

Estimating F_{MSY} assuming a variety of Stock-Recruitment relationships

During the 2nd Preparatory Conference, held in Cali, Colombia, the Preparatory Conference requested the Science Working Group to consider a number of points related to Jack Mackerel stock assessment and Management. Among these, the SWG was requested to look at '*Catch levels likely to achieve particular fishing mortality and/or biomass reference points, within particular time frames*'. Within this study, an attempt has been made to provide insights into the reference points of F_{MSY} and B_{MSY}.

Key to determining F_{MSY} and B_{MSY} reference points is the inclusion of a stock-recruitment model inside a population age structured simulation model. The equilibrium situation of the population model is primarily determined by the productivity of the SR-model. However, in many instances, as well as in this case at first sight, a clear relationship between Spawning Stock Biomass and Recruitment is lacking and on biological grounds no stock-recruitment model can be assigned such as a Ricker or Beverton and Holt curve. As this information is lacking, and to refrain from making arbitrary choices, a multiple stock assessment approach has been taken, as described by Simmonds et al. (2011), and applied to the Jack Mackerel stock.

Materials & Methods

As indicated above, the methods applied to the Jack Mackerel stock follow closely the methods as described by Simmonds et al. (2011). Simmonds et al. however assumes 6 types of curves, and fits these models with each 3 different residual distributions (normal, lognormal, gamma), while in this study we only consider 3 models, the Ricker, the Beverton and Holt and Segmented regression model, fitted assuming normally distributed residuals, as shown in their mathematical form below.

Beverton and Holt	$\alpha \cdot S / (\beta + S)$
Ricker	$\alpha \cdot S \cdot \exp(-\beta \cdot S)$
Segmented Regression	$\text{if } S \leq \beta \text{ then } \alpha \cdot S \text{ else } \alpha \cdot \beta$

At first, each model was fitted to the data, and based on the variance-co-variance matrix, and a multi-dimensional random distribution, 3000 new parameter sets were generated for each of the models. For each of these newly generated models, the likelihood fit was calculated. The harmonic mean of the likelihood by model type was calculated from these fits, and up to 1% of the models was removed if they influenced the harmonic mean to a large extend.

For simulation purposes, only 1000 models were needed, hence, some of the 9000 models available in total had to be dropped (see figure 1). The harmonic mean ratio between the models finally determined which proportion of the 1000 models was going to be represented by what model type (e.g. if model 1 to 3 has a likelihood of resp. -10, -15 and -25, the first model will make up 10/40th of the 1000 models etc.). The total of 1000 models were used in a population age structured simulation model to estimate F_{MSY}. Population characteristics as maturity-at-age and weight-at-age were obtained from last year's Jack Mackerel assessment, as well as the most recent F_{pattern} as estimated in

2010. For each simulation, calculations were run into equilibrium where F , SSB and yield were calculated based on the population equilibrium conditions. The population was scanned for 100 F multiplier values (0 to 100) which represents an F range of approximately 0 to 1.

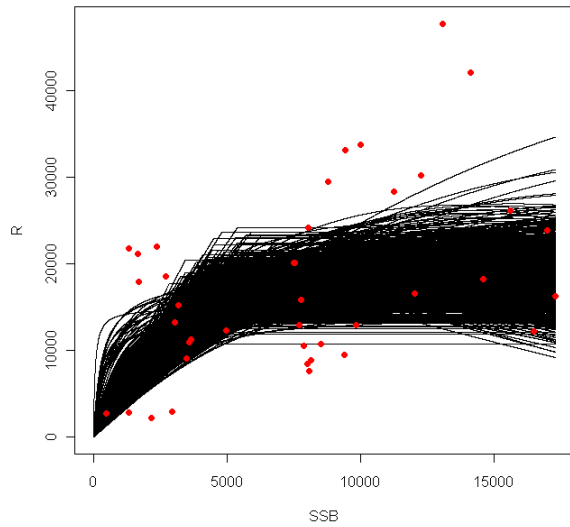


Figure 1: Graphical representation of the 1000 models that have been selected. Black solid lines represent selected models, red dots represent SSB -Recruitment points as observed for Jack Mackerel.

Results

Two main results can be distilled from this study. At first, yield is plotted against fishing mortality to estimate F_{MSY} , as is shown in figure 2.

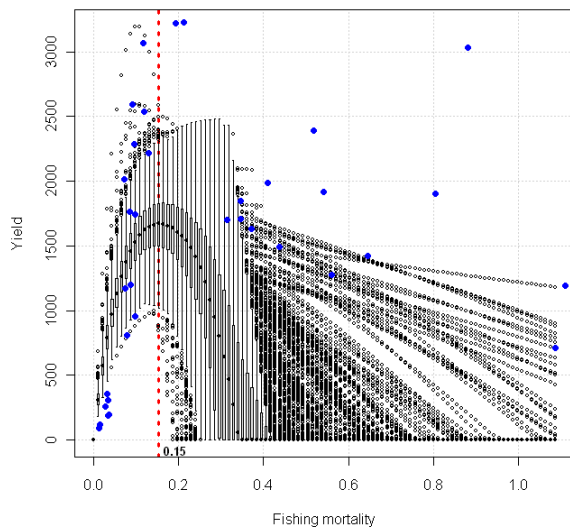


Figure 2: Yield plotted against fishing mortality for all 1000 runs, where the spread in the boxplot indicates the spread in the 1000 models. The median of the 1000 models is given by a small black dot, inside the dark grey boxes. The blue points represent the observed yield versus fishing mortality values as obtained from the assessment. The vertical red dotted line indicates the top of the curve, F_{MSY} .

From figure 2 we can obtain an F_{MSY} value, which lies in the top of the curve. There is little doubt about the top of the curve, with specific reference to the median top of the curve. This is estimated to lie at $F = 0.15$.

In a similar approach, also SSB can be shown against Fishing mortality (see figure 3).

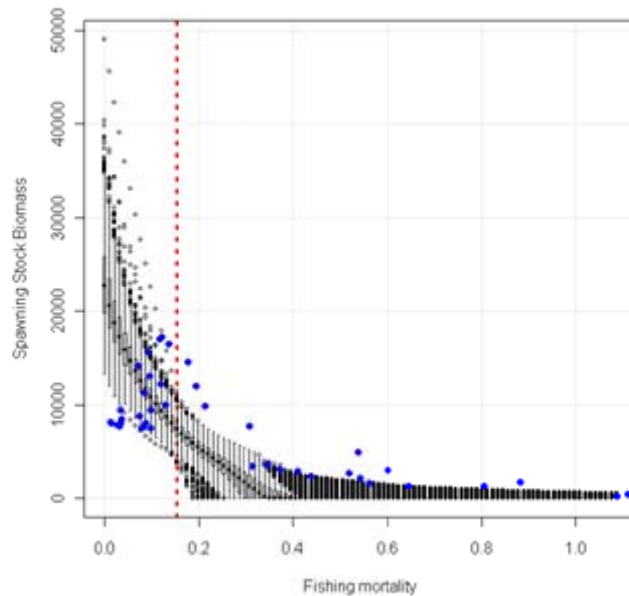


Figure 3: Spawning Stock biomass plotted against fishing mortality for all 1000 runs, where the spread in the boxplot indicates the spread in the 1000 models. The median of the 1000 models is given by a small black dot, inside the dark grey boxes. The blue points represent the observed SSB versus fishing mortality values as obtained from the assessment. The vertical red dotted line indicated the top of the yield-curve and is introduced in this figure to refer to B_{MSY} .

Based on the SSB calculations, we obtain the median B_{MSY} value of 7.4 million tonnes which corresponds with an F of 0.15, F_{MSY} .

Conclusions

Based on a first attempt to estimate F_{MSY} and B_{MSY} the values of 0.15 and 7.4 million tonnes respectively were obtained.

References

Simmonds, E.J., Campbell, A., Skagen, D., Roel, B.A., Kelly, C., Development of a stock–recruit model for simulating stockdynamics for uncertain situations: the example of Northeast Atlantic mackerel (*Scomber scombrus*), ICES Journal of Marine Science 68(5), 848-859