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Fish Health Index *See* Coastal and Estuarine Environments

Fisheries Management

S J D Martell, University of British Columbia, Vancouver, BC, Canada

Introduction

The role of ecological models in fisheries science is primarily for stock assessment, and stock assessment is about making quantitative predictions about population change in response to alternative management choices. A stock assessment model is actually a collection of several submodels that deal with specific components of the entire system, and the level of complexity of each of these submodels can range from simple with very few unknown parameters to very complex with thousands of unknown parameters. Regardless of the level of complexity among competing models, there are three basic objectives that we hope to obtain in fisheries stock assessment:

1. Stock status: to specifically assess the current level of exploitation (the fraction of the total population that is being removed each year) and the current abundance relative to some management target.
2. Stock productivity: to specifically assess the shape of the underlying production function and the level of exploitation deemed sustainable. Also, to determine which harvest policies should be used to ensure sustainability.
3. Stock reconstruction: to specifically assess how the components of population change (recruitment, mortality, net migration) have varied over time, and whether or not these variations are related to fishing and/or environmental changes.

A typical modern-day stock assessment usually begins with the third objective in order to examine the first two objectives.

The basic structure for any assessment model requires at least five key components (Figure 1), and each of these components are linked such that a simple change in the data or assumption about the model structure could ultimately redefine the management objective. Overall, there are two key parameters of interest in fisheries stock assessment models: (1) a parameter that defines the overall population scale (i.e., how large is the population), and (2) a parameter that defines the underlying production function (i.e., the intrinsic rate of growth or how resilient the population is to disturbance). The interplay between these two parameters ultimately defines the suitable range of alternative harvest policies.

The essential components of a fisheries stock assessment model outlined in Figure 1 will form the basic outline for this article. We will begin with a description of the types of data that are frequently encountered and used in fisheries stock assessment. Then we provide a few examples of the types of population dynamics models and error structures that are used to make inference about components of population change over time. Following this, we will discuss how the population models are used to generate predicted observations in order to proceed with the next step of the assessment – comparing

Essential components of a fisheries stock assessment model	*Detailed components of fisheries stock assessment models*
(1) Data	Abundance indices Mortality information Composition information
(2) Population models	Surplus production models Age or stage based models Multispecies or multistock models
(3) Observation models	Trend comparisons Size selectivity and composition comparison
(4) Statistical model	Parameter estimation Assessing model fit or lack of fit Quantifying uncertainty
(5) Management advice	Harvest policies Alternative hypotheses and decision tables Management objectives

Figure 1 The essential components of a fisheries stock assessment model. There are at least five essential components in a fisheries stock assessment model, and modern fisheries stock assessment models integrate all of this information into a single framework that is ultimately used for providing management advice.

predicted and observed values using a variety of statistical approaches. Lastly, we discuss how this information is used to formulate yield recommendations and management advice.

Before proceeding with a detailed description of the various components of a modern fisheries stock assessment model, it is worth mentioning that many of the components or submodels of a modern assessment have now been integrated into a single modeling framework. By analogy, this evolution of fisheries stock assessment is similar to the evolution of a modern bread maker, where all of the ingredients for a loaf of bread are simply tossed into a machine and four hours later the final product is produced. This has both advantages and disadvantages; uncertainty in each of the components (e.g., uncertainty in estimation of natural mortality) is carried forward into the management advice and is advantageous because a more precautionary or conservative strategy may be warranted due to additional uncertainty. A disadvantage is that such model integration may also create structural confounding that obfuscates the underlying production function, which ultimately gives rise to correct policy advice. Returning to the bread maker, this would be equivalent to the addition of unwanted ingredients that result in a brick of flour rather than a loaf of bread.

Data

Trend Information

Fisheries stock assessment models rely on historical time-series information to make inferences about how fishing activities have affected the stock. There are three main types of data that are commonly used in fisheries stock assessments: (1) a time series of abundance (absolute or relative abundance estimates), (2) information on mortality, and (3) compositional information on age, size, or sex ratios. It is not necessary to have all three types of data in order to proceed with estimating historical impacts, but at least one of these types is necessary.

Abundance information (relative abundance or absolute abundance) is frequently obtained from fisheries-dependent sources, and perhaps the most common statistic is the catch rate information or catch per unit effort (CPUE). The basic notion is that the rate at which fish are removed from the population is a function of the abundance and this rate is usually assumed to be directly proportional to abundance. This assumption presumes that spatial allocation of fishing operations is randomly distributed with respect to the spatial distribution of the target species, an assumption that is almost always violated. However, in many industrial fisheries around the world, this is the only information that is available to make inferences on the relative change in population abundance. Most often fisheries-dependent CPUE data are assumed to be proportional to stock size, and the underlying error structure is assumed to be log-normally distributed. This can be represented as a simple equation:

$$\mathrm{CPUE}_t = qB_t \exp(\varepsilon_t) \quad [1]$$

Where B_t is the biomass of the stock, q is the catchability coefficient (a scaling term) and ϵ_t is the error term. Equation [1] assumes that trends in the CPUE index are proportional to trends in stock biomass. In general, there have been two strong objections to the use of commercial CPUE indices, the first being a violation of the proportionality assumption (i.e., the trends in CPUE are not directly proportional to trends in B_t). Fishery-dependent CPUE indices are most likely to be hyperstable (i.e., catch rates decline at a much slower rate than the stock size). The second major objection owes to the variability in CPUE indices among a fishing fleet. Most often, commercial CPUE indices are derived from an entire fishing fleet (e.g., $\mathrm{CPUE} = \sum C_k / \sum E_k$, where k is an index for individual fishing vessels, C is the catch by any individual vessel, E is the individual fishing effort, and CPUE is the mean catch rate over the entire fleet). Variability in individual catch rates or relative improvements in fishing technologies over time, or even the composition of the fishing fleet each year can change the interpretation of the CPUE index. Some people just catch more fish than others, whether it is due to better fishing gear, knowing where the fish are, or having a bigger boat. This inherent variability becomes problematic when the less apt fishermen drop out of the fishery altogether and as a result the mean CPUE increases.

When alternative abundance indices are available, such as those derived from fisheries-independent surveys, it is normally wise to severely discount or ignore indices that are derived from fisheries-dependent sources. If however, the fisheries-dependent CPUE information is the only available abundance index then standardization of the CPUE index is recommended. CPUE standardization is a fairly active research area in fisheries science, and it attempts to remove individual variability in catch rates as well as interannual variation in catch rates that are associated with changes in fishing technology, fleet composition, environmental covariates and other associated factors that could potentially affect catch rates. The standardization process is usually carried out using generalized linear models (GLMs) where the covariates may be both categorical variables (e.g., individual boats, capture method, area fished) and continuous variables (e.g., water temperature, price of fish, fuel cost). Recently, this standardization process has also been integrated into the whole stock assessment framework, where the coefficients in the GLMs are jointly estimated along with all other parameters.

Fisheries-independent surveys most often employ a stratified random sampling design; therefore, trend information is much more likely to be proportional to stock size. However, fisheries-independent surveys are also capable of generating estimates of absolute abundance, primarily by using area-swept information and spatial interpolation. This approach will generate an estimate of mean density (e.g., number of fish per unit area) and multiply this density by the total area over which the stock is distributed. There are two main technologies employed to generate absolute abundance estimates over large spatial scales: (1) bottom trawls for benthic species, and (2) hydroacoustic technologies for pelagic species. Bottom trawls generate density estimates over a survey grid, and spatial statistics (e.g., bicubic splines or Kriging methods) are used to interpolate between survey points (see blue crab example in **Figure 2**). Hydroacoustic technologies use sound to measure the amount of backscatter in the water column, this backscatter corresponds to

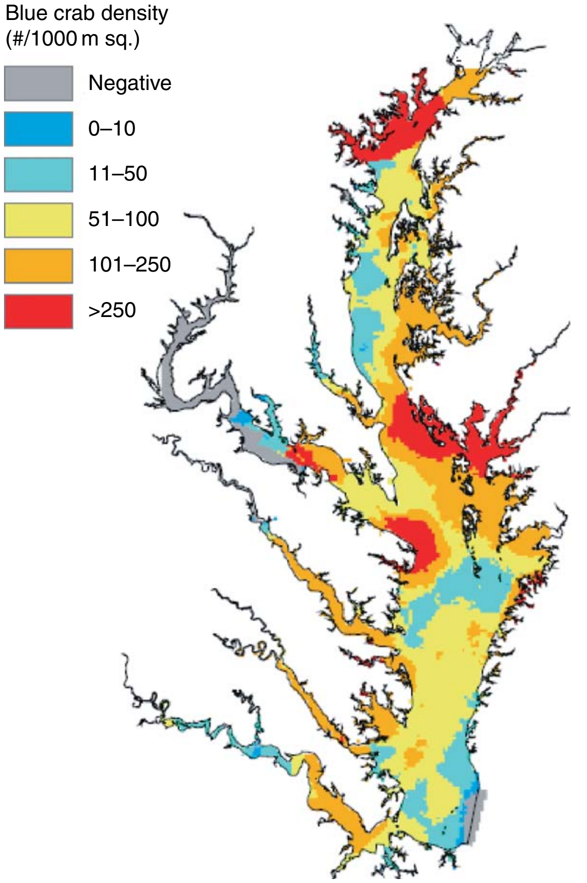

Figure 2 An example of geostatistical techniques for estimating absolute abundance of blue crabs in the Chesapeake Bay based on Kriging methods for interpolation of trawl survey data. Kindly provided by Olaf P. Jensen (University of Wisconsin).

individual fish and the technology is now sufficient to estimate the size of individual targets.

Mortality Information

There are two main data sources in which mortality information can be derived, age or size composition information and information from tagging programs. To demonstrate the utility of age composition information, consider following a single cohort of fish over time. The survival of this single cohort from one year to the next can be described using a simple equation:

$$N_{a+1} = N_a \exp(-Z) \qquad [2]$$

where N_a is the number of individuals at age a, and Z is the instantaneous total mortality rate. Solving eqn [2] for Z leads to the simple expression:

$$Z = \ln(N_{a+1}) - \ln(N_a) \qquad [3]$$

Thus, the total mortality rate can be obtained from information on the proportions at age in the population. It is not necessary to know the absolute abundance of each cohort, only the relative proportions of each cohort in the population. The method can also be extended to size composition data; however, information on fish growth must also be known. There are two main problems in using this simple approach to obtain independent information on total mortality rates: (1) it is often difficult to collect a representative sample that reflects the true population age structure due to sampling difficulties (e.g., sampling gears are almost always size-selective), and (2) the method assumes that annual recruitment to the population is nearly constant.

Estimates of mortality rates from tagging programs are based on the same general principle as that for age or size composition data; however, in this case total mortality rates are determined by following the fate of a tagged population over time. There are two assumptions in tagging programs that must be met in order to use this information to estimate mortality: (1) assume no tagging-related mortality or the tagging mortality rate is known, and (2) assume no tag loss, or the loss rate is known. There is also a third assumption that must be met if the sampling program relies on commercial or recreational fisheries for the recovery of tags – that all recaptured tags are reported. Tagging programs have proved to be invaluable for the estimation of mortality as well as many other demographic parameters; however, violations of this last assumption have been problematic in fisheries stock assessment.

Compositional Information

As previously mentioned, compositional information (age-structure or size-structure information) form very valuable demographic data for making inferences about total mortality rates. Compositional information has also been used to make inferences about the relative cohort strengths, and more recently, information on the relative abundances of juvenile fish is now being used to improve the short-term forecasts of stock abundance. Other potentially useful types of compositional information include mean body weight, mean length, or mean age information. These simple measures of population composition are usually easier to obtain and are more cost-effective in terms of the information they provide relative to the cost of obtaining detailed age composition information.

Most often, composition information is obtained by randomly sampling the catch from commercial or recreational fisheries. Individual fish are then measured using hard bony structures (fin rays and more commonly otoliths or earbones). These aging structures lay down annual growth rings (annuli) much like the rings in a tree and the fish can be aged by simply counting the number of rings. Age composition can also be inferred directly from size composition data, where a length–frequency distribution is converted to an age–frequency distribution using an age–length key.

Population Models

Population models are an essential part of the stock assessment framework because they provide three essential elements: (1) a theoretical framework for understanding the dynamics of a natural population, (2) a quantitative framework to make inferences about the historical and current status of a population, and (3) a framework to make quantitative predictions about the effects of future harvest on the status of the population. There are literally hundreds of different types of population models that have been developed to describe the dynamics of a single population, and even dozens of models that have been developed to describe the dynamics of whole communities. Here, we restrict the descriptions to three general types of population models: (1) production models, (2) age- or stage-based models, and (3) multispecies or multistock models. A common thread among all of the population models and the ecological basis of sustainable harvesting is the concept of density dependence.

The dynamics of any natural population is determined by four vital rates: mortality, births (or recruitment), immigration, and emigration. In fisheries stock assessment, it is common to assume a unit stock, or a closed population, and simply ignore the effects of immigration and emigration; therefore, there are only two important vital rates of concern (mortality and recruitment). The ecological basis for sustainable harvesting requires that either recruitment rate increases or natural mortality rate must decrease, otherwise the population will head toward extinction once harvesting has initiated. In other words, the recruitment rate must increase or the mortality rate must decrease as the density of fish decreases, or these rates are simple density dependent. There is very little empirical evidence in fish of density-dependent mortality rates; however, there is a tremendous amount of evidence for density-dependent recruitment rates.

Production Models

Production models are the simplest form of population dynamics models used in fisheries stock assessment. The detailed processes of new recruitment and mortality are condensed into two terms that describe the intrinsic rate of growth (denoted by r) and the populations' carrying capacity (denoted by K). Change in population biomass over time can be described using a very simple differential equation:

$$\mathrm{d}B/\mathrm{d}t = rB(1-B/K)^{(m-1)} - Y \qquad [4]$$

where B is a measure of population biomass or density, Y is the yield removed by the fishery, and m is a parameter that describes the population density at which production is maximized (**Figure 3**).

The simplest form of the basic production model is to assume that production is maximized at ½ of the population carrying capacity (i.e., $m=2$ in eqn [4]). In fisheries science, this is usually referred to as the Schaefer or logistic production model. Equation [4] forms the underlying theoretical basis for sustainable harvest and a quantitative basis for determining the level of harvest that will maximize yields. If we assume equilibrium conditions (i.e., $B_{t+1}=B_t$ or $\mathrm{d}B/\mathrm{d}t=0$ in eqn [4] and fix $m=2$ for simplification), then the equilibrium yield is obtained by

$$Y = rB(1-B/K) \qquad [5]$$

and the yield is maximized by setting

$$\mathrm{d}Y/\mathrm{d}B = r(1-B/K) - rB/K = 0 \qquad [6]$$

from which the population size that maximizes the yield is found by solving eqn [6] for B:

$$B_{\max} = K/2 \qquad [7]$$

Equation [7] can then be substituted back into eqn [5] to determine the maximum yield:

$$Y_{\max} = rK/4 \qquad [8]$$

Regardless of the complexity of the population models, these simple algebraic manipulations of equations (that represent the dynamics of an exploited population) are used to determine how much should be harvested to ensure long-term sustainability.

Age- or Stage-Based Models

The simple production model described in the previous sections assumes that all individuals in the population are more or less equals (e.g., the mean egg production per individual does not change over time, or the mean weight of each individual landed in the fishery does not change over time). In reality, there are additional demographic affects associated with the population age- or size-structure that could influence the dynamics of a given population. For example, older, larger fish contribute more eggs, or provide better parental care, etc., than younger, smaller fish. Furthermore, nearly all fishing gears are size-selective (i.e., small fish are less likely to be captured on large fish hooks, or the fishery operates in an area where only large fish reside) and it may take several years (even decades) for individual fish to grow to sufficient size that they become vulnerable to the fishing gear. These delays in production (production as seen by the fishery) are not sufficiently captured by simple production models and are better represented by age-structured or stage-structured models. The term stage-based model is used to represent specific life-history stages (e.g., larvae, juvenile, adult) or length classes rather than calendar ages, as it is not always possible to obtain age information (e.g., invertebrates are difficult to age because they lack permanent bony

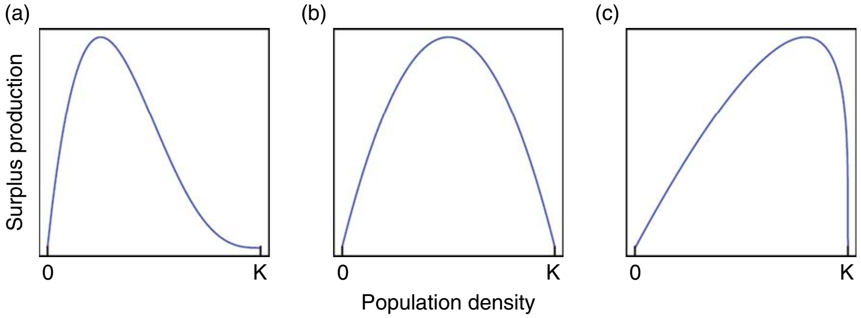

Figure 3 Three basic forms of the surplus production model where (a) production is maximized at less than ½ of the carrying capacity ($m=1.25$ in eqn [4]), (b) production is maximized at ½K (logistic growth model), and (c) where production is maximized at population densities that are greater than ½K ($m=4$ in eqn [4]).

structures such as otoliths that are used to determine age). Population models based on life-history stages operate on the same basic principle as age-based models, where the principal difference is the time it takes to graduate from one stage to the next stage.

There are two basic approaches for the use of age-structured models in fisheries stock assessment: (1) a virtual population method that reconstructs the populations' number-at-age backwards in time, and (2) a synthetic population that reconstructs the populations' numbers-at-age forward in time. These two approaches are usually referred to as virtual population analysis (VPA) and statistical catch-at-age analysis (SCA), respectively. Both approaches rely extensively on catch-at-age data to estimate population parameters; however, it is not always necessary to have complete catch-age composition information for SCA approach. The basic equations that are used to describe the changes in numbers-at-age over time are given by

$$N_{a+1,t+t} = S\left(N_{a,t} - C_{a,t}\right) \qquad [9]$$

$$C_{a,t} = v_{a,t} U_t N_{a,t} \qquad [10]$$

where $N_{a,t}$ is the numbers-at-age in year t, S is the annual survival rate (assumed to be constant and independent of age in this case), $C_{a,t}$ is the catch-at-age, $v_{a,t}$ is the proportion-at-age that are vulnerable to exploitation, and U_t is the overall exploitation rate in year t.

In the VPA case, the system of equations is actually solved backward in time (**Figure 4**) where the numbers-at-age in the last year and the numbers in the oldest age group for every year are unknown quantities that must be estimated from the data. For the unknown numbers in the oldest age group, it is usually assumed that no fish lives longer than the oldest age class, thus the number of fish in the oldest age class is simply the number caught in the fishery divided by the exploitation rate in that year. For the terminal numbers-at-age, estimates are usually obtained by solving eqn [10] for $N_{a,t}$ and specifying and exploitation rate in the terminal year (U_{term}). The VPA then proceeds to back-calculate the numbers at age by adding the $C_{a,t}$ information to $N_{a+1,t+1}$ and dividing by the survival rate. Therefore, it is essential that catch-at-age information be specified for each year. The vulnerability-at-age schedule ($v_{a,t}$) in the terminal year must be specified in order to determine the abundance of incomplete cohorts (see **Figure 4**). These vulnerabilities are usually determined by examining the historical vulnerability-at-age patters in earlier years.

In the SCA case, the system of equations is solved forward in time (**Figure 4**) and the unknown quantities consist of the initial age-structure in the population and the new recruits each year (**Figure 4**). The unknowns in the SCA can be treated as unknown parameters that are estimated by fitting the model to observed catch-at-age information and time-series data on relative abundance. Alternatively, the new recruits each year may also be derived from a spawner–recruit relationship (e.g., a Beverton-Holt or Ricker type stock recruitment model), and the initial age-structure determined from an estimated initial recruitment and a survivorship curve defined by the initial total mortality rate. A major difference between the SCA and the VPA is that a vulnerability-at-age matrix ($v_{a,t}$) must be specified or estimated from the available data in the SCA case and often this adds many additional parameters to the estimated parameter set and increases the uncertainty in the stock size estimate.

Entire book chapters and several thousand primary publications have been devoted to VPA and SCA modeling approaches and it is impossible to discuss all of the pros and cons of either method in such a short article. However, there are two primary concerns in using either of these

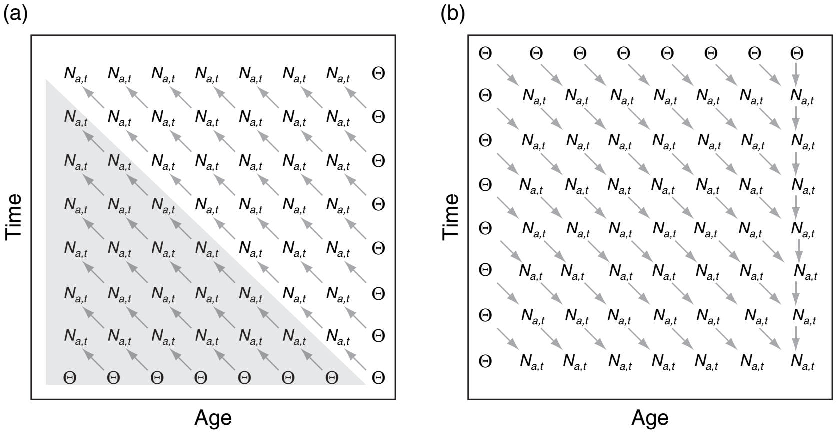

Figure 4 A graphical representation of how the numbers-at-age are updated in (a) a VPA, and (b) an SCA. The Θ symbols represent unknown parameters or quantities that must be estimated in each of the approaches. In a VPA, these unknowns correspond to abundances in the terminal year and terminal age in all years. The shaded region represents the incomplete cohorts (those cohorts that are still remaining in the fishery). In an SCA, the unknowns are the initial age composition and the initial recruits in each year.

approaches that should be considered: (1) effects of aging error and (2) assumptions about vulnerability-at-age. In the VPA case, aging errors are propagated backward with expanded effect over time. For example, a simple error in the estimating of proportion-at-age in an older age class is propagated backward in time and is amplified by successive division of the survival rate *S*. This effect is dampened in the SCA case because the error is successively reduced by multiplication of the survival rate over time. The vulnerability-at-age schedule (i.e., the fraction of fish of a certain age class that is vulnerable to exploitation) is usually assumed to be constant over time (or perhaps over blocks of time that represent periods of certain types of fishing activities). Temporal changes in the vulnerability-at-age associated with changes in fishing locations or gear types can be interpreted as just that, or they can also be interpreted as strong year classes that have entered or disappeared from the fishery. For example, if fishermen learn that smaller fish fetch a higher value, they begin to target smaller fish relative to larger fish (i.e., $v_{a,t}$ increases for younger fish) and this information is not passed on to the stock assessment scientist, then the interpretation of the data is that a strong cohort is about to enter the fishery and the stock size will be severely overestimated. As a result, stock forecasts will be very optimistic. This scenario occurred in northern cod stocks of the east coast of Canada in the late 1970s and early 1980s (**Figure 5**).

Stock–Recruitment Models

The stock–recruitment relationship is one of the most critical components in fisheries models. The role of the stock–recruitment model is twofold: (1) to provide short-term forecasts about future recruitment based on estimates of current spawning abundance, and (2) to provide a biological basis for the underlying production function in the model. Ultimately the stock–recruitment relationship defines just how much we can safely harvest and at what rate this should occur. There are many different analytical stock–recruitment models in use, but the two most commonly used models are the Ricker and the Beverton-Holt models:

- Ricker model: $R_t = E_t \exp(a - bE_t)$
- Beverton-Holt model: $R_t = aE_t/(1 + bE_t)$

where E_t is a measure of egg production (which is often assumed to be proportional to spawning stock biomass), a is the maximum juvenile survival rate, and b represents density-related effects on juvenile survival. The Ricker model is frequently used to describe the production dynamics of salmon populations, and the Beverton-Holt model more frequently used in the assessment of pelagic and benthic marine fishes. Both of these models predict a compensatory response or improvement in the juvenile survival rate from egg (E_t) to recruit (R_t) as egg production or spawning stock biomass is reduced. Stock–recruitment models are often integrated into statistical catch-at-age models and the unknown parameters (a,b) of the model are estimated (or derived from other model parameters) simultaneously with all other model parameters.

Multispecies or Multistock Models

There are many fisheries that engage in multispecies fisheries around the world, or single fishing fleets that target several distinct populations or stocks of fish of the same species. That is, a single fishing vessel is permitted

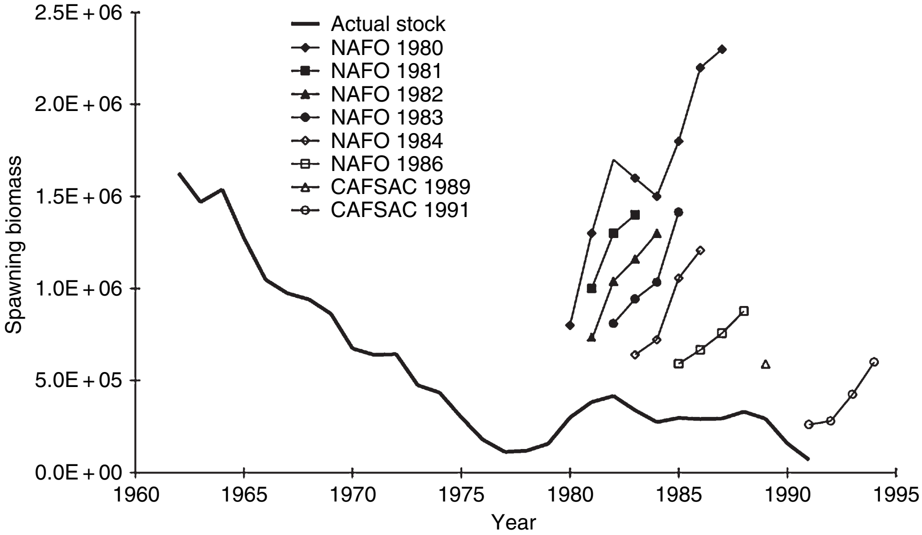

Figure 5 Estimated biomass of northern cod of the east coast of Canada (2J3KL) stocks and the biomass forecasts produced by the stock assessment models (VPA-based assessment models) in the late 1970s and early 1980s.

to catch and land an array of different species or several different stocks of the same species. For example, the trawl fishery for groundfish off the west coast of British Columbia deliberately targets about 19 different species of fish. The Fraser River sockeye salmon fishery can harvest 20 or more distinct sockeye salmon populations that spawn in particular watersheds. Pelagic long-line fisheries that target tuna are also permitted to harvest billfish, sharks, and other small pelagics. In comparison to the single-species realm, there have been very few stock assessment applications that simultaneously model multiple species or multiple stocks.

There have been two general approaches to modeling the multispecies or multistock fisheries: (1) data aggregation approaches, and (2) explicit modeling of each species or stock. Data aggregation approaches involve the use of a single model to represent the dynamics of a collection of species or stocks of the same species. In these cases, the mean life-history characteristics and demographics parameters are represented by a simple population dynamics model (e.g., logistic production model). The principal problem with this approach is often the subjective nature of how the data are aggregated and interpreted. For example, the CPUE indices are assumed to be proportional to abundance, but the CPUE index itself cannot be used to track changes in community composition because the effort index lacks information about changes in targeting. The second approach involves integrating several population dynamics models into a single framework, where the fishing mortality rates for each species are explicitly modeled using information on targeting (usually inferred using assumptions about ideal free distribution and economic variables such as the relative price differences in each species and/or cost of fishing in certain areas).

Observation Models

There are two general types of observation models that are commonly used in fisheries stock assessment: (1) models for comparing trend information, and (2) models for comparing composition information. Examples of trend information include the CPUE index described in the data section for trends in relative abundance, trends in absolute abundance, and trends in mean age or mean body weight. Relative abundance indices are not always informative about the underlying population parameters in the population dynamics models. CPUE indices that do not vary over time (e.g., catch rates are relatively constant) provide no contrast in which to inform model parameters. This is nearly equivalent to performing a regression analysis in which there is no variation in the independent variable. Furthermore, CPUE indices that display a one way trip (either a continuous decline or continuous increase over time) do not allow for separation of variables in the population model. That is, in one-way trip data, we cannot distinguish between a small productive population or a very large unproductive population.

The basic observation model for trend information is defined by eqn [1], and it is common to assume that observation errors are multiplicative and thus log-normally distributed. Given an estimate of abundance from the population model (e.g., B_t conditioned on the observed catch history or effort and initial guesses for the population parameters) we can reexpress eqn [1] in terms of the residuals:

$$\varepsilon_t = \ln(\mathrm{CPUE}) - \ln(qB_t) \qquad [11]$$

where q is a scalar term, or an observation model parameter. Equation [11] forms the statistical criterion (e.g., as least-squares criterion) in which to evaluate alternative parameter combinations (both population model parameters and observation model parameters). It is also possible to eliminate the nuisance parameters (e.g., scalar parameters such as q) by computing the maximum-likelihood estimate of the parameter conditional on other model parameters (see 'Further reading'). In cases where the index is an absolute measure of biomass or mean body weight, etc., it is not necessary to include the scaling term (q) into the parameter set, and estimation of model parameter proceeds by making direct comparisons.

Compositional information such as catch-at-age or size–frequency data are assumed to come from a multinomial distribution. To utilize these types of data to estimate model parameters an age-structured or stage-structured population model is necessary to compute the predicted proportions. Thus, the observation model is simply the population model that generates the predicted proportions-at-age or proportions-at-length and the assumed sample size. It is common to use the actual number of fish measured or aged as the effective sample size for the multinomial distribution; however, many studies have demonstrated that this approach tends to overweight the compositional information and has the potential to produce strong biases or confounding in the parameter estimates. The effective sample size for the multinomial distribution is nearly always much less than the total number of fish aged (or measured), and it is often thought that the number of vessels sampled or the number of sampling trips conducted to collect the information is a better approximation of the effective sample size.

Statistical Criterion and Parameter Estimation

The most widely used statistical approach for parameter estimation in fisheries stock assessment is the maximum-likelihood approach and the second most common and becoming more popular is Bayesian analysis. We will not discuss the Bayesian analysis here, other than to say that likelihood forms the foundation for Bayesian analysis. The concept of using likelihood and maximum-likelihood methods for estimating model parameters is to recognize that the data are known (we observed them) and the hypothesis is unknown (we do not know the model parameters). The notation or jargon that is used in likelihood methods is a simple statement such as:

$$L(\text{data}|\text{hypothesis}) \qquad [12]$$

which reads as "the likelihood of the data given the hypothesis." The data can be relative abundance indices, compositional information, tagging data, etc., and the hypotheses (plural) are the unknown model parameters which we are interested in estimating. The likelihood itself is simply a probability distribution (e.g., normal distribution, multinomial distribution, Poisson distribution, etc.).

To illustrate the concept of maximum-likelihood parameter estimation, consider the following 10 observations (the data denoted by Y_i):

$$Y_i = (4.76 \;\; 5.08 \;\; 4.93 \;\; 4.89 \;\; 5.20 \;\; 4.95 \;\; 5.16 \;\; 4.85 \;\; 4.95 \;\; 4.96)$$

Here we are interested in determining the mean and standard deviation of the data (i.e., the unknown parameters), and it is a fairly straightforward exercise to simply compute the mean and standard deviation ($\mu = 4.973$, $\sigma = 0.136$). In a maximum-likelihood sense, we are interested in computing the likelihood of the data given hypotheses about various combinations of μ_m and σ_m (where m is an index for alternative hypotheses). To do this, we must first specify the probability distribution from which these data were derived – for now let us assume they arose from a normal distribution. Given that the data were assumed to come from a normal distribution, the likelihood of the data given a hypothesis is computed using

$$L(Y_i|\mu_m, \sigma_m) = \frac{1}{\sqrt{2\pi}\,\sigma_m} \exp\left[\frac{(Y_i - \mu_m)^2}{2\sigma_m^2}\right] \qquad [13]$$

The total likelihood of all of the data is then given by the product of eqn [13] applied to each of the 10 observations. This product of individual likelihoods raises a potential concern; if there are a large number of observations, then the product of several tiny numbers results in numbers that become so small that modern-day computers cannot distinguish this number from 0. Therefore, it is common practice to estimate parameters using log-likelihoods and simply sum the log-likelihoods for all observations. To estimate the most likely parameters that describes the data set, simply calculate the likelihood of the data over a systematic grid of values for μ_m and σ_m and find the combination of μ_m and σ_m values that maximizes the sum of log-likelihoods. Such a grid search approaches work fine for small-dimensional problems (e.g., three unknown parameters). In higher-dimensional problems (e.g., >3 unknown parameters) it is usually much more efficient to use a quasi-Newton nonlinear search routine (e.g., Solver in the Microsoft Excel software).

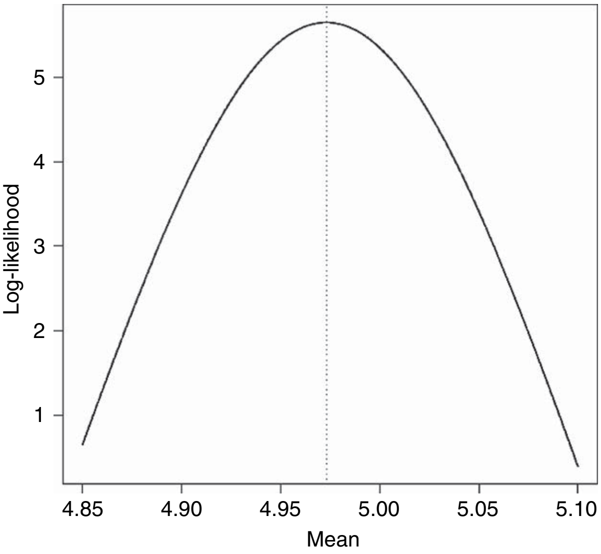

Figure 6 An example of a likelihood profile for assessing the odds of alternative hypotheses. The most likely value is indicated by the vertical dotted line, and the solid line represents the likelihood of alternative hypotheses about the population mean.

The basic concept of computing the likelihood of the data given the parameter values and searching for parameter values that maximize the log-likelihood (either using a simple grid search or a nonlinear search algorithm) is the basic engine that is used in estimating model parameters for fisheries stock assessment. Assessing how well the model fits the data (or how well the parameters describe the data) is determined by the ratio of log-likelihoods. Moreover, uncertainty in the parameter estimates can be readily obtained by examining the likelihood profile (see example in Figure 6).

Management Advice

The ability to provide informative management advice is the final product of the stock assessment model. There are three important considerations for providing management advice (Figure 1), and of those the most important is a clear specification of the management objectives. Lacking a clear management objective is akin to playing darts without a dartboard. Second, harvest policies should be designed such that they can be used to achieve management objectives. Finally, all of the alternative hypotheses and the uncertainty associated with alternative hypotheses should be considered in the decision-making process.

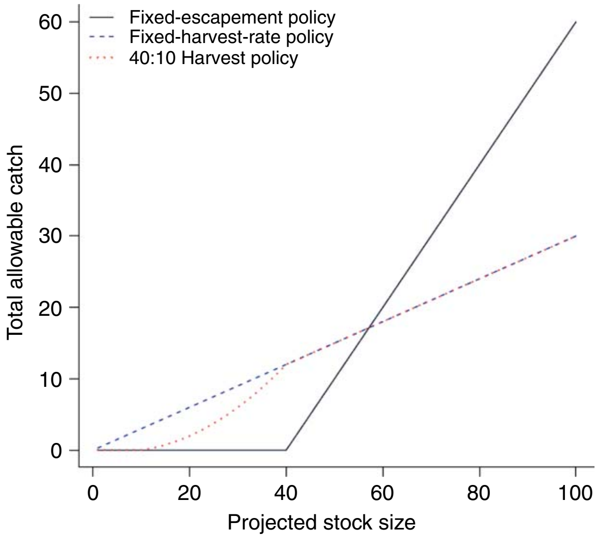

Figure 7 Examples of three different harvest policies. A fixed escapement policy harvests all available surplus beyond some escapement target (shown here as the intercept with the *x*-axis), a fixed-harvest-rate policy harvests a fixed proportion of the projected stock each year. The 40:10 harvest rule is a combination of both the fixed escapement and fixed-harvest-rate policies (see text for further description).

Management objectives can be fairly simple, such as to harvest a population with sufficient effort such that the maximum sustainable yield is extracted each year, or they can be incredibly complex where other social, political, and ecological interactions are examined simultaneously. In some countries, management objectives are defined by law and formal definitions of overfished and overfishing are provided such that even lawyers can make significant profits in a fishery. Whatever the circumstance, management objectives are essential to define the 'targets' in which harvest policies can be developed.

There are two general categories of harvest policies in practice, usually referred to as fixed-exploitation-rate policies and fixed-escapement policies (Figure 7). Fixed-escapement policies attempt to harvest all available surplus above some target stock size. For example, in Figure 7, the fixed escapement level is 40 units of abundance and if the stock is greater than 40 units the total allowable catch (TAC) is the surplus minus the escapement target (e.g., $\mathrm{TAC} = (X_t - 40)$, where X_t is an estimate of the abundance in the upcoming fishing season). Under the fixed-escapement policy, if the stock is below the escapement level then the fishery is closed. A fixed-exploitation-rate policy removes a constant fraction of the projected abundance each year (i.e., $\mathrm{TAC} = uX_t$, where u is the target exploitation rate). Under this policy, the fishery is never closed, even when the stock becomes relatively scarce. A combination of the two policies, called the 40:10 harvest rule, allows for a fixed-exploitation-rate strategy when the stock is deemed to be greater than 40% of its unfished state, the fishery is closed if the stock is deemed to be less than 10% of its unfished state, and the harvest rate must decline proportionally when the stock is between 10% and 40% of its unfished state. Regardless of which harvest rule is adopted, the two key pieces of information that must be determined in the stock assessment process are the projected biomass for the upcoming fishing season, and the optimal harvest rate or escapement level that ensures long-term sustainability.

Even if there are clear management objectives and well-defined harvest rules for setting annual total allowable catches, the underlying statistical models that are used to interpret historical observations and make short-term predictions about future abundance contain a considerable amount of uncertainty. Furthermore, alternative model structures or assumptions about the underlying error distributions can fit the time-series data equally well (from a statistical perspective), but the short-term forecasts about future abundance could be substantially different. Faced with this uncertainty and alternative hypotheses, decision makers have moved toward the use of decision tables. The purpose of the decision table is to create a logical process in which to weigh the alternative hypothesis (e.g., use the likelihood of the data given the model and its associated parameters) against alternative policy options. It is now becoming standard practice in fisheries stock assessments to include such decision tables into the assessment document; this is usually referred to as the yield recommendations.

See also: Fish Growth; Lake Models; River Models; Wetland Models.

Further Reading

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Fishery Models

K W Shertzer, M H Prager, D S Vaughan, and E H Williams,
National Oceanic and Atmospheric Administration, Beaufort, NC, USA

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Introduction

Because of the substantial economic value of fisheries, population dynamics of fish (here taken to include similarly exploited living resources such as crustaceans, mollusks, reptiles, and marine mammals) is one of the oldest realms in quantitative population ecology. For over 100 years, scientists have been developing mathematical models of fish populations.

Any such field will have given rise to specialized terms. In fish population dynamics, this includes the term 'stock', which for practical purposes is synonymous with the biological term 'population'. In this article, the terms stock and population are used interchangeably.

The goals of much work in fish population dynamics are to evaluate the effects of fishing and to provide advice for policy makers on whether fishing should be increased or decreased. For that reason, special attention has been given to estimating the fishing mortality rate and whether it is above or below some optimal value. This focus is also relevant biologically because in many exploited stocks, the strongest force of mortality on adult fish is fishing.

Basic Forces

The simplest representation of the dynamics of a fish stock, represented in units of biomass, is that due to Russell:

$$B_{t+1} = B_t + (G_t + R_t) - (Y_t + D_t) \qquad [1]$$

where B is stock biomass, t denotes time (conventionally measured in years), G is somatic growth of individuals, R is biomass increase due to recruitment (addition of young individuals to the stock), Y is yield (catch in weight) from fishing, and D is loss of biomass from deaths due to other causes. These are the four basic forces considered in models of fish population dynamics.

An equation parallel to eqn [1] can be written for stock size in numbers. Notably, it would omit the term expressing somatic growth.

Generally, external influences such as environmental forcing are either assumed unimportant or modeled as modifying one of the four basic forces. Because eqn [1] models a closed stock, migration in or out is excluded by definition. Stock mixture is usually modeled as exchange between two otherwise independent stocks.

Time

Treatment of time in fish population dynamics is flexible. By convention, stock size in number or weight N_t or B_t refers to the start (however defined) of year t. Yield Y_t and catch in numbers C_t are annual sums. Recruitment R_t is usually an annual number, though it may be an annual biomass, and is typically modeled as occurring at a discrete point during the year, rather than as a continuous process. This may reflect the origin of much fish population dynamics theory in higher latitudes, where seasonality is pronounced, as are the corresponding biological processes.

Models of individual growth (see section titled 'Growth of individuals') are usually continuous in time, but size at age is often simplified to an annual average, rather than a continuously varying measure. In modeling