SMS, A STOCHASTIC AGE–LENGTH–STRUCTURED MULTISPECIES MODEL APPLIED TO NORTH SEA AND BALTIC SEA STOCKS

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by

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Overview

SMS (Stochastic Multi Species model) is a fish stock assessment model in which includes estimation of predation mortalities from observation of catches, survey indices and stomach contents. Estimation of predation mortality is based on the theory for predation mortality as defined by Andersen and Ursin (1977) and Gislason and Helgason (1985). SMS is a "forward running" model that operates with a chosen number of time steps (e.g. quarters of the year). The default SMS is a one-area model, but the model has options for spatial explicit predation mortality given a known stock distribution.

Model parameters are estimated using maximum likelihood (ML) technique. Uncertainties of the model parameters are estimated from the Hessian matrix and confidence limits of derived quantities like historical fishing mortalities and stock abundances are estimated from the parameter estimates and the delta-method. SMS can be used to for forecast scenarios and Management Strategy Evaluations, where fishing mortalities are estimated dynamically from Harvest Control Rules.

This document describes the model structure and the statistical models used for parameter estimation.

1 Model Structure

1.1 Survival of the stocks

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

$$N_{s,a,y,q+1} = N_{s,a,y,q} \, e^{-Z_{s,a,y,q}} \qquad\qquad \text{Eq. 1}$$

or

$$N_{s,a+1,y,+1,q=1} = N_{s,a,y,q=last\ season} \, e^{-Z_{s,a,y,q=last\ season}} \qquad \text{Eq. 2}$$

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; predation mortality ($M2$), fixed residual natural mortality ($M1$) and fishing mortality (F):

$$Z_{s,a,y,,q} = M1_{s,a,q} + M2_{s,a,y,q} + F_{s,a,y,q}$$

For non-assessment species which act as predators (e.g. grey seal and horse mackerel) stock numbers are assumed known and must be given as input.

1.2 Fishing mortality

Fishing mortality, $F_{s,a,y,q}$ is modelled from an extended separable model including age, year and season 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:

$$F_{a,y,q} = F^1_{Y,A1} \ F^2_y \ F^3_{Y,A2,q} \qquad\qquad \text{Eq. 3}$$

where indices $A1$ and $A2$ are grouping of ages, (e.g. ages 1-3, 4-7 and 8-9) and Y is grouping of years (e.g. 1975-1989, 1990-2011).

Eq. 3 defines that the years included in the model can be grouped into a number of period clusters (Y), in 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 particular year. The grouping of ages for age selection, $A1$, and season selection, $A2$, can be defined independently.

1.2.1   Options for year effect

Given a good relationship between F and effort the fishing mortality can be calculated from the observed effort.

$$F_{a,y,q} = F^1_{Y,A1} \ EFFORT_y \ F^1_{Y,A2,q}$$

1.3 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.

M2 of a prey species, *prey*, with size group l_{prey} due to a predator species, *pred*, with size group l_{pred} is calculated as suggested by Andersen and Ursin (1977) and Gislason and Helgason (1985).

$$M2_{prey,l_{prey},y,q} = \sum_{pred} \sum_{l_{pred}} \frac{\bar{N}_{pred,l_{pred},y,a} \ RA_{pred,l_{pred},y,q} \ S_{prey,pred,q}(l_{prey}, l_{pred})}{AB_{pred,l_{pred},y,a}} \qquad \text{Eq. 4}$$

where RA denotes the total food ration (weight) of one individual predator per time unit, where S denotes the food suitability defined in section 1.3.2 and where AB is the total available (suitable) biomass. AB is defined as the sum of the biomass of preys weighted by their suitability. This total 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 are combined into one group, such that the total available prey biomass becomes:

$$AB_{pred,l_{pred},y,q} = \sum_{prey} \sum_{l_{prey}} \left(\bar{N}_{prey,l_{prey},y,q} \ W_{prey,l_{prey},y,q} \ S_{prey,pred,q}(l_{prey}, l_{pred}) \right) + OF_{pred,} \ S_{OF,pred,q}(l_{pred}) \qquad \text{Eq. 5}$$

$M2$ cannot directly be calculated from Eq. 4 because $M2$ also is included in the right hand term in Eq. 6 to calculate $\bar{N}$.

$$\bar{N} = \frac{N\ (1 - e^{-(M1+M2+F)})}{M1 + M2 + F} \qquad \text{Eq. 6}$$

As no analytical solution for $M2$ exists, $M2$ has to be found numerically. If the time step considered is sufficiently small, for instance a quarter, $M2$ becomes small and can optionally be approximated by replacing the average number during the season, $\bar{N}$, on the right hand side of Eq. 4 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 Eq. 4 where AB (Eq. 5) is modified correspondingly.

1.3.1   Use of size distribution by age

The equations outlined in the section above provides M2 at size groups. However, predation mortality by age is needed as well because F and catches are age-structured. If just one size group per age group of predators and preys is assumed Eq. 4 can be used directly where the age index substitutes the size group index in stock numbers ($\bar{N}_{prey,a,y,q} = \bar{N}_{prey,l_{prey},y,q}$)

Given more size groups per age, the calculation of M2 at age requires age-length-keys to split N at age to N at size group.

$$N_{s,l_s,y,q} = \sum_{a} N_{s,a,y,q} \ ALK_{s,a,l_s,y,q} \qquad \text{Eq. 7}$$

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

Assuming that F and $M1$ depends only of the age and that $M2$ only depends of the length, $M2$ at age is estimated by: (leaving out the species, year and quarter indices)

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

where

$$\bar{N}_{a,l} = N_{a,l} \frac{1 - e^{-(F_{a,l}+M1_{a,l}+M2_{a,l})}}{F_{a,l} + M1_{a,l} + M2_{a,l}} = N_{a,l} \frac{1 - e^{-(F_a+M1_a+M2_l)}}{F_a + M1_a + M2_l}$$

and where

$$D_a = \sum_l \bar{N}_{a,l} \left(F_a + M1_a + M2_l \right)$$

denotes the number of individuals at age died within a season.

1.3.2   Food suitability

As suggested by Andersen and Ursin (1977) and Gislason and Helgason (1985) the size dependent food suitability of prey entity j for predator entity i is defined as the product of a species dependent vulnerability coefficient, $\rho_{i,j}$, a size preference coefficient $\varrho_{i,j}(l_i, l_j)$, and an overlap index $o_{i,j,q}$. Suitability is then defined as:

$$S_{pred,prey,q}\left(l_{pred}, l_{prey}\right) = \rho_{pred,prey} \; \varrho_{pred,prey}(l_{pred}, l_{prey}) \; o_{pred,prey,q} \qquad \text{Eq. 8}$$

For the "other food" part suitability is defined as

$$S_{OF,pred,q}\left(l_{pred}\right) = \rho_{OF,pred} \; o_{OF,pred,q} \; \exp\left(v_{pred} \; \log\left(W_{pred,l_{pred},q} / \overline{W}_{pred} \right) \right) \qquad \text{Eq. 9}$$

Where $\overline{W}_{pred}$ is the average size of the predator species. Eq. 9 extends the original equation, to allow size dependent suitability for other food, for values of v_{pred} different from zero. The overlap index may change between seasons, but is assumed independent of year and sizes.

1.3.2.1   log-normal distributed size selection

Several functions can be used for size preference of a prey. 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:

$$\varrho_{pred,prey}\left(l_{pred}, l_{prey}\right) = \exp\left(- \frac{\left(\log\left(\frac{W_{l_{pred}}}{W_{l_{prey}}} \right) - \eta_{PREF\;pred} \right)^2}{2 \; \sigma^2_{PREF\;pred}} \right) ; 0 < \varrho \leq 1 \qquad \text{Eq. 10}$$

Where η_{PREF} is the natural logarithm of the preferred size ratio, σ^2_{PREF} is the "variance" of relative preferred size ration, expressing how selective a predator is with respect to the size of a prey and where W_{l_s} is the mean weight for a species size group.

The basic size selection equation (Eq. 10) has been extended by modifying the preferred size ratio parameter.

$$\varrho_{pred,prey}\left(l_{pred}, l_{prey}\right)$$
$$= \exp\left(- \frac{\left(\log\left(\frac{W_{l_{pred}}}{W_{l_{prey}}} \right) - \left(\eta_{PREF\;pred} + \xi_{prey} + \varpi_{pred} \; \log\left(W_{l_{pred}} \right) \right) \right)^2}{2 \; \sigma^2_{PREF\;pred}} \right) \qquad \text{Eq. 11}$$

Where ξ_{prey} specify a prey specific adjustment term for the preferred size ratio, and where ϖ_{pred} specifies how the preferred size range can change by predator size.

1.3.2.2   Uniform size selection

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

$$\varrho_{pred,prey}\left(l_{prep}, l_{prey}\right) = \begin{cases} 1 & \text{for } \eta_{MIN_{pred,prey}} \leq \dfrac{W_{l_{pred}}}{W_{l_{prey}}} \leq \eta_{MIN_{pred,prey}} \\ 0 & \text{for values outside observed range} \end{cases} \qquad \text{Eq. 12}$$

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

1.3.2.2.1 Constraint uniform size selection

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 (Floeter and Temming, 2005; Sharft et al., 2000). A way to account for that is to assume that the fixed minimum and maximum constants, η_{MIN} and η_{MAX}, depend on the predator size:

$$\varrho_{pred,prey}\left(l_{pred}, l_{prey}\right)$$
$$= \begin{cases} 1 & \text{for } U1_{pred,prey} + U2_{pred,prey} \log(W_{l_{pred}}) \leq \log\left(\dfrac{W_{l_{pred}}}{W_{l_{prey}}}\right) \leq U3_{pred,prey} + U4_{pred,prey} \log(W_{l_{pred}}) \\ 0 & \text{for values outside regression range} \end{cases} \quad \text{Eq. 13}$$

The regression parameters are estimated externally by quantile regression (e.g. Koenker and Bassett 1978) using e.g. the 2.5% and 97.5% percentiles of stomach content data. Figure 1 shows an example of such regression.
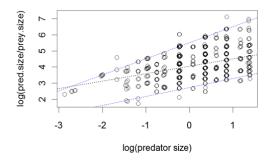

Figure 1. Quantile regression of stomach contents observations (Baltic cod eating cod), with 2.5%, 50% and 97.5 % lines shown. Predator and prey size in weight.

1.4 Adjustment of age–size keys

For the North Sea configuration, age length keys were obtained from the IBTS surveys where the same gear (i.e. the GOV trawl) has been used in the period considered. This allows an adjustment of the observed ALK's to account for mesh size selection. Using a logistic length dependent selection function, selection is defined as:

$$SL_s(l) = 1/\left(1 + e^{(S1_s - S2_s * l)}\right)$$

Where $S1_s$ and $S2_s$ are species specific gear selection parameters.

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

$$ALK_{s,l_s,a,y,a} = \text{ObservedALK}_{s,l_s,a,y,q} / SL_{s,l_s}$$

which finally has to be standardised to 1 for each age before used in Eq. 7.

1.5 Growth

Not implemented yet!

1.6 Food ration

Food ration, *RA*, pr. time step is given as input or estimated from mean weight by size group assuming an exponential relationship between ration and body weight *W*

$$RA_{pred,l_{pred},q} = \gamma_{pred,q} \; W_{pred,l_{pred}}^{\varsigma_{pred}} \qquad\qquad \text{Eq. 14}$$

where the coefficient γ and ς are assumed to be known.

Body weight at size group l_pred is estimated from mean length within the size group and a length weight relation.

1.7 Area based SMS

SMS has three area explicit options:

1. Default one area model. Both F and M2 are calculated for the entire stock area

2. M2 by area. M2 is calculated by sub-areas, but F is assumed global

3. M2 and F by area. Both M2 and F are calculated by area (forecast only)

1.7.1   Stock distribution

For the area based models the stock is assumed redistributed between areas between each seasonal time step.

$$N_{s,a,y,q}^{area} = N_{s,a,y,q} \; DIST_{s,a,y,q,area}$$

Where DIST is a stock distribution key that sums up to 1

$$\sum_{area} DIST_{s,a,y,q,area} = 1$$

The calculation of M2 for Option 1) is provided in the previous section

The method for option 3) is very similar, but the calculations must be done by each sub-area separately.

$$Z_a^{area} = F_a^{area} + M1_a^{area} + M2_a^{area}$$

where $M2^{area}$ is calculated as given in Eq. 4

Option 2) is the hybrid, where F is global but M is calculated by area.

$$Z_a^{area} = F_a + M1_a^{area} + M2_a^{area}$$

$\bar{N}$ in an area is calculate in the usual way

$$\bar{N}_a^{area} = N_a^{area} \frac{1 - e^{-Z_a^{area}}}{Z_a^{area}}$$

The total number of individuals died due to predation mortality (DM2) then becomes

$$DM2_a = \sum_{area} M2_a^{area} \ \bar{N}_a^{area}$$
<div align="right">Eq. 15</div>

M2 for the whole stock can be estimated from

$$M2_a = \log\left(\frac{N_a}{N_a - D_a}\right) \frac{DM2_a}{D_a}$$

where

$$D_a = \sum_{area} DF_a^{area} + DM1_a^{area} + DM2_a^{area}$$

and DF and DM1 are the number died due to fishery and residual mortality (M1) and are calculated in similar ways as specified for DM2 (Eq. 15).

1.7.2   Area based suitability parameters

For the "one area" SMS suitability is defined by Eq. 8.

The area based version of suitability uses an area specific vulnerability and overlap index, while the size preference (ϱ) is assumed independent of area.

$$S_{pred,prey,q}^{area}\left(l_{pred}, l_{prey}\right) = \rho_{pred,prey}^{area} \ \varrho_{pred,prey}(l_{pred}, l_{prey}) \ o_{pred,prey,q}^{area}$$

2   Statistical models

Three types of observations are considered: Total international catch at age; survey abundance indices and relative stomach content. 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.

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_{CATCH}, associated with the catches is

$$L_{CATCH} = \prod_{s,a,y,q} \frac{1}{\sigma_{CATCH\ s,a,q}\ \sqrt{2\pi}}\ exp\left(-\frac{\left(\log(C_{s,a,y,q}) - E\left(\log(C_{s,a,y,q})\right)\right)^2}{2\ \sigma^2_{CATCH\ s,a,q}}\right)$$ Eq. 16

Where

$$E\left(\log(C_{s,a,y,q})\right) = \log(F_{s,a,y,q}\ \bar{N}_{s,a,y,q})$$

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

$$l_{CATCH} = -\log(L_{CATCH}) \propto NOY \sum_{s,a,q} \log(\sigma_{CATCH\ s,a,q}) + \sum_{s,a,y,q} \left(\log(C_{s,a,y,q}) - E\left(\log(C_{s,a,y,q})\right)\right)^2 / 2\sigma^2_{CATCH\ s,a,q}$$ Eq. 17

Where NOY is the number of years in the time series.

2.1.1 Annual catches

Catch at age numbers by quarter have not been available for some of the demersal North Sea stocks in recent years. For use in the default SMS configuration of the North Sea, where quarterly time step is used, it is assumed that the seasonal distribution (the F^3 parameter in Eq. 3) is known and given as input. The likelihood function is modified to make use of the observed annual catches.

$$E\left(\log(C_{s,a,y})\right) = \log\left(\sum_{q} F_{s,a,y,q}\ \bar{N}_{s,a,y,q}\right)$$

$$L_{CATCH} = \prod_{s,a,y} \frac{1}{\sigma_{CATCH\ s,a}\ \sqrt{2\pi}}\ exp\left(-\frac{\left(\log(C_{s,a,y}) - E\left(\log(C_{s,a,y})\right)\right)^2}{2\ \sigma^2_{CATCH\ s,a}}\right)$$ Eq. 18

2.2 Survey indices

Similarly to the catch observations, survey indices, $CPUE_{survey,s,a,y,q}$ are assumed to be log-normally distributed with mean

$$E\left(\log(CPUE_{survey,s,a,y,q})\right) = \log(Q_{survey,a}\ \bar{N}_{SURVEY\ s,a,y,q})$$ Eq. 19

where Q denotes catchability by survey and $\bar{N}_{SURVEY}$ is mean stock number during the survey period. Catchability may depend on a single age or groups of ages. Similarly, the variance of log $CPUE$, , σ^2_{SURVEY} may be estimated individually by age or by clusters of age groups. The negative log likelihood is on the same form as Eq. 16.

$$l_{SURVEY} = -\log(L_{SURVEY})$$
$$\propto NOY_{survey,s} \sum_{survey,s,a} \log(\sigma_{SURVEY\ survey,s,a})$$
$$+ \sum_{survey,s,a,y} \left(\log(CPUE_{survey,s,a,y}) - E\left(\log(CPUE_{survey,s,a,y})\right)\right)^2 / 2\sigma^2_{SURVEY\ s,a}$$ Eq. 20

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, $STOM_{pred,l_{pred},prey,l_{prey},y,q}$, are given for combinations of prey and predator species and size classes. In the following we use entity i for a combination of predator species and predator size class (e.g. saithe 50-60 cm) and entity j for the combination of prey species and prey size class eaten by entity i. Model observations therefore becomes $STOM_{i,j,y,q}$

$STOM$ are assumed to be stochastic variables subject to sampling and process variations. For a given predator entity the observations across prey entities i are continuous variables which sum to one. Thus, the probability distribution of the stomach observations for a given predator including all prey/length groups 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. Leaving out the year and season index, the Dirichlet density function for a predator entity i with k observed diet proportions $STOM_{i,1}, \dots STOM_{i,k-1} > 0$ and the parameters $p_1, \dots, p_k > 0$ has the probability density given by

$$f_i = f\left(STOM_{i,1}, \dots, STOM_{i,k-1} \mid p_{i,1}, \dots, p_{i,k}\right) = \frac{\Gamma(p_i)}{\prod_{j=1}^{k} \Gamma(p_{i,j})} \prod_{j=1}^{k} STOM_{i,j}^{p_{i,j}-1} \qquad \text{Eq. 21}$$

Where

$$STOM_{i,k} = 1 - \sum_{j=1}^{k-1} STOM_{i,j}$$

and

$$p_i = \sum_{j=1}^{k} p_{i,j}$$

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

$$E\left(STOM_{i,j}\right) = \frac{p_{i,j}}{p_i}$$

$$Var\left(STOM_{i,j}\right) = \frac{E\left(STOM_{i,j}\right)\left(1 - E\left(STOM_{i,j}\right)\right)}{p_i + 1} \qquad \text{Eq. 22}$$

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

$$E\left(STOM_{i,j}\right) = \frac{\bar{N}_j \ W_j \ S_{i,j}(l_i, l_j)}{\sum_j \left(\bar{N}_j \ W_j \ S_{i,j}(l_i, l_j)\right) + OF_i \ S_{OF,i}(l_i)} = \frac{p_{i,j}}{p_i} \qquad \text{Eq. 23}$$

where the food suitability function, S, is defined by Eq. 8 and Eq. 9. We make the same assumption as made for the calculation of M2 (Eq. 4) that the small time steps used in the model, allows a replacement of $\bar{N}_j$ by N_j in Eq. 23.

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:

$$Var\left(STOM_{i,j,y,q}\right) = \frac{E\left(STOM_{i,j,y,q}\right)\left(1 - E\left(STOM_{i,j,y,q}\right)\right)}{V_{pred}\ U_{i,y,q}} \qquad \text{Eq. 24}$$

where $U_{i,y,q}$ is a known quantity reflecting the sampling level of a predator entity, e.g. the number of hauls containing with stomach samples of a given predator and size class. V_{pred} is a predator species dependent parameter linking the sampling level and variance. Equating Eq. 22 and Eq. 24 implies that

$$P_{i,y,q} = V_{pred}\ U_{i,y,q} - 1 \qquad \text{Eq. 25}$$

Insertion of Eq. 25 into Eq. 23 results in that

$$P_{i,j,y,q} = \left(V_{pred}\ U_{i,y,q} - 1\right) \frac{\bar{N}_j\ W_j\ S_{i,j}\left(l_i, l_j\right)}{\sum_j\left(\bar{N}_j\ W_j\ S_{i,j}\left(l_i, l_j\right)\right) + OF_i\ S_{OF,i}\left(l_i\right)}$$

The parameters, $p_{i,j,y,q}$ 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 derived from Eq. 21:

$$l_{STOM} = -\log(L_{STOM}) = -\sum_{i,j,y,q} \log\left(f_{i,j,y,q}\right) \qquad \text{Eq. 26}$$

2.3.1 Modification of the stomach contents model

The stomach contents observations, $STOM_{prey,l_{prey},pred,l_{pred},y,q}$ are given for combinations of prey and predator species and size classes. For a diet consisting of a large proportion "other food" and several species and prey size classes, the proportion of the individual combination of species and size becomes small (less than 0.1%) for several prey entities. Very small proportions, in combination with a modest sampling size per stratum, make the estimation of parameters impossible in some cases. To overcome the problem SMS has an option to let the likelihood use proportion summed over all size classes for a given prey species such that the prey entity equals the species.

The same grouping of all sizes from a prey is applied when the uniform size selection option (Eq. 12 and Eq. 13) is used, as   The likelihood function is the same as used for stomach observations which include prey size.

2.4 Stock-recruitment

In order to enable estimation of recruitment in the last year for cases where survey indices catch from the recruitment age is missing (e.g. saithe), and to estimate parameters for forecast use, a stock-recruitment relationship $R_{s,y} = R\left(SSB_{s,y}|\ \alpha_s, \beta_s\right)$ penalty function is included in the likelihood function.

Recruitment to the model takes place in the same season ($recq$) and at the same age (fa) for all species. It is estimated from the Spawning Stock Biomass (SSB) in the first season (fq) of the year, and a stock recruitment relation. SSB is calculated from stock numbers, proportion mature (PM) and mean weight in the sea.

$$SSB_{s,y} = \sum_a N_{s,y,a,q=recq} \; PM_{s,y,a,q=recq} \; W_{s,y,a,q=recq} \qquad \text{Eq. 27}$$

At present the Ricker (Eq. 28), the Beverton & Holt (Eq. 29), segmented regression (Eq. 30) and geometric mean are implemented.

$$R_{s,y} = \alpha_s \, SSB_{s,y-fa,fq} \; e^{(\beta_s \, SSB_{s,y-fa,fq})} \qquad \text{Eq. 28}$$

$$R_{s,y} = \frac{\alpha_s \, SSB_{s,y-fa,fq}}{1 + \beta_s \, SSB_{s,y-fa,q}} \qquad \text{Eq. 29}$$

$$R_{s,y} = \begin{cases} \alpha_s \, SSB_{s,y-fa,fq} & \text{for } SSB_{s,y-fa,fq} < \beta_s \\ \alpha_s \, \beta_s & \text{for } SSB_{s,y-fa,fq} < \beta_s \end{cases} \qquad \text{Eq. 30}$$

Assuming that recruitment is lognormal distributed, the negative log likelihood, l_{SR}, equals

$$l_{SR} = -\log(L_{SR}) \propto NOY \sum_s \log(\sigma_{SR\,a}) \; + \sum_{s,a,y} \left(\log\left(N_{ss,a=fa,y,q=recq}\right) - E\left(\log(R_{s,y})\right)\right)^2 / 2\sigma_{SR\,s}^2 \qquad \text{Eq. 31}$$

Where NOY gives the number of years selected and where Eq. 32 gives the expected recruitment for the Ricker case.

$$E(\log(R_s)) = \log\left(\alpha_s \, SSB_{s,y-fa,fq} \; e^{(\beta_s \, SSB_{s,y-fa,fq})}\right) \qquad \text{Eq. 32}$$

3   Total likelihood function and parameterisation

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 uniquely determined parameters it is necessary to fix part of them. For the F at age model (Eq. 3) the year selection in the beginning of each year range (Y) has been fixed to one ($F^2_{y=\text{first year in each group of years}} = 1$). The season effect in the last season of all years and ages is also fixed ($F^3_{y,a,q=\text{last season}} = 1/\text{number of seasons}$).

Eq. 4 and Eq. 8 indicate that it is only possible to determine relative vulnerability parameters, $\rho_{pred,prey}$. 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 (e.g. at 1 million tonnes) for each predators. The actual value by predator was chosen to obtain estimates of vulnerability parameters for the fish prey at

around 1. Other parameters than suitability are practically unaffected of the actual choice of biomass of other food.

In the food suitability function (Eq. 8 and Eq. 9) vulnerability and overlap effects cannot be distinguished. Hence the overlap parameters were must be fixed for at least one season. In practice, several combinations of overlap have however to be fixed (at e.g. 1).

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 Eq. 1 and Eq. 2.

The year effect ($F_{y,s}^2$) in the separable model for fishery mortality (Eq. 3) takes one parameter per species for each year in the time series which sum up to a considerable number of parameters. To reduce this high number of parameters, the year effect can optionally be model from a cubic spline function which requires fewer parameters. The number of knots must be specified if this option is used.

Another way to reduce the number of parameters is to substitute the parameters σ_{CATCH}, σ_{SURVEY} and σ_{SR} used in the likelihood functions by their empirical estimates. This optional substitution has practically no effect on the model output and the associated uncertainty.

Appendix 1 gives an overview of parameters and variables in the model.

The parameters are estimated using maximum likelihood (ML) i.e. by minimizing the negative log likelihood, l_{TOTAL}. The variance/covariance matrix is approximated by the inverse Hessian matrix. Uncertainties of functions of the estimated parameters (such as biomass and mean fishing mortality) are calculated using the delta method.

4 SMS forecast

SMS as specified in section 1 is a forward running model and can as such easily be used for forecast scenarios and Management Strategy Evaluation (MSE). SMS used the estimated parameters to calculate the initial stock numbers and exploitation pattern used in the forecast. Exploitation pattern are assumed constant in the forecast period, but is scaled to a specified average F, derived dynamically from Harvest Control Rules (HCR). Recruits are produced from the stock/recruitment relation, input parameters and a noise term.

4.1 Recruitment

Recruitment is estimated from the available stock recruitment relationships, f(SSB), (se section 2.4) and optionally a log normal distributed noise term with standard deviation std.

$$R = f(SSB)\ e^{(std\ NORM(0,1))} \qquad\qquad \text{Eq. 33}$$

Where NORM(0,1) is a random number drawn from a normal distribution with mean=0 and standard deviation 1. A default value for std can be obtained from the estimated variance of stock recruitment relationship, $\sigma_{SR_s}^2$ (Eq. 31)

Application of the noise function for the lognormal distributed recruitment gives on average a median recruitment as specified by f(SSB). Optionally, recruitment can be adjusted with half of the variance, to obtain, on average, a mean recruitment given by f(SSB).

$$R = f(SSB)\ e^{(std\ NORM(0,1))}\ e^{\left(-(std^2/2)\right)} \qquad\qquad \text{Eq. 34}$$

4.2 Harvest Control Rules

Several HCR have been implemented, e.g. constant F and the ICES interpretation of management according to MSY for both short and long-lived species. Selected, more complex management plans in force for the North Sea and Baltic Sea species have also been implemented.

5   Model validation

Model validation (in the years 2004-2009) was focused on the performance of the model using simulated data from an independent model and simulated data produced by the SMS model itself. The independent model was implemented using the R-package (R Development Core Team. 2011) and include a medium complex North Sea configuration (9 species, of which 4 are predators and 8 species preys). The simulation model follows the SMS model specification with an addition of von Bertalanffy growth curves to model mean length at age. Variance around mean length at age was assumed to increase by increasing age. This combined age-length approach made it possible to simulate all the data needed for model verification. Test data set from the simulation model included 20 years of catch data, one survey times series per species covering all years and ages, and 4 quarterly stomach samples in year 10 including stomach observations for all predator length groups. Data from the independent simulation model was used to verify that the SMS model actually works as intended and to investigate model sensitivity with respect to observation errors on catch, survey CPUE and stomach data.

To test if model parameters were identifiable when uncertainties estimated from real data were applied, the SMS model was modified to produce observations with the estimated observation noise of catch, survey and stomach data. The experiment consists of the following steps:

1. Estimate model parameters using the SMS model and available North Sea data.
2. Generate 100 set of input data from SMS output (expected catch numbers, survey indices and stomach observations) and their associated variance of these values) .
3. Let SMS estimate 100 sets of parameters from the 100 sets of input data.

This procedure results in one set of "true parameters", $\theta = (\theta_1, \dots, \theta_k)$ and 100 sets of estimated parameters, $\hat{\theta}_j = (\hat{\theta}_{1,j}, \dots, \hat{\theta}_{k,j})$, $j = 1, \dots, k$. Based on the 100 repetitions and for each of the k parameters the mean and the standard deviation of the mean $\bar{\hat{\theta}}_i$ and σ_i and hence the 95% confidence limits, was calculated. Finally the proportion of the parameters was calculated for which θ_i lies in the 95% confidence interval of $\bar{\hat{\theta}}_i$.

The test showed that parameters are identifiable for most "real" North Sea configurations. For some species with relatively few diet observations, size selection parameters (Eq. 11) and the variance parameter (V) linking the stomach sampling level to the variance of Dirichlet distribution (Eq. 24 and Eq. 25) , were outside the 95% confidence interval of $\bar{\hat{\theta}}_i$. (MORE TEXT to be added

A more informal testing of the model has been done by simply using the model. SMS has been applied to produce the so-called key-run for both the species rich North Sea system (10 species with stock number estimation including 7 prey species, and 16 species of "other predators") (ICES WGSAM 2011) and the species poor Baltic Sea (cod, herring and sprat, one predator and three prey species) (WGSAM, 2008, WKMAMPEL 2009). In addition the model has been used in single species mode for the ICES advice of blue whiting in the North East Atlantic (WGWIDE, 2011) since 2005 and several sandeel stocks in the North Sea since 2009 (WGNSSK, 2011). For MSE purposes the model has been applied for sandeel and Norway pout in the North Sea (AGSANNOP 2007), blue whiting and pelagic stocks in the Baltic (WKMAMPEL 2009) in both single and multi species mode.

SMS is essentially an extension of the statistical models normally used for single species stock assessment. This allows the use the long list of available diagnostics tools, e.g. residuals plots, and retrospective analysis, developed for model testing of sub-models for catch at age and survey indices. For stomach observations however, fewer established methods are available. To apply reliable residual

plots for stomach observations residuals need to be independent, which are not the case for the stomach contents model as the observations with respect to prey entity sum to one. Instead we do the following: Let the predator entity, year and quarter be given and consider the stomach contents observations following the Dirichlet distribution:

$$STOM_r = (STOM_{r,1}, \ldots, STOM_{r,k-1}) \sim Dir(p_{r,1}, \ldots, p_{r,k})$$

Where r is the combined entity of predator entity, year and quarter and where $p_{r,j}, j = 1, \ldots, k$ are the Dirichlet parameters estimated. Instead of considering the weight proportions, $STOM$, we consider absolute weight in the stomachs, $W_{r,j}, \; j = 1, \ldots, k$, where

$$STOM_{r,j} = \frac{W_{r,j}}{\sum_j W_{r,j}}$$

If we assume that $W_{r,j}, \; j = 1, \ldots, k$ are independent and follow gamma distributions with the same scale parameter, θ_r, i.e.

$$W_{r,j} \sim \Gamma(p_{r,j}, \theta_r) \; j = 1, \ldots, k$$

it is well known that $STOM_r$ follows the Dirichlet distribution. We now assume that opposite is the case (we have to prove that!) and hence assume that the absolute weights, $W_{r,j}$ are independent gamma distributed variables. We then transform these observations to obtain normal distributed residuals: Leaving out the indices we get that $U = pgamma(W, p, \theta)$, where pgamma is the distribution function of the gamma distribution, is uniform distributed. To obtain normal distributed variables U is finally transformed to $V = qnorm(U)$, where qnorm is the inverse of the distribution function of the standardized normal distribution. This mean that V is our new residuals for stomach contents observations.

To obtain the absolute weight of the prey entities form the relative stomach content, $STOM$, we have to know the total stomach weight for the predator entity. We have not extracted those from the basic observations, but simply assumed that the total weight in the stomach is proportional to the number of stomachs sampled for a given predator entity.

6   Implementation

The SMS-OP has been implemented using the AD Model Builder (Fournier *et al.*, 2011), which is freely available from ADMB Foundation (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 are 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 M2.

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 however in general makes the estimation process more robust as extreme values and system crash are avoided.

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Appendix 1. Notation.

Indices
a age
area   area with specific predation mortality
A_1, A_2 group of ages
Fa   first age group in the model
i prey entity, combination of prey species and prey size group
j predator entity, combination of predator group and predator size group
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
recq   recruitment season
s species
survey survey identifer
y year
Y group of years

Parameters and variables
AB   available (suitable) 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
D   number died
DM1   number died due to M1
DM2   number died due to M2
DF   number died due to F
F   instantaneous rate of fishing mortality.
F^1 age effect in separable model for fishing mortality. Estimated parameter
F^2 year effect in separable model for fishing mortality. Estimated parameter
F^3 season effect in separable model for fishing mortality. Estimated parameter
M1   instantaneous rate of residual natural mortality. Input
M2   instantaneous rate of predation mortality estimated in the model
N   stock number
$N_{s,a,y=first\ year,q=1}$. Stock number in the first year of the model. Estimated parameters.
$N_{s,a=fa,q=recq}$. Stock numbers at youngest age (recruitment). Estimated parameter.
OF   Biomass of other food for a predator. Input
Q   catchability, proportion of the population caught by one effort unit. Estimated
$R_{s,y}$ recruitment calculated from stock recruitment model
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. Estimated
SSB   spawning stock biomass
STOM weight proportion of prey i found in the stomach of predator j. Observations

U	sampling intensity of stomachs. Observation
V	variance of diet observations in relation to sampling intensity. Estimated Parameter
W	body weight. Input
Z	instantaneous rate of total mortality
α	stock recruitment parameter. Estimated
β	stock recruitment parameter. Estimated
ϱ	prey size preference of a predator. Estimated parameter
γ	food ration coefficients. Input
ς	food ration exponent. Input
υ	parameter for size dependent preference for other food. Estimated parameter
η_{PREF}	natural logarithm of the preferred predator prey size ratio. Estimated 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. Estimated parameter
ρ	coefficient of species vulnerability. Estimated parameter
σ_{CATCH}	standard deviation of catch observations. Estimated 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. Estimated parameter
σ_{STOM}	standard deviation of stomach content observations (used with log normal distribution)
σ_{SURVEY}	standard deviation of survey cpue observations. Estimated parameter

Appendix 1. Option file for SMS.

This appendix shows an option file for Baltic Sea SMS.

```
# 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
#
0
##########################################
# Produce output for SMS-OP program. 0=no, 1=yes
1
##########################################
# Single/Multispecies mode (option VPA.mode)
# 0=single species mode
# 1=multi species mode, but Z=F+M (used for initial predation parm. estimation)
# 2=multi species mode, Z=F+M1+M2
0
##########################################
# Number of areas for multispecies run (default=1)
1
#&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&
# single species parameters
#&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&
#
## first year of input data (option first.year)
1974
##########################################
## last year of input data (option last.year)
2010
##########################################
## last year used in the model (option last.year.model)
2010
##########################################
##  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)
3
##########################################
# Species names, for information only. See file species_names.in
#  Cod Herring Sprat
##########################################
## 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)
8
##########################################
```

```
## 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. Esimate F year effect from effort data. 0=no, 1=yes
# 5. Last age included in the catch at age likelihood (normally last age)
# 6. plus group, 0=no plus group, 1=plus group
# 7. predator species, 0=no, 1=VPA predator, 2=Other predator
# 8. prey species, 0=no, 1=yes
# 9. 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)
##
8 2 5 0 8 1 1 1 95000  # 1 Cod
8 1 5 0 8 1 0 1 1  # 2 Herring
7 1 4 0 7 0 0 1 1e+06  # 3 Sprat
#########################################
## use input recruitment estimate (option use.known.rec)
#   0=estimate all recruitments,
#   1=yes use input recruitment from file known_recruitment.in
0
#########################################
## adjustment factor to bring the beta parameter close to one (option beta.cor)
#        Cod       Herring       Sprat
       1e+06       1e+06        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       Herring       Sprat
         1989          -1        1990
# last year by species
#          Cod       Herring       Sprat
          -1          -1          -1
#########################################
## Objective function weighting by species (option objective.function.weight)
# first=catch observations,
# second=CPUE observations,
# third=SSB/R relations
# fourth=stomach observations
##
1 1 1 1  # 1 Cod
1 1 1 0  # 2 Herring
1 1 1 0  # 3 Sprat
#########################################
## 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.y.spline (year effect in F model, implemented as spline function)
-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)
```

```
0.1
#######################################
## minimum CV of catch SSB-recruitment relation used in ML-estimation
0.1
#######################################
## Use proportion landed information in calculation of yield (option calc.discard)
#     0=all catches are included in yield
#     1=yield is calculated from proportion landed (file proportion_landed.in)
#          Cod      Herring       Sprat
             1          0            0
#######################################
## 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 C with annual time steps or seasonal C with seasonal time steps
#     1=annual C 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      Herring       Sprat
             0          0            0
#######################################C
# catch observations: number of separate catch variance groups by species
#          Cod      Herring       Sprat
             3          3            4
#  first age group in each catch variance group
2 3 7  #  Cod
1 2 3  #  Herring
1 2 3 4      #  Sprat
#######################################
##
# catch observations: number of separate catch seasonal component groups by species
#          Cod      Herring       Sprat
             2          3            2
#  first ages in each seasonal component group by species
2 3    #  Cod
1 2 3  #  Herring
1 2    #  Sprat
#######################################
## first and last age in calculation of average F by species (option avg.F.ages)
4 7  # Cod
3 6  # Herring
3 5  # Sprat
#######################################
# catch observations: number of year groups with the same age and seasonal selection
#          Cod      Herring       Sprat
             3          3            3
#  first year in each group
1975 1996 2005      #  Cod
1975 1990 2000      #  Herring
1975 1983 1996      #  Sprat
#######################################
##
# number of nodes for year effect Fishing mortality spline
# 1=no spline (use one Fy for each year), >1 number of nodes
#          Cod      Herring       Sprat
             1          1            1
#  first year in each group
1976   #  Cod
1976   #  Herring
1976   #  Sprat
#######################################
## year season combinations with zero catch (F=0) (option zero.catch.year.season)
# 0=no, all year-seasons have catchs, 1=yes there are year-season combinations with
# no catch. Read from file zero_catch_seasons_ages.in
0
```

```
##########################################
## season age combinations with zero catch (F=0) (option zero.catch.season.ages)
# 0=no, all seasons have catchs, 1=yes there are seasons with no catch. Read from
# file zero_catch_season_ages.in
0
##########################################
## Factor for fixing last season effect in F-model (default=1) (fix.F.factor))
#         Cod     Herring      Sprat
             1          1          1
##########################################
## Uncertanties for catch, CPUE and SSB-R observations (option calc.est.sigma)
#  values: 0=estimate sigma as a parameter (the right way of doing it)
#          1=Calculate sigma and truncate if lower limit is reached
#          2=Calculate sigma and use a penalty function to avoid lower limit
#  catch-observation, CPUE-obs, Stock/recruit
             2          2          2
##########################################
# Read HCR_option file (option=read.HCR) default=0
#  0=no  1=yes
1
##########################################
#
#&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&
#
# multispecies parameters
#
#&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&
#
# Exclude year,season and predator combinations where stomach data are not
# included (option incl.stom.all)
#   0=no, all stomach data are used in likelihood
#   1=yes there are combinations for which data are not included in the likelihood.
#     Read from file: incl_stom.in
1
##########################################
##  N in the beginning of the period or N bar for calculation of M2 (option use.Nbar)
#  0=use N in the beginning of the time step (default)
#  1=use N bar
0
##########################################
## Maximum M2 iterations (option M2.iterations) in case of use.Nbar=1
5
##########################################
## 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
##########################################
## Usage of age-length-keys for calc of M2 (option simple.ALK))
#  0=Use only one sizegroup per age (file lsea.in or west.in)
#  1=Use size distribution per age (file ALK_all.in)
0
##########################################
## Usage of food-rations from input values or from size and regression parameters
#  0=Use input values by age (file consum.in)
#  1=use weight at age (file west.in) and regression parameters (file consum_ab.in)
#  2=use length at age (file lsea.in), l-w relation and regression parameters
#       (file consum_ab.in)
#  3=use mean length at size class (file ALK_all.in), l-w relation and regression
#        parameters (file consum_ab.in)
0
##########################################
## Size selection model based on (option size.select.model)
```

```
#  1=length:
#      M2 calculation:
#          Size preference:
#            Predator length at age from file: lsea.in
#            Prey     length at age from file: lsea.in
#          Prey mean weight is weight in the sea from file: west.in
#      Likelihood:
#          Size preference:
#            Predator mean length per length group (file:
#                  stom_pred_length_at_sizecl.in)
#            Prey mean length per ength group (file stomlen_at_length.in
#          Prey mean weight from mean weight per prey length group (file:
#                  stomweight_at_length.in
#  2=weight:
#      M2 calculation:
#          Size preference:
#            Predator weight at age from file: west.in
#            Prey     weight at age from file: west.in
#          Prey mean weight is weight in the sea from file: west.in
#      Likelihood:
#          Size preference
#            Predator mean weight is based on mean length per predator length group
#                (file: stom_pred_length_at_sizecl.in)
#                and l-w relation (file: length_weight_relations.in),
#            Prey mean weight per prey length group (file: stomweight_at_length.in)
#          Prey mean weight from mean weight per prey length group (file:
#            stomweight_at_length.in
#  3=weight:
#      M2 calculation: Same as option 2
#      Likelihood:
#          Size preference:
#            Predator mean weight is based on mean length per predator length group
#                (file: stom_pred_length_at_sizecl.in)
#                and l-w relation (file: length_weight_relations.in),
#            Prey mean weight per prey length group (file: stomlen_at_length.in) and
#                l-w relation (file:length_weight_relations.in)
#          Prey mean weight from prey mean length per prey length group (file:
#                stomlen_at_length.in) and l-w relation (file:
#                 length_weight_relations.in)
#  4=weight:
#      M2 calculation:
#          Size preference:
#            Predator mean weight from file lsea.in (length in the sea) and l-w
#                 relation (file: length_weight_relations.in)
#            Prey mean weight from file lsea.in (length in the sea) and l-w relation
#                  (file: length_weight_relations.in)
#      Likelihood:  Same as option 3
#  5=weight in combination with simple.ALK=1:
#      M2 calculation:
#          Size preference:
#            Predator weight based on length from file ALK_all.in (length distribution
#                  at age) and l-w relation (file: length_weight_relations.in)
#            Prey weight based on length from file ALK_all.in (length distribution at
#                  age) and l-w relation (file: length_weight_relations.in)
#          Prey mean weight based on length from file ALK_all.in (length distribution
#                  at age) and l-w relation (file: length_weight_relations.in)
#      Likelihood: Same as for option 2
#  6=weight in combination with simple.ALK=1:
#      M2 calculation: Same as option 5
#      Likelihood: Same as option 3
2
#########################################
# Adjust Length at Age distribution by a mesh selection function (option L50.mesh)
#  Please note that options simple.ALK shoud be 1 and option
#  size.select.model should be 5
# 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     Herring        Sprat
             -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
#   11=normal distribution size selection, but sum of all prey sizes used in
#      likelihood
#   3=Gamma distribution size distribution
#   4=no size selection, but range defined by input min and max regression parameters
#      (file pred_prey_size_range_param.in)
#   5=Beta distributed size distribution, within observed size range
#   6=log-Beta size distributed, within observed size range
#
# by predator
#          Cod
            0
#########################################
## 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
#          Cod
            0
#########################################
## Minimum observed relative stomach contents weight for inclusion in ML estimation
(option min.stom.cont)
#          Cod
        0.0001
#########################################
## Upper limit for number of samples used for calculation of stomach observation
#    variance
#          Cod
          1000
#########################################
## Max prey size/ pred size factor for inclusion in M2 calc
#          Cod
          0.3
#########################################
## 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
# prefered size ratio (default=2) (option phase.pref.size.ratio)
-1
# predator size ratio adjustment factor (default=-1)
-1
# prey species size adjustment factor (default=-1)
-1
# variance of prefered size ratio (default=2) (option phase.var.size.ratio)
-1
# season overlap (default=-1) (option phase.season.overlap)
-1
# Stomach variance parameter (default=2) (option phase.Stom.var)
2
# Mesh size selection of stomach age length key (default=-1)
-1
```

##