**FISH 559: Example Application IV (Length-structured model)**

Many of the world’s fish and (particularly) invertebrate stocks are assessed using size-structured population dynamics models because either there are no data on the age-composition of the population or growth is indeterminate. This example has two steps: (a) fit a (simple; 6 stage) size-structured population dynamics model and (b) project into the future under various levels of fishing intensity to implement a rebuilding strategy.

**Step A: Population assessment**

**A.1 Population dynamics model**

The basic dynamics of the population are:

 (1)

where  is the vector of numbers-at-stage at the start of year *y*, **X** is the growth transition matrix (assumed to be lower triangular), **S**y is the survival matrix for year *y*, and  is the vector of recruits for year *y* (with zeros on all elements except the first). The matrix **S**y is diagonal with elements:

 (2)

where  is the instantaneous rate of natural mortality (assumed to be time-and size-invariant),  is selectivity on animals in size-class *i*, and  is the fully-selected fishing mortality rate during year.

Recruitment occurs to the first size-class only and is modelled as 

The catch in numbers and by weight are given by:

 (3a)

 (3b)

where  is the weight of animals in size-class *i*.

**A.2 Parameterization**

The parameters of model are the numbers-at-size at the start of the first year, the parameters which define selectivity and growth, the fully-selected fishing mortalities, median recruitment, , and the deviations in recruitment about mean recruitment, . Fishery selectivity as a function of length is modelled as a logistic function of length with lengths at 50% and 95% selectivity of 40 and 70cm while survey selectivity is modelled as a logistic function with lengths at 50% and 95% selectivity of 20 and 60cm. The growth transition matrix is pre-specified (see EX4A.DAT). The only parameters which are included in the ADMB non-linear search are the numbers-at-size at the start of the first year, the fully-selected fishing mortalities and the parameters which define annual recruitment (the vaklue for the catchability coefficient is estimated analystically).

The data available for assessment purposes are the catches in weight, the size-composition of the catches and an index of survey-selected biomass. The contributions of each of the data sources to the negative of the logarithm of the negative likelihood function are:

 (4)

where  is the observed catch-in-weight for year *y*,  is the standard deviation of the logs of the catches in weight (assumed to be 0.05).

 (5)

where  is the index of abundance for year *y*,  is the pre-specified standard deviation of the logarithm of  (0.2),  is the biomass corresponding to :

 (6)

 is survey selectivity for animals in size-class *i*, *q* is a constant of proportionality.

 (7)

where  is the effective sample size (set to 100),  is the observed proportion which animals in size-class *i* constitute of the catch in numbers during year *y*, and  is the model estimate corresponding to:

 (8)

A penalty is placed on the deviations in recruitment about mean recruitment:

 (9)

where  is the standard error of the  (assumed to be 0.6).

**A.3 Problem statement**

Update the provided code and estimate the values for the parameters of the model. Use the MCMC module within ADMB construct a posterior distribution. Implement the MCMC algorithm by running 1,000,000 cycles, saving every 10,000th vector. Based on the samples from the posterior (ignore the first 100 of 1000) construct a posterior distribution for the time-trajectory for . Hints:

* You want a PIN file
* I suggest treating the logarithms of average recruitment, annual fishing mortality and initial numbers as parameters to ensure they stay positive.
* Set the value for *q* to the maximum likelihood estimate.
* You need to include an mceval\_phase() to output *B*y for each draw from the posterior.

**Step B: Risk Analysis**

The aim of this step is to find the constant level of *F*y which if implemented over the next 20 years will result in *B*y rebuilding to 1000t with 0.5 probability by year 46, i.e. P(*B*46>1000t)=0.5. You need to extend the code you developed for step A so that recruitment deviations are generated for years 26 to 46 and so that projections can be conducted for 20 years under a pre-specified value for *F*y. You should use R to link to the ADMB program to automatically search for the *F*y such that the probability that *B*46 exceeds 1000t is closest to 0.5. For “bonus points” plot the future *F* as a function of P(*B*46>1000t).

Hints:

* Create a file which R updates which lists the *F* you wish to project the model forward for. This value needs to be read into the program (which you can rename from the one you used to conduct the assessment).
* Extend the set of estimated recruitment deviations so they are estimated for years 26 to 46 as well as the years with data (so uncertainty in future recruitment is captured) – note that this means re-running the MCMC algorithm.
* Use the mceval phase to output the time-series of biomass values for each MCMC sample and read this into R to compute the probability.