TECHNICAL MEASURES IN FISHERIES MANAGEMENT

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Restrictions on size of fish that are caught are used as one of a number of measures considered for the sustainable management of fish stocks all over the world. The simple logic behind this conservation principle is to provide chance to the younger ones to grow, mature and reproduce at least once and contribute to the population before they are taken away in the catch. In many countries, there are legally implemented size (or length) limits for different species in the catch in the fishery including recreational fishing. Such size limits are arrived based on scientific research about the species especially its reproductive features. Though in most cases size restrictions are for the minimum size, there are restrictions on maximum size in some species were larger individuals contribute more to the population growth (example: Asian seabass younger ones are males and become females and spawn when they grow larger).

Advantages of implementing minimum legal size in a fishery

- Reduce juvenile fishing which results in economic loss
- Prevent growth over-fishing which is detrimental to the stock
- Maintain spawning stocks
- Ensures enough fish survive to grow and spawn
- Conservation of heavily exploited stocks
- Share catch more equally
- Reduce illegal marketing of fish
- Promote ethical and responsible fisheries
- Maximize marketing and economic benefits
- Promote aesthetic values of fish

In aquaculture the ultimate aim is to produce as many fish as possible in the shortest possible time which could be achieved *through* increased growth rate. an increased growth rate most probably will be accompanied by a subsequent decrease in age and size at sexual maturity. Since it is not economical to rear the species beyond sexual maturity, size at maturity is important for aquaculture also.

Information on size and reproductive behaviour of the species are necessary for a management regime to ensure that sufficient number of juveniles reach maturity and contribute to the growth of the population. An individual in a population is said to be fit when it survives to sexual maturity and contribute to the gene pool of the population and collectively, those surviving individuals determine the survival of the population. Thus it is very important to study about the reproductive biology of the fish for better understanding and management of an exploited ecosystem. As the reproductive behaviour vary highly from species to species

Some of the key measurements used for size regulation in fish include size at first maturity or size at which 50% of fish are mature (L50) and minimum size at maturity or size of the smallest mature fish. Proper estimation of these size measurements is very useful for fish stock management. Different methods have been proposed to estimate L50 and other measures of maturity size. According to a very useful study, each individual fish should be identified as reproductive or non reproductive. Although diverse methods are available for assessment of L50, most of the researchers apply some kind of logistic functions.

Thus restrictions on size of the animals that are caught is extensively used as one of the different means necessary for conservation of fish stocks. Accurate estimates of female age or length at maturity are thus critical for conservation of exploited fishery resources. Information on age and length at maturity based on histological evaluation of maturity status is therefore needed for different species. Fishery biologists prefer to conceive size at first maturity as the average size at which 50% of the individuals are mature. Size at 50% maturity (L50%) is commonly evaluated for wild populations as a biological reference point.

To estimate (L50%), a sample of organisms known to have just reached sexual maturity could be made available and their arithmetic mean size can be used as an estimator. One accepted method of estimating the size at first maturity is by sampling the mature animals from the population following a suitable sampling design. But the sample needed to obtain such a design based estimator (Sampling Design) for wild populations might be too expensive and would involve time-consuming histological procedures. With this conception, the estimator is usually not based on a sampling design but on a statistical model of the relation between body size and the number of individuals that are mature from a total number at each of many size intervals.

The most preferred model is the Logistic regression model to fit sigmoid curves to the proportion mature by length. The mathematical expression for a logistic regression model is

$$P(x) = \frac{e^{b_0 + b_1 x}}{1 + e^{b_0 + b_1 x}}$$

Here p(x) is the probability that a fish is mature in a given length *x*. The parameters in the model b0 and b1 determine the shape and location of the sigmoid curve. Once estimates of the parameters of the model are available we can workout the length corresponding to any required proportion (size of the animal for which a given percentage of the animals will be mature) using the expression (except for 0 and 100%)

$$x = \frac{ln\left(\frac{p}{1-p}\right) - \widehat{b_0}}{\widehat{b_1}}$$

where $\hat{b}_0$ and $\hat{b}_1$ are the estimates of the parameters in the logistic regression model.

Logistic regression model parameters can be estimated by adopting different statistical procedures. One method is through regression analysis after linearising the model by log transformation as shown below where *p* is the proportion mature having length *x* in the observed data.

$$x = \frac{ln\left(\frac{p}{1-p}\right) - \widehat{b_0}}{\widehat{b_1}}$$

The above method create estimation problems when the observed data have samples with proportions 0, 0.5 and 1.0 as the left hand side of the above equation become indeterminate or not defined for these cases. Some authors have suggested some adjustments in the observed data to handle this situation. A well accepted method is to use the statistically popular method of maximum likely hood which requires specific statistical softwares. Another alternative is to use Bayesian estimation for the logistic regression model which is explained here using the OpenBUGS computer software.

Bayesian methods are widely used in fisheries for stock assessment to obtain posterior probability densities of parameters of interest. Two important advantages of Bayesian inference are i) it provides estimates of posterior probability densities of unknown parameters of the model rather than the usual point estimates (ii) prior knowledge about the model parameters can be incorporated into the estimation process.

OpenBUGS is an open source version of WinBUGS, a statistical software for Bayesian analysis using Markov Chain Monte Carlo (MCMC), which is downloadable from www.openbugs.net. It is the windows version of the original DOS version BUGS (Bayesian inference Using Gibbs Sampling) software developed by MRC Biostatistics Unit, Cambridge, and Imperial College School of Medicine, London in 1989.

Practical Example

The source of data used for demonstration of Bayesian estimation using OpenBUGS is from the following publication accessed on line:

INFORMATION REPORTS NUMBER 2009-04, "Length and age at maturity of female yelloweye rockfish (*Sebastes rubberimus*) and cabezon (*Scorpaenichthys marmoratus*) from Oregon waters based on histological evaluation of maturity" by Robert W. Hannah, Matthew T. O. Blume and Josie E. Thompson, Oregon Department of Fish and Wildlife Marine Resources Program, 2040 Southeast Marine Science Drive, Newport, Oregon 97365, U.S.A

Number of female yelloweye rockfish sampled, number and proportion mature, by length (cm)

Length	Observed Number	Number Matured	Proportion	Length	Observed Number	Number Matured	Proportion
31	1	0	0.00	51	3	3	1.00
32	4	0	0.00	52	5	5	1.00
33	2	0	0.00	53	5	5	1.00
34	3	0	0.00	54	2	2	1.00
35	2	0	0.00	55	0	0	
36	4	2	0.50	56	1	1	1.00
37	5	2	0.40	57	4	4	1.00
38	4	1	0.25	58	2	2	1.00
39	4	2	0.50	59	0	0	
40	5	2	0.40	60	3	3	1.00
41	7	6	0.86	61	2	2	1.00
42	7	6	0.86	62	1	1	1.00
43	6	6	1.00	63	0	0	
44	8	7	0.88	64	1	1	1.00
45	5	5	1.00	65	2	2	1.00
46	19	19	1.00	66	0	0	
47	9	8	0.89	67	1	1	1.00
48	9	9	1.00	68	1	1	1.00
49	7	6	0.86	69	0	0	
50	3	3	1.00	70	1	1	1.00

OpenBUGS code for the logistic model

Download the OpenBUGS software (Version 3.0.3 or higher) from the website "http://www.mrc-bsu.cam.ac.uk/bugs" and install it on a computer system. Start the software and proceed with the following steps.

1. Open a new OpenBUGS page by choosing 'New' from the File Menu and copy the given code into the blank page (the portion from 'model' to the last line starting with 'list'.
2. Replace the input sample data portion (do not disturb the structure) with the original data where the x portion is for the lengths of samples, n portion is for the number of samples of each length observed and r is the numbers that are mature corresponding to each sample.
3. From the Model menu open the specification tool
4. Double click on the word "model" in the open page containing the code to select it and click on the check model button in the specification tool box. At the bottom left corner of the open page "model is syntactically correct" message should appear.
5. Double click on the word 'list' in the data portion of the open page to select it and click on the load data button in the specification tool box. At the bottom left corner of the open page "data loaded" message should appear.
6. Click on the compile button in the specification tool box. At the bottom left corner of the open page "model compiled" message should appear.

```
model
     {for ( i in 1 : N ) {
          r[i] ~ dbin(p[i],n[i])
     logit(p[i]) <- b0.star + b1 * (x[i] - mean(x[]))
          rhat[i] <- n[i] * p[i]
          culmative.r[i] <- culmative(r[i], r[i])}
         b0 <- b0.star - b1 * mean(x[])
         b1 ~ dnorm(0.0,0.001)
         b0.star ~ dnorm(0.0,0.001) }
#
# Input sample data
#
list ( x = c(31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
     ,46,47,4
8,49,50,51,52,53,54,56,57,58,60,61,62,64,65,67,68,70),
n    =   c(1,4,2,3,2,4,5,4,4,5,7,7,6,8,5,19,9,9,7,3,3,5,5,2,
         1,4,2,3,2,1,1,2,1,1,1),
r    =   c(0,0,0,0,0,2,2,1,2,2,6,6,6,7,5,19,8,9,6,3,3,5,5,2,1,
         4,2,3,2,1,1,2,1,1,1), N = 35)
#
# Initial values for parameters
#
list(b0.star=0, b1=0)
```

7. Double click on the word 'list' in the initialization portion of the open page (last line) and click on the load inits button in the specification tool box. At the bottom left corner of the open page "model is initialized" message should appear.

8. Now close the specification tool box.

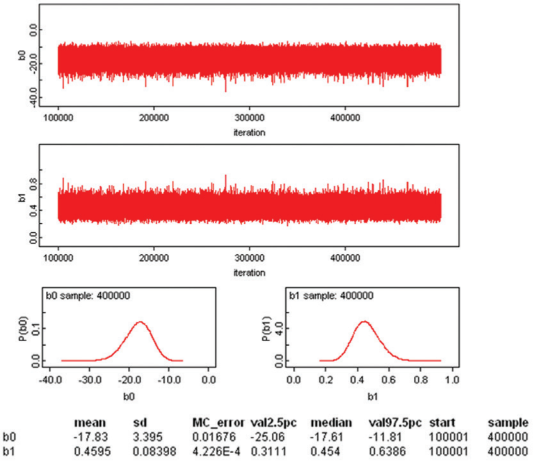
9. Open the sample monitor tool box from the inference menu. Type the parameter names (b0, b1,b0.star,rhat) one at a time in the box against node and press the set button. Repeat it with other parameter names and close the sample monitor tool box once finished.

10. Open the update tool box from model menu. Replace the number in the update box with your choice number of updates (say, 100000 or more for good results) and click on the update button. The MCMC algorithm starts and the number of updates completed will be displayed in the iteration box. Close the update tool box one the iteration/updating is complete.

11. Open the sample monitor tool box from the inference menu again. Select the parameter name by clicking on the down arrow against the node (* for all set parameters) and click on the respective buttons to get information about the MCMC results. The important items are

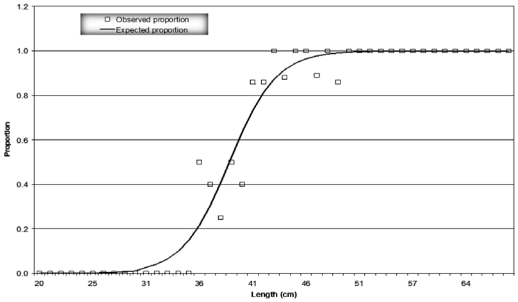
Name on the Button	Purpose
History	Graphical display of iteration history
Density	Graphical display of the probability density
Stat	Summary of statistics estimated

Here, for each parameter, the estimation history and posterior probability density plot should be examined before accepting the estimates displayed when 'stat' button is pressed. The history plot should be oscillating steadily in an acceptable range and the density plot should be smooth. For the sample data, the history plots, posterior probability density plots and summary statistics for the two parameters in the model obtained with 5,00,000 updations, omitting the initial 1,00,000 are given below.



```
        mean     sd       MC_error  val2.5pc  median   val97.5pc  start    sample
b0      -17.83   3.395    0.01676   -25.06    -17.61   -11.81     100001   400000
b1      0.4595   0.08398  4.226E-4  0.3111    0.454    0.6386     100001   400000
```

The Bayesian estimates of the parameters of the logistic regression model for the sample data are $\hat{b}_0 = -17.83$ and $\hat{b}_1 = 0.4595$ and the plot of the observed proportions and the fitted sigmoid curve are given below. From the fitted model, the estimates of L25, L50 and L75 (lengths corresponding to 25%, 50% and 75% are mature) for the species are 36.4cm, 38.8cm and 41.2cm respectively.



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