

D2.6 Sub-model SMS including user guide

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1. INTRODUCTION

SMS is a stochastic multispecies model describing stock dynamics of interacting stocks linked together by predation. It operates on annual or seasonal time steps. The model consists of sub-models of survival, fishing mortality, predation mortality, survey catchability and stock-recruitment. SMS uses maximum likelihood to estimate parameters and the total likelihood function consists of four terms related to observations of international catch at age, survey catch per unit effort (cpue), stomach contents observation, and a stock-recruitment (penalty) function. Uncertainties of parameters and biological key parameters (biomass and average fishing mortality) are estimated from the inverse Hessian matrix, or alternatively using the Marco Chain Monte Carlo (MCMC) methodology (e.g. Gilks *et al.*, 1996)

The model developed is a mixture of age and size structured models. The catch model has been chosen to be age-structured while the food preference model is size based because preference depends on size rather than age. This also applies to the fishery mortality model as well, but catch data by size classes are not available for the North Sea. The mixed age-size structure implies that data by age groups are transformed to sizes using age-length keys.

SMS can be used as assessment model, where parameters and the historical stock dynamic are estimated. As forecast model, SMS uses the parameter estimates and terminal stock sizes to forecast stock dynamic in short or long term, given harvest control rules for the individual stocks.

The notation is given in Appendix 1.

The SMS manual, code and interface are available to download from

<http://www.meece.eu/Library.aspx>

1.1 Model description

1.1.1 Population dynamics model

Survival of the stocks

The survival of the stock s is described by the standard exponential decay equation of stock numbers (N)

$$N_{s,a,y,q+1} = N_{s,a,y,q} \exp(-Z_{s,a,y,q}) \quad (1)$$

or

$$N_{s,a+1,y+1,q=1} = N_{s,a,y,q=\text{last season}} \exp(-Z_{s,a,y,q=\text{last season}}) \quad (2)$$

Likewise the MSVPA approach, the instantaneous rate of total mortality, $Z(s, a, y, q)$, by species s , age-group a , year y and season q , is divided into three components; an predation mortality ($M2$), a fixed residual natural mortality ($M1$) and an fishing mortality (F):

$$Z_{s,a,y,q} = M1_{s,a,q} + M2_{s,a,y,q} + F_{s,a,y,q} \quad (3)$$

If both $M1$ and $M2$ are assumed to be known quantities, the model described so far is a stochastic single species assessment model, where the dynamic of each of the species is independent of each other.

Stock numbers are normally estimated within the model. A special case – for which observations are not available - is the so-called “other predators”, which is a group of important predator species for which the stock number at age or size class is assumed known from external sources. For the North Sea, such species includes for example sea birds, marine mammals or fish species without an analytical assessment, e.g. grey gurnards (*Eutrigla gurnardus*) or assessed, but widely distributed species with a highly variable proportion of the stock within the model area, e.g. mackerel (*Scromber scrombus*) and horse mackerel (*Trachurus trachurus*).

Fishing mortality

Fishing mortality, $F(s,a,y,q)$, is modelled as an extended separable model including age, year and seasonal effects. However, as these effects may change over time a more flexible structure is assumed allowing for such changes for specified periods. For convenience the species index is left out in the following:

$$F_{a,y,q} = F_1(Y, A) F_2(y) F_3(Y, A_2, q) \quad (4)$$

where indices A_1 and A_2 are grouping of ages, (e.g. ages 1-6 and 7-9) and Y is grouping of years (e.g. 1975-1989, 1990-2000).

Model (4) defines that the years included in the model can be grouped into a number of period clusters (Y), for which the age selection (F_1) and seasonal selection (F_3) are assumed constant. F_2 is the year effect, specifying the overall level of F for a year. The grouping of ages for age selection, A_1 , and season selection, A_2 , can be defined independently.

Natural Mortality

Natural mortality is divided into two components, predation mortality ($M2$) caused by the predators included in the model and a residual natural mortality ($M1$), which is assumed to be known and is given as input.

The predation mortality of a prey with length l_{prey} due to a predator with length l_{pred} is calculated as suggested by Andersen and Ursin (1977) and Gislason and Helgason (1985):

$$M2_{prey,l_{prey},y,q} = \sum_{pred,l_{pred}} \frac{\bar{N}_{pred,l_{pred},y,q} RA_{pred,l_{pred},y,q} S_{prey,pred,q}(l_{prey},l_{pred})}{AB_{pred,l_{pred},y,q}} \quad (5)$$

where RA denotes the food ration per time unit, where S denotes the food suitability coefficient defined below and where AB is the total available biomass. AB is defined as the sum of the biomass of preys weighted by its suitability. This prey biomass includes also the so-called “other food” (OF), which includes all prey items not explicitly modelled, e.g. species of invertebrates and non commercial fish species. Other food species is combined into one group, such that the total available prey biomass becomes:

$$AB_{pred,l_{pred},y,q} = \sum_{prey,l_{prey}} \bar{N}_{prey,l_{prey},y,q} w_{prey,l_{prey},y,q} S_{prey,pred,q}(l_{prey},l_{pred}) + OF_{pred,l_{pred}} S_{other,pred,l_{pred},q}$$

$\bar{N}_{prey,l_{prey},y,q}$ is not directly being estimated in the model for which stock numbers and fishing mortality have been parameterised through the age. Using age-length-keys (ALK) stock numbers at length is obtained by

$$N_{prey,l_{prey},y,q} = \sum_a N_{prey,a,l_{prey},y,q} \sum_a N_{prey,a,y,q} ALK_{prey,l_{prey},a,y,q} \quad (6)$$

where $ALK_{s,l_s,a,y,q}$ denote the observed proportion of size class l_s for a given species and age group, i.e. $\sum_{l_s} ALK_{s,l_s,a,y,q} = 1$

Predation mortality by age is needed as well because the catch model is age-structured. Assuming that F and $M1$ depends only of the age and that $M2$ only depends of the length and leaving out the species, year and quarter indices $M2$ at age is estimated by

$$M2_a = Z_a * \frac{\sum_l \bar{N}_{a,l} * M2_{a,l}}{D_a} = \log\left(\frac{N_a}{N_a - D_a}\right) * \frac{\sum_l \bar{N}_{a,l} * M2_l}{D_a}$$

where

$$N_{a,l} = N_{a,l} * \frac{(1 - \exp(-(F_{a,l} + M1_{a,l} + M2_{a,l})))}{F_{a,l} + M1_{a,l} + M2_{a,l}} = N_{a,l} * \frac{(1 - \exp(-(F_a + M1_a + M2_l)))}{F_a + M1_a + M2_l}$$

and where

$$D_a = \sum_l \bar{N}_{a,l} * (F_a + M1_a + M2_l) = \text{the number of individuals died within a time step.}$$

$M2$ cannot directly be calculated from equation (5) because $M2$ also is included in the right hand term in equation (5) as (leaving out all indices)

$$\bar{N} = \frac{1 - \exp(-M1 - M2 - F)}{M1 + M2 + F} N$$

As no analytical solution for $M2$ exists, $M2$ has been found numerically. If the time step considered is sufficiently small, for instance a quarter, $M2$ becomes small and can be approximated by replacing the average number during the season, \bar{N} , on the right hand side of equation (5) by the stock at the beginning of the season, N . As the right hand side of equation now is independent of $M2$ this quantity can be calculated directly from equation (5), where AB is modified correspondingly.

Food suitability

As suggested by Andersen and Ursin (1977) and Gislason and Helgason (1985) the size dependent food suitability is defined as the product of a species dependent vulnerability coefficient $\rho_{i,j}$, a size preference coefficient $g_{i,j}(l_i, l_j)$ and an overlap index, $o_{i,j,q}$ to describe the seasonal variability of predator prey habitat overlap such that suitability is defined as:

$$S_{prey,pred,q}(l_{prey}, l_{pred}) = \rho_{prey,pred} g_{prey,pred}(l_{prey}, l_{pred}) o_{prey,pred,q} \quad (6)$$

where *pred* and *prey* denote predator and prey species, and where l_{prey} denote *prey* and l_{pred} *pred* dependent size classes.

The overlap index may change between seasons, but is assumed independent of year and sizes.

Several functions can be used for size preference. Andersen and Ursin (1977) assumed that a predator has a preferred prey size ratio and that a prey twice as big as the preferred size is as attractive as another half the prey size. This was formulated as a log-normal distribution:

$$g_{prey,pred}(l_{prey}, l_{pred}) = \exp\left(-\frac{(\log(\frac{lm_{pred}}{lm_{prey}}) - \eta_{PREF\ pred})^2}{2\sigma_{PREF\ pred}^2}\right); \quad 0 < g \leq 1 \quad (7)$$

where η_{PREF} is the logarithm of the preferred size ratio and σ_{PREF}^2 , the "variance" of relative preferred size ration, expressing how particular a predator is about the size of a prey. lm_{pred} and lm_{prey} are the mean size of the size classes l_{pred} and l_{prey} .

Alternatively, a uniform size preference can be assumed within the range of the observed size ratio and zero selection outside that ratio:

$$g_{prey,pred}(l_{prey}, l_{pred}) = \begin{cases} 1 & \eta_{MIN\ pred,prey} \leq \frac{lm_{pred}}{lm_{prey}} \leq \eta_{MAX\ pred,prey} \\ 0 & \text{outside observed range} \end{cases}$$

where η_{MIN} and η_{MAX} are the observed minimum and maximum size ratios.

The uniform size preference does not take into account that the preferred predator/prey size ratio might change by size, such that larger individuals select relatively smaller preys. A way to implement this, the constants η_{MIN} and η_{MAX} are substituted by functions where the relative size range is dependent on predator size:

$$g_{prey,pred}(l_{prey}, l_{pred}) = \begin{cases} 1 & c_{pred,prey} + d_{pred,prey} \log(lm_{pred}) \leq \log\left(\frac{lm_{pred}}{lm_{prey}}\right) \leq e_{pred,prey} + f_{pred,prey} \log(lm_{pred}) \\ 0 & \text{outside regression range} \end{cases}$$

The regression parameters are estimated by quantile regression (Koenker and Bassett 1978) using the 2.5% and 97.5% percentiles of stomach content data.

Adjustment of age-size keys and estimation of food ration

The age length keys were obtained from the IBTS surveys using the same gear (i.e. the GOV trawl) in the period considered. Hence the observed ALK's were adjusted to account for the effect of mesh size selection. This was done using a logistic selection function

$$SL(s,l) = \frac{1}{1 + (\exp(S1_s - S2_s * lm_{s,l}))}$$

where $lm_{s,l}$ denotes the mean length of length class l and $S1$ and $S2$ species specific gear selection parameters.

The adjusted ALK can then be derived from the observed ALK by:

$$ALK_{s,l,s,a,y,q} = \text{Observed} ALK_{s,l,s,a,y,q} / SL_{s,l,s}$$

which finally has to be standardised to 1 for each age before used in equation (6).

Food ration pr. time unit was estimated assuming an exponential relationship between ration and body weight w :

$$RA_{pred,l,pred,y,q} = \gamma_{pred,q} w_{pred,l,pred,y,q}^{\delta_s}$$

Where the weight w is estimated from the standard equation $w = a l^b$ and the coefficients a , b , γ and δ are assumed to be known.

1.2 Statistical models

Three types of observations are considered: Total international catch at age; research survey cpue and stomach content observations. For each type a stochastic model is formulated and the likelihood function is calculated. As the three types of observations are independent the total log likelihood is the sum of the contributions from three types of observations. A stock-recruitment (penalty) function is added as a fourth contribution.

1.2.1 Catch-at-age

Catch-at-age observations are considered stochastic variables subject to sampling and process variation. The probability model for these observations is modelled along the lines described by Lewy and Nielsen (2003):

Catch at age is assumed to be lognormal distributed with log mean equal to log of the standard catch equation. The variance is assumed to depend on age and season and to be constant over years. To reduce the number of parameters, ages and seasons can be grouped, e.g. assuming the same variance for age 3 and age 4 in one or all seasons. Thus, the likelihood function, L_C , associated with the catches is

$$L_{CATCH} = \prod_{s,a,y,q} \frac{1}{\sigma_{CATCH\ s,a,q} \sqrt{2\pi}} \exp\left(-\frac{(\log(C_{s,a,y,q}) - E(\log(C_{s,a,y,q})))^2}{2\sigma_{CATCH\ s,a,q}^2}\right) \quad (9)$$

Where

$$E(\log(C_{s,a,y,q})) = \log\left(\frac{F_{s,a,y,q}}{Z_{s,a,y,q}} N_{s,a,y,q} (1 - e^{-Z_{s,a,y,q}})\right) \quad (10)$$

Leaving out the constant term, the negative log-likelihood of catches then becomes:

$$l_{CATCH} = -\log(L_{CATCH}) \propto NOY \sum_{s,a,q} \log(\sigma_{CATCH\ s,a,q}) + \sum_{s,a,y,q} (\log(C_{s,a,y,q}) - E(\log(C_{s,a,y,q})))^2 / (2\sigma_{CATCH\ s,a,q}^2) \quad (11)$$

1.2.2 Survey indices

Similarly, the survey indices, $CPUE(survey,s,a,y,q)$, are assumed to be log-normally distributed with mean

$$E(\log(CPUE_{survey,s,a,y,q})) = \log(Q_{survey,s,a} \bar{N}_{SURVEY\ s,a,y,q}) \quad (12)$$

where Q denotes catchability by survey and \bar{N}_{SURVEY} mean stock number during the survey period. Catchability may depend on a single age or groups of ages. Similarly, the variance of log CPUE, $\sigma(survey,a)$, may be estimated individually by age or by clusters of age groups. The negative log likelihood is on the same form as equation (11):

$$l_{SURVEY} = -\log(L_{SURVEY}) \propto \sum_{survey,s,a} NOY_{survey,s} \sum_{survey,s,a} \log(\sigma_{SURVEY\ survey,s,a}) + \sum_{survey,s,a,y} (\log(CPUE_{survey,s,a,y}) - E(\log(CPUE_{survey,s,a,y})))^2 / (2\sigma_{SURVEY\ survey,s,a}^2) \quad (13)$$

1.2.3 Stomach contents

The stomach contents observations, which are the basis for modelling predator food preference, consist of the average proportions by weight of the stomach content averaged over the stomach samples in the North Sea. The model observations, $STOM_{prey,pred,y,q}(l_{prey}, l_{pred})$ are given for combinations of prey and predator species and size classes.

STOM are assumed stochastic variables subject to sampling and process variations. The observations across prey/size sum to one Thus, the probability distribution of the stomach observations for a given predator including all prey/length groups in principle needs to be a multivariate distribution defined on the simplex. As far as the authors know the Dirichlet distribution is the only distribution fulfilling this requirement. The Dirichlet density function of the observed diet proportions in a given year and quarter is

$$f_{pred,y,q} = f((STOM_{prey\ j_{prey},pred,l_{pred},y,q})_{prey\ j_{prey}} | (p_{prey\ j_{prey},pred,l_{pred},y,q})_{prey\ j_{prey}}) = \frac{\Gamma(p_{pred\ j_{pred},y,q})}{\prod_i \Gamma(p_{prey\ j_{prey},pred,l_{pred},y,q})} \prod_{prey\ j_{prey}} STOM_{prey\ j_{prey},pred,l_{pred},y,q}^{p_{prey\ j_{prey},pred,l_{pred},y,q}-1} \quad (14)$$

where

$$p_{pred\ j_{pred},y,q} = \sum_{prey\ j_{prey}} p_{prey\ j_{prey},pred,l_{pred},y,q}$$

The mean and variance of the observations in the Dirichlet distribution are

$$E(STOM_{prey,l_{prey},pred,l_{pred},y,q}) = \frac{P_{prey,l_{prey},pred,l_{pred},y,q}}{P_{pred,l_{pred},y,q}} \quad (15)$$

$$V(STOM_{prey,l_{prey},pred,l_{pred},y,q}) = \frac{E(STOM_{prey,l_{prey},pred,l_{pred},y,q})(1 - E(STOM_{prey,l_{prey},pred,l_{pred},y,q}))}{P_{pred,l_{pred},y,q} + 1} \quad (16)$$

The expected value of the stomach contents observations is modelled using the theory developed by Andersen and Ursin (1977):

$$E(STOM_{prey,l_{prey},pred,l_{pred},y,q}) = \frac{N_{prey,l_{prey},y,q} W_{prey,l_{prey},y,q} S_{prey,pred,q}(l_{prey},l_{pred})}{\sum_{prey,l_{prey}} N_{prey,l_{prey},y,q} W_{prey,l_{prey},y,q} S_{prey,pred,q}(l_{prey},l_{pred}) + OF_{pred} S_{other,pred,q}} \quad (17)$$

$$= \frac{P_{prey,l_{prey},pred,l_{pred},y,q}}{P_{pred,l_{pred},y,q}}$$

where the food suitability function, S, is defined by equation (6). Assuming that the seasonal stomach sampling has taken place uniformly over the seasons $\bar{N}_{prey,l_{prey},y,q}$ at the right hand side of equation (17) in principle should be replaced by $\bar{N}_{prey,l_{prey},y,q}$. However, as this would increase the running time of the programme substantially (because M2 is included in the expression $\bar{N}_{prey,l_{prey},y,q}$) without changing the results, the use of equation (17) is justified.

Using equation (8) average stock numbers of prey by size is approximated from stock numbers at age using age-length-keys.

$$N_{s,l_s,y,q} = \sum_a N_{s,a,y,q} ALK_{s,l_s,a,y,q}; \quad \sum_{l_s} ALK_{s,l_s,a,y,q} = 1 \quad (18)$$

Regarding the variance of stomach contents observations unpublished analyses of the present authors of data from the North Sea stomach sampling project 1991 (ICES, 1997) indicate that the relationship between the variance and the mean of the stomach contents may be formulated in the following way:

$$VAR(STOM_{prey,l_{prey},pred,l_{pred},y,q}) = \frac{E(STOM_{prey,l_{prey},pred,l_{pred},y,q})(1 - E(STOM_{prey,l_{prey},pred,l_{pred},y,q}))}{V_{pred} U_{pred,l_{pred},y,q}} \quad (19)$$

where V_{pred} are predator species dependent parameters and where the known quantity $U_{j,y,q}$ reflects the sampling level of a predator entity, e.g. the number of hauls containing the predator/size in the stomach sampling programme. Equating eq. (16) and (19) implies that

$$P_{pred,l_{pred},y,q} = V_{pred} U_{pred,l_{pred},y,q} - 1 \quad (20)$$

Insertion of (20) into (17) results in that

$$P_{prey,l_{prey},pred,l_{pred},y,q} = (V_{pred} U_{pred,l_{pred},y,q} - 1) \frac{\bar{N}_{prey,l_{prey},y,q} W_{prey,l_{prey},y,q} S_{prey,pred,q}(l_{prey},l_{pred})}{\sum_{prey,l_{prey}} (\bar{N}_{prey,l_{prey},y,q} W_{prey,l_{prey},y,q} S_{prey,pred,q}(l_{prey},l_{pred})) + OF_{pred} S_{other,pred,q}} \quad (21)$$

The parameters, $P_{prey,l_{prey},pred,l_{pred},y,q}$, are uniquely determined through stock numbers, total mortality, suitability parameters and V_{pred} .

Assuming that the diet observations for the predator/length groups are independent the negative log likelihood function including all predators/length groups are:

$$l_{STOM} = -\ln(L_{STOM}) = - \sum_{prey,l_{prey},pred,l_{pred},y,q} \ln(f_{prey,l_{prey},pred,l_{pred},y,q}) \quad (22)$$

1.2.4 Stock-recruitment

In order to enable estimation of recruitment in the last year for cases where survey cpue and catch from the recruitment age is missing (e.g. saithe) a stock-recruitment relationship $R_{s,y} = R_s(SSB_{s,y} | \alpha_s, \beta_s)$ penalty function is included in the likelihood function. Assuming that recruitment takes place at the beginning of the third quarter of the year and that recruitment is lognormal distributed the parameters the log penalty contribution, l_{SR} , equals

$$l_{SR} = -\log(L_{SR}) \propto NOY \sum_s \sigma_{SR_s} + \sum_{s,y} ((\log(N_{s,a=0,y,q=3}) - E(\log(R_{s,y})))^2 / 2\sigma_{SR_s}^2) \quad (23)$$

where

$E(\ln(R_{s,y})) = \ln(\alpha_s SSB_{s,y} \exp(-\beta_s SSB_{s,y}))$ for the Ricker case. Other stock recruitment relations (Beverton & Holt and ‘‘Hockey stick’’) and stock independent geometric mean recruitment have also been implemented. As indicated in equation (23) recruitment at age zero in the beginning of the third quarter was considered.

Total likelihood function and parameterization

The total negative log likelihood function, l_{TOTAL} , is found as the sum of the four terms:

$$l_{TOTAL} = l_{CATCH} + l_{SURVEY} + l_{STOM} + l_{SR}$$

To ensure unique determined parameters it is necessary to fix part of them. For the F at age model (equation 4) the year selection in the beginning of each year range has been fixed to one ($F_2(y = \text{first year in each group of year } Y) = 1$). The season effect in the last season is also fixed ($F_3(Y, q = \text{last season}, A) = 1/NOS$).

Equations (5) and (6) indicate that it is only possible to determine relative vulnerability parameters, $\rho_{prey,pred}$. We have chosen to fix the vulnerability of other food for all predators to 1.0.

Similarly the biomass of other food OF_{pred} has arbitrarily been set to 1 million tonnes for all predators except mackerel for which 10 million tonnes were used. The actual value by predator was chosen to obtain estimates of vulnerability parameters for the fish prey at around 1. The other parameters are unaffected of this choice.

In the food suitability function (equation (6)) the vulnerability and overlap effects cannot be distinguished. Hence the overlap parameters were initially set to 1 for at last one season.

Initial stock size, i.e. the stock numbers in the first year and recruitment over years are used as parameters in the model while the remaining stock sizes are considered as functions of the parameters determined by equations (1) and (2). Appendix 1 gives an overview of parameters and variables in the model.

The parameters are estimated by minimizing the negative log likelihood, l_{TOTAL} . The variance/covariance matrix is approximated by the inverse Hessian matrix. The variance of functions of the estimated parameters (such as biomass) has been calculated using the delta method or Markov Chain Monte Carlo.

1.3 Forecast

When SMS is used as a forecast program, the stock is projected forward in time using the maximum likelihood estimate of the model parameters and the population in the terminal year as initial stock size. The age and season effect from the F-model is kept constant and a year factor is derived dynamically from a Harvest Control Rule. Recruits are produced from the stock/recruitment relation and estimated parameters. For a stochastic projection, the number of recruits calculated is altered by a factor drawn from a truncated normal distribution with a known standard deviation. By making a high numbers of projection, mean and variance of future stock numbers, SSB yield etc. can be calculated. Application of HCRs can be based on a perfect knowledge of the present stock status and F, or simulate the real life condition where the TAC for the following year is set based on output from the assessment.

Uncertainties in stock assessment and forecast

The approach taken in this implementations of HCR is based on the framework for evaluation of management strategies as described by ICES study group on management strategies (ICES 2005/ACFM:09, 2006/ACFM:15) and used for a range of stocks, e.g. presented in the report of the ICES *ad hoc* group on long term advice (ICES 2005/ACFM:25).

The SMS approach does not simulate the full annual cycle of assessment and projection. Instead, it is assumed that the true stock size can be “observed” with some bias and noise and it is this “perceived” stock that makes the basis for the use of HCR and estimation of a TAC. The true stock size is assumed known in the first projection year and is later updated annually by recruitment and catches derived from application of HCR on the “perceived” stock.

Figure 1 gives an overview of the method.

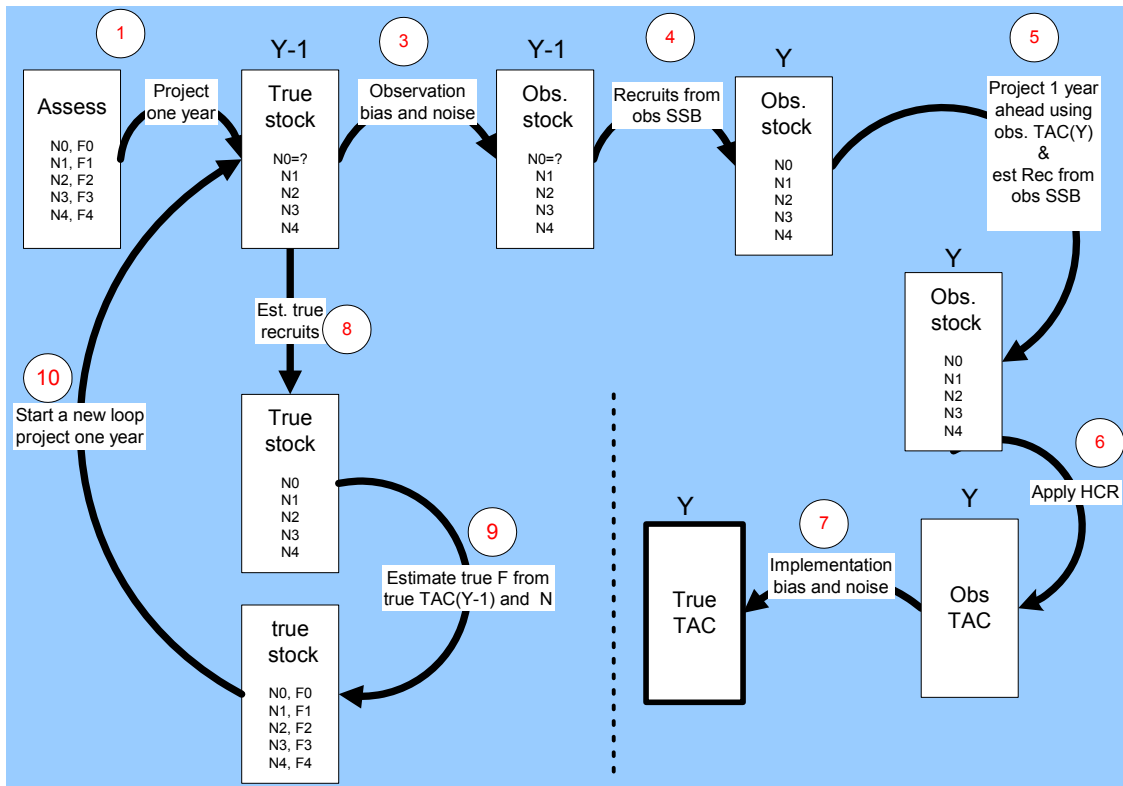


Figure1. Overview of the SMS method for management plan evaluation. Numbers in circles refer to the text below.

Step 1:

Make an assessment with terminal year Y-2 to estimate “true” stock numbers

Step 2:

Project the true stock forward one year using F and M for year Y-2. This will produce the true stock for year Y-1.

Step 3

Step 3 simulates the assessment done. The “observed” or perceived stock which makes the basis for the TAC is made on the basis of the true stock and an observation noise and bias:

$$N(a)_{obs} = N(a)_{true} * Bias * e^{(std * NORM(0,1))} * e^{-(std^2 / 2)}$$

The bias factor (default=1) and the standard deviation (std) are given as input. The same random number drawn from NORM(0,1) are used for all ages, giving a correlation of one between the observed stock numbers. Alternatively random number drawn from NORM(0,1) can be drawn for each age, producing uncorrelated noise.

Step 4

Recruitment for the observed stock is estimated as a point estimate from the specified stock recruitment relation. The result is observed stock numbers for all ages.

Step 5

The observed N at age is projected one year ahead using the observed TAC value for the year. This TAC is given as input for the first two years of simulations or calculated from a previous iteration in step 7. The observed recruitment in the TAC year (Y) is estimated as a point estimate from the stock recruitment relation. Step 5 results in observed stock numbers in the start of the TAC year, such that observed SSB in year Y can be calculated on the basis of the HCR.

Step 6

Apply the HCR to estimate the observed TAC(Y)

Step 7

Step 7 estimates the true TAC(Y) by adding implementation noise and bias to the observed TAC(Y). in a similar way as done for N in step 3.

Step 8

Step 8 estimates recruits for the true stock (N(Y-1)) using the stock recruitment relation and the noise function.

Recruitment (referred to as N0 in the figure) is estimated from a specified stock recruitment relationship (f(x)) and a log normal distributed noise term with standard deviation, std.

$$R_{obs} = f(x) * e^{(std * NORM(0,1))} * e^{-(std^2 / 2)}$$

Step 9

Step 9 projects the true stock one year ahead by using the true stock (N(Y-1)), true TAC(Y-1), exploitation pattern and mean weight at age in the catch W(a).

Step 10

The result of step 10 is the true stock number, which goes into a new simulation loop.

2. IMPLEMENTATION

The SMS model is implemented using the AD Model Builder software, ADMB, (Otter Research Ltd, 2003), freely available from ADMB Foundation and can be downloaded from www.admb-project.org. ADMB is an efficient tool including automatic differentiation for Maximum likelihood estimation of many parameters in nonlinear models.

SMS configurations may contain more than 1000 parameters of which less than 5% are related to predation mortality. It is not possible to estimate all parameters simultaneously without sensible initial parameter values. Such values were obtained in three phases:

1. Estimate “single species” stock numbers, fishing mortality and survey catchability parameters assuming that natural mortality (M1+M2) are fixed and known (i.e. as used by the ICES single species assessments).

2. Fix all the “single species” parameters estimated in step 1 and use the fixed stock numbers to estimate initial parameter values for the predation parameters.
3. Use the parameter values from step 1 and 2 as initial parameter values and re-estimate all parameters simultaneously in the full model including estimation of predation mortality M_2 .

Optimisation might potentially be dependent on the initial parameter values, however the same final result was obtained using the three steps above or using a configuration where step two is omitted. Using step two makes however in general the estimation process more robust as extreme values and estimation crash are avoided.

2.1 How to run SMS

SMS is a program for multispecies stock assessment and forecast. It is a compiled C++ program which reads ASCII files as input, process data and writes the results as ASCII files:

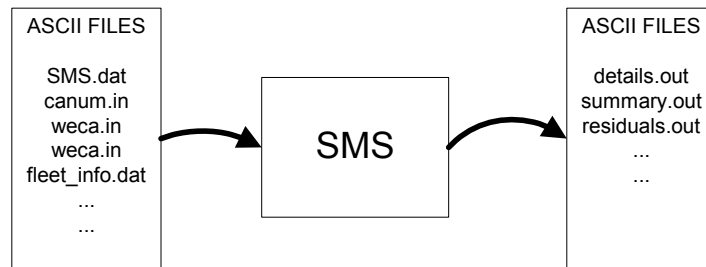


Figure 2. Schematic data flow of SMS data

Few of the output files can be used directly. To create useful output and graphics The R package and several R-scripts can be used.

2.1.1 Initial setup

SMS makes use of the R-Package to make SMS runs and for presentations of results. R can be downloaded from the internet <http://cran.r-project.org> . You also need to install the following R-packages: FLCore and FLAssess from <http://r-forge.r-project.org/projects/flr/> .

For an easy interface to R, I will suggest to use the editor “Tinn-R”. Tinn-R” can be installed from the internet <http://www.sciviews.org/Tinn-R/> (select “old stable version 1.17.2.4”).

Organization of the SMS package

The SMS package is organized in a number of directories:

```

SMS                                     # main directory for the SMS package
-   \R-prog                             # R-scripts for processing output, etc.
-   -   \Functions                       # R-functions
-   -   \FLSMS                           # Functions to link SMS and FLR
-   \Program                             # the SMS program files
-   \MyStock1                            # SMS configuration for your stock
-   \MyStock2                            # SMS configuration for your stock
  
```

2.2 SMS parameter estimation and assessment

2.2.1 Data and files for SMS assessments

There are two types of input files for SMS. Files with the extension “in”, e.g. canum.in, contains input data and files with the extension “dat” includes options for the run. All the files must be present in the directory for the species configuration, e.g. the “MyStock” directory.

Option files

The file SMS.dat includes the configuration and options for the run. In addition the file_info.dat file gives options for survey indices.

The SMS.dat file is heavily annotated, however it might be difficult to get it right the first time!

The text table below shows a configuration for a single species run using annual time steps. Annex 2 presents a more complex multispecies configuration using quarterly time steps.

Text table 1. Example of option file SMS.dat for one species (blue whiting) only.

```

# the character "#" is used as comment character, such that all text and numbers after #
# are skipped by the SMS program
#
#####
# Produce test output (option test.output)
# 0 no test output
# 1 output file SMS.dat and file fleet.info.dat as read in
# 2 output all single species input files as read in
# 3 output all multi species input files as read in
# 4 output option overview
#
# 11 output between phases output
# 12 output iteration (obj function) output
# 13 output stomach parameters
# 19 Both 11, 12 and 13
#
# Forecast options
# 51 output HCR_option.dat file as read in
# 52 output prediction output summary
# 53 output prediction output detailed
0
#####
# Single/Multispecies mode (option VPA.mode)
# 0=single species mode
# 1=multi species mode, but Z=F+M (used for initial food suitability parameter estimation)
# 2=multi species mode, Z=F+M1+M2
0
#
#####
# single species parameters
#
#####
## first year of input data (option first.year)
1981
#####
## last year of input data (option last.year)
2008
#####
## last year used in the model (option last.year.model)
2008
#####
## number of seasons (option last.season). Use 1 for annual data
1
#####
## last season last year (option last.season.last.year). Use 1 for annual data
1
#####
## number of species (option no.species)

```

```

1
#####
# Species names, for information only. See file species_names.in
# Blue whiting
#####
## first age all species (option first.age)
1
#####
## recruitment season (option rec.season). Use 1 for annual data
1
#####
## maximum age for any species(max.age.all)
10
#####
## various information by species
# 1. last age
# 2. first age where catch data are used (else F=0 assumed)
# 3. last age with age dependent fishing selection
# 4. Last age included in the catch at age likelihood (normally last age)
# 5. plus group, 0=no plus group, 1=plus group
# 6. predator species, 0=no, 1=VPA predator, 2=Other predator
# 7. prey species, 0=no, 1=yes
# 8. Stock Recruit relation, 1=Ricker, 2=Beverton & Holt, 3=Geom mean,
#           4= Hockey stick, 5=hockey stick with smoother,
#           >100= hockey stick with known breakpoint (given as input)
##
10 1 8 10 1 0 0 3
#####
## adjustment factor to bring the beta parameter close to one (option beta.cor)
1e+08
#####
## year range for data included to fit the R-SSB relation (option SSB.R.year.range)
# first (option SSB.R.year.first) and last (option SSB.R.year.last) year to consider.
# the value -1 indicates the use of the first (and last) available year in time series
# first year by species
-1
# last year by species
-1
#####
## Objective function weighting by species (option objective.function.weight) (default=1)
# first=catch observations,
# second=CPUE observations,
# third=SSB/R relations
# fourth=stomach observations
##
1 1 0.01 0
#####
## parameter estimation phases for single species parameters
# phase.rec (stock numbers, first age) (default=1)
1
# phase.rec.older (stock numbers, first year and all ages) (default=1)
1
# phase.F.y (year effect in F model) (default=1)
1
# phase.F.q (season effect in F model) (default=1)

```

```

1
# phase.F.a (age effect in F model) (default=1)
1
# phase.catchability (survey catchability) (default=1)
1
# phase.SSB.R.alfa (alfa parameter in SSB-recruitment relation) (default=1)
1
# phase.SSB.R.beta (beta parameter in SSB-recruitment relation) (default=1)
-1
#####
## minimum CV of catch observation used in ML-estimation (option min.catch.CV)
0.05
#####
## minimum CV of catch SSB-recruitment relation used in ML-estimation (option min.SR.CV)
0.3
#####
## use seasonal or annual catches in the objective function (option combined.catches)
# do not change this options from default=0, without looking in the manual
# 0=annual catches with annual time steps or seasonal catches with seasonal time steps
# 1=annual catches with seasonal time steps, read seasonal relative F from file F_q_ini.in
(default=0)
0
#####
## use seasonal or common combined variances for catch observation (option
seasonal.combined.catch.s2)
# seasonal=0, common=1 (use 1 for annual data)
0
#####
##
# catch observations: number of separate catch variance groups by species
4
# first age group in each catch variance group
1 2 3 7
#####
##
# catch observations: number of separate catch seasonal component groups by species
1
# first ages in each seasonal component group by species
1
#####
## first and last age in calculation of average F by species (option avg.F.ages)
3 7
#####
## minimum 'observed' catch, (option min.catch). You cannot have zero catch at age!
#
# negative value gives percentage (e.g. -10 ~ 10%) of average catch in age-group for input #
catch=0
# negative value less than -100 substitute all catches by the option/100 /100 *average
# catch in the age group for catches less than (average catch*-option/10000
#
# if option>0 then will zero catches be replaced by catch=option
#
# else if option<0 and option >-100 and catch=0 then catches will be replaced by
# catch=average(catch at age)*(-option)/100
# else if option<-100 and catch < average(catch at age)*(-option)/10000 then catches will

```

```

# be replaced by catch=average(catch at age)*(-option)/10000
1
#####
##
# catch observations: number of year groups with the same age and seasonal selection
2
# first year in each group
1981 1999
#####
## year season combinations with zero catch (F=0) (option zero.catch.year.season)
# 0=no, all year-seasons have catches, 1=yes there are year-season combinations with no catch.
Read from file zero_catch_seasons_ages.in
# default=0
0
#####
## season age combinations with zero catch (F=0) (option zero.catch.season.ages)
# 0=no, all seasons have catches, 1=yes there is seasons with no catch. Read from file
zero_catch_seasons_ages.in
# default=0
0
#####
## Factor for fixing last season effect in F-model (default=1) (fix.F.factor))
1
#####
## use penalty function or truncation for var below input limit (option var.penalty.trunc)
# values: 0=penalty 1=truncation, 2= init bounded
# catch-observation, CPUE-obs Stock/recruit
0 2 0
#####
# Read HCR_option file (option=read.HCR) default=0
# 0=no 1=yes
0
#

```

The examples can be used as template for your own configuration. Alternatively the R-code below can be modified and used to produce a SMS.dat file with default option values.

```

a<-FLSMS.control(first.year=1976,last.year=2008,no.species=3, first.age=0,
max.age.all=10, no.other.predators=1,no.VPA.predators=1,
species.names=c('Cod','Herring','Sprat'))

```

```

write.FLSMS.control(a,file=file.path(MyPath,'SMS.dat'))

```

Input files

The input files to the SMS assessment are presented below:

Tabel 3. Input to SMS assessment.

File nr	Data file	Variable and description	Sorted by
1	SMS.dat	Configuration and option file	
2	Fleet_info.dat	Configuration for abundance indices (tuning) fleets)	

3	canum.in	Catch at age numbers	Species, year, season, age
4	Natmor.in	Natural mortality at age	Species, year, season, age
5	Weca.in	Mean weight at age in the catch	Species, year, season, age
6	west.in	Mean weight at age in the sea	Species, year, season, age
7	Species_names.in	Name of the species	Species
8	Fleet_catch.in	Abundance indices. Effort and catch at age by tuning fleet	Species, fleet, year, age
9	Fleet_names	Name of the tuning fleets	Species, fleet
10	Reference_points.	Biological reference points. Used for output only	Species
11	Just_one.in	A file with a lot of "1",used to compensate bad programming	
19	natmor1.in	Natural residual mortality, M1	Species, year, age
20	lsea.dat	Mean length at age in the sea	Species, year, age
21	Consum.in	Food ration, biomass eaten, by an individual predator	Predator, year, age
22	season_overlap.in	Relative stomach contents by predator and prey entity	Predator, prey, season
28	other_food.in	Biomass of other food by predator species	Predator
29	Length_weight_relations.in	Length to weight relation parameters	Species
30	ALK_stom.in	Age - Length distribution for years with stomach data	Special 1
31	N_haul_at_length.in	Number of hauls by predator entity (species and species length)	Special 1
32	stomcon_at_length.in	Relative stomach contents by predator and prey entity	Special 1
33	stomlen_at_length.in	Mean prey length by predator and prey entity	Special 1
34	stomweight_at_length.in	Prey mean weight by predator and prey entity	Special 1
35	stom_pred_length_at_sizecl.in	Predator mean length by predator entity	Special 1
36	stom_struc_at_length.in	Data structure file for "stomach" files above	Special 1

Input files are on ASCII format, which means that it can be read by most programs, editors and spreadsheets. Values within the file must be separated by "blanks". The "#" mark is used for

comments, such that all text that follows a “#” in a line can be used for comments and is ignored as input.

Example 1: Hypothetical of catch at age numbers (canum.in) including one species and 1 season (annual data)

```
# catch at age data, Sandeel in the North Sea, 2005-2008
# age-0 age-1 age-2 age-3 age-4
1527400 58500000 14782800 3245100 4997700 # 2005
5343600 40728500 1654000 4677700 483100
5343600 2293500 481700 416400 68000 #2007
# Preliminary data for 2008
76123 18391900 5615400 408900 487800
```

Example 2: Hypothetical of catch at age numbers (canum.in) including three species and four seasons

```
# COD year: 1974
# age 1-8
0 1 2149 45005 22558 10264 2739 1107 740
0 0 1001 9527 15184 8289 2420 836 487
0 0 2379 10713 5171 2478 934 204 124
0 1 5228 13155 6908 3188 806 166 97
# COD year: 1975
0 1 2606 56121 37534 10429 2674 702 592
0 0 1849 31670 23088 5929 1883 465 225
0 0 2036 14394 8740 2879 1016 110 59
0 241 4597 18744 11454 3443 726 74 64
# HER year: 1974
# age 0-8
0 35592 337969 261472 230434 94646 41419 20193 72120
0 88555 715303 645533 692745 218044 131761 102765 192289
1421 165289 214024 200429 158344 364695 125476 46668 232057
3407 257760 355470 323913 315562 249868 96221 58187 177581
# HER year: 1975
0 57979 280179 217448 147575 143916 30533 22652 82430
0 80883 685208 646759 422021 407849 111911 66896 225174
3345 123822 181522 183685 136452 423418 136981 47597 253223
73773 468469 269607 229112 149047 251518 74426 39071 126718
# SPR year: 1974
#age 0-7
0 128150 1695967 3297727 1378903 198132 154350 145368 0
0 545350 1228683 2710808 1101411 259147 215380 115744 0
6425 24527 467561 1216291 400373 99086 55751 50482 0
168982 1118371 943827 2310125 441911 237629 145413 137297 0
# SPR year: 1975
162244 2322245 2140760 1389053 451943 278105 171025 23333 0
0 509768 568985 1208578 1068725 306883 165626 98495 0
0 800 558657 1012423 995002 296988 151582 87087 0
0 26596 543147 1031330 482561 158657 165903 132761 0
```

In example 2 above, the number of age groups differs between species. The overall matrix of catch at age numbers has however to be defined from the maximum age range of all species (option `max.age.all` in `SMS.dat`). For cod that means that zero catches have to be inserted for the 0-group. For sprat, zero catches must be inserted for age 8.

2.2.2 R-script for running SMS

SMS can be run from the command line using the options available for the program. A list of available options is obtained by the command “SMS –help”.

There is an R-script (se below) that configures the options for the SMS run in an easy way.

```
do.a.full.SMS.run(
  label="run_",      # label for output
  do.single=T,      # run SMS in single species mode
  do.multi.1=F,     # Make preliminary estimate of "predation parameters"
  do.multi.2=F,     # Run the full model, with simultaneously estimation of all
                    # parameters except the stomach variance parameter
  do.multi.2.redo=F, # Run the full model, with simultaneously estimation of all
                    # parameters
  do.multi.2.redo.Nbar=F, # As above, but use mean stock numbers (Nbar) for predation
  do.hessian=F,     # Make the Hessian matrix and estimate uncertainties
  do.MCMC=F,       # Prepare for MCMC analysis
  mcmc=1,mcsave=1, # Options for MCMS analysis
  do.prediction=F, # Make a prediction
  pause=F,         # Make a pause between each stage
  Screen.show=F,   # show the output on screen, or save it in file
  do.run=T,        # Make the run immediately, or make the batch file for the run
  deleteFiles=NA) # clean up in files before the run is made
```

As described in section 4, the run must be made sequentially. The first run is in single species mode (`do.single=TRUE`). The script takes the `SMS.dat` option file as input and configures it, such that it fit to the state of the estimation. For each of the “do...” command three files are produced where the names begins with the label (“run_”) you specified in the command above. Example, for the `do.single=TRUE` three files are produced:

- `run_ms0.dat`: actual configuration of the `SMS.dat` used to this run.
- `Run_ms0.rep`: the report file for the configuration
- `Run_ms0.par`: the estimated parameters for the configuration. These are used for initialisation of the next (`do.multi.1=TRUE`) run.

If you want to change an option you must do it in the `SMS.dat` file, and re-run the script again. As SMS stores the intermediate results, you don’t need to re-run SMS in single species mode and you can set `do.single=F`. You can also make the runs in a stepwise manner, one “do...=TRUE” at time.

2.2.3 SMS assessment output

SMS produces a lot of output files. A few of them are formatted for directly use, however most of the files are intended for further manipulation by e.g. R-scripts.

Formatted output

SMS.rep: The file SMS.rep includes an overview of the model diagnostics and estimates of the main parameters

details_ICES.out: This file includes the standard ICES tables for Catch numbers, F and stock numbers at age

summary_table.out: File with a stock overview table

Output for further processing

A lot of files with the file extension “out” are produced. All of them are intended to be read into R for further processing.

Data file	Variable and description	Sorted by
Catch_residuals.out	Residuals (log(Obs. catch)-log(Expec. catch)).	Spreadsheet format
Survey_residuals.out	Residuals for survey CPUE	Spreadsheet format
Catch__survey_residuals.out	Residuals for both catch and survey CPUE	Data frame
Par_exp.out	File used to link parameter names and index like species and fleet	Data frame
SSB_R.out	Parameters for stock recruitment relation	Data frame
Summary.out	File including most of the input and output “single species” variable	Data frame
Summary_stom.out	File including most of the input and output “multi species” variable	Data frame
objective_function.out	Likelihood contributions by submodel	Species

ADMB standard output.

SMS is implemented using the AD Model Builder packages. It produces a several files with new name of the application (in this case SMS and a specific file extension). The most useful files are:

SMS.par: Parameter estimates

SMS.cor: Parameter correlation matrix

SMS.std: Standard deviation of the estimated parameters and derived values (e.g. SSB)

2.2.4 R-scripts for processing output

Several R-scripts can be used for analysis and presentation of SMS input and output:

R-script	Description
Chi_2_test.R	Template for log ratio test
compare_runs.R	Comparison of various runs: SSB recruitment and F
compare_runs_M2.R	Comparison of various runs: M2 at age
compare_runs_pre_y_size_selection.R	Comparison of various runs: Prey size selection
compare_SSB_R_parameters.R	Comparison of various runs: Stock recruitment parameters
consum.R	Tabulation of food ration
correlation.R	Tabulation of correlation matrix
CV.R	Various tables and graphs including uncertainties of parameters and derived values
HCR_output_histo.R	Distribution (histogram) of key output from stochastic forecasts
HCR_output_multi.R	Presentation of key output variable from forecast
HTML.R	HTML tables of SMS key output
Tabulation of key values Part_M2.R	Graphs and tables with partial predation mortalities. Who eats whom
Plot_catch_residuals_bubble.R	Residual plot for catch at age observations
plot_M2_uncertainty.r	Plot of predation mortalities and confidence limits
Plot_obs_model_catch.R	Plot of observed and calculated expected yield
plot_other_predators.R	Various tables and plots for "Other predators"
Plot_size_preference.R	Plots of prey size selection
Plot_SSB_rec.R	Various plot for stock recruitment relation
Plot_stomach_data.R	A very long list of scripts to present and input and output of stomach (predation) related data.
Plot_summary_ICES_multi.R	"Summary plot" SSB, recruitment, F and Yield
Plot_survey_residuals_bubbles.R	Residual plot of survey observations
Retrospective_single_sp.R	Script for making and presenting "retrospective analysis"
Weighting_factor_single_sp.R	Script of analysing effect of various a priori weighting and presentation of results
XSA2SMS.R	Transformation of data on Lowestoft (XSA) format into SMS format

2.3 SMS forecast

2.3.1 Data and files for SMS forecast

Forecast data are mainly extracted directly from output file produces by SMS assessment, however values ca be changed from additional input.

Option files

Options for forecast are specified in the file "HCR_options.dat" . An example with three species (Eastern Baltic) is presented below:

```
# HCR_oprion.dat option file
# the character "#" is used as comment character, such that all text and numbers
# after # in a line are skipped by the SMS program
#
#####
# last year in prediction
2040
#####
# no of iteration within each MCMC prediction (default=1)
1000
#####
# first and last year for calc of mean weight in the sea
#   Cod   Herring   Sprat
#   2005   2005     2005
#   2007   2007     2007
#####
# first and last year for calc of mean weight in the catch
#   Cod   Herring   Sprat
#   2005   2005     2005
#   2007   2007     2007
#####
# assumed F year adjustment factor for 'missing' seasons in the last assessment year
(default=1)
#   Cod   Herring   Sprat
#     1     1       1
#####
# truncation of standardised normal distribution used to produce noise on recruitment
# lower and upper
# (values -15.0 and 15.0 give no truncation, -2 and 2 give approximately 95% of the distribution)
#   Cod   Herring   Sprat
#    -2    -2      -2
#     2     2       2
#####
# use recruitment noise from input parameters
# 0=no, estimate from input R/SSB parameters
# 1=yes, read residuals from file recruit_residuals.in
#   Cod   Herring   Sprat
#     0     0       0
#####
# option HCR :
# 1=constant F
```

```

# 2=constant TAC
# 10=F from trigger T1&T2 and SSB in the beginning of the TAC year
# 11=TAC from trigger T1&T2 and SSB in the beginning of the TAC year
#
# 15=F from target SSB (target.SSB) in the beginning of the TAC year+1
#
# Real time-monitoring:
# 20= F from trigger T1&T2 and N1 in the beginning of the TAC year
# 21=TAC from trigger T1&T2 and N1 in the beginning of the TAC year
# 22= F from target SSB (target.SSB) in the beginning of the TAC year+1,
#     derived from real time N1
# 23=TAC from target SSB (target.SSB) in the beginning of the TAC year+1,
#     derived from real time N1
# 30= F from trigger T1&T2 and TSB in the beginning of the TAC year
# 31=TAC from trigger T1&T2 and TSB in the beginning of the TAC year
#
# Baltic cod:
# 44= Reduce F by 10% per year until target F (at 0.3 East, or 0.6 West) is reached
#     & apply a +-15% TAC constrain if F is below 0.6 (East) or 1.0 (West)
#     & target F must be given as constant.F
#     & F reduction rate (e.g. 0.1) must be given as FT1a
#     & upper limit F for TAC constraint must be given as T1
#
# North Sea and Kattegat cod:
# 47= Reduce F by 25% per year if SSB < T1 (blim)
#     & reduce by 15% per year if SSB < T2 (bpa), however minimum F=0.4 (constantF)
#     & reduce by 10 per year if SSB > T2 (bpa), however minimum F=0.4 (constantF)
#     & apply a +-20% TAC constraint (TAC.constraints) in all cases
#
# Blue whiting:
# 334=2008 management plan
#
#
#     Cod   Herring   Sprat
#     44     10       10
#####
# option T1. Trigger 1, (SSB, TSB, F or stock N depending on HCR in use)
# option T2. Trigger 2, (SSB, TSB, F or stock N depending on HCR in use)
#     Cod   Herring   Sprat
#     0.6   2e+05    8e+05
#     3.85e+05  2e+05    4e+05
#####
# options FT1a and FT1b. a1 and b1: intercept and slope for regression to calc
#     max F or TAC for observed values below T1.
#     e.g.  F =a1+b1 * SSB using HCR=10 and SSB in TAC year
# options FT12a and FT12b. a2 and b2: intercept and slope for regression to calc
#     max F or TAC for observed values above T1 but below T2.
#     e.g.  F = a2+b2 *(SSB-T1) using HCR=10 and SSB in TAC year
# options FT2a and FT2b. a3 and b3: intercept and slope for regression to calc
#     max F or TAC for observed values above T2.
#     e.g.  F = a3+b3 *(SSB-T2) using HCR=10 and SSB in TAC year
# one column gives a1, b1, a2, b2, a3, and b3
#     Cod   Herring   Sprat
#     0.1   0.01     0.01
#     0     0        0

```

```

0    0.01    0.01
0    5.301e-07    2e-06
0    0.22    0.4
0    0    0
#####
# option HCR.F.TAC. Implement HCR result F as effort (option=0) or use TAC (option=1) to
estimate real F
#    Cod    Herring    Sprat
#    1    1    1
#####
# value constant.F. F for constant F scenarios (HCR=1)
# A value >0 gives absolute F, a value<0 gives fraction of F status quo
# e.g. option=-0.5 gives F=0.5*Fsq
#    Cod    Herring    Sprat
#    0.3    0    0
#####
# value constant.TAC. TAC for constant TAC scenarios (HCR=2). Values as for constant.F
#    Cod    Herring    Sprat
#    0    0    0
#####
# option target.SSB. Target SSB, if relevant (for HCR options in 15, 16, 22 or 23)
#    Cod    Herring    Sprat
#    0    0    0
#####
# option real.time.F. Mean F to obtain real time estimate, if relevant
#    Cod    Herring    Sprat
#    0    0    0
#####
# option cap.TAC Max TAC(true) irrespective of HCR and constraints (=0 is no max TAC)
#    Cod    Herring    Sprat
#    0    0    0
#####
# option cap.F Maximum F(true) irrespective of HCR and constraints (=0 is no max F)
#    Cod    Herring    Sprat
#    1.5    0.6    1
#####
# ##### %%%%%%%%%%% constraints %%%%%%%%%%% ###
# options min.F.change and max.F.change
# min and max variation in F between years calculated as
(F_forecast_year/F_forecast_previous_year)
# 0=no constrains
#    Cod    Herring    Sprat
#    0    0    0
#    0    0    0
#####
# options min.yield.change and max.yield.change
# min and max variation in YIELD between years calc.
# as (YIELD forecast year/YIELD forecast previous year)
# 0=no constrains
#    Cod    Herring    Sprat
#    0.85    0.85    0.8
#    1.15    1.15    1.2
#####
# options min.SSB.change and max.SSB.change
# min and max variation in SSB between years calc.

```

```

#      Cod   Herring   Sprat
#      0     0       0
#      0     0       0
#####
#### %%%%%%%%%% 'observation and implementation errors'
%%%%%%%%%%%%###
# options obs.noise.lower and obs.noise.upper
# truncation of standardised normal distribution used to produce noise on observations
# lower and upper
# (values -15.0 and 15.0 give no truncation, -2 and 2 give approximately 95% of the distribution)
#      Cod   Herring   Sprat
#      -2    -2      -2
#      2     2       2
#####
# options real.T.dist and real.T.bias and real.T.std
# real time monitoring stock numbers observation uncertainties:
# 1. distribution model (-1=not used, 0=normal, 1=log normal)
# 2. mean (mean is mean bias factor, mean=1 produces no bias)
# 3. std dev for log normal dist, or CV for normal dist
# 4. same noise. Use same noise for all ages (same noise=1)
#    or independent noise per age(same noise=0)
# special for HCR 334 (Normally used for real-time monitoring, see above)
# 1. annual decrease percentage in F until target has been reached
# 2. HCR when target has been reached
# 3. adjustment factor for TAC constraints in rebuilding (init) phase.
#    i.e. factor=x. Init min.yield.change=0.85 and max.yield.change=1.15
#    are change to 0.85*x and 1.15/x
# 4. not relevant
#      Cod   Herring   Sprat
#      -1    -1      -1
#      1     1       1
#      0     0       0
#      0     0       0
#####
# options survey.dist and survey.bias and survey.std
# (used for Real Time monitoring options)
# survey indices observation uncertainties:
# 1. distribution model (-1=not used, 0=normal, 1=log normal)
# 2. mean (mean is mean bias factor, mean=1 produces no bias)
# 3. std dev for log normal dist, or CV for normal dist
# 4. same noise. Use same noise for all ages (same noise=1)
#    or independent noise per age(same noise=0)
#      Cod   Herring   Sprat
#      -1    -1      -1
#      1     1       1
#      0     0       0
#      0     0       0
#####
# options assess.error.dist and assess.bias and assess.std
# assessment observation uncertainties (on stock numbers)
# 1. distribution model (-1=not used, 0=normal, 1=log normal)
# 2=log normal using covariance matrix from file covariance_N.in)
# 2. mean (mean is mean bias factor, mean=1 produces no bias)
# 3. std dev for log normal dist, or CV for normal dist
# 4. same noise. Use same noise for all ages (same noise=1) or

```



```

0      0      0
#####
# factor to adjust expected recruits (adjust.recruits)
#   Cod   Herring   Sprat
#     1     1     1
#####
# adjust recruitment with half of the variance (factor exp(-(CV^2)/2) option adjust.recruit.CV
# 0=no adjustment, 1=do adjustment
#   Cod   Herring   Sprat
#     0     0     0
#####
# read SSB recruitment parameters from file SSB_R.in
# (0=no use estimated parm, 1=yes, read in new parameters)
0
#####
#### %%%%%%%%%% various for output %%%%%%%%%% ####
#   F     M2     Z     N     C     FLR   constraints   closure
# 0=no output, 1=output
#     0     1     0     0     0     0     0     0
#####
#### %%%%%%%%%% various for predicted N (for FLR operating model)
%%%%%%%%%% ####
# read prediction stock numbers incl. recruits from file predict_stock_N.in
# first and last year for including stock numbers
# use years before first prediction year for no inclusion of data= use values from assess.
# first and last year
#     2000    2000
#####
# number of initial population (default=1)
1
#####
#### %%%%%%%%%% various for F and exploitation pattern
%%%%%%%%%% ####
# read F/exploitation pattern from file exploitation_pattern.in
# first and last year for including values
# use years before first prediction year for no inclusion of data,
# that is to use values from exploitation pattern and HCR
#
#     2000    2000
#####
# use values from file exploitation_pattern.in as
# 0 = absolute F (without applying HCR afterwards) or 1=exploitation pattern
1
#####
#### %%%%%%%%%% various for other predators
%%%%%%%%%% ####
# annual change factor for population number
# first year (relative to first prediction year) year of change (-1 is no change)
# last year (relative to first prediction year) of change (-1 is no change)
# other predator stock numbers
#   Cod
#     -1
#     -1
#     -1

```

The examples can be used as template for your own configuration. Alternatively the R-code below can be modified and used to produce a HCR_options.dat file with default option values.

```
SMS.control<-read.FLSMS.control(file=file.path(data.path,'SMS.dat'))
HCR<-FLSMS.predict.control(
  first.prediction.year=2009,
  last.prediction.year=2014,
  no.species=3, no.other.predators=0,
  species.names=c('Cod','Herring','Sprat')
)
write.FLSMS.predict.control(HCR,SMS=SMS.control,file='HCR_options.dat')
```

Input files

The main input to forecast are automatically taken from the SMS assessment output. It is however possible to overwrite some of the values with data from external files:

File	Description
Exploitation_pattern.in	Exploitation pattern (relative F at age)
Predict_stock_N.in	Stock number at age
SSB_rec.in	(Alternative) parameters for stock recruitment relations
Covariance_N.in	Covariance matrix for stock N

Output files

A stochastic projection is made on the basis of a large number of projections where recruitments and other values are drawn from a specified distribution. It is possible to dump detailed output for each time step for all the projections, which can result in very large output files. Alternatively SMS can calculate a mean values and standard deviations of key output variables.

Text table. Output from SMS forecast.

File	Contents
MCout_average_mean_F.out	Average and standard deviation of Mean F by time step
MCout_average_recruits.out	Average Recruits
MCout_average_TSB.out	Average Total Stock biomass
MCout_average_SSB.out	Average Spawning stock biomass
MCout_average_Yield.out	Average Yield
MCout_F.out	F at age by projection and time step
MCout_N.out	Stock numbers at age
MCout_M2.out	Predation mortality at age
MCout_C.out	Catch at age
MCout_meanF.out	Mean F
MCout_recruits.out	Recruitment

MCout_TSB.out	Total Stock biomass
MCout_SSB.out	Spawning Stock Biomass
MCout_Yield.out	Yield

See section 6.4 for R-scripts to process and present output from SMS forecast.

3. MODEL CODE

The SMS code is open to sharing. SMS.tpl and executable SMS.exe can be downloaded from the Model Library on the MEECE Project website (www.meece.eu) or requested from Morten Vinther (mv@aqu.dtu.dk). SMS is AdModel Builder program and requires the ADMB library to compile and link.

ADMB can freely be downloaded from <http://admb-project.org/>.

4. References

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Appendix 1. Notation.

Indices

a, b	age
A_1, A_2	group of ages
i	prey entity
j	predator entity
l	species size class
l_{pred}	predator size class
l_{prey}	prey size class
$other$	other food “species”
$pred$	predator species
$prey$	prey species
q	season of the year, e.g. quarter 1
RS	recruitment season. Input
s	species
$survey$	survey identifier
y	year
Y	group of years

Parameters and variables

c, d, e and f are size preference parameters depending of the prey and predator

AB	available prey biomass for a predator
ALK	proportion at size for a given age group. Input
C	catch in numbers. Observations
$CPUE$	catch in numbers per unit of effort. Observations
F	instantaneous rate of fishing mortality.
$g_{prey, pred}(l_{prey}, l_{pred})$	prey size preference of a predator. Estimated
lm_{pred}	mean size of size class l_{pred} . Input
lm_{prey}	mean size of size class l_{prey} . Input
$M1$	instantaneous rate of residual natural mortality. Input
$M2$	instantaneous rate of predation mortality estimated in the model

N	stock number
NOA	number of ages. Input
NOS	number of seasons. Input
NOY	number of years. Input
OF	Biomass of other food for a predator. Input
of	Biomass of other food available for a predator size class
Q	catchability, proportion of the population caught by one effort unit. Parameter
$R_{s,y}$	recruitment, number of the youngest fish entering the model, $N_{s,a=0,y,q=3}$. Parameters
$N_{s,a,y=first\ year,q=1}$	Parameters.
RA	food ration, biomass consumed by a predator. Input
S	suitability of a prey entity as food for a predator entity
$S1, S2$	mesh selection parameters.
SSB	spawning stock biomass
$STOM$	weight proportion of prey i found in the stomach of predator j . Observations
U	sampling intensity of stomachs. Input
V	variance of diet observations in relation to sampling intensity. Parameter
W	body weight. Input
Z	instantaneous rate of total mortality
α	stock recruitment parameter
β	stock recruitment parameter
γ and δ	food ration coefficients. Input
r and p	length weight coefficients. Input
η_{PREF}	natural logarithm of the most suitable relative prey size for a predator. Parameter
η_{MIN}	observed minimum relative prey size for a predator species. Input
η_{MAX}	observed maximum relative prey size for a predator species. Input
o	spatial overlap between predator and prey species in season q . Mainly input
ρ	coefficient of species vulnerability. Parameter
σ_{CATCH}	standard deviation of catch observations. Parameter
σ_{PREF}	parameter expressing how particular a predator is about the size of its prey. Parameter
σ_{SR}	standard deviation of stock recruitment estimate. Parameter
σ_{STOM}	standard deviation of stomach content observations
σ_{SURVEY}	standard deviation of survey cpue observations. Parameter

Appendix 2. Example of SMS.dat option file used for multispecies analysis of the North Sea.

```

# SMS.dat option file
# the character "#" is used as comment character, such that all text and numbers after # are
# skipped by the SMS program
#
#####
# Produce test output (option test.output)
# 0 no test output
# 1 output file SMS.dat and file fleet.info.dat as read in
# 2 output all single species input files as read in
# 3 output all multi species input files as read in
# 4 output option overview
#
# 11 output between phases output
# 12 output iteration (obj function) output
# 13 output stomach parameters
# 19 Both 11, 12 and 13
#
# Forecast options
# 51 output HCR_option.dat file as read in
# 52 output prediction output summary
# 53 output prediction output detailed
0
#####
# Single/Multispecies mode (option VPA.mode)
# 0=single species mode
# 1=multi species mode, but Z=F+M (used for initial food suitability parameter estimation)
# 2=multi species mode, Z=F+M1+M2
0
#
#####
# single species parameters
#
#####
## first year of input data (option first.year)
1975
#####
## last year of input data (option last.year)
2000
#####
## last year used in the model (option last.year.model)
2000
#####
## number of seasons (option last.season). Use 1 for annual data
4
#####

```

```

## last season last year (option last.season.last.year). Use 1 for annual data
4
#####
## number of species (option no.species)
9
#####
# Species names, for information only. See file species_names.in
# W Mackerel NS Mackerel Cod Whiting Haddock Saithe Herring Sandeel Nor. pout
#####
## first age all species (option first.age)
0
#####
## recruitment season (option rec.season). Use 1 for annual data
3
#####
## maximum age for any species(max.age.all)
10
#####
## various information by species
# 1. last age
# 2. first age where catch data are used (else F=0 assumed)
# 3. last age with age dependent fishing selection
# 4. Last age included in the catch at age likelihood (normally last age)
# 5. plus group, 0=no plus group, 1=plus group
# 6. predator species, 0=no, 1=VPA predator, 2=Other predator
# 7. prey species, 0=no, 1=yes
# 8. Stock Recruit relation, 1=Ricker, 2=Beverton & Holt, 3=Geometric mean,
#           4= Hockey stick, 5=hockey stick with smoother,
#           >100= hockey stick with known breakpoint (given as input)
##
1 0 0 0 0 2 0 0 # W Mackerel
6 0 0 0 0 2 0 0 # NS Mackerel
10 1 7 9 1 1 1 150000 # Cod
8 0 7 8 1 1 1 225000 # Whiting
10 0 7 9 1 1 1 3 # Haddock
10 2 8 10 1 1 0 75000 # Saithe
7 0 5 7 1 0 1 1 # Herring
4 0 2 4 1 0 1 430000 # Sandeel
3 0 2 3 0 0 1 1 # Nor. pout
#####
## adjustment factor to bring the beta parameter close to one (option beta.cor)
#   Cod   Whiting   Haddock   Saithe   Herring   Sandeel   Nor. pout
#   1e+06   1e+06   1e+06   1e+05   1e+05   1e+05   1e+06
#####
## year range for data included to fit the R-SSB relation (option SSB.R.year.range)
# first (option SSB.R.year.first) and last (option SSB.R.year.last) year to consider.
# the value -1 indicates the use of the first (and last) available year in time series
# first year by species
#   Cod   Whiting   Haddock   Saithe   Herring   Sandeel   Nor. pout
#   -1   -1   -1   -1   -1   -1   -1
# last year by species
#   Cod   Whiting   Haddock   Saithe   Herring   Sandeel   Nor. pout
#   -1   -1   -1   -1   -1   -1   -1
#####
## Objective function weighting by species (option objective.function.weight) (default=1)

```

```

# first=catch observations,
# second=CPUE observations,
# third=SSB/R relations
# fourth=stomach observations
##
0 0 0 1 # W Mackerel
0 0 0 1 # NS Mackerel
1 1 1 1 # Cod
1 1 1 1 # Whiting
1 1 1 1 # Haddock
1 1 1 1 # Saithe
1 1 1 0 # Herring
1 1 1 0 # Sandeel
1 1 1 0 # Nor. pout
#####
## parameter estimation phases for single species parameters
# phase.rec (stock numbers, first age) (default=1)
1
# phase.rec.older (stock numbers, first year and all ages) (default=1)
1
# phase.F.y (year effect in F model) (default=1)
1
# phase.F.q (season effect in F model) (default=1)
1
# phase.F.a (age effect in F model) (default=1)
1
# phase.catchability (survey catchability) (default=1)
1
# phase.SSB.R.alfa (alfa parameter in SSB-recruitment relation) (default=1)
1
# phase.SSB.R.beta (beta parameter in SSB-recruitment relation) (default=1)
1
#####
## minimum CV of catch observation used in ML-estimation (option min.catch.CV) (default=0.2)
0.2
#####
## minimum CV of catch SSB-recruitment relation used in ML-estimation (option min.SR.CV)
(default=0.2)
0.2
#####
## use seasonal or annual catches in the objective function (option combined.catches)
# do not change this options from default=0, without looking in the manual
# 0=annual catches with annual time steps or seasonal catches with seasonal time steps
# 1=annual catches with seasonal time steps, read seasonal relative F from file F_q_ini.in
(default=0)
0
#####
## use seasonal or common combined variances for catch observation (option
seasonal.combined.catch.s2)
# seasonal=0, common=1 (use 1 for annual data)
#      Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
#      1      1      1      0      0      0      0
#####
##
# catch observations: number of separate catch variance groups by species

```

```

#      Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
      4      4      5      3      3      2      3
# first age group in each catch variance group
1 2 4 7 # Cod
0 1 2 5 # Whiting
0 1 2 5 7 # Haddock
2 3 6 # Saithe
0 1 2 # Herring
0 1 # Sandeel
0 1 3 # Nor. pout
#####
##
# catch observations: number of separate catch seasonal component groups by species
#      Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
      4      4      3      3      3      2      2
# first ages in each seasonal component group by species
1 2 3 5 # Cod
0 1 2 3 # Whiting
0 1 2 # Haddock
2 3 4 # Saithe
0 1 2 # Herring
0 1 # Sandeel
0 1 # Nor. pout
#####
## first and last age in calculation of average F by species (option avg.F.ages)
2 6 # Cod
2 6 # Whiting
2 6 # Haddock
3 6 # Saithe
2 6 # Herring
1 2 # Sandeel
1 2 # Nor. pout
#####
## minimum 'observed' catch, (option min.catch). You cannot have zero catch at age!
#
# negative value gives percentage (e.g. -10 ~ 10%) of average catch in age-group for input
catch=0
# negative value less than -100 substitute all catches by the option/100 /100 *average catch in
the age group for catches less than (average catch*-option/10000
#
# if option>0 then will zero catches be replaced by catch=option
#
# else if option<0 and option >-100 and catch=0 then catches will be replaced by
catch=average(catch at age)*(-option)/100
# else if option<-100 and catch < average(catch at age)*(-option)/10000 then catches will be
replaced by catch=average(catch at age)*(-option)/10000
#      Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
      -500  -500  -500  -500  200  1  5000
#####
##
# catch observations: number of year groups with the same age and seasonal selection
#      Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
      2      2      2      1      3      2      1
# first year in each group
1975 1993 # Cod

```

```

1975 1991      # Whiting
1975 1985      # Haddock
1975          # Saithe
1975 1978 1983      # Herring
1975 1990      # Sandeel
1975          # Nor. pout
#####
##
# catch observations: number of years with zero catch for all seasons and ages
#   Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
#     0    0      0      0      0      0      0
# first year in each group
0      # Cod
0      # Whiting
0      # Haddock
0      # Saithe
0      # Herring
0      # Sandeel
0      # Nor. pout
#####
## season age combinations with zero catch (F=0) (option zero.catch.season.ages)
# 0=no, all seasons have catches, 1=yes there is seasons with no catch. Read from file
zero_catch_seasons_ages.in
# default=0
1
#####
## Factor for fixing last season effect in F-model (default=1) (fix.F.factor)
#   Cod  Whiting  Haddock  Saithe  Herring  Sandeel  Nor. pout
#     3    2      2      1      2      0.5    2
#####
## use penalty function or truncation for variances below input limit (option var.penalty.trunc)
# values: 0=penalty 1=truncation, 2= init bounded
# catch-observation, CPUE-obs Stock/recruit
#     1    2      1
#####
# Read HCR_option file (option=read.HCR) default=0
# 0=no 1=yes
0
#
#####
# multispecies parameters
#
#####
## N in the start of the period or N bar for calculation of M2 (option use.Nbar)
# 0=use N in the start of the time step (default)
# 1=use N bar
0
#####
## Maximum M2 iterations (option M2.iterations) in case of use.Nbar=1
3

```

```
#####
## convergence criteria (option max.M2.sum2) in case of use.Nbar=1
# use max.M2.sum2=0.0 and M2.iterations=7 (or another high number) to make Hessian
0
#####
## stomach contents variance model (option stomach.variance)
# 1=log normal distribution
# 2=normal distribution
# 3=Dirichlet distribution
3
#####
## Use age-length-keys for calc of M2 (option simple.ALK))
# 0=Use only one sizegroup per age (file lsea.in or wsea.in)
# 1=Use size distribution per age (file ALK_all.in)
0
#####
## Use food-rations from input values or from size and regression parameters (option consum)
# 0=Use input values by age (file consum.in)
# 1=use weight at age (file wsea.in) and regression parameters (file consum_ab.in)
# 2=use length at age (file lsea.in), length-weight relation and and regression parameters (file
consum_ab.in)
# 3=use mean length at size class (file ALK_all.in), length-weight relation and and regression
parameters (file consum_ab.in)
2
#####
## Size selection model based on (option size.select.model)
# 1=length:
# M2 calc: Size preference is based on predator and prey length at age from input file: lsea.in
# Prey weight is weight in the sea from input file: west.in
# Likelihood: Size preference is based on mean length per predator length group (input file:
stom_pred_length_at_sizecl.in)
# and prey mean length per prey length group (input file stomlen_at_length.in)
# Prey mean weight from mean weight per prey length group (input file:
stomweight_at_length.in)
# 2=weight:
# M2 calc: Size preference is based on predator and prey weight from input file: wsea.in
# Prey weight is weight in the sea from input file: west.in
# Likelihood: Size preference is based on mean length per predator length group (input file:
stom_pred_length_at_sizecl.in)
# and lenth-weight relation (input file: length_weight_relations.in),
# and prey mean weight per prey length group (input file: stomweight_at_length.in)
# Prey mean weight from mean weight per prey length group (input file:
stomweight_at_length.in)
# 3=weight:
# M2 calc: Size preference is based on predator and prey weight from input file: wsea.in
# Prey weight is weight in the sea from input file: west.in
# Likelihood: Size preference from mean length per predator length group (input file:
stom_pred_length_at_sizecl.in) and length-weight relation
# (input file: length_weight_relations.in)
# and prey mean length per prey length group (input file: stomlen_at_length.in) and
length-weight relation (input file:
# length_weight_relations.in)
# Prey mean weight from mean weight per prey length group (input file:
stomweight_at_length.in)
# 4=weight:
```

```

# M2 calc: Size preference is based on predator and prey weight, from input file lsea.in
(length in the sea) and length-weight relation
# (input file: length_weight_relations.in)
# Prey weight based on length from input file lsea.in and length-weight relation (input
file: length_weight_relations.in)
# Likelihood: Size preference from mean length per predator length group (input file:
stom_pred_length_at_sizecl.in) and length-weight relation
# (input file: length_weight_relations.in)
# and prey mean length per prey length group (input file: stomlen_at_length.in) and
length-weight relation #
# (input file: length_weight_relations.in)
# Prey mean weight from prey mean length per prey length group (input file:
stomlen_at_length.in) and length-weight relation
# (input file: length_weight_relations.in)
# 5=weight in combination with simple.ALK=1:
# M2 calc: Size preference is based on predator and prey weight, from input file file ALK_all.in
(length at age and size in the sea)
# and length-weight relation (input file: length_weight_relations.in)
# Prey weight based on length from input file lsea.in and length-weight relation (input
file: length_weight_relations.in)
# Likelihood: Size preference from mean length per predator length group (input file:
stom_pred_length_at_sizecl.in) and length-weight relation
# (input file: length_weight_relations.in)
# and prey mean length per prey length group (input file: stomlen_at_length.in) and
length-weight relation
# (input file: length_weight_relations.in)
# Prey mean weight from prey mean length per prey length group (input file:
stomlen_at_length.in) and
# length-weight relation (input file: length_weight_relations.in)
5
#####
# Adjust Length at Age distribution by a mesh selection function (option L50.mesh)
# L50 (mm) is optional given as input. Selection Range is estimated by the model
# L50= -1 do not adjust
# L50=0, estimate L50 and selection range
# L50>0, input L50 (mm) and estimate selection range
# by VPA species
# Cod Whiting Haddock Saithe Herring Sandeel Nor. pout
# -1 -1 -1 -1 -1 -1 -1
#####
## spread of size selection (option size.selection)
# 0=no size selection, predator/preys size range defined from observations
# 1=normal distribution size selection
# 3=Gamma distribution size distribution
# 4=no size selection, but range defined by input min and max regression parameters (file
pred_pre_y_size_range_param.in)
# 5=Beta distributed size distribution, within observed size range
# 6=log-Beta size distributed, within observed size range
#
# by predator
# W Mackerel NS Mackerel Cod Whiting Haddock Saithe
# 0 0 1 1 0 1
#####
## Scaling factor (to bring parameters close to one) for relation between no of stomachs sampling
and variance

```

```

# value=0: use default values i.e. 1.00 for no size selection and otherwise 0.1 (option
var.scale.stom)
# W Mackerel NS Mackerel    Cod    Whiting    Haddock    Saithe
#    0.1    0.1    0.1    0.1    0.1    0.1
#        1        1        1        1        1        1
#####
## other food suitability size dependency (option size.other.food.suit)
# 0=no size dependency
# 1=yes, other food suitability is different for different size classes
# W Mackerel NS Mackerel    Cod    Whiting    Haddock    Saithe
#        0        0        0        0        0        0
#####
## Minimum observed relative stomach contents weight for inclusion in ML estimation (option
min.stom.cont)
# W Mackerel NS Mackerel    Cod    Whiting    Haddock    Saithe
#    0.0001  0.0001  0.0001  0.0001  0.0001  0.0001
#####
## Max prey size/ pred size factor for inclusion in M2 calc (option prey.pred.size.fac)
# W Mackerel NS Mackerel    Cod    Whiting    Haddock    Saithe
#    0.13    0.13    0.5    0.5    0.13    0.2
#####
## use overlap input values by year and season (use.overlap)
# 0: overlap assumed constant
# 1: overlap index from file overlap.in (assessment only, use overlap from last year in forecast)
# 2: overlap index from file overlap.in (assessment and forecast)
0
#####
## parameter estimation phases for predation parameters
# the number gives the phase, -1 means no estimation
#
# vulnerability (default=2) (phase phase.vulnera)
2
# other food suitability slope (default=-1) (option phase.other.suit.slope)
-1
# preferred size ratio (default=2) (option phase.pref.size.ratio)
2
# predator size ratio adjustment factor (default=-1) (option phase.pref.size.ratio.correction))
-1
# prey species size adjustment factor (default=-1) (option phase.prey.size.adjustment)
-1
# variance of preferred size ratio (default=2) (option phase.var.size.ratio)
2
# season overlap (default=-1) (option phase.season.overlap)
2
# Stomach variance parameter (default=2) (option phase.Stom.var)
2
# Mesh size selection of stomach age length key (default=-1) (option phase.mesh.adjust)
-1
#####

```