will have two morphs, one for each gender. More complex set-ups will include multiple morphs for each gender so the differential effects of size-selective mortality on fast-growing versus slow-growing morphs can be assessed.

The population is also sub-divided into geographic regions and numbers at age for each morph are tracked within region. The areas are considered all part of a meta-population with a common larval pool; spawning biomass is summed across areas to calculate the expected total number of recruits, and the recruits are apportioned back out to the areas in proportions that are independent of the proportion of spawners occurring in that area. Presently, the code does not contain full algorithms for moving fish between areas, so area subscripts on arrays and issues regarding movement of fish between areas is deferred to a future version of the model.

The population dynamics are projected using a seasonal time step with catch removed in the middle of each season. The time index t increments one unit per season, and is calculated by (1.1). Thus, each value of t is associated with a particular season in a particular year. Where the season index s or the year index y are used in the equations below, they refer to season and year associated with the particular time step t.

a age for $0 \leq a \leq A$

f is the index of fishery or survey for $1 \leq f \leq A_f$

g index for growth morph for $1 \leq g \leq A_g$

l is the index for length bin for $1 \leq l \leq A_l$,

γ is the index for gender for $1 \leq \gamma \leq A\gamma$ (where $A\gamma = 1$ or 2),

y year for $Y_1 \leq y \leq Y_2$

s is the index of season in $1 \leq s \leq A_s$,

δ_s is the duration of the season s corresponding to time step t in decimal years, and

t is the index of time combining year and season, calculated as,

$$t = Y_1 + (y - Y_1)A_s + s - 1. \tag{1.1}$$

Numbers at Age

The numbers at age in the initial year is calculated from equilibrium conditions described below in (3.4). In subsequent years, conventional age-structured dynamics are used to update the population numbers. The number at age a in growth morph g in the middle of time step t is given by:

$$\tilde{N}_{tga} = N_{tga} e^{-0.5 M_{ga} \delta_s}, \tag{1.2}$$

The number at age a in growth morph g in the beginning of each time step is incremented as:

$$N_{t+1,ga} = \left(\tilde{N}_{tg,a-s_0} - \sum_{f=1}^{A_f} \sum_{l=1}^{A_l} C_{ftg,a-s_0,l} \right) e^{-0.5 M_{ga} \delta_s}, \tag{1.3}$$

where:

M_{ga} is the natural mortality at age a in growth morph g, given by (2.1), and

C_{tfgal} is the calculated number in the catch by each fishery in time step t at age a, length l, and growth morph g, as calculated in (1.11), and

s_0 is an indicator of the first season. It accounts for the convention that fish progress to the next age on Jan 1. It is calculated as,

$$s_0 = \begin{cases} 1 & \text{if } s = 1, \\ 0 & \text{else,} \end{cases} \tag{1.4}$$

When the time step t corresponds to the last season of the year, (1.3) is only used for ages $a > 0$. For $a = 0$, the number in the first season of the next year is given by the equation for recruitment (1.6).

Spawning Biomass

Spawning biomass is calculated as the sum across all morphs at the beginning of the season designated as the spawning season:

$$S_t = \sum_{g=1}^{A_g} \sum_{a=0}^{A} N_{tga} w'_{tga} \tag{1.5}$$

where:

w'_{tga} is the average spawning output at time t of age a and growth morph g (which will only be non-zero for growth morphs which are female). w'_{tga} is calculated in XXX

Recruitment

For each time step t corresponding to the first season of a year, the expected level of recruitment of age zero fish on Jan 1 is given by the Beverton-Holt spawner-recruitment relationship as modified by <Mace&Doonan?>:

$$\hat{R}_y = \frac{4hR_0 S_y}{S_0(1-h) + S_y(5h-1)} e^{h'V_y}, \tag{1.6}$$

where:

h is the parameter for steepness of the stock-recruitment function, where the value of h specifies the ratio of R_y to R_0 when $S_y = 0.2S_0$. Thus, the parameter, h, is bounded by 0.2 and 1.0.

R_0 is the initial recruitment,

S_0 is the unfished equilibrium spawning biomass corresponding to the recruitment level R_0

S_y is the spawning biomass at the beginning of the spawning season in year y

h' is the parameter for linkage to an environmental data series

V_y is the value of the environmental data series in year y. Note that no offset is included in the linkage relationship, so the $\{ V_y \}$ must be scaled appropriately.

For years in which recruitment residuals are not estimated, the level of total recruitment R_y is set equal to $\hat{R}_y$.

For years in which recruitment residuals are estimated, the level of total recruitment is given by:

$$R_y = \hat{R}_y e^{-0.5\sigma_R^2} e^{\tilde{R}_y}, \tag{1.7}$$

where:

σ_R is the standard deviation for recruitment in log space

$\tilde{R}_t$ is the lognormal recruitment deviation in year y.

The level of σ_R scales the log-bias adjustment so that the expected arithmetic mean of the set $\{R_y\}$ is equal to the mean of the $\hat{R}_y$ for the same years. However, when a model is set up to estimate recruitment deviations in years much before the advent of data, the log-bias adjustment can cause a difference between the single maximum likelihood (ML) population estimate and the mean of the MCMC estimates. This occurs because the ML estimation tends to draw the data-poor recruitment deviations to the log-bias adjusted level, which is the median of the recruitment distribution. Because there is no variability among these data-poor recruitment estimates, there are no large positive deviates to bring the mean up to the correct value. On the other hand, in the MCMC estimation, each of these data-poor recruitment estimates takes on a pdf that has the correct mean and median. Because the level of biomass depends upon the total number of recruits, the ML and MCMC estimates will have different levels of biomass early in the time series which will influence the estimated values of many other model parameters. Further investigation of this phenomenon is underway.

The total recruitment is distributed among growth morphs each year according to:

$$R_{yg} = g'_g R_y, \tag{1.8}$$

where:

g'_g is the parameter defining the proportion of the recruitment allocated to growth morph g. The vector g' is re-scaled to sum to 1.0.

Fishing Mortality and Catch

The harvest rate is based on the ratio of observed catch biomass to the mid-season biomass available to the fishery. This ratio uses the observed and expected catch that is retained by the fishery because it is more common to have a complete and accurate time series of retained (landed) catch than it is to have complete information on total catch. The error in the estimate of observed, retained catch is assumed to be negligible, so the harvest of fishery f at time step t is computed as,

$$F_{tf} = C_{tf} / B_{tf} \tag{1.9}$$

where:

C_{tf} is the retained catch at time step t by fishery f.

And the vulnerable retainable biomass at time step t for fishery f is given by:

$$B_{tf} = \sum_{l=1}^{A_l} \sum_{\gamma=1}^{A_\gamma} w_{l\gamma} b_{ltf\gamma} \beta_{ltf\gamma} \sum_{a=1}^{A} \beta_{atf\gamma} \sum_{g\in\gamma} \phi_{tgal} \tilde{N}_{tga} \,, \tag{1.10}$$

where:

$g \in \gamma$ denotes the set of growth morphs which are associated with the gender γ.

$w_{l\gamma}$ is the mean weight of individuals in length bin l and gender γ, Note that if the catch is in terms of numbers of fish, then this weight term is omitted from the calculation of available, retainable abundance,

$\beta_{ltf\gamma}$ is the length-based selectivity for length bin l, time step t, fishery f and gender γ,

$\beta_{atf\gamma}$ is the age-based selectivity for age a, time step t, fishery f and gender γ,

$b_{tfl\gamma}$ is the length-specific fraction of the catch in length bin l, time step t, for fishery f, gender γ that is retained

$\tilde{N}_{tga}$ is the number at age a in growth morph g in the middle of time step t, and

Although the harvest rate calculation is based on the retained catch, the resultant mortality must take into account total catch. The harvest rate F calculated from retained catch is applied to the total available numbers to calculate the expected number in the total catch by each fishery f in time step t at age a, length l, and growth morph g:

$$C_{tfgal} = F_{tf} \beta_{ltf\gamma} \beta_{atf\gamma} \phi_{tgal} \tilde{N}_{tga} \,, \tag{1.11}$$

where the gender γ in the selectivity functions is that which is associated with the growth morph g. This estimated level of removals is used in equation (1.3). Note that removals are summed across lengths for each morph and age. When a retention function is not used, or is set to retain all fish, then the retained catch computations above are identical to total catch calculations.

Also, there is no provision to account for the possibility that some of the discarded fish are alive. Such a provision could be complicated. For example, the discarded fish tend to be smaller than the retained fish, but among the discarded fish, it may be that the larger fish are more likely to survive.

The nature of the harvest rate calculation creates the possibility that the catch would be greater than the available biomass during some model iterations while it is searching for the best parameter combination. The possibility of negative abundance is even greater for individual ages when there are multiple fisheries causing mortality. A penalty function is necessary to keep the model from crashing when it temporarily encounters these negative abundance situations. This penalty is described in XXX.

Biological Factors

Natural Mortality

For age a and growth morph g, the rate of natural mortality is given by:

$$M_{ga} = \begin{cases} M_{1g} & \text{for } a \le a_1, \\ M_{1g} + \dfrac{(a-a_1)(M_{2g}-M_{1g})}{a_2 - a_1} & \text{for } a_1 < a < a_2, \\ M_{2g} & \text{for } a \ge a_2, \end{cases} \qquad (2.1)$$

where:

    M_{1g} is the natural mortality for age 0 in growth morph g,

    M_{2g} is the natural mortality for age A in growth morph g,

    a_1 is the last age for natural mortality equal to M_1 for all growth morphs, and

    a_2 is the first age for natural mortality equal to M_2 for all growth morphs.
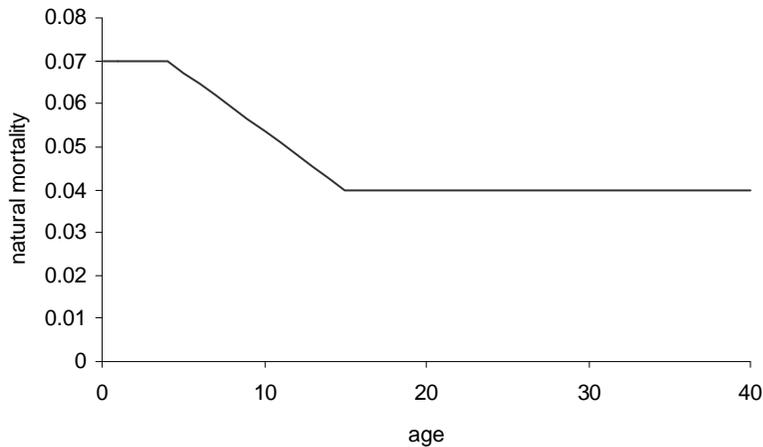
Figure 2.1. Example of age-specific natural mortality function.

Growth

    For all ages in the first season of the start year, mean size-at-age is calculated from:

$$L_{ga} = L_{\infty g} + (L_{1g} - L_{\infty g})e^{-K_g(a-a_3)}, \qquad (2.2)$$

where:

    L_{ga} is the mean size at age a for growth morph g,

    a_3 is a reference age near the youngest age well represented in the data,

    L_{1g} is the mean size of growth morph g at age a_3,

K_g is the growth coefficient for growth morph g, and

$L_{\infty g}$ is the mean asymptotic size, calculated from,

$$L_{\infty g} = L_{1g} + \frac{L_{2g} - L_{1g}}{1 - e^{-K(a_4 - a_3)}}, \tag{2.3}$$

where:

a_4 is a reference age near the oldest age well represented in the data, and

L_{2g} is the mean size of growth morph g at age a_4.

The mean size at the beginning of each season for each growth morph is incremented across time steps as:

$$L_{t+1,g,a} = L_{t,g,a-s_0} + \left(L_{t,g,a-k} - L_{\infty g} \right) \left(e^{-K_g \delta_s} - 1 \right), \tag{2.4}$$

The mean size in the middle of each season for each growth morph is calculated from the size at the beginning of the season as:

$$\tilde{L}_{tga} = L_{tga} + \left(L_{tga} - L_{\infty g} \right) \left(e^{-0.5 K_g \delta_s} - 1 \right). \tag{2.5}$$

The coefficient of variation in length changes linearly with size-at-age between parameters specified for ages a_3 and a_4 for each growth morph. The standard deviation of length at age for each growth morph is given by:

$$\sigma_{0ga} = \begin{cases} \tilde{L}_{ga} \left(CV_{1g} \right) & \text{for } a \leq a_3, \\[2mm] \tilde{L}_{ga} \left(CV_{1g} + \frac{(\tilde{L}_{ga} - L_{1g})}{(L_{2g} - L_{1g})} \left(CV_{2g} - CV_{1g} \right) \right) & \text{for } a_3 < a < a_4,, \\[2mm] \tilde{L}_{ga} \left(CV_{2g} \right) & \text{for } a \geq a_4, \end{cases} \tag{2.6}$$

where:

CV_{1g} is the coefficient of variation for length in growth morph g at age a_3, and

CV_{2g} is the coefficient of variation for length in growth morph g at age a_4.

σ_{0ga} is the standard deviation of length at age a in each growth morph g.

The σ_{0ga} are calculated only in the first year and are not updated if growth parameters change later in the time series

Age-Length Population Structure

In order to calculate the dynamics of size-specific mortality, the numbers at age for each growth morph are distributed across the defined length bins. The proportion in length bin l for age a and growth morph g at time step t is calculated as:

$$\phi_{tgal} = \begin{cases} \Phi\left(\dfrac{L'_{min} - \tilde{L}_{tga}}{\sigma_{ga}}\right) & \text{for } l = 1 \\[2ex] \Phi\left(\dfrac{L'_{l+1} - \tilde{L}_{tga}}{\sigma_{ga}}\right) - \Phi\left(\dfrac{L'_l - \tilde{L}_{tga}}{\sigma_{ga}}\right) & \text{for } 1 < l < A_l , \\[2ex] 1 - \Phi\left(\dfrac{L'_{max} - \tilde{L}_{tga}}{\sigma_{ga}}\right) & \text{for } l = A_l \end{cases}$$

(2.7)

where:

Φ is the standard normal cumulative density function,

L'_l is the lower limit of length bin l,

L'_{min} is the lower limit of the smallest length bin,

L'_{max} is the lower limit of the largest length bin,

$\tilde{L}_{tga}$ is the mean length in the middle of time t for growth morph g. It is calculated from equation (2.2) and subsequent equations, and

σ_{ga} is the standard deviation of length at age a in each growth morph g, calculated from (2.6).

When t corresponds to the spawning season ϕ_{tgal} is computed using the length at the beginning of the time step, L_{tga}, rather than the length in the middle of the time step, $\tilde{L}_{tga}$, in (2.7).

Body Weight

Body weight at length is calculated using the mid-value of each length bin, with separate parameters for females and males.

$$w_{l\gamma} = \Omega_1 L_l^{\Omega_2} \quad \text{for females}$$
$$w_{l\gamma} = \Omega_6 L_l^{\Omega_7} \quad \text{for males}$$

(2.8)

Maturity and Fecundity

The fecundity at age for each female morph combines the frequency distribution of length at age; fraction of females that are mature calculated from a logistic function

using the mid-value of each length bin; eggs per kg as a linear function of body weight; and body weight at length:

$$\varphi'_l = (1 + e^{\Omega_3(L_l - \Omega_4)})^{-1} \qquad \text{Fraction mature}$$

$$\varphi''_l = \Omega_5 + \Omega_6 w_{l\gamma} \qquad \text{Eggs per kg} \tag{2.9}$$

$$w'_{tga} = \sum_{l=1}^{A_l} \phi_{tgal} \varphi'_l \varphi''_l w'_l \qquad \text{Fecundity at age}$$

Initial Conditions

Virgin Age Structure

The age structure of the virgin population is given by:

$$N'_{0ga} = g'_g R_0 \prod_0^{a-1} e^{-M_{g,.}} \qquad \text{for } a = 1 \text{ to } A\text{-}1 \tag{3.1}$$

where:

R_0 is the initial recruitment[1],

g'_g is proportion of the recruitment allocated to growth morph g, and

M_{ga} is the natural mortality at age a in growth morph g, given by (2.1).

In the calculating of the age structure of the virgin and initial equilibrium populations, the last age is considered a plus group. Thus, the number at age $a = A$ in growth morph g is given by:

$$N'_{0gA} = N'_{0g,A-1} \frac{e^{-M_{g,A-1}}}{1 - e^{-M_{gA}}} \, . \tag{3.2}$$

Initial Age Structure with Equilibrium Catch

The initial equilibrium catch is set only in terms of total catch. There is no provision to base the calculation on retained catch. Also, the initial equilibrium is calculated using only an annual time step; there is no provision to invoke seasonality of the fishery or to calculate spawning biomass at a time other than Jan 1.

The number at age 0 in growth morph g at the beginning of the equilibrium year is given by:

$$N_{0ga} = g'_g R_1 e^{-0.5 M_{ga}} \, , \tag{3.3}$$

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[1] The parameter for initial recruitment is estimated in log space: $\ln(R_0)$.

where:

R_1 is the initial equilibrium recruitment, defined as an offset from R_0 but typically set equal to R_0.

The number at each age greater than 0 in growth morph g at the beginning of the equilibrium year is calculated using the iterative equation:

$$N_{0g,a+1} = \left(N_{0ga}e^{-0.5M_{ga}} - \sum_{f=1}^{A_f}\sum_{l=1}^{A_l} C_{0fgal} \right) e^{-0.5M_{ga}} , \tag{3.4}$$

where:

C_{0fgal} is the number removed by the equilibrium catch from length bin l and age a in growth morph g, calculated as:

$$C_{0fgal} = \sum_{f=1}^{A_f} F_{0f}\beta_{l,Y1,fg}\beta_{a,Y1,fg}\phi_{0gal}\tilde{N}_{0ga} , \tag{3.5}$$

where:

F_{0f} is the parameter for the fraction of the selected biomass removed at equilibrium by fishery f,

$\beta_{l,Y1,fg}$ is the selectivity for length bin l in the start year for fishery f and growth morph g

$\beta_{a,Y1,fg}$ is the selectivity for age a in the start year for fishery f and growth morph g,

ϕ_{0gal} is the proportion in length bin l for age a and growth morph g in the middle of the equilibrium year,

$\tilde{N}_{0ga}$ is the number at age a in growth morph g in the middle of the equilibrium year, calculated from the numbers at the beginning of the year as:

$$\tilde{N}_{0ga} = N_{0ga}e^{-0.5M_{ga}} \tag{3.6}$$

For the accumulator age A, an approximation is based on the overall survivorship in age *A-1*:

$$N_{0g,A} = \cfrac{t1}{1 - \cfrac{t1}{N_{0g,A-1}}}$$

where:

$$t1 = \left(\tilde{N}_{0g,A-1} - \sum_{f=1}^{A_f} \sum_{l=1}^{A_l} C_{0fg,A-1,l} \right) e^{-0.5M_{g,A-1}}$$

(3.7)

The total expected equilibrium catch in biomass for fishery f is given by:

$$\hat{C}_{0f} = \sum_{a=0}^{A} \sum_{l=1}^{A_l} \sum_{\gamma=1}^{A_\gamma} w_{l\gamma} \sum_{g \in \gamma} C_{0fgal} .$$

(3.8)

Virgin and Initial Spawning Biomass

The virgin mature female biomass (or egg production) is calculated as:

$$S_0 = \sum_{g=1}^{A_g} \sum_{a=0}^{A} N'_{0ga} w'_{0ga}$$

(3.9)

where:

w'_{0ga} is the initial average spawning output of age a and growth morph g (which will only be non-zero for growth morphs which are female).

The initial mature female biomass under the initial equilibrium catch is calculated as:

$$S_1 = \sum_{g=1}^{A_g} \sum_{a=0}^{A} N_{0ga} w'_{ga}$$

(3.10)

Note that these equilibrium spawning biomass values are calculated using annual time steps, so the spawning biomass corresponds to Jan 1.

First Year Recruitment

The expected level of recruitment in the first year is given by equation (1.6) using the initial equilibrium spawning biomass S_1 to produce these recruits. Note that if the initial equilibrium catch is more than a trivial level and the steepness of the spawner-recruitment curve is less than 1.0, then the starting year of the model will influence the biomass level early in the time series. For example, if the model is started in 1950 with an initial equilibrium catch of 500 mt it will have a higher biomass in 1950 than if it is started in 1940 with an initial equilibrium catch of 500 mt and a catch of 500 mt for each year during 1941-1949. This difference is due to the model using R_0 all the way through

1950 in the first setup, but in the second setup the spawner-recruitment curvature causes the expected recruitment level during the 1940s to decline below R_0.

Selectivity And Retention

The selectivity for each fishery and survey contains length and age-based selectivity functions, each of which must be specified but either can be set to a null level (constant selectivity for all sizes or ages). The age and length selectivities can be selected to be one of several patterns, including a constant at 1 and a mirror of the selectivity of another fishery or survey. The coding requires a vector of selectivity parameters, β_i, the length of which and their specific interpretation is in context of the selectivity pattern. These selectivity parameters can be fixed or estimated quantities, and can also be time-varying. Selectivity is indexed by time step t in this documentation for consistency with other variables, but the selectivity function for a given fishery and gender will be the same for all seasons in each year.

$\beta_{ltf\gamma}$ is the length-based selectivity for length bin l, time step t, fishery or survey f and gender γ,

$\beta_{atf\gamma}$ is the age-based selectivity for age a, year y, fishery or survey f and gender γ.

l is the index for length bin for $1 \leq l \leq A_l$,

γ is the index for gender for $1 \leq \gamma \leq A\gamma$ (where $A\gamma = 1$ or 2),

L_l is the midpoint of length bin l,

L_{min} is the midpoint of the smallest length bin,

L_{max} is the midpoint of the largest length bin, and

For simplicity, the equations below do not include the indices for either year, fishery, or gender, so selectivity of length bin l will simply be denoted β_l.

Length-based selectivity functions

Pattern 0: Constant (0 parameters)

$$\beta_l = 1 \tag{4.1}$$

Pattern 1: Logistic (2 parameters)

$$\beta_l = \left(1 + e^{-\log(19)(L_l - \beta_1)/\beta_2}\right)^{-1} \tag{4.2}$$

where the parameters are:

β_1 is the length at 50% selectivity

β_2 is the difference between the length at 95% selectivity and the length at 50% selectivity
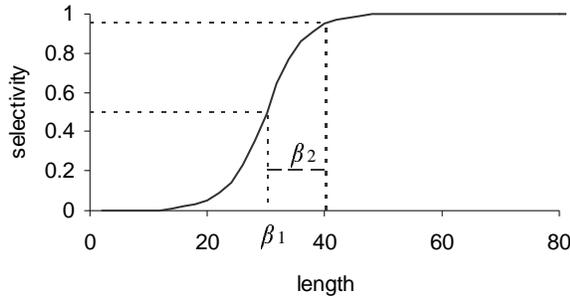
Figure 4.1: An example of type 1 selectivity (logistic).

Pattern 2: Double-Logistic (8 parameters)

Not documented here; same as Pattern 7, except uses IF statements rather the logistic joins.

Pattern 3: Flat middle, power up, power down (6 parameters)

$$\beta_l = \begin{cases} T_3 + \left(\left(L_l - L_{min}\right)/\left(T_1 - L_{min}\right)\right)^{(1+\beta_5)(1-T_3)} & \text{for } L_l < T_1 \\ 1 & \text{for } T_1 \leq L_l \leq T_2 \\ 1 + \left(\left(L_l - T_2\right)/\left(L_{max} - T_2\right)\right)^{(1+\beta_6)(T_4-1)} & \text{for } L_l > T_2 \end{cases}$$

(4.3)

where the parameters are:

β_1 is the parameter determining start of selectivity = 1.0

β_2 is the parameter determining end of selectivity = 1.0

β_3 is the parameter determining selectivity at the minimum size

β_4 is the parameter determining selectivity at the maximum size

β_5 is the power parameter for the increase

β_6 is the power parameter for the decrease,

and where the derived quantities are:

T_1 is the length to get to 1.0, given by:

$$T_1 = L_{min} + \left(1 + e^{-\beta_1}\right)^{-1}\left(L_{max} - L_{min}\right)$$

(4.4)

T_2 is the length to begin the decline from 1.0, given by:

$$T_2 = T_1 + \left(1 + e^{-\beta_2}\right)^{-1}\left(L_{max} - T_1\right)$$

(4.5)

T_3 is the selectivity at the minimum size given by:

$$T_3 = \left(1 + e^{-\beta_3}\right)^{-1} \qquad (4.6)$$

T_4 is the selectivity at the maximum size given by:

$$T_4 = \left(1 + e^{-\beta_4}\right)^{-1} \qquad (4.7)$$
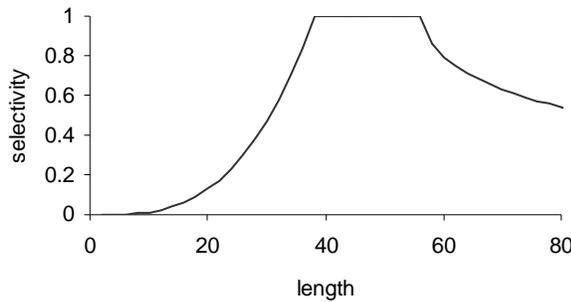
Figure 4.2: An example of Type 3 selectivity (flat middle, power up, power down)

Pattern 4: Size selectivity equals female maturity (0 parameters)

Selectivity function is set equal to female fecundity-at-length. Note that this selectivity function builds in the effect of weight-at-length, so the survey observations must be identified as if they are in numbers, otherwise the weight-at-length effect would be accounted twice.

Pattern 5: Mirror another selectivity function (2 fixed parameters)

Selectivity function is set equal to a subset of a selectivity function for a lower numbered survey or fishery type. The 2 parameters are used to indicate the minimum and maximum size bin to be included in the subset.

Pattern 6: Linear segments (N segments + 2 parameters)

Pattern 7: Double logistic with smooth transitions (8 parameters). This function is composed of 4 sections: an ascending curve for small fish (*asc*), a flat-top at which selectivity equals 1.0 (*peak*), a descending curve for large fish (*dsc*), and constant selectivity (*final*) at or above a final size. The four sections have three intersections. At each intersection, the sections are joined using a pair of complementary, steep logistic functions *j*.

$$sel = ((asc \bullet j_1^- + peak \bullet j_1^+) \bullet j_2^- + dsc \bullet j_2^+) \bullet j_3^- + final \bullet j_3^+ \qquad (4.8)$$

where:

maxL is either L_{max}, or the mean length of an age A fish from morph 1 in the first year.

The 8 parameters are:

β_1 is the peak, the size at which selectivity=1.0 begins

β_2 is the selectivity at L_{min}

β_3 and β_4 define the *asc* curve by interpolating on the basis of logistic transformed length according to:

$$asc = \beta_2 + (1-\beta_2) \cdot \left(\frac{\left(\left(1 + e^{-\beta_4(L_l - t1)} \right)^{-1} - t2 \right)}{t3 - t2} \right)^{t4}$$

$$t1 = L_{min} + \left(1 + e^{-\beta_3} \right)^{-1} \cdot (\beta_1 - L_{min})$$

$$t2 = 0.9999 \left(1 + e^{-\beta_4(L_{min} - t1)} \right)$$

(4.9)

$$t3 = 1.00001 \left(1 + e^{-\beta_4(\beta_1 - t1)} \right)$$

$$t4 = \frac{\log(0.5)}{\log\left(\frac{(0.5 - t2)}{(t3 - t2)} \right)}$$

β_5 sets the *final* selectivity using a logistic transformation according to:

$$final = (1 + e^{-B5})^{-1}$$

(4.10)

β_6 and β_7 define the *dsc* curve according to:

$$dsc = 1 + (final - 1) \cdot \left(\frac{\left(\left(1 + e^{-\beta_7(L_l - t5)} \right)^{-1} - t6 \right)}{t7 - t6} \right)^{t8}$$

$$t5 = (\beta_1 + \beta_8) + \left(1 + e^{-\beta_6} \right)^{-1} \cdot \left(\max L - (\beta_1 + \beta_8) \right)$$

$$t6 = 0.9999 \left(1 + e^{-\beta_7((\beta_1 + \beta_8) - t5)} \right)$$

(4.11)

$$t7 = 1.00001 \left(1 + e^{-\beta_7(\max L - t5)} \right)$$

$$t8 = \frac{\log(0.5)}{\log\left(\frac{(0.5 - t6)}{(t7 - t6)} \right)}$$

β_8 sets the width of the *peak*. Normally this is not estimated and is set equal to 1 or 2 multiples of the binwidth.

The joins at β_1 (and similarly at $\beta_1 + \beta_8$ and at *maxL*) are calculated from:

$$j_1^- = (1 + e^{-10(l-B_1)})^{-1}$$
$$j_1^+ = (1 + e^{+10(l-B_1)})^{-1} \qquad\qquad (4.12)$$

This approach to joining the four sections of the pattern makes the entire pattern a continuous function, which makes it differentiable with respect to the parameter β_1. Note that parameters β_3, β_5 and β_6 are internally transformed according to a logistic function so that the operational value will be in the interval {0,1}.

A typical resulting shape is shown in the figure below:
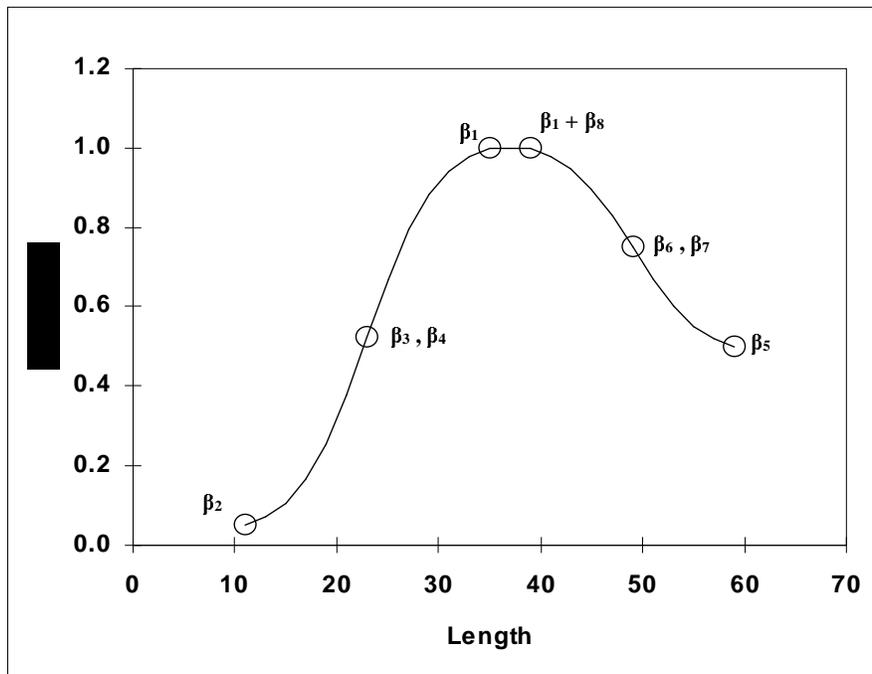
Age-based selectivity functions

Pattern 10: Constant (0 parameters)

$$\beta_a = 1 \qquad\qquad (4.13)$$

Pattern 11: Age selectivity equals 1 within a range of ages (2 fixed parameters)

$$\beta_a = \begin{cases} 1 & \text{if } \beta_1 \le a_1 \le \beta_1 \\ 0 & \text{otherwise} \end{cases} \qquad\qquad (4.14)$$

where the parameters[2] are:

β_1 is the first age of selectivity equal to 1,

---

[2] While input to the model as parameters for consistency in coding, the values for Type 11 Selectivity would never be estimated in the model.

β_2 is the last age of selectivity equal to 1.

Pattern 12: Logistic (2 parameters)

$$\beta_a = \left(1 + e^{-\log(19)(a-\beta_1)/\beta_2}\right)^{-1} \tag{4.15}$$

where the parameters are:

β_1 is the age at 50% selectivity

β_2 is the difference between the age at 95% selectivity and the age at 50% selectivity

Pattern 13: Double logistic (8 parameters)

***NEED TO ADD THIS

Pattern 14: each age (nages + 1 parameters)

***NEED TO ADD THIS

Pattern 15: Mirror another age selectivity function (0 parameters)

Age selectivity function is set equal to a previously specified age selectivity function.

Pattern 16: ascending Gaussian (2 parameters)

Pattern 17: augmented logistic (5 parameters)

Pattern 18: Double logistic with smooth transition (8 parameters)

Male selectivity

The selectivity of males is defined relative to the selectivity of females. If differential male selectivity is invoked for any type of fishery or survey, then 4 additional parameters are included to define the male selectivity.

β_0 is the age or size at a transition from the left to the right side of the function;

β_1 is log of male selectivity relative to female selectivity at the minimum size, L_{min}, or minimum age, 0;

β_2 is log of male selectivity relative to female selectivity at the transition size, or age;

β_3 is log of male selectivity relative to female selectivity at the maximum size, L_{max}, or maximum age, 0;

$$\log(\beta_l) = \begin{cases} \beta_1 + \dfrac{(L_l - L_{\min})}{(\beta_0 - L_{\min})}(\beta_2 - \beta_1) & \text{if } L_l \le \beta_0 \\[3mm] \beta_2 + \dfrac{(L_l - \beta_0)}{(L_{\max} - \beta_0)}(\beta_3 - \beta_2) & \text{otherwise} \end{cases} \tag{4.16}$$

and for age:

$$\log(\beta_a) = \begin{cases} \beta_1 + \dfrac{(a - 0)}{(\beta_0 - 0)}(\beta_2 - \beta_1) & \text{if } a \le \beta_0 \\[3mm] \beta_2 + \dfrac{(a - \beta_0)}{(A - \beta_0)}(\beta_3 - \beta_2) & \text{otherwise} \end{cases} \tag{4.17}$$

where:
β_1 is log of male size selectivity relative to female size selectivity;
β_a is log of male age selectivity relative to female age selectivity;

If male selectivity is greater than 1.0 for any size (age), then the combined vector of male and female selectivity at size (age) is rescaled to have a maximum of 1.0.

Retention

A retention function can be used for each fishery. Each retention function is logistic with a specified asymptote (not necessarily 1), and the male inflection size can be an arithmetic offset to the female inflection size. Thus 4 parameters are required. If the retention function is not used then fisheries are assumed to retain all catch. When retention is used, then data for each fishery can be designated as discarded, retained, or combined catch. The index m for market category is used to designate between these data types.

$b_{tfl\gamma m}$ is the fraction of the catch in length bin l, time step t, for fishery f, gender γ, and market category m. It is calculated as:

$$b_{tfl\gamma m} = \begin{cases} 1 & \text{for } m = 0 \text{ (combined catch)} \\[2mm] 1 - \beta_3\left(1 + e^{-(L_l - (\beta_1 + \beta_4))/\beta_2}\right)^{-1} & \text{for } m = 1 \text{ (discarded catch)} \\[2mm] \beta_3\left(1 + e^{-(L_l - (\beta_1 + \beta_4))/\beta_2}\right)^{-1} & \text{for } m = 2 \text{ (retained catch)} \end{cases} \tag{4.18}$$

where the parameters, which can be specific to each time step, fishery and gender are:

β_1 is the length at the point of inflection in the retention function,

β_2 is the parameter determining the slope at the point of inflection,

β_3 is the asymptotic fraction retained.

B_4 is 0 for females and is the offset value for males.

OBSERVATION MODEL

Survey Characteristics

Every fishery or survey is a potential source of an observation. There are several kinds of observations that can be taken from each fishery or survey. These include:

- Abundance
  - Retained biomass or numbers,
  - relative index (catchability unconstrained, as for a fishery CPUE or egg&larval index) or a calibrated index (catchability fixed or with a tight prior as for an acoustic or some bottom trawl surveys)
  - lognormal error
- Length composition
  - Multiple observations per time period and source allowed
  - Multinomial error
- Age composition
  - Multiple observations per time period and source allowed
  - with a specified degree of ageing imprecision
  - for all lengths or for a specified subset of length bins
  - multinomial error
- Mean length-at-age
  - Multiple observations per time period and source allowed
  - accounting for a specified degree of ageing imprecision
  - normal error
- Mean body weight
  - Normal error
- Discard
  - as fraction of total catch or as an amount
  - normal error

Observations have several general characteristics. Observations are area and season-specific. Each type of fishery or survey is designated to occur in one geographic area, if the model is set up to contain multiple areas. Each type of fishery or survey is designated to occur at a specified fraction of the way through a specified season. For fishery observations, most can be taken from the discarded, retained, or total catch. For length and age composition data, the observations can be from combined genders, a single gender, or a joint distribution across both genders. The fish available to an observation are calculated from:

$$\tilde{N}_{tf\gamma al} = \sum_{g \in \gamma} \phi_{tgal} \beta_{ltf\gamma} \beta_{atf\gamma} \left(N_{tga} e^{-M_{ga}\delta_s\delta_f} - \delta_f \sum_{l=1}^{A_t} C_{ftgal} \right) \tag{5.1}$$

where:

δ_f is the fraction of the season elapsed before the observation is taken. This same fraction is used for the fraction of the catch that occurs before the observation is taken.

Abundance Index

The expected abundance index is based upon the retained numbers from (5.1) summed over length, age, and gender. The total can be in terms of weight as shown here, or in numbers by omitting the body weight-at-length term:

$$B_{tf} = \sum_{l=1}^{A_l} \sum_{\gamma=1}^{A_\gamma} \sum_{a=1}^{A} w_{l\gamma} b_{ltf\gamma} \tilde{N}_{tf\gamma al} \tag{5.2}$$

The expected abundance index *G* is related to the available population abundance by:

$$G_{tf} = Q_f B_{tf}^{1+Q'_f} \varepsilon_{1tf}, \tag{5.3}$$

where:

Q_f is the catchability coefficient for fishery or survey *f*, and which can be set to be a function of an environmental time series;

Q'_f is the power parameter for catchability. It usually is set to 0.0, and

ε_{1tf} is the abundance index error that is assumed to be lognormally distributed as:

$$\ln(\varepsilon_{1tf}) \sim N(-0.5\sigma_{1tf}^{2}, \sigma_{1tf}^{2}),$$

where:

σ_{1tf} is the standard error of $\ln(G_{tf})$.

If the catchability coefficient Q_f is calculated internally, it can be assumed to be either a mean unbiased index or a median unbiased index. If Q_f is considered a mean unbiased index then it is calculated as,

$$Q_f = \exp\left(\frac{\dfrac{n_{0f}}{2} + \sum_t \ln(G_{tf} / B_{tf}^{1+Q'_f}) / \sigma_{1tf}^{2}}{\sum_t 1/\sigma_{1tf}^{2}} \right),$$

where:

n_{0f} is the number of observations of abundance for fishery or survey *f*.

If Q_f is considered a median unbiased index then it is calculated as

$$Q_f = \exp\left(\frac{\sum_t \ln(G_{tf}/B_{tf}^{1+Q_f'})/\sigma_{1tf}^2}{\sum_t 1/\sigma_{1tf}^2}\right).$$

The objective function component for fishery catch, fishery CPUE or fishery effort observation, or for a survey abundance observation is defined as:

$$\mathcal{L}_{1f} = 0.5\sum_t\left(\frac{\ln(G_{tf}) - \ln(\hat{G}_{tf})}{\sigma_{1tf}}\right)^2 \tag{5.4}$$

Discards

The expected discarded biomass for fishery f in time step t is:

$$\hat{D}_{tf} = E(D_{tf}) = \sum_{l=1}^{A_l}\sum_{\gamma=1}^{A_\gamma} w_{l\gamma}(1-b_{tfl\gamma 1})\sum_{a=1}^{A}\sum_{g\in\gamma} C_{tfgal}, \tag{5.5}$$

where:

$w_{l\gamma}$ is the mean weight of individuals in length bin l and gender γ,

$b_{tfl\gamma 1}$ is the retention fraction

C_{0fgal} is the number removed by the equilibrium catch from length bin l and age a in growth morph g, and

ε_{2tf} is the discard error for fishery f at time t.

The discard is assumed to be normally distributed as:

$$\varepsilon_{2tf} \sim \mathrm{N}(-0.5\sigma_{2tf}^2, \sigma_{2tf}^2), \tag{5.6}$$

where:

σ_{2tf} is the standard error of D_{tf}.

The contribution to the objective function for discarded biomass is given by:

$$\mathcal{L}_{2f} = 0.5\sum_t\left(\frac{D_{tf} - \hat{D}_{tf}}{\sigma_{2tf}}\right)^2 \tag{5.7}$$

When discard data is input as a fraction rather than absolute biomass, the expected discard fraction is given by:

$$\hat{D}'_{tf} = \hat{D}_{tf}/(\hat{D}_{tf} + C_{tf}), \tag{5.8}$$

and this fraction is used in place of $\hat{D}_{tf}$ in (5.7).

Mean Body Weight

The expected mean weight of the catch in discard/retained partition m by fishery f at time t is given by:

$$\hat{\bar{w}}_{tfm} = E(\bar{w}_{tfm}) = \frac{\sum\limits_{l=1}^{A_l}\sum\limits_{\gamma=1}^{A_\gamma} w_{tl\gamma} b_{tfl\gamma m} \sum\limits_{a=0}^{A}\sum\limits_{g\in\gamma} C_{tfgal}}{\sum\limits_{l=1}^{A_l}\sum\limits_{\gamma=1}^{A_\gamma} b_{tfl\gamma m} \sum\limits_{a=0}^{A}\sum\limits_{g\in\gamma} C_{tfgal}} . \tag{5.9}$$

where:

$\quad v \qquad$ is the index of the observation

$\quad \varepsilon_{3tfmv} \qquad$ is the error for mean weight observation v of market category m and fishery f at time t.

The error for mean weight is assumed to be normally distributed as:

$$\varepsilon_{3tfmv} \sim N(0, \sigma_{3tfmv}{}^2) , \tag{5.10}$$

where:

$\quad \sigma_{3tfmv} \qquad$ is the standard error of the observation, $\bar{w}_{tfmv}$.

The contribution to the objective function for mean weight is given by:

$$\mathcal{L}_{3f} = 0.5 \sum_v \sum_t \sum_m \left(\frac{\bar{w}_{tfm} - \hat{\bar{w}}_{tfm}}{\sigma_{3tfm}} \right)^2 \tag{5.11}$$

Composition Data

Length Compositions

The observations of the length composition are assumed to have a multinomial distribution. The observed proportions can be compressed at the tails. The compression occurs observation by observation following the general formula:

$$p_{1tfl\gamma} = \begin{cases} 0 & \text{for } l < l_{1\gamma} \\[2mm] \displaystyle\sum_{l \le l_{1\gamma}} p_{1tfl\gamma} & \text{for } l = l_{1\gamma} \\[3mm] p_{1tfl\gamma} & \text{for } l_{1\gamma} < l < l_{2\gamma}, \\[2mm] \displaystyle\sum_{l > l_{2\gamma}} p_{1tfl\gamma} & \text{for } l = l_{2\gamma} \\[3mm] 0 & \text{for } l > l_{2\gamma} \end{cases} \qquad (5.12)$$

where:

$p_{1tfl\gamma m}$ is the observed proportion of the catch in length bin l at time step t for fishery or survey f, gender γ, and market category m, and

$l_{1\gamma}$ is the accumulator length bin for a the lower tail for gender γ in a given observation, and

$l_{2\gamma}$ is the accumulator length bin for the upper tail for gender γ in the same observation.

The accumulator length bins are chosen for each observation as the length bins which will contain a proportion greater than p_{min}, a specified minimum proportion which is fixed across all observations. The proportions computed for each length bin have a specified constant ε added for computational purposes, after which they are renormalized as,

$$p_{1tfl\gamma} = \frac{p_{1tfl\gamma} + \varepsilon}{\displaystyle\sum_{l=1}^{A_l}(p_{1tfl\gamma} + \varepsilon)} . \qquad (5.13)$$

The corresponding expected proportion of the catch in length bin l at time step t for fishery or survey f, gender γ, and market category m is calculated as:

$$\hat{p}_{1tfl\gamma m} = \frac{b_{tfl\gamma m}\displaystyle\sum_{a=0}^{A}\sum_{g\in\gamma}C_{tfgal}}{\displaystyle\sum_{l=1}^{A_l}\sum_{\gamma=1}^{A_\gamma}b_{tfl\gamma m}\sum_{a=0}^{A}\sum_{g\in\gamma}C_{tfgal}} . \qquad (5.14)$$

For observations that combine genders, the expected proportions are summed across genders. When an observation of the length composition has been compressed at the tails then the expected length composition is likewise compressed using the same accumulator length bins for the upper and lower tails. The expected proportions computed for each length bin have a specified constant ε added for computational purposes, after which they are renormalized.

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The contribution to the objective function for length composition is defined as:

$$\mathcal{L}_{4f} = \sum_t \sum_m \sum_{\gamma=1}^{A_\gamma} n_{1tf\gamma m} \sum_{l=1}^{A_i} p_{1tfl\gamma m} \ln(p_{1tfl\gamma m} / \hat{p}_{1tfl\gamma m})$$ (5.15)

where:

$n_{1tf\gamma m}$ is the number of observed lengths in the catch at time step t for fishery or survey f in length bin l, gender γ, and market category m.

Ageing Error

The proportion of age a assigned to age bin i under ageing error of type k is:

$$\Omega_{kia} = \begin{cases} \Phi\left(\dfrac{\tilde{a}_i - \mu_{ka}}{\sigma_{ka}}\right) & \text{for } i=1 \\[2ex] \Phi\left(\dfrac{\tilde{a}_{i+1} - \mu_{ka}}{\sigma_{ka}}\right) - \Phi\left(\dfrac{\tilde{a}_i - \mu_{ka}}{\sigma_{ka}}\right) & \text{for } 1 < i < A_i \ , \\[2ex] 1 - \Phi\left(\dfrac{\tilde{a}_i - \mu_{ka}}{\sigma_{ka}}\right) & \text{for } i = A_i \end{cases}$$ (5.16)

where:

Φ is the standard normal cumulative density function,

μ_{ka} is the mean age assigned to age a under ageing error of type k,

$\tilde{a}_i$ is the lower limit of age bin i,

σ_{ka} is the standard deviation of ageing error at age a for ageing error type k.

Mean Size at Age

Observations of mean size in age bin i in time step t for fishery f in gender γ, associated with ageing error type k are assumed to be:

$$\overline{L}_{tf\gamma imk} = \frac{\sum_{a=0}^{A} \Omega_{kia} \sum_{l=1}^{A_i} b_{tfl\gamma m} L_l \sum_{g \in \gamma} C_{tfgal}}{\sum_{a=0}^{A} \Omega_{kia} \sum_{l=1}^{A_i} b_{tfl\gamma m} \sum_{g \in \gamma} C_{tfgal}} + \varepsilon_{6tf\gamma imk} \ ,$$ (5.17)

where:

i is the index for age bin in $1 \le i \le A_i$,

k is the index for the type of ageing error in $1 \le k \le A_k$,

Ω_{kia} is the proportion of age a assigned to age bin i under ageing error of type k,

L_l is the midpoint of length bin l, and

$\varepsilon_{6tf\gamma imk}$ is the error for mean size in age bin i and market category m in time step t for fishery or survey f in gender γ, associated with ageing error type k.

The error for mean size at age is assumed to be normally distributed as:

$$\varepsilon_{6tf\gamma imk} \sim \mathrm{N}\left(0,(\sigma_{6tf\gamma imk}/n_{6tf\gamma imk})^2\right), \tag{5.18}$$

where:

$n_{6tf\gamma imk}$ is the number of observed ages in age bin i and market category m in time step t for fishery or survey f in gender γ, associated with ageing error type k, and

$\sigma_{6tf\gamma imk}$ is the standard error of the expected mean size in age bin i and market category m in time step t for fishery or survey f in gender γ, associated with ageing error type k, calculated from,

$$\sigma_{6tf\gamma imk} = \sqrt{\frac{\displaystyle\sum_{a=0}^{A}\Omega_{kia}\sum_{l=1}^{A_l}b_{tfl\gamma m}L_l^2\sum_{g\in\gamma}C_{tfgal}}{\displaystyle\sum_{a=0}^{A}\Omega_{kia}\sum_{l=1}^{A_l}b_{tfl\gamma m}\sum_{g\in\gamma}C_{tfgal}} - \left(\frac{\displaystyle\sum_{a=0}^{A}\Omega_{kia}\sum_{l=1}^{A_l}b_{tfl\gamma m}L_l\sum_{g\in\gamma}C_{tfgal}}{\displaystyle\sum_{a=0}^{A}\Omega_{kia}\sum_{l=1}^{A_l}b_{tfl\gamma m}\sum_{g\in\gamma}C_{tfgal}}\right)^2}. \tag{5.19}$$

The expected mean size in each age bin is computed for each gender in each fishery or survey for which there is data of this type. For data that combine genders, the expected proportions are summed across genders. Ageing error is included in the calculation of the size and age composition so that the expected proportions approximate the processes that produced the observed values as closely as possible. The mean size at age is computed using the ageing error matrix type appropriate for the associated observed data.

The expected mean size in age bin i in time step t for fishery f in gender γ, associated with ageing error type k is calculated as:

$$\hat{\bar{L}}_{tf\gamma imk} = E(\bar{L}_{tf\gamma imk}) = \frac{\displaystyle\sum_{a=0}^{A}\Omega_{kia}\sum_{l=1}^{A_l}b_{tfl\gamma m}L_l\sum_{g\in\gamma}C_{tfgal}}{\displaystyle\sum_{a=0}^{A}\Omega_{kia}\sum_{l=1}^{A_l}b_{tfl\gamma m}\sum_{g\in\gamma}C_{tfgal}}. \tag{5.20}$$

The contribution to the objective function for the mean size at age is given by:

$$\mathcal{L}_{6f} = \sum_{t}\sum_{m}\sum_{k}\sum_{\gamma=1}^{A_\gamma}\sum_{i=1}^{A_i}\left(\frac{\bar{L}_{tf\gamma imk} - \hat{\bar{L}}_{tf\gamma imk}}{\sigma_{6tf\gamma imk}/n_{6tf\gamma imk}}\right)^2. \tag{5.21}$$

Age Compositions

Like the observed length compositions, the observed age compositions are assumed to have a multinomial distribution. The tails of the age compositions are compressed within each gender in the same manner as the length compositions in (5.12) and are renormalized after the addition of a constant as in (5.13).

The expected proportion of the catch in each age bin is computed for each gender in each fishery or survey for which there is data of this type. For data that combine genders in a two sex model, these proportions are summed across genders.

The expected proportion in age bin i in time step t for fishery or survey f in gender γ, associated with ageing error type k is calculated as:

$$\hat{p}_{2tfi\gamma mk} = \frac{\sum\limits_{a=0}^{A} \Omega_{kia} \sum\limits_{l=1}^{A_l} b_{tfl\gamma m} \sum\limits_{g \in \gamma} C_{tfgal}}{\sum\limits_{i=1}^{A_i} \sum\limits_{\gamma=1}^{A_\gamma} \sum\limits_{a=0}^{A} \Omega_{kia} \sum\limits_{l=1}^{A_l} b_{tfl\gamma m} \sum\limits_{g \in \gamma} C_{tfgal}} . \tag{5.22}$$

The contribution to the objective function for the age compositions is given by:

$$\mathcal{L}_{5f} = \sum_t \sum_m \sum_k \sum_{\gamma=1}^{A_\gamma} n_{2tf\gamma mk} \sum_{i=1}^{A_i} p_{2tfi\gamma mk} \ln(p_{2tfi\gamma mk} / \hat{p}_{2tfi\gamma mk}) \tag{5.23}$$

where:

$n_{2tf\gamma mk}$ is the number of observed ages in the catch at time step t for fishery or survey f, gender γ, market category m, associated with ageing error type k.

STATISTICAL MODEL

Objective Function Components

The objective function $\mathcal{L}$ is the weighted sum of the individual components indexed by kind j, and fishery f for those observations that are fishery specific (Table 1):

$$\mathcal{L} = \sum_{j=1}^{7}\sum_{f=1}^{A_f} \omega_{jf}\mathcal{L}_{jf} + \omega_R\mathcal{L}_R + \sum_{\theta}\omega_\theta\mathcal{L}_\theta + \sum_{P}\omega_P\mathcal{L}_P \tag{6.1}$$

where:

$\mathcal{L}$ is the total objective function,

j is the index for objective function component,

$\mathcal{L}_{jf}$ is the objective function component of kind j, and fishery and survey f, and

ω_{jf} is a weighting factor for each objective function component.

Table 1. Components of objective function

index	Source	Kind	Error Structure
1,f	fishery or survey f	CPUE or abundance index	lognormal
2,f	fishery f	Discard biomass	normal
3,f	fishery or survey f	Mean body weight	normal
4,f	fishery or survey f	Length composition	multinomial
5,f	fishery or survey f	age composition	multinomial
6,f	fishery or survey f	Mean size at age	normal
7,f	Fishery – all	Initial equilibrium catch	normal
R		recruitment deviations	lognormal
P		random parameter time series deviations	normal
Θ		parameter priors	Normal or Beta
	Fishery – all	Negative abundance penalty	N/A

Recruitment Deviations

The contribution to the objective function for the deviations in recruitment is defined as:

$$\mathcal{L}_{8f} = \frac{1}{2\sigma_R^2}\sum_{t}\tilde{R}_t^{\,2} + n_R\ln(\sigma_R) \tag{6.2}$$

where:

$\tilde{R}_t$ is the deviation in recruitment, which is lognormally distributed with expected value equal to the deterministic stock-recruitment curve given by (1.6) and (1.7),

σ_R is the standard deviation for recruitment, and

n_R is the number of years for which recruitment is estimated

Parameter Deviations

When parameters for natural mortality, growth, and selectivity are allowed to vary over time, the contribution to the objective function for deviations in these parameters is defined as:

$$L_P = \frac{1}{2\sigma_P^2} \sum_t \tilde{P}_t^2 \tag{6.3}$$

where:

$\tilde{P}_t$ is the exponential deviation of the parameter P at time t, and

σ_P is the standard deviation for the time series of random parameter deviates.

Parameter Priors

Normal distributions can be used for all estimated parameters. The selectivity and stock-recruit parameters can also have a beta prior.

The normal priors distribution for a parameter θ has the form:

$$L_\theta = 0.5 \left(\frac{\theta - \mu_\theta}{\sigma_\theta} \right)^2 \tag{6.4}$$

where:

θ is the parameter,

μ_θ is the prior mean value of the parameter, and

σ_θ is the standard deviation for the parameter's prior.

The contribution to the objective function for the beta priors is given by:

$$L_\theta = \left(\ln(1-\theta') - \ln(1-\mu_\theta') \right)\left(\theta_A - 1\right) + \left(\ln(\theta') - \ln(\mu_\theta') \right)\left(\theta_B - 1\right) \tag{6.5}$$

where:

$\theta' = \dfrac{\theta - \theta_{min}}{\theta_{max} - \theta_{min}}$ is the parameter θ rescaled into [0, 1],

$$\mu'_\theta = \frac{\mu_\theta - \theta_{min}}{\theta_{max} - \theta_{min}} \text{ is the prior mean value rescaled into } [0, 1],$$

$\mu_\theta \qquad$ is the input prior value,

$\sigma_\theta \qquad$ is the standard deviation after rescaling into $[0, 1]$,

$$\theta_B = \frac{(1 - \mu_\theta)\mu_\theta{}^2}{\sigma_\theta{}^2} - \mu_\theta \text{ is a derived quantity, and}$$

$$\theta_A = \frac{\theta_B}{\mu_\theta} - \theta_B \text{ is a derived quantity.}$$

Penalties

In addition to the objective function components above, there is a penalty function whenever the harvest rate for a particular fishery is above a user-specified value, typically 0.9. This penalty function also traps for negative abundance of a particular age occurring due to the cumulative removals from several fisheries.

MANAGEMENT QUANTITIES

Fishing Intensity

Although a major goal of this model is to measure the intensity of fishing mortality, a single quantitative measure of the intensity of fishing mortality can be difficult to define. A single value that represents the level of fishing mortality is ambiguous except in the simple case of a single fishery and with all age classes above a particular age having selectivity equal to 1.0. All other cases involve some degree of approximation or blurring of details: multiple fleets with different selectivity patterns and varying allocations between fleets over time; size-selectivity causes different fleets to have different weights-at-age; dome-shaped selectivity patterns, etc. A weighted average across ages and fleets will involve some degree of approximation and subjective decisions regarding these details.

In SS2, all of the complexity of each fleet's age and/or size selectivity is used to calculate the age and size component of the population that is "available" to the fleet at the instant of the middle of the season. The fleet's harvest rate is then simply calculated as the ratio of catch to available population. This is a standard measure of fishing intensity for that fleet, but combining harvest rates across fleets that have different selectivity patterns would require specification of a somewhat subjective weighting scheme. Typically, the target level of residual spawners per recruit is set, say at 45% of the unfished level, and the level of fishing intensity is scaled to produce this target SPR while taking into account the details of selectivity, fleet allocations, weights-at-age, etc. Once this fishing intensity index is calculated, it can be compared to the current,

comparably calculated fishing mortality index to determine if overfishing is occurring or to set quotas or other management action. The shortcoming of this approach is that the fishing mortality index may not be a meaningful measure of the actual mortality; it can be interpreted only in the context of the details of selectivity and life history.

Because of this difficult with a weighted average harvest rate, an alternative coarse measure of total fishing intensity might be constructed simply as the total catch for the year from all fisheries divided by the population biomass at the beginning of the year for an age range of the population selected to represent the ages that are reasonably represented in the fishery. But this simple exploitation rate also would entail subjective decisions, such as the age range of the population to select for the denominator.

Another way to characterize fishing mortality is to focus on the impact to the residual population. This is already routinely done when target fishing mortality rates are gauged in terms of their impact on residual spawning output per recruit (references, including Prager et al (1987)). The modification implemented in SS2 is to keep the focus strictly on the expected residual spawning output per recruit, or spawning potential ratio (SPR, reference). This one number incorporates all aspects of multi-fleet fishing intensity and the life history of the stock with no subjectivity in the weighting of each age and fishery. The value is directly comparable to the value set as the fishery target or limit. Each year in the time series, the value is calculated as the ratio of the equilibrium spawning output per recruit (SBR_f) under fished conditions to the spawning output per recruit under no fishing (SBR_0). The current year's selectivity patterns and harvest rates influence the numerator and the current year's population size-at-age and fecundity-at-length influence both the numerator and denominator. The program outputs both the SPR value and the associated yield per recruit.

Note that time-varying growth and maturity are taken into account in this calculation, although no attempt is made here to provide a conceptual framework for including time-varying life history parameters in the setting of target levels of exploitation. Time-varying maturation is evaluated annually, so any time-varying changes will have an immediate impact on this SPR calculation. However, time-varying growth will not have an immediate complete impact on this calculation because the current year's length-at-age is used, rather than the length-at-age that would occur if the current year's growth parameters had existed for the A previous years. This situation regarding time-varying growth will be addressed in the future.

Maximum Sustainable Yield

The calculation of deterministic, equilibrium Maximum Sustainable Yield combines the yield per recruit and spawning biomass per recruit calculations with the recruitment levels calculated from the model's recruitment-spawner curve. The model searches for the fishing intensity multiplier that will maximum the product of yield per recruit and recruitment. The search algorithm is simple, it reverses direction and halves the search step each time the current calculation is less than the previous calculation for a fixed number of steps: 50. With the Beverton-Holt spawner-recruitment curve, the equilibrium values are calculated from:

$$S_{msy} = a \cdot \frac{S'_{fmsy}}{R_0} - b$$

$$R_{msy} = \frac{4hR_0 S_{msy}}{S_0(1-h) + S_{msy}(5h-1)}$$

where:

S'_f is equilibrium spawning output with fishing intensity, f_{msy}

(7.1)

$$a = \frac{(4hR_0)}{(5h-1)}$$

$$b = \frac{S_0(1-h)}{(5h-1)}$$

For the Ricker curve, the values are calculated from:

$$S_{msy} = S_0 \left(1 + \frac{\log\left(\frac{R_0}{S_0}\right) + \log\left(S'_{fmsy}\right)}{h} \right)$$

(7.2)

$$R_{msy} = \frac{R_0 S_{msy}}{S_0} e^{h\left(1 - \frac{S_{msy}}{S_0}\right)}$$

The model calculates deterministic, equilibrium management quantities based on the selectivity and life history characteristics at the ending year of the time series. However, S0 is based on life history characteristics at the beginning of the time series. The management quantities also depend upon the relative harvest rates among the various fishing fleets. These can be specified as user input, or designated to match the relative harvest rates in the last year of the time series. The management quantities produced by the model are:

Variable	Description	Per Recruit	Total
R_0	Unfished Recruitment	1	7446
S_0	Unfished Spawning Output	7.376	54925
BIO_0	Unfished summary biomass	18.703	139269
H	Spawner-recruitment steepness	0.428	
$SPR = S_{fmsy} / S_0$	SPR at MSY	0.592	
MSY/BIO_{fmsy}	Exploitation Index at MSY	0.026	
R_{msy}	Recruitment at MSY	0.654	4870
S_{msy}	Spawning Output at MSY	4.369	21278
S_{msy}/S_0	Depletion at MSY	0.387	
MSY	MSY Yield	0.482	2346
BIO_{fmsy}	Summary biomass at MSY	12.119	90244
SPR_{target}	Target SPR for forecast	0.500	
Y_{target}/BIO_{target}	Exploitation Index at target	0.054	
S_{target}	Spawning Output at target	3.688	
Y_{target}	Yield at target	0.575	
BIO_{target}	Summary biomass at target	10.591	

These deterministic quantities should be augmented with information from stochastic simulations of the stock's dynamics (references AgePRO, others). The lognormal distribution of recruitment means that these mean-based quantities will occur less than 50% of the time. This is a relevant consideration when these mean based quantities are used to calculate rebuilding targets that are to be achieved with 50% probability. The degree of difference between a mean and median biomass level is less than the difference between mean and median recruitment because biomass is a weighted sum of a sequence of recruitments. However, as a stock is fished, the contribution of older age groups diminishes and the variability in stock biomass will increase towards the level of variability in recruitment itself.

Forecast

The forecast module provides the capability to do a projection for a user-specified number of years that is directly linked to the model's ending conditions, and associated uncertainty, and to a specified level of fishing intensity. The forecast requires information on life history, fishery selectivity, relative harvest rate between fleets, overall fishing intensity, and recruitment.

- The life history and fishery selectivity characteristics in the ending year are used throughout the forecast. Note that this could have unexpected consequences if there is a recent change in growth which causes an anomaly in the length-at-age vector in the ending year. It also would be problematic if the fishery selectivity in the ending year is allowed to be overly responsive to noisy data.
- The relative harvest rate between fleets for the forecast can be specified by user input or designated to match the relative harvest rates in the last year of the time series. These same relative harvest rates are used in the calculation of the fishing intensity that would produce the target SPR.

- The overall level of fishing intensity is set equal to the target SPR level calculated in the management quantities module. In the forecast, this overall level is multiplied by the relative harvest rates between fleets to get the actual harvest rate value for each fleet during the forecast. Alternatively, the user can specify actual levels of landed catch for particular fleets in particular time periods. In this case, the model calculates the actual harvest rate needed to take that amount of catch just as it does during the estimation phase for the data time series.

- The level of recruitment during the forecast is estimated as random deviations from the estimated spawner-recruitment function. Because there are no data influencing these forecast recruitment deviations, their maximum likelihood estimate is a value of zero with a standard deviation equal to the sigmaR, the designated level of recruitment variability. Thus forecasts of future catch and stock abundance will inherit variance from these estimated parameters. When the model is operating in MCMC mode, these future recruitments will be resampled throughout the full range of the lognormal probability density. There are, however, several caveats and additional control features for implementing this forecast recruitment feature:

  - If environmental influence on expected recruitment is used, this will influence the recruitment through the end year, but there is no provision to provide a forecast of future environmental conditions with which to alter the expected value of future recruitments.

  - The starting year for forecast recruitments is the year after the last year with recruitment deviations during the time series. This is necessary because some model configurations will not estimate recruitment deviations all the way through the end year due to inadequate recent data. If the forecast recruitments were not allowed to start during this period, the uncertainty in the forecast would be underestimated.

  - The vector of forecast recruitment deviations is estimated during an additional model estimation phase. If this vector starts before the ending year of the time series, then the estimates of these recruitments will be influenced by the data in these final years. This is problematic, because the original reason for not estimating these recruitments at the end of the time series was the poor signal/noise ratio in the available data. It is not that these data are worse than data from earlier in the time series, but the low amount of data accumulated for each cohort allows an individual datum to dominate the model's fit. Thus, an additional control is provided so that forecast recruitment deviations during these years can receive an extra weighting in order to counter-balance the influence of noisy data at the end of the time series.

  - An additional control is provided for the fraction of the log-bias adjustment to apply to the forecast recruitments. Recall that R is the expected mean level of recruitment for a particular year as specified by the spawner-recruitment curve and R' is the geometric mean recruitment level calculated by discounting R with the log-bias correction factor $e^{-0.5s^2}$. Thus a lognormal distribution of recruitment deviations centered on R' will produce a mean level of recruitment equal to R. During the modeled

time series, the virgin recruitment level and any recruitments prior to the first year of recruitment deviations are set at the level of R, and the lognormal recruitment deviations are centered on the R' level. For the forecast recruitments, the fraction control can be set to 1.0 so that 100% of the log-bias correction is applied and the forecast recruitment deviations will be based on the R' level. This is certainly the configuration to use when the model is in MCMC mode. Setting the fraction to 0.0 during maximum likelihood forecasts would center the recruitment deviations, which all have a value of 0.0 in ML mode, on R. Thus would provide a mean forecast that would be more comparable to the mean of the ensemble of forecasts produced in MCMC mode. Further work on this topic is underway.

LITERATURE CITED

APPENDIX A: NOTATION

This section contains a complete list of quantities referred to in the text and equations of this report. The quantities are grouped into six categories. For the last 3 categories, the type of quantity is identified as P = parameter that can be kept constant at its input value or estimated by the model fitting procedure, I = fixed input coefficient, blank = internally calculated quantity.

Indices and index ranges

a	age
A	maximum age
A_f	number of fishing fleets
A_g	number of growth morphs
A_i	number of age bins
A_γ	number of genders
A_l	number of length bins
A_s	number of seasons
δ_s	is the duration of the season s
g	is the index for growth morph
γ	is the index for gender
i	is the index for age bin
j	is the index for objective function component
l	is the index for length bin
m	is the market category of the catch (1 = discarded, 2 = retained, 3 = combined)
v	is the index of observation within a given data type
y	year
Y_1	first year in model
Y_2	last year in model

Data

D_{tf}	is the observed discarded biomass at time t for fishery f
G_{tf}	is the observed abundance index for fishery or survey f at time t

$\overline{L}_{tf\,\gamma imk}$ is the observed mean size in age bin i in time step t for fishery or survey f in gender γ, associated with ageing error type k

n_{0f} is the number of observations of abundance for fishery or survey f.

$n_{1tf\,\gamma m}$ is the number of observed lengths in the catch at time step t for fishery or survey f in length bin l, gender γ, and market category m

$n_{2tf\,\gamma mk}$ is the number of observed ages in the catch at time step t for fishery or survey f in length bin l, gender γ, market category m, associated with ageing error type k

$n_{6tf\,\gamma imk}$ is the number of observed ages in age bin i in time step t for fishery or survey f in gender γ, associated with ageing error type k

n_R is the number of years for which recruitment is estimated

$p_{1tfl\,\gamma m}$ is the observed proportion of the catch in length bin l at time step t for fishery or survey f, gender γ, and market category m

$p_{2tfi\gamma mk}$ is the observed proportion of the catch in age bin i at time step t for fishery or survey f, gender γ, and market category m, associated with ageing error type k

$\overline{w}_{tfm}$ is the observed mean weight of the catch in market category m by fishery f at time t

Parameters and quantities used in estimation

$\mathcal{L}$ is the total objective function

ω_{jf} is a weighting factor for each objective function component

$\mathcal{L}_{jf}$ is the objective functions component of kind j, and fishery and survey f.

Biological Characteristics

		TYPE
a_1	is the last age for natural mortality equal to M_1 for all growth morphs	P
a_2	is the first age for natural mortality equal to M_2 for all growth morphs	P
a_3	is a reference age near the youngest age well represented in the data	

a_4	is a reference age near the oldest age well represented in the data	I
$\tilde{a}_i$	is the lower limit of age bin i	I
g'_g	is proportion of the recruitment allocated to growth morph g	I
L_l	is the midpoint of length bin l	
L_{min}	is the midpoint of the smallest length bin	
L_{max}	is the midpoint of the largest length bin	
L'_l	is the lower limit of length bin l	
L'_{min}	is the lower limit of the smallest length bin	
L'_{max}	is the lower limit of the largest length bin	
L_{1g}	is the mean size of growth morph g at age a_3	P
L_{2g}	is the mean size of growth morph g at age a_4	P
$L_{\infty g}$	is the mean asymptotic size of growth morph g	
L_{0ga}	is the mean length in the beginning of the equilibrium year for growth morph g	
$\tilde{L}_{0ga}$	is the mean length in the middle of the equilibrium year for growth morph g	
L_{tga}	is the mean size at age a at the beginning of season t for growth morph g	
$\tilde{L}_{tga}$	is the mean size at age a in the middle of season t for growth morph g	
K_g	is the growth coefficient for growth morph g	P
m_{gal}	is the fraction of which are mature at age a in length bin l and growth morph g	
M_{1g}	is the natural mortality for youngest age for growth morph g	P
M_{2g}	is the natural mortality for oldest age for growth morph g	P
μ_{ka}	is the mean age assigned to age a under ageing error of type k	I
Ω	is the vector of 7 biological parameters for weight and fecundity	P

Population States and Processes

<div align="right">

TYPE

</div>

$b_{lyf\gamma}$	is the fraction retained in length bin l, year y, fishery f, and gender γ	

B_{tf} The vulnerable biomass at time step t for fishery f

$\beta_{lyf\gamma}$ is the length-based selectivity for length bin l, year y, fishery or survey f and gender γ

$\beta_{atf\gamma}$ is the age-based selectivity for age a, year y, fishery or survey f and gender γ

β_1- β_7 are selectivity parameters specific to a given selectivity type   P

C_{tf} is the catch at time step t by fishery f

$C_{tfal\gamma}$ is the expected number in the catch by each fishery or survey in time step t at age a, length l, and gender γ

CV_{1g} is the coefficient of variation for length in growth morph g at age 0   I

CV_{2g} is the coefficient of variation for length in growth morph g at age A I

$\hat{D}_{tf}$ is the expected discarded biomass for fishery f in time step t

$\hat{D}'_{tf}$ is the expected fraction of the catch discarded for fishery f in time step t

F_{tf} is the harvest rate of fishery f at time step t

ϕ_{0gal} is the proportion in length bin l for age a and growth morph g in the middle of the equilibrium year

ϕ_{tgal} is the proportion in length bin l for age a and growth morph g at time t

$\hat{G}_{tf}$ is the abundance index for fishery or survey f at time t

h is the parameter for steepness of the stock-recruitment function   P

N_{0ga} is the number at age a in growth morph g at the beginning of the equilibrium year

$\tilde{N}_{0ga}$ is the number at age a in growth morph g in the middle of the equilibrium year

N_{tga} is the number at age a in growth morph g at the beginning of time step t

$\tilde{N}_{tga}$ is the number at age a in growth morph g in the middle of time step t

$\tilde{P}_t$ is the exponential deviation of the parameter P at time t

Q_f is the catchability coefficient for fishery or survey f P

Q'_f is the power parameter for catchability of the fishery or survey f P

R_0 is the initial recruitment (parameter is $\ln(R_0)$) P

R_1 is the equilibrium recruitment, defined as an exponential offset from R_0 P

R_{tg} is the recruitment to growth morph g at time step t

$\hat{R}_{tg}$ is the expected value of the lognormally distributed recruitment residuals for growth morph g at time step t

$\tilde{R}_t$ is the deviation in recruitment, which is lognormally distributed with expected value equal to the deterministic stock-recruitment curve

S_0 is the virgin spawning biomass

S_1 is the spawning biomass in the under the initial equilibrium catch

w_{gal} is the mean weight of individuals at age a in length bin l and growth morph g

$\hat{\bar{w}}_{tf}$ is the expected mean weight of the catch by fishery f at time t

$\hat{\bar{w}}'_{tf}$ is the expected mean weight of the retained catch by fishery f at time t

$\hat{\bar{w}}''_{tf}$ is the expected mean weight of the discarded catch by fishery f at time t

Standard Deviation

|		TYPE
σ_R	is the standard deviation for recruitment	P
σ_{0ga}	is the standard deviation of length at age a in growth morph g	P
σ_{1tf}	is the standard error of the log of the observed abundance index, $\ln(G_{tf})$	I
σ_{2tf}	is the standard error of the log of the observed discarded biomass, $\ln(D_{tf})$	I
σ_{3tf}	is the standard error of the observed mean weight, $\bar{w}_{tfm}$	I
$\sigma_{6tf\gamma imk}$	is the standard error of the expected mean size in age bin i in time step t for fishery or survey f in gender γ, associated with ageing error type k	
σ_θ	is the standard deviation for the parameter prior on parameter θ	I
σ_P	is the standard deviation for the time series of random parameter deviates	I
σ_{ka}	is the standard deviation of ageing error at age a for ageing error type k.	I

Appendix B – Example Application

An example application was created to demonstrate the model's basic capabilities with data comparable to that available for west coast groundfish. This is a simple test in that the growth, natural mortality and form of selectivity patterns were set to be identical to that in the model used to generate the data. Nevertheless, the demonstration shows to ability of the model to correctly deal with variability in data. The data set spanned 1971-2001. There was a single fishery with a constant logistic selectivity pattern over time and with age and size composition data each year. Natural mortality was set at 0.1 and the accumulator age in the population was set at 40 years. There was a triennial fishery-independent survey during 1977-2001 with associated abundance index, age and size composition. There was also an annual recruitment index for each year 1990-2001. Recruitment followed a Beverton-Holt spawner-recruitment relationship with steepness of 0.7 and standard deviation of residuals equal to 0.8. In order to demonstrate the ability of the model to achieve size-specific survivorship the following morph structure was adopted: there was one male growth morph and five female growth morphs; the male growth morph and the middle female growth morph had identical mean size-at-age; the male growth curve had a broad variability of size-at-age and each female growth morph had a narrower variability, but the set of female growth morphs together produced an unfished size-at-age distribution that was identical to the male distribution. Twenty parametric bootstrap data sets were generated by SS2 from one population realization. Male size-at-age is one broad morph; female size-at-age is composed of five narrower morphs..
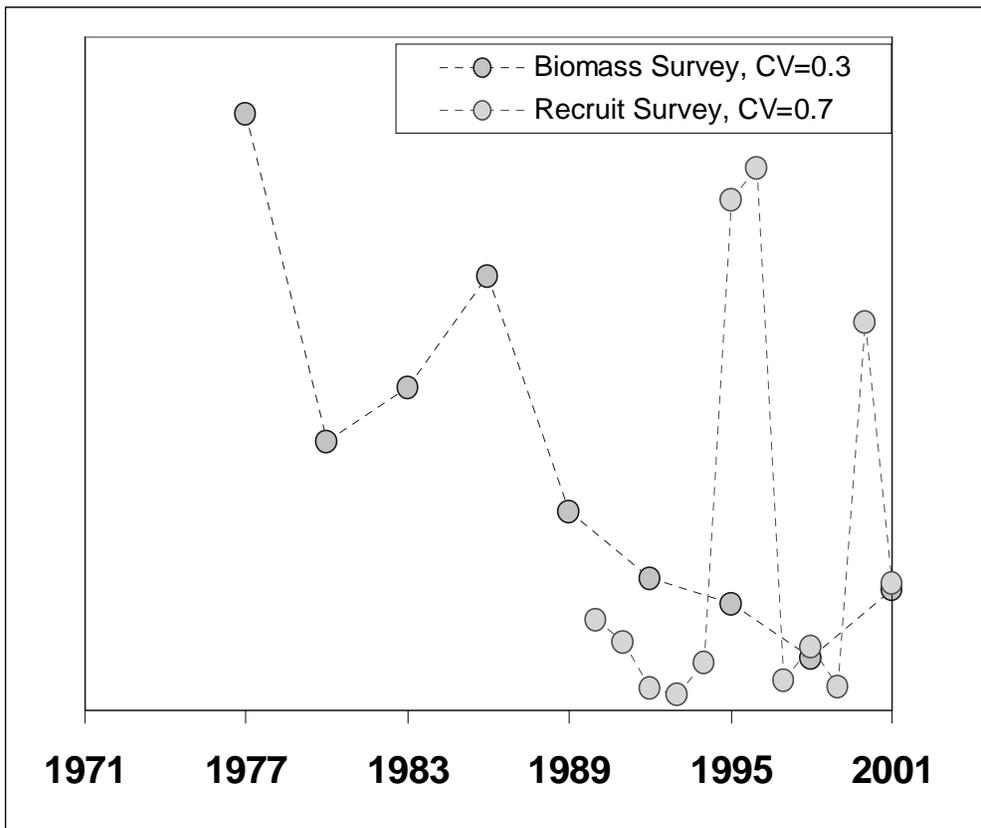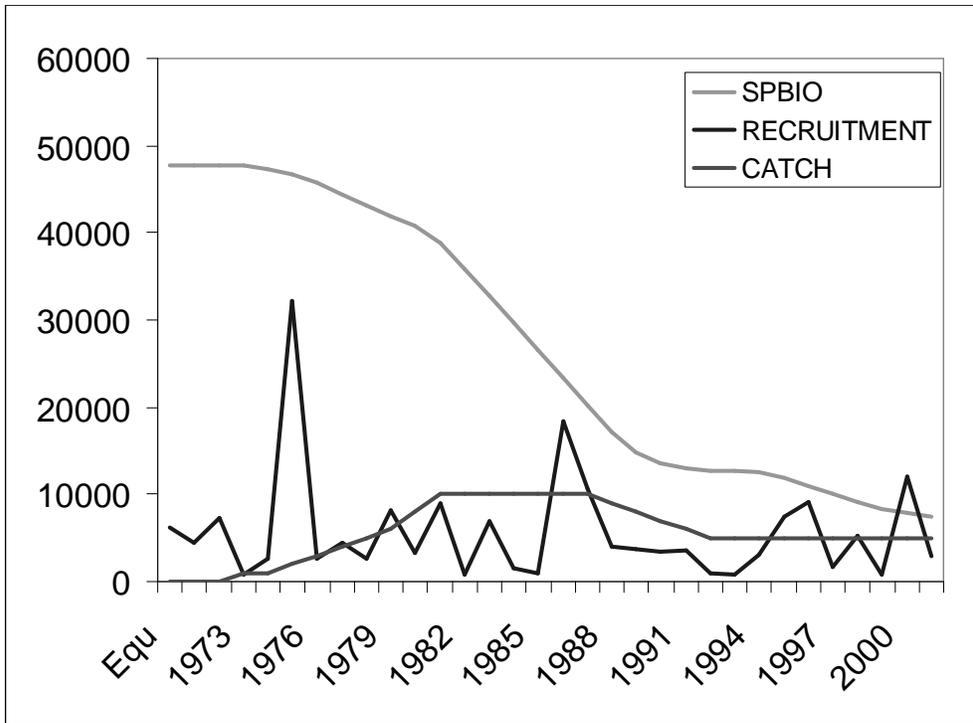
Typical parametric bootstrap data set of the 20 sets generated.
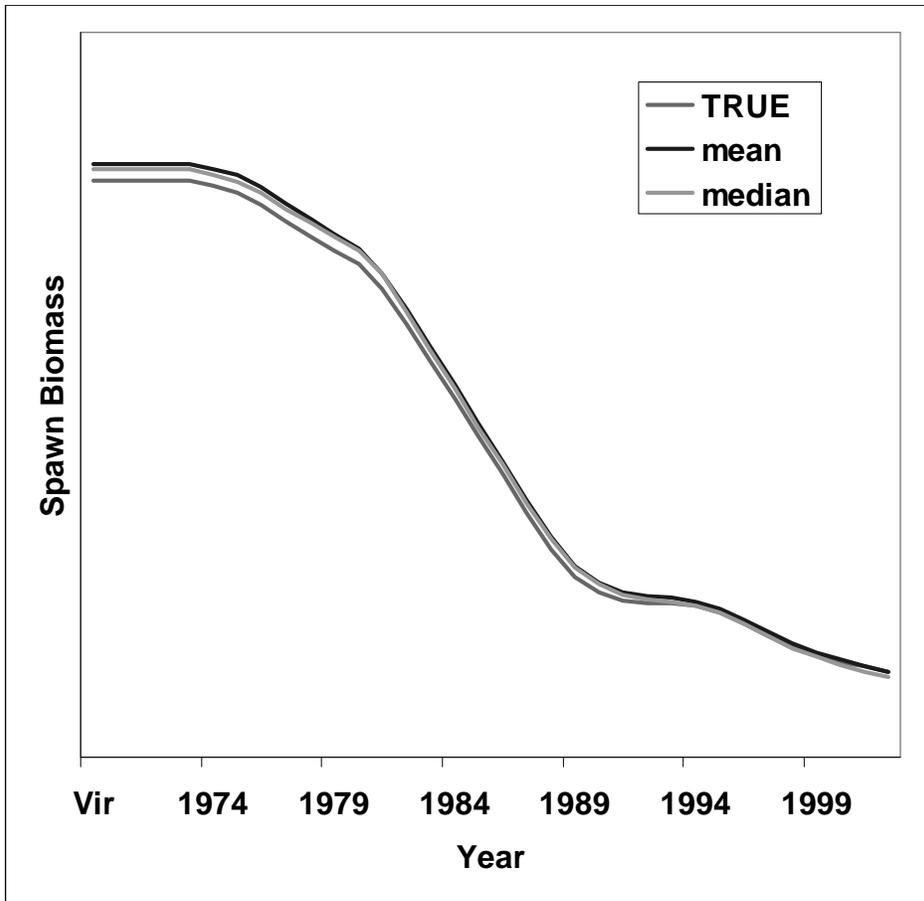
The average estimate of spawning biomass among the fits to the 20 data sets is nearly identical to the true level.
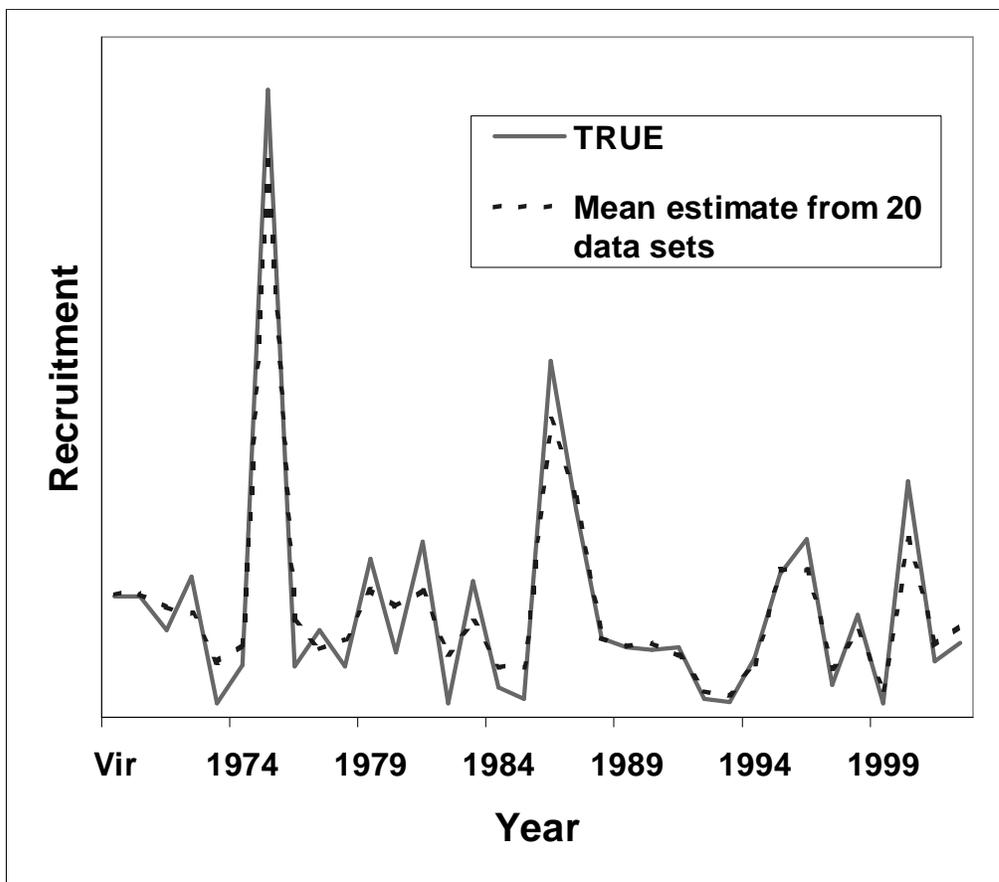
The average estimate of recruitment slightly undershoots the true range of variability.
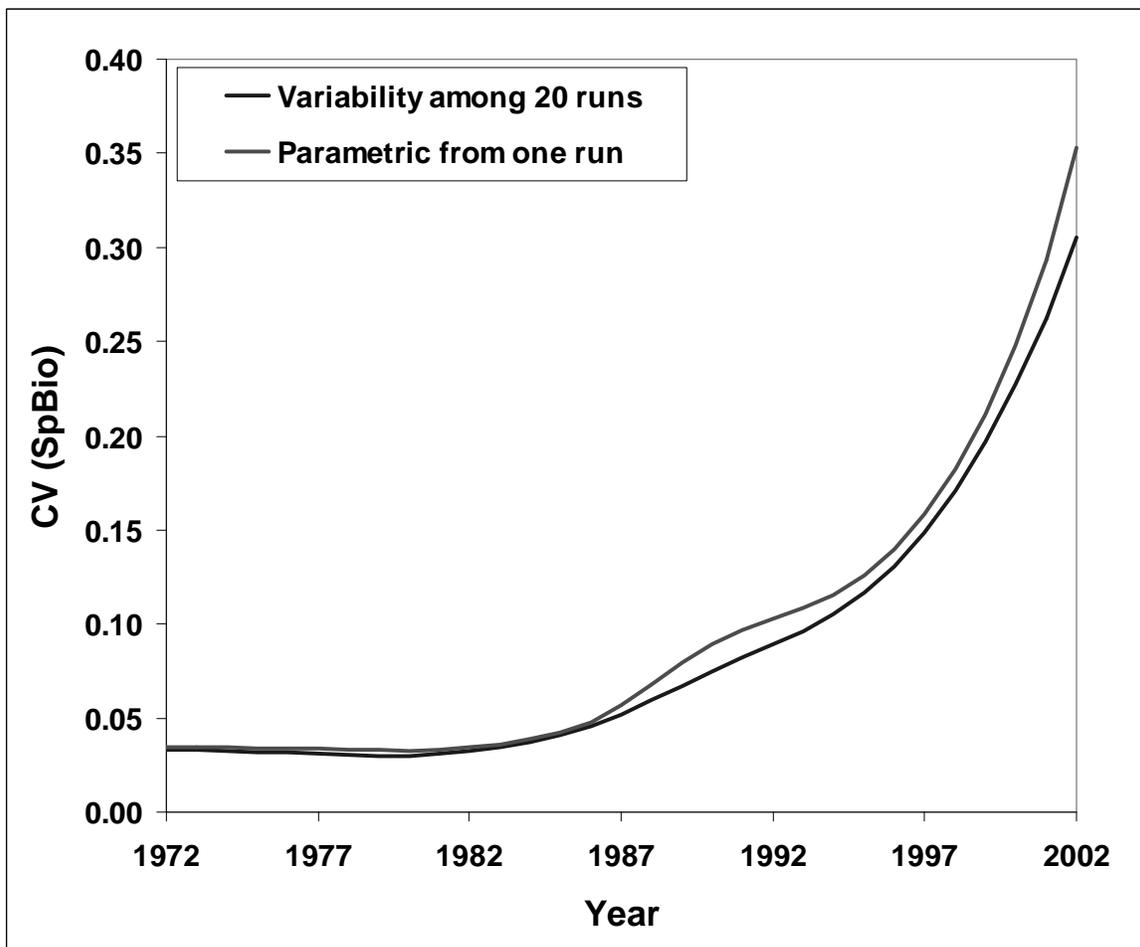
Parametric estimate of variance in spawning biomass estimate from ADMB's inverse Hessian is nearly identical to the vaiability among the fits to the 20 data sets.
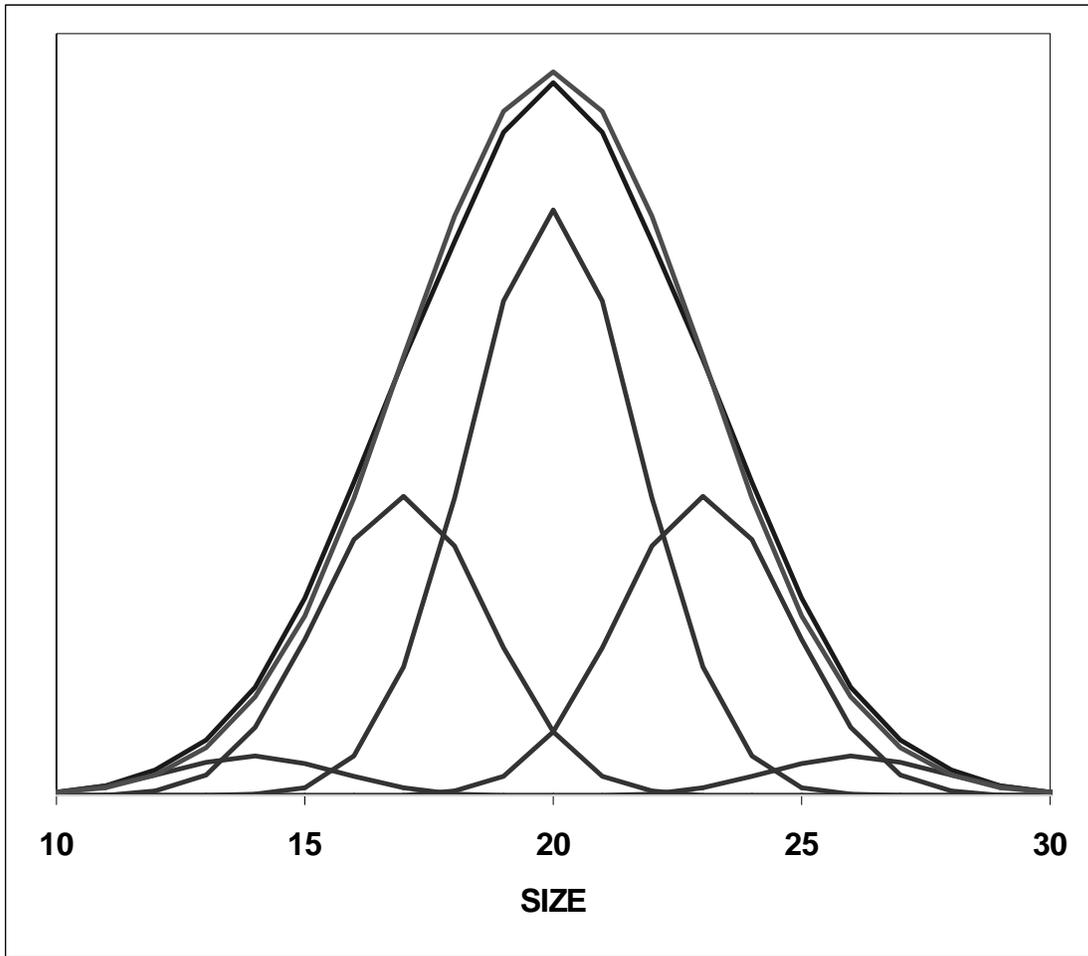
Size at age of females (blue) is built up from 5 normal curves (purple) to produce an oveall distribution comparable to males (red).
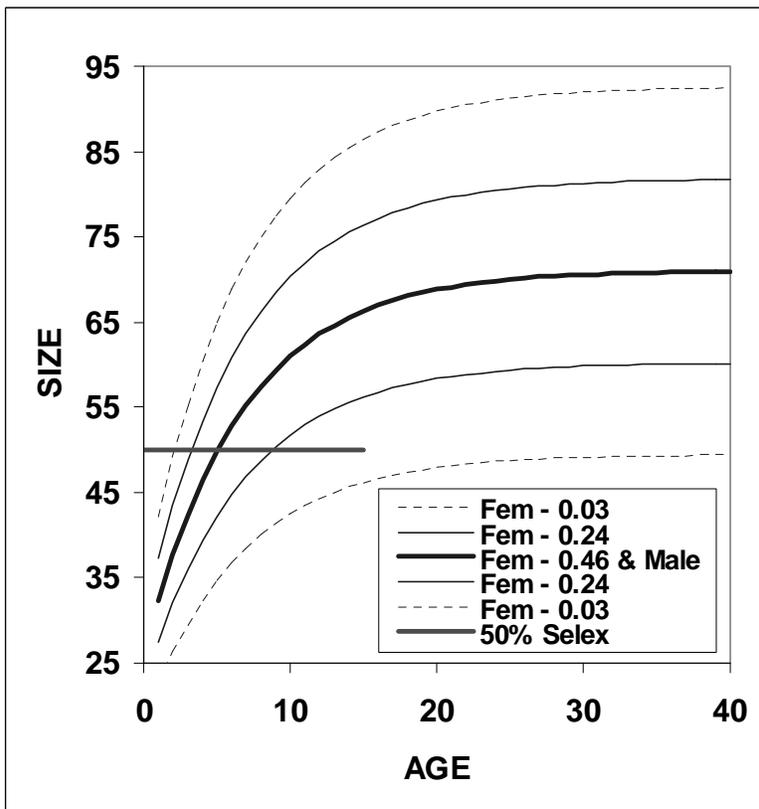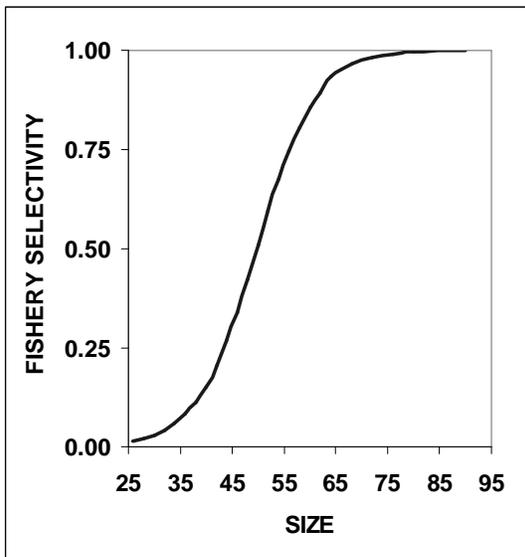
Fishery size-selectvity causes differential mortality between the five female growth morphs.
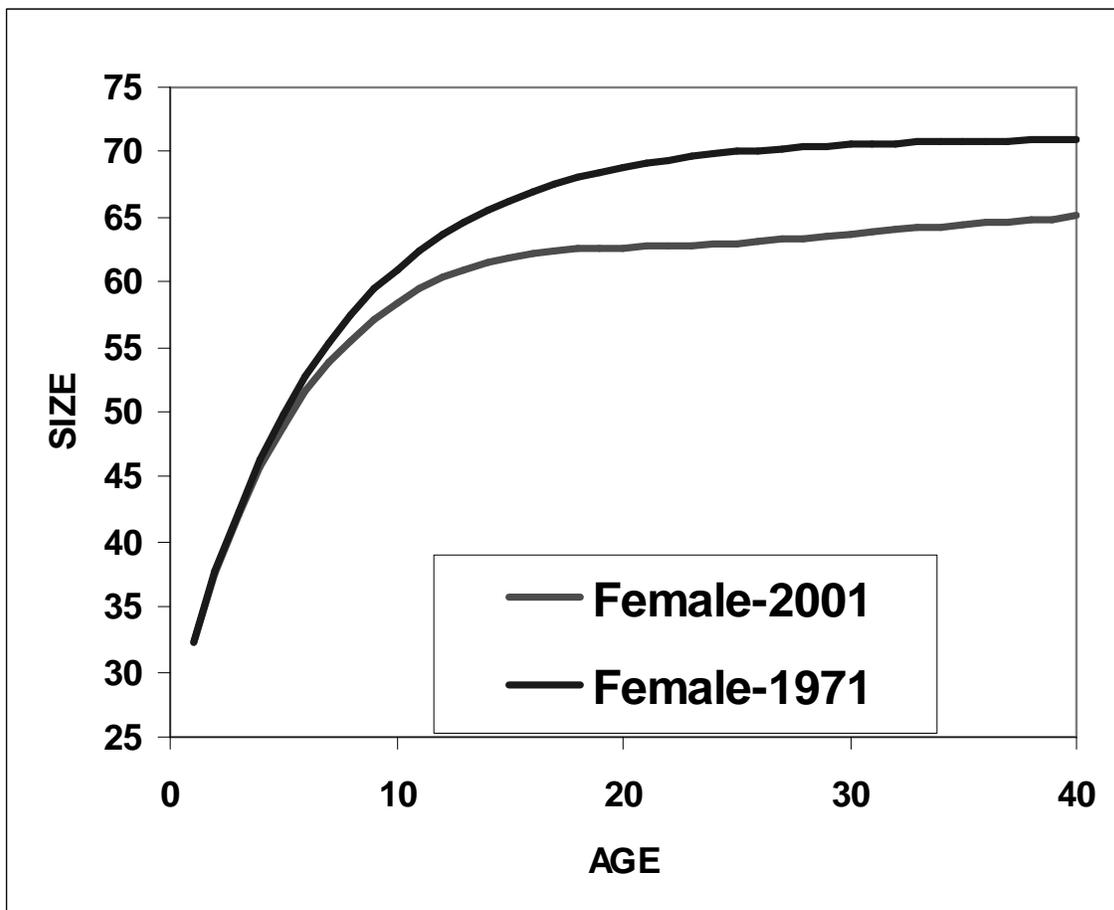
The result of morph specific survivorship is that the mean size-at-age of females, summed across all 5 morphs, declines substantially over the time series. Males, which have just one morph, have mean size-at-age constant over the time series.