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Critical review and analysis of existing risk-based techniques for determining sustainable mortality levels of bycatch species

Examen et analyse critiques des techniques existantes fondées sur le risque pour déterminer les niveaux de mortalité durables des espèces faisant l'objet de prises accessoires

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ABSTRACT

This document describes available techniques for the assessment of the status of bycatch species. For all the approaches discussed, we provide data requirements, caveats, assumptions, recommendations, and comments on their accuracy and precision, when available. First, we review the direct (i.e., based on catch data) and indirect methods (i.e., based on meta-analytical models) for estimating natural mortality that are applicable to bycatch species. Second, we describe how natural mortality estimates and other demographic methods can be used to estimate sustainable fishing mortality rates, and other reference points.

RÉSUMÉ

Le présent document décrit les techniques existantes pour évaluer l'état des espèces faisant l'objet de prises accessoires. Pour chaque approche examinée, nous indiquons les exigences en matière de données, les mises en garde, les hypothèses, les recommandations et les commentaires sur l'exactitude et la précision lorsqu'ils sont disponibles. Tout d'abord, nous étudions les méthodes directes (p. ex. : fondées sur les données sur les prises) et indirectes (p. ex. : fondées sur des modèles méta-analytiques) d'estimation de la mortalité naturelle qui sont appliquées aux espèces faisant l'objet de prises accessoires. Nous décrivons ensuite comment il est possible d'utiliser les estimations de la mortalité naturelle et d'autres méthodes démographiques pour estimer les taux de mortalité par la pêche durable et d'autres points de référence.

1 DETERMINING NATURAL MORTALITY RATES

1.1 BACKGROUND

In fisheries assessment the total mortality of fish (Z) is typically partitioned into two main processes: mortality due to natural causes and that from fishing. Instantaneous natural mortality (M) is the rate at which that portion of a population dies, due to causes other than fishing. Natural mortality encompasses senescence, disease, and other events, mostly mediated by predation. Likewise, instantaneous fishing mortality (F) is the rate at which that portion of a population is removed due to fishing. In order to make mortality rates comparable amongst different populations as well as being able to easily add and subtract them, these mortality rates are exponentiated:

$$N_t = N_0 e^{-Zt} \tag{1}$$

As per unit of time:

$$N_{t+1} = N_t e^{-Z} \tag{2}$$

where N_{t+1} is the number of fish at a later time step $t+1$, N_t is the number of fish at the earlier time step t, and Z is total mortality. As $Z = M + F$, the equation can be rewritten as:

$$N_{t+1} = N_t e^{-(M+F)} \tag{3}$$

We can convert total mortality (Z) back into percentage survival (S) using the following equation:

$$S = e^{-Z} \tag{4}$$

Mortality can be estimated directly using mark-recapture data, fisheries-independent surveys, and even from abundance differences inside and outside of marine reserves (Willis and Millar 2005). However, these methods are usually time consuming and expensive. Given the difficulties of directly estimating M directly, a number of indirect methods of estimating M have been created based on its relationship with life history parameters. One approach to estimate M is to first calculate total mortality Z and then partition it into fishing F and natural mortality M. This is typically done by calculating and accounting for natural mortality leaving F as a remainder.

We begin by firstly describing methods estimating total mortality Z directly and how to split estimates of Z into fisheries (F) and natural mortalities (M), followed by indirect methods of estimating natural mortality, which can be subdivided into age-independent methods (i.e., with an average estimate of M across their whole lifespan) and age- or size-dependent methods (i.e., with varying M with ontogenetic growth). All estimates of instantaneous mortality rates shown in this review have a unit of year^{-1}.

1.2 ESTIMATING TOTAL MORTALITY Z FROM CATCH-AT-LENGTH DATA

Total mortality Z can be estimated from catch data by comparing abundances among cohorts. Three methods are described here, one based on generalizations derived from mean length in catch, and two methods which use catch abundances across cohorts; one comparing all cohorts within a time-step (catch curves), and a second method which tracks a single cohort through different time steps (year-class curves).

1.2.1 Mean length in catch

When a large number of length-frequency data are available from a given stock, by a given gear, total mortality Z can be estimated from the mean length ($\bar{L}$) in the catch from a given population:

$$Z = \frac{k\ (L_\infty - \bar{L})}{\bar{L} - L_C} \tag{5}$$

Where k and L_∞ are the von Bertalanffy growth parameters, $\bar{L}$ is the mean length in the catch, and L_C is the mean length at first capture for the species with the gear (Pauly 1980b). Another equation provided that allows the estimation of Z using mean length in catch is:

$$Z = \frac{nk}{(n+1)\log\frac{L_\infty - L_C}{L_\infty - \bar{L}}} \tag{6}$$

In addition to the parameters defined above, *n* is the number of individuals used for the estimation of $\bar{L}$. The same equation can be written in terms of asymptotic weight W_∞, a parameter from a weight-at-age von Bertalanffy growth function:

$$Z = \frac{nk}{(n+1)\log\frac{\sqrt[3]{W_\infty} - \sqrt[3]{W_C}}{\sqrt[3]{W_\infty} - \sqrt[3]{\bar{W}}}} \tag{7}$$

1.2.2 Estimating Z using catch at age - Catch curve analysis

When catch data are available, total mortality Z can be determined from the decrease in observed number of individuals across the age-structure of the population, which is assumed to be caused by mortality (rather than emigration). The key assumption is that recruitment is constant across years (and hence age classes). In order to estimate Z from catch data, knowledge of the age of individuals is required which can be estimated indirectly using age-length or age-weight conversion equations. A key consideration is in the choice of those age classes fully-selected by the fishery to be included in the estimation of the regression slope (Figure 1). Most catch curves have an ascending part in the youngest age classes due to low gear selectivity, and the slope of the descending limb of the fully selected age classes can be used to calculate – Z.

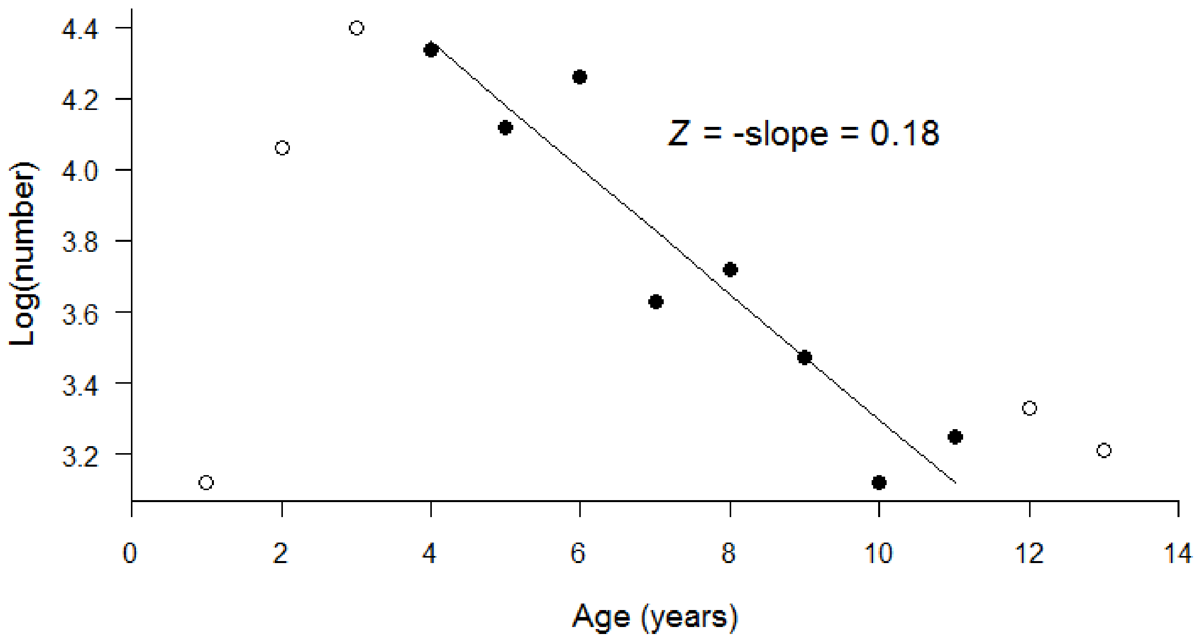

Figure 1. Catch curve from hypothetical catch at age data. The slope is estimated with least squares regression fitted only to fully selected age classes between 4 and 11 (solid circles), while ages one to three, 12, and 13 were not used for the estimation of the slope (open circles).

This approach makes a number of important assumptions: (1) accurate age determination, (2) aged individuals are representative of the population age structure, (3) total mortality is constant through the age classes used to fit the regression, (4) **constant recruitment through the years** (perhaps the most important assumption), and (5) that all age classes are equally as likely to be caught in the fishing gear.

This method is applicable to bycatch when there is knowledge of age or length-age relationships of a species, and the age structure of catch data is likely to represent the age structure of the population. Catch curve analysis can be calculated using the FSA package based on the statistical software language R (R Development Core Team 2010).

1.2.3 Estimating Z using catch at age - Year-class curves

The year-class curve (also known as longitudinal catch-curve analysis) is a method that also estimates total mortality Z, but unlike a catch curve it is fitted to the successive ages of one year class – a cohort - rather than successive year classes at their respective ages in one catch (Cotter 2007). This overcomes the limitation of the key assumption of traditional catch curve analysis – that of constant recruitment. Mortality is calculated from the log Catch Per Unit Effort (CPUE) versus age for a single class cohort, and it is derived from equation (1) taking the form:

$$\log N_{a,c} = \log N_{0,c} + Zage \tag{8}$$

where $N_{a,c}$ is the number (or abundance index) of fish aged *a* from age class c, $N_{0,c}$ is the initial numbers (or abundance) for age class c, and Z_a is total mortality for age a (Equation 8). This is the simplest form of the year-class curve model, however in practice it usually has a few added parameters to account for error and non-linearity in catchability of different age classes:

$$\log N_{a,c} = \log N_{0,c} + Za + \beta \log(a + 1) + \varepsilon_{a,c} \qquad (9)$$

where log (a + 1) is a term added to the model that allows for lower catchability (i.e., adds non-linearity) of younger age classes to survey methods, and $\varepsilon_{a,c}$ is an error term of mean = 0 and variance = σ^2 (see Cotter 2001 for more explanation on how to derive the error term). The year-class curve model can be further specified to account for differences between survey methods by adding an inter-calibration factor S_s for each survey s:

$$\log N_{a,c,s} = \log N_{0,c} + Za + S_s + \beta \log(a + 1) + \varepsilon_{a,c,s} \qquad (10)$$

This method requires catch data for a number of cohorts spanning several years. It also allows for the implementation of differential recruitment (e.g., youngest age classes being under-represented by survey methods) as well as providing an estimate of uncertainty (ε) around the computed value.

The year-class curve analysis makes many of the same assumptions as the previous catch curve model: (1) accurate age determination, (2) aged individuals are representative of the population age structure, (3) total mortality is constant through the age classes used to fit the regression, and (4) that all age classes are equally as likely to be caught in the fishing gear. Year-class curve analysis also assumes that a cohort can be accurately followed between years. The FSA package in R can also compute year-class curves (labeled as longitudinal catch curves).

1.2.4 Partitioning Z into M and F

It is possible to partition Z into M and F when estimates of Z are available for several years with varying annual fishing effort, thus M can be obtained given that:

$$F = q * f \qquad (11)$$

where q is catchability and f is fishing effort. Thus by replacing equation 11 into the equation for Z ($Z = M + F$):

$$Z = M + qf \qquad (12)$$

Which, when fitted to points of Z and f from different years, is an equation of the form of a linear regression with an intercept M and slope = q. This approach is recommended only for used for relatively unexploited stocks.

1.3 INDIRECT METHODS OF ESTIMATING NATURAL MORTALITY M

Even though it is one of the most important parameters in fisheries modelling, instantaneous natural mortality M is usually the least well-estimated one (Vetter 1988). Natural mortality M is typically treated as an overall population or species-level trait and should be considered separately from the survivorship schedule of mortality across age or size classes within a population or species. Broadcast-spawning fishes are typically thought to follow a type III survivorship curve whereby mortality is highest in small size classes and decreases as fish grow larger, due to higher mortalities of earlier life stages and decreasing predation with increasing size. Given that it can be difficult, costly, and time consuming to directly estimate natural mortality rates (M) for marine stocks, it has become a common practice to indirectly derive M

from a number of different published models derived from cross-species comparative analyses. These models are based on fitting regressions through the relationship between estimated and measured M values and a range of life history parameters. Indirect estimates of natural mortality are prone to provide substantial error in their predictions thus propagating error (uncertainty) in these models is key for their effective use (Pascual and Iribarne 1993). Uncertainty from empirical estimates of M comes from three main sources: (1) the quality of life history traits estimated which are used to calculate M for the stock of interest (trait error), (2) the variability of values between stocks which were used to construct the empirical relationships (coefficient error), and (3) uncertainty associated with the nature of the empirical model (model error) (Quiroz et al 2010). Trait error can be propagated by accounting for variability or uncertainty in input life history values for each model (i.e., providing distributions of input values rather than point estimates). Coefficient error can be propagated by providing a distribution of values for each coefficient. In this case it is important to account for the correlation structure of coefficients in a model, given that these are usually highly correlated with each other. Therefore drawing coefficient values should be done from a single multivariate distribution rather than from a number of separate univariate distributions. The function *M.empirical()* in the fish methods package in R (Nelson 2011) computes the values of M, but not the coefficient uncertainties, for most of the indirect models outlined below.

1.3.1 Age-independent methods (average M)

1.3.1.1 Reciprocal of lifespan

Assuming mortality is similar in each age class, the simplest way of estimating natural mortality M is by relating it to the inverse of the maximum age or lifespan ($\alpha_{\max}$). Beverton and Holt originally suggested that $M \sim 1/\alpha_{\max}$. This approach has been generalised to:

$$M \approx \frac{C}{\alpha_{max}} \tag{13}$$

where C is a constant, which has been traditionally set at 3 for blue crab (*Callinectes sapidus*) stock assessments (Hewitt and Hoenig 2005). Hewitt and Hoenig (2005) suggested setting this constant as $C = 4.22$. For example, for a population with a maximum age of 10 years, using the updated value of $C = 4.22$ and equation (3) in order to translate instantaneous mortality into survival, the average proportion of animals dying in each year is: $1 - S = 1 - e^{-4.22/10}$ which equates to 34.4% of the population dying each year on average.

1.3.1.2 Comparative analysis of longevity and mortality by Hoenig (1983)

Using a cross-species comparative analysis from molluscs, cetaceans, and fishes, Hoenig (1983) related M to lifespan (α_{max}) using least squares regression. The first equation is applicable for all three taxa previously mentioned:

$$\log M = 1.44 - 0.982 \log \alpha_{max} \tag{14}$$

When using data from fishes only the equation is:

$$\log M = 1.46 - 1.01 \log \alpha_{max} \tag{15}$$

The Hoenig (1983) model is one of the most commonly used indirect estimators of natural mortality given its sound theoretical basis. It is based on the idea that only a small fraction (around 1.5%) of the population reaches the last year of life (α_{max}), thus it can be used to calculate the average mortality rate that will result in the death of most individuals before reaching the maximum lifespan.

1.3.1.3 Comparative analysis of temperature, VBGF, and mortality by Pauly (1980a)

Pauly's (1980a) methodology uses the von Bertalanffy growth parameters (k, L_∞ or W_∞), as well as mean annual water temperature (T, in °C) to estimate natural mortality in fishes. Equations linking growth, temperature to mortality were estimated from least squares regression fits to comparative data spanning 175 fish stocks. The equation for weight-derived growth parameters is as follows:

$$\log M = -0.2107 - 0.0824 \log W_\infty + 0.6757 \log K + 0.4627 \log T \tag{16}$$

The equation for length-derived growth parameters is:

$$\log M = -0.0066 - 0.279 \log L_\infty + 0.6543 \log K + 0.4634 \log T \tag{17}$$

Pauly's equation has also been widely used for estimating M for a wide range of species, particularly due to the wide availability of von Bertalanffy growth parameters in marine species.

1.3.1.4 Jensen (1996)

By optimization of the tradeoffs between survival and fecundity, Jensen (1996) provided the following equation to calculate M, based on age at maturity (α):

$$M = \frac{1.65}{\alpha} \tag{18}$$

1.3.1.5 Recommendations

There is broad scope of error in all indirect methods of estimating natural mortality. While the Pauly (1980a) method was broadly used shortly after its publication, the Hoenig (1983) equation is more widely used at present for estimating average M. Whenever possible, we recommend using a number of different equations for estimating average M and using a multi-model approach to account for uncertainty in model choice. In its simplest form, this would consist of using a range of values between the lowest and highest estimates of average M for a given stock. Distributions of M value can be produced with this approach is also taking into account other sources of uncertainty (e.g., coefficient error or trait error). Multi-model approaches can be applied using Monte Carlo simulation or a Bayesian framework.

1.3.2 Size-dependent methods

Size-dependent models calculate M based on the observation that, in general, natural mortality rate decreases with size due to reduced predation. Whereas some methods use von Bertalanffy growth parameters to estimate size-dependent natural mortality (Chen and Watanabe 1989, Gislason et al. 2010), others calculate natural mortality as a function of weight (Peterson and Wroblewski 1984, McGurk 1986, Lorenzen 1996). It is important to know that both these weight-based methods for estimating M exhibit power relationships consistent with metabolic theory of ecology where biological rates, such as mortality, should scale with body mass to the power of -1/4 (Brown et al. 2004).

1.3.2.1 Chen and Watanabe (1989)

Chen and Watanabe (1989) modelled M based on the von Bertalanffy growth parameters (k and t_0) using two separate functions: an age-specific one for the ages prior to the onset of senescence ($t \leq t_m$) and an age-independent model for ages after the onset of senescence ($t \geq t_m$). This model describes a bathtub (U-shaped) mortality curve consisting on decreasing mortality with increasing size which increases at the end of the organism's lifespan due to senescence. The two part model is as follows:

$$M(t) = \begin{cases} \dfrac{k}{1-e^{-k\,(t-t_0)}}, & t \leq t_M \\ \dfrac{k}{a_0 + a_1(t-t_M) + a_2(t-t_M)^2}, & t \geq t_M \end{cases} \tag{19}$$

where the upward mortality trend observable in this model is provided by the following three a coefficients:

$$\begin{gathered} a_0 = 1 - e^{-k(t_M - t_0)} \\ a_1 = ke^{-k(t_M - t_0)} \\ a_2 = \frac{1}{2}k^2 e^{-k(t_M - t_0)} \end{gathered} \tag{20}$$

and the point at which the reproduction and senescence phases meet and mortality begins to increase (t_M), thus providing the "bathtub" shaped curve, is defined as:

$$t_M = -\frac{1}{k}\ln\left(1 - e^{kt_0}\right) + t_0 \tag{21}$$

1.3.2.2 Gislason et al.(2010)

Another methodology to estimate length-based mortality in marine and brackish water fishes was recently developed by Gislason et al. (2010), which builds upon the comparative analysis developed by Pauly (1980a). Based on a thorough data selection process which eliminated all but the most robust estimates of M the comparative analysis of 168 estimates of M from 70 publications is as follows:

$$\log M_L = 0.55 - 1.61 \log L + 1.44 \log L_\infty + \log k \tag{22}$$

where M_L is mortality at length L, and k and L_∞ are the von Bertalanffy growth parameters for the stock in question.

The Gislason et al. (2010) model has been adopted since its publication (e.g., Le Quesne and Jennings 2012). However, while this equation realistically shows that mortality declines ontogenetically with increasing size, it does not realistically capture the lower overall mortality observed in larger species (compared with smaller ones).This anomaly led to Charnov et al. (in press) to re-analyze the same data but from a more mechanistic basis founded in life history optimality theory. These authors conclude that the coefficients for L and L_∞ are not statistically different and find that a common exponent of 1.5 provides a better fit to the data and conclude that the Gislason et al. (2010) equation can be generalized as:

$$M = \left(\frac{L}{L_\infty}\right)^{-1.5} \times k \tag{23}$$

Furthermore, this equation is more consistent with life history optimisation and tradeoffs than the phenomenologically derived Gislason et al. (2010) one.

1.3.2.3 Peterson and Wroblewski (1984)

Peterson and Wroblewski (1984) created a size-specific equation for estimating mortality in pelagic marine fishes using weight (in grams):

$$M_W = 1.92\, W^{-0.25} \tag{24}$$

where M_W is natural mortality rate at weight W in grams. Their analysis is based on the idea that predation is the chief process driving natural mortality. However, their model underestimated mortality of the early larval stages of pelagic fishes. McGurk (1986) noted this, and came up with an updated model to predict egg and larval natural mortality, discussed below.

1.3.2.4 McGurk (1986)

By acknowledging that patchiness of eggs and larvae can have an effect on their mortality, McGurk (1986) proposed an equation based on the work of Peterson and Wroblewski (1984) that estimates natural mortality for eggs and larvae of pelagic fish for weight (in grams):

$$M_W = 0.0803\, W^{-0.85} \tag{25}$$

where M_W is natural mortality rate at weight W in grams. This equation should not be extrapolated to adult fishes; in that case equation (21) provides a better estimate of M (McGurk 1986).

1.3.2.5 Lorenzen (1996)

Lorenzen derived an equation for estimating M in fish based on their individual weight, using a comparative analysis data from 308 estimates of M from fish in both freshwater and marine ecosystems.

$$M_W = 3.00\, W^{-0.288} \tag{26}$$

where M_W is natural mortality rate at weight W in grams. When analysing only values from marine fishes (n = 113), the equation is as follows:

$$M_W = 3.69\, W^{-0.305} \tag{27}$$

Lorenzen’s (1996) equations explicitly exclude egg and larval stages from their analyses, thus they should not be used to predict natural mortality for those stages.

1.3.2.6 Recommendations

As with size-independent models, quantifying performance of indirect estimates of mortality can be difficult due to the paucity of direct estimates of *M* in the literature. If there is enough life history data available, we recommend the use of a multi-model approach to account for uncertainty in model selection. A multi-model approach accounts for model uncertainty and provides a range of values for *M* instead on a single deterministic estimate with no uncertainty associated with it.

2 ESTIMATING SUSTAINABLE FISHING MORTALITY RATES

In this section we highlight three methods that use life history theory to calculate a series of target and limit reference points for fishing mortality, including: (a) Euler-Lotka derived limit reference points (F_{crash}, F_{extinct}), (b) yield-per-recruit target reference points ($F_{\max}$, $F_{0.1}$), and (c) spawner per recruit-derived target reference points (F_{40}).

2.1 BROAD GENERALIZATIONS

The simplest generalization for estimating sustainable harvest rates is derived from observations by Tiurin (1962) where, in the absence of density dependence, the fishing mortality rate that will provide maximum sustainable yield (F_{msy}) equals the natural mortality rate *M*:

$$F_{MSY} = M \tag{28}$$

From this equation, it follows that the maximum sustainable yield is a proportion of virgin biomass B_0. For logistic growth with linear density-dependence in births and deaths this takes the form:

$$B_{MSY} = 0.5\ B_0 \tag{29}$$

These extremely broad generalization has been widely criticized, with numerous authors pointing out that equating F_{msy} to M is extremely risky, while some suggesting to use 0.8Minstead of 1M (Thompson 1993). Gulland (1970) used the two previous equations in order to obtain a generalized equation for catch at *MSY*:

$$MSY = 0.5\ M\ B_0 \tag{30}$$

This equation is commonly used as a proxy for sustainable harvest rates. For example, in the Depletion-Corrected Average Catch methodology (DCAC, section 4.4) they use a more conservative version of this equation as an approximation of potential yield at MSY using a coefficient of 0.4 instead of 0.5 of the virgin biomass B_0.

2.2 $\mathbf{F_{CRASH}}$

The fishing mortality that will make a population become extinct in the long term (F_{crash}) is a parameter that is a useful upper limit for fishing mortality of a stock. Theoretically, it is equivalent to F_{extinct} (section 3.5.3) but is derived from different analyses. The simplest approximation for F_{crash} is an extension of equation 28 above, where F_{crash} is twice F_{MSY} so that:

$$F_{MSY} = 2\ M \tag{31}$$

This method, albeit very broad and prone to large uncertainties, is still being used for current fisheries assessment models (Zhou and Griffiths 2008).

A second proxy for F_{crash} can be obtained from an equation derived from a delay-difference model by Deriso (1982):

$$u_{upper} \leq \sqrt{\frac{1}{\rho l^2 rv}} \tag{32}$$

where u_{upper} is the upper bound for exploitation rate (which was considered equivalent to $\mathrm{u}_{\mathrm{crash}}$, with F_{crash} = - log(1 - u_{upper}) , ρ is the Brody's growth coefficient (equivalent to von Bertalanffy k), l is the annual natural survival fraction for adults [$l = \mathrm{e}^{(-M)}$], and $rv = [(1-\rho l)(1-l)]^{-1}$.This proxy was also used by Zhou and Griffiths (2008) assessment model.

2.3 YIELD-PER-RECRUIT MODELS

Yield-per-recruit models (YPR) are based on the idea that the total biomass of a cohort increases as individual fish grow in weight but mortality in numbers mean that the average yield per individual recruit reaches a maximum values at an intermediate length. Subjecting these cohorts to different rates of age-specific fishing mortality can give differing overall yield. This approach ignores recruitment; instead the calculations begin by applying growth, and mortality to a fixed number of individuals. The method requires a growth curve, age at first capture, and an idea of for the mortality schedules for each cohort.

2.3.1 F_{max} and $F_{0.1}$

The primary target reference point obtainable from yield-per-recruit models is F_{max}, which is the fishing mortality at which yield is maximized, and should be equivalent to MSY. Due to the limit nature of F_{max}, stochastic processes in catch, recruitment, and mortality can drive stocks to be overfished even when fished at F_{max}. Thus a more conservative reference point: $F_{0.1}$ was suggested, which is the fishing mortality at which the increase in yield per unit of fishing mortality increases at 10% of its initial yield (i.e., yield at lowest levels of F). (*Assumptions, caveats and performance will be expanded upon later*)

2.4 SPAWNER PER RECRUIT MODELS

Spawner per recruit models are an extension of yield-per-recruit models which take into account recruitment dynamics while assessing catch and assess the effect of fishing on the spawning potential of a stock (Gabriel et al. 1989). Spawner per recruit models are based in the spawning stock biomass (SSB) equation proposed by Beverton and Holt (1957), which was then parameterized by Pope et al. (2000) as:

$$SSB = R \cdot e^{[-M(t_c - t_r) - Z(t_\alpha - t_c)]} \cdot a \cdot L_\infty^3 \cdot \sum_{i=0}^{3} U_i \left[\frac{(1-h)^i}{1 - e^{(-Z-ik)}} \right] \tag{33}$$

where SSB is the spawning stock biomass of a year class of R recruits that recruit at age t_{r}, are then captured at age t_{c} and mature at age t_{a}, M is instantaneous natural mortality, Z is instantaneous total mortality, and U_{i} is the cubic expansion to convert from length to weight and U_{i} = +1, -3, +3, -1 for *i* = 0, 1, 2, 3, respectively. From this general equation a series of target and limit references points can be calculated.

2.4.1 $F_{\%SPR}$

By investigating the relationship in stock-recruitment curves between optimum F and life history parameters, Clark (1991) noted that a yield just under MSY could be achieved by applying a fishing pressure which would reduce the biomass per recruit to around 35% of its unfished level.

The ratio between biomass per recruit (SSB) and virgin biomass per recruit is known. This Spawning Potential Ratio (SPR) can be defined as:

$$SPR = \frac{SSB_{exploited}}{SSB_{unexploited}} \qquad (34)$$

where $SSB_{\text{exploited}}$ and $SSB_{\text{unexploited}}$ are the spawning stock biomass at the exploited and virgin levels, respectively. Values ranging from F_{35} to F_{40} are thought to represent a reliable proxy for F_{MSY} (Clark 1991, Clark 1993, Mace 1994, Mace and Sissenwine 2003, Ault et al. 2008), while values ranging from F_{20} to $F_{30}$are thought to represent recruitment overfishing thresholds (Goodyear 1993, Rosenberg et al. 1994). Restrepo et al. (1998) suggested using proxies ranging from F_{35} for highly resilient stocks to F_{60} for stocks with low productivity (such as elasmobranchs).

2.4.2 F_{jeopardy} (F_{φ})

Based on the spawner per recruit framework, Pope (2000) came up with a model to calculate the fishing mortality that will reduce the spawning potential ratio (SPR) below certain threshold or jeopardy level, or $F\varphi$. Here, Pope arbitrarily chose a jeopardy level, $\varphi$of 5% corresponding to a 95% decline in SPR. This approach is mathematically equivalent to the F_{40}approach originally proposed by Clark (1991). However, $F\varphi$ is meant to be used as a risk measure or limit reference point instead of a safe fishing level or target reference point, which is the objective of F_{40}. The threshold suggested by Pope is φ, thus $F\varphi = F_{05}$, which is a limit threshold, rather than a target one, like F_{40}. The F_{jeopardy} model is:

$$\varphi = 100 \cdot \{-F_{\varphi} \cdot (t_{\alpha} - t_c)\} \cdot \frac{\sum_{i=0}^{3} U_i \left[\frac{(1-h)^i}{1-e^{(-Z-ik)}}\right]}{\sum_{i=0}^{3} U_i \left[\frac{(1-h)^i}{1-e^{(-M-ik)}}\right]} \qquad (35)$$

where t_c is age at capture, t_{α} is age at maturity, M is instantaneous natural mortality, Z is instantaneous total mortality, and the cubic expansion of the VBGF to convert from length to weight is U_i = +1, -3, +3, -1 for i = 0, 1, 2, 3, respectively.

2.5 USE OF LIFE HISTORY RELATIONSHIPS TO PARAMETERIZE YIELD MODELS

Relationships among life history parameters can be used to predict unknown parameters such as natural mortality rate, and thus, can be useful to predict vital rates in situations where there is minimal data. These correlations are derived from life history theory; an area of study whose primary premise is that the biological trait of any given population is constrained by evolutionary trade-offs. These life history trade-offs, also known as life-history invariants, were first discovered by Beverton and Holt (1959) half a century ago. They noted that the ratios between certain life history parameters were relatively constant amongst a given taxon (i.e., invariant ratios). The calculation and use of invariants as predictive tools has been increasingly investigated in recent years (Charnov 1993, Jensen 1996, Frisk et al 2001, amongst others). The most commonly-used example of its use comes from the equations used for the indirect estimation of natural mortality (e.g., Pauly 1980a, Chen and Watanabe 1989, Jensen 1996, Gislason et al 2010). Aside for predicting natural mortality, invariant relationships have been created to predict reproductive effort (Charnov 2008, Gislason et al. 2008), age at maturity (Gislason et al. 2008), and growth coefficients (Le Quesne and Jennings 2012), amongst others. Most assessments of the status of a fish population will use, to varying degrees, estimates derived from trends between life history parameters.

These methods are widely applicable to any taxa from which basic life history data is available. In the absence of such equations, sufficient life history parameters need to be gathered in order to calculate the relationships between them.

As mentioned above, most of the tools for estimating natural mortality indirectly come from life history correlates. Furthermore, correlates have been used to completely parameterize demographic models in data-poor situations, including elasmobranchs (Frisk et al. 2001) and for target and bycatch species in research trawl surveys(Le Quesne and Jennings 2012) gathered a number of life-history relationships (Table 1) and applied them to most of species caught (target and bycatch) North Sea bottom trawl fishery in order to parameterize an age structured yield-per-recruit (YPR) model using only known maximum size.

Table 1. Life history relationships used by Le Quesne and Jennings (2012) to parameterize age-structured spawner per recruit models using only maximum size.

	Unit	Relationship	Source
Function			
Asymptotic length	cm	$\log_{10}(L_\infty) = 0.044 + 0.9841 * \log_{10}(L_{max})$	Froese & Binohlan (2000) equation 5
Weight	g	$W_t = 0.01 * L_t^3$	Gislason et al. (2008) equation 14
Natural mortality rate	per year	$M_t = \exp(0.55 - 1.61 * \log(L_t) + 1.44 * \log(L_\infty) + \log(k))$	Gislason et al. (2010) equation 2
Relative reproductive output		$R = L_t^{3.75}$	Le Quesne & Jennings (2012) appendix S1
Teleosts			
von Bertalanffy *k*	per year	$k = 2.15 * L_\infty^{-0.46}$	Le Quesne & Jennings (2012)
Length at first maturity	cm	$L_{mat} = 0.64 * L_\infty^{0.95}$	Gislason et al. (2008) Table 1
Elasmobranchs			
von Bertalanffy *k*	per year	$k = -0.17 * \log(L_{max}) + 0.97$	Frisk et al. (2001) Fig. 6
Length at first maturity	cm	$L_{mat} = 0.7 * L_{max} + 3.29$	Frisk et al. (2001) Fig. 1

This approach is very desirable due to its potential for very small data requirements and simplicity of use. These methods are very flexible in that they allow for the parameterization of even the most data-thirsty models based on life history parameters by predicting these using invariant relationships, thus allowing for a quick analysis of a vast number of species.

By modeling life history parameters, these approaches are usually accompanied by large uncertainties in their outputs which are seldom accounted for. A commonly overlooked source of uncertainty in these models comes from the coefficients in the equations used to predict life history relationships: rather than being point estimates these always vary (and covary), and as such, their uncertainty should be propagated throughout the hierarchical framework (Pardo et al. 2010). Also, these models are based on the main trends observed between life history parameters and as such are unable to predict exceptions (Le Quesne and Jennings 2012).

2.6 DEMOGRAPHIC APPROACHES

2.6.1 Euler-Lotka equation

The Euler-Lotka population equation is the basis of most modern demographic analyses. It is based on the concept that in a stable population, based on survival and reproductive rates varying with ontogeny, an individual produces on average one offspring to replace itself:

$$\sum_{x=\alpha}^{w} l_x m_x e^{rx} = 1 \tag{36}$$

where l_x is survival at age x, m_x is annual reproductive output at age x, and r is the intrinsic rate of population increase.

2.6.2 Au and Smith (1997) rebound potential

From this equation, Au and Smith (1997) created a simplified version in order to estimate rebound potential r which accounting for density dependence:

$$e^{-(M+r)} + l_\alpha b e^{-rx}\left[1 - e^{-(M+r)(w-a+1)}\right] = 1 \tag{37}$$

where α is age at maturity, w is maximum reproductive age, M is adult instantaneous natural mortality, b is average number of female pups per adult female, and l_α is pre-adult survival. If not obtainable through other means, pre-adult survival can be defined as:

$$l_\alpha = e^{-M(w-a)} \tag{38}$$

Furthermore, in order to obtain an estimate of r that accounts for density dependence, the modified Euler-Lotka equation is solved for Z instead of M, and assuming $Z = M + F = 2M$ when the stock is around MSY it should be stable, r is set to zero:

$$e^{-(Z)} + l_{\alpha,Z}\left[1 - e^{-Z(w-a+1)}\right] = 1 \tag{39}$$

Now, a new estimate of pre-adult survival $l_{\alpha,Z}$ is obtained, which then replaces $l_\alpha$in the original equation in order to estimate a depleted stock rebound potential r_Z. Thus this growth potential $\underline{r_Z}$ can be defined as the minimum possible fishing mortality that will maintain a population, albeit at extremely low biomass. Thus, it is used as a limit reference point rather than a target one.

2.6.3 $F_{extinct}$

The Euler-Lotka equation is typically used to calculate r the intrinsic rate of population increase. In the absence of density dependence r is the same as F_{extinct}, the fishing mortality that will drive the population to extinction. Hence this approach can be used to calculate F_{extinct}, or the fishing mortality that will drive a species to extinction (Myers and Mertz 1998):

$$b = e^{\left(F_{extinct}(\alpha_{mat} - \alpha_{sel} + 1)\right)}\left(1 + e^{-(M + F_{extinct})}\right) \tag{40}$$

where b is annual reproductive output α_{mat} is age at maturity, α_{sel} is the age of selectivity into the fishery, and M is natural mortality. Annual reproductive output b is calculated from litter size (l) and interbirth interval (i) for females only:

$$b = \frac{l}{i} \times 0.5. \tag{41}$$

This equation ignores density dependence and hence is most applicable to species with low rates of reproduction or depleted stocks, and as such it can be used as a proxy for $r_{\max}$, (J. Carlson, *pers. comm.*). Thus, parameters used as input into the equation also need to be derived from depleted scenarios.

2.6.4 **Recommendations**

Demographic approaches provide useful limit reference points (i.e., the minimum sustainable levels of mortality) for species which have been severely exploited as they provide an idea of the intrinsic rate of increase in the absence of density dependence. They can be easily calculated with basic life history information, and allow for quick comparison between species, which is why they have been used in ecosystem-based approaches (Simpfendorfer et al. 2008, see section 5.4).

3 ESTIMATING SAFE BIOLOGICAL LIMITS FROM CATCH DATA

3.1 ORCS REPORT METHODS

Only Reliable Catch Stocks, or ORCS, is a classification of a fishery for which only catch data and possibly a few parameters derived from life history relationships are available (Berkson et al. 2011). A recent review of methods of assessing ORCS was compiled by Berkson et al. (2011), and the following section summarize these methods with particular focus on their application to bycatch stocks. The four methods outlined below are ordered from least data requirements to greatest data needs.

3.2 SCALAR MULTIPLIED BY THE ABC OF THE TARGET SPECIES, WHEN ORCS ARE BYCATCH SPECIES

In certain data-poor fisheries, bycatch quotas (in the form of Acceptable Biological Catch, ABC) are calculated as a proportion of the targeted stock’s ABC. The ABC of the target is multiplied by a scalar value that is determined by expert judgment and usually is precautionary in nature. The only data required is the quota for the target species. Scalars that have been used in fisheries have ranged between 5 and 16% of the target fishery (Berkson et al. 2011). Monitoring programs (e.g., estimates of species composition in landings, observer data, and fishery-independent surveys) are required when using this approach to ensure the sustainable management of bycatch species because the appropriate scalar cannot be known before it is applied.

This method is as simple as it is uncertain in its outcome. However, when applied to species or species groups that are experiencing only minimal fishing-related mortality, it is likely that the risk of overfishing is low (Berkson et al. 2011).

3.3 NATURAL MORTALITY-BASED APPROACH

This method, developed for ORCS in New Zealand (Anon 2009) is a variant of the scalar approach. It is based on the following formula:

$$MCY = c \times Y_{ave} \tag{42}$$

where MCY is maximum constant yield, c is the natural variability factor, and Y_{ave} is the average catch over a specified period of time. The relationship between natural variability factor c and natural mortality as used in New Zealand is defined in Table 2. Stocks with higher natural mortality are expected to have fewer age classes, thus a lower natural variability factor coefficient is assigned to counteract the effect of greater biomass fluctuations derived from fast life histories. If Y_{ave} is determined from a period of time when the stock was fully exploited, then $Y_{\text{ave}} \approx MAY$ (Maximum Average Yield) and should provide a good estimate of MCY. If on the other hand, the stock was under-exploited, a conservative estimate of MCY is obtained.

Table 2. Values for the natural variability factor c as determined by natural mortality values (M) based on method developed for New Zealand stocks (Anon 2009).

M	***c***
< 0.05	1.0
0.05 - 0.15	0.9
0.15 - 0.25	0.8
0.26 - 0.35	0.7
> 0.35	0.6

An adequate period of time from which to base Y_{ave} estimates is required, as is knowledge of the fishery. The period upon which Y_{ave} is based should ideally contain no systematic changes in fishing mortality, no systematic changes in fishing effort if it correlates with M, and no systematic changes in catch. The period should also be at least half the exploited lifespan (i.e., the number of year classes which are removed by the fishery) of the species being assessed. If the period shows a systematic increase in catch then it will result in an under-estimate of *MCY*; the method will produce an overestimate if the trend is decreasing. An estimate of natural mortality is also required to assign a value for c (See table 2).

This approach assumes that the stock is stable and that the fishery is at or near sustainable levels of removal. Thus, for fisheries where effort is highly variable or the stock is being overfished, this approach might not be appropriate.

3.4 DEPLETION-CORRECTED AVERAGE CATCH (DCAC)

When a reliable long-term catch time series are available, sustainable catch can be estimated using a methodology developed by MacCall (2009), based on the work by Restrepo et al. (1998). This approach consists in accounting for increases in catch that result from reduction in standing stock, and as the name implies, correcting catch values accordingly. This methodology provides estimates of a sustainable yield, rather than MSY, which might be of importance to some fisheries managers.

By assuming that biomass at MSY is a proportion of virgin biomass $B_{\text{MSY}} = 0.4B_0$, and that F_{MSY} is proportional to natural mortality (M), $F_{\text{MSY}} = cM$, where c is a tuning adjustment, the potential maximum sustainable yield, in this case called potential yield, Y_{pot}, is a more conservative equivalent of equation 30 and can be expressed as:

$$Y_{pot} = 0.4cMB_0 \tag{43}$$

A one-time windfall harvest can be taken to deplete a stock from B_0 to B_{msy}, thereafter only a smaller sustainable yield Y_{pot} can be taken. Assuming also that windfall harvest W can be expressed as the difference in biomass between the first and last years, i.e., $W = B_{\text{FYR}} - B_{\text{LYR}}$, relative decline in abundance Δ, can be expressed as:

$$\Delta = \frac{B_{FYR} - B_{LYR}}{B_0} \tag{44}$$

Therefore by replacement, the ratio W/Y_{pot} which expresses the magnitude of the windfall harvest relative to a single year of potential yield, and forms the basis for depletion correction, can be expressed as:

$$\frac{W}{Y_{pot}} = \frac{\Delta B_0}{0.4cMB_0} = \frac{\Delta}{0.4cM}, \tag{45}$$

thus removing virgin biomass (a “data rich” parameter) from the equation. By assuming that on average each year one unit of annual sustainable yield is produced, the resulting catch can be expressed as the sum of two components; one derived from sustainable annual production, and the other from a one-time windfall harvest. Therefore, for a catch series C of length n, the yield that could potentially have been sustained (Y_{sust}) during that period can be calculated by:

$$Y_{sust} = \frac{\sum C}{n + W/Y_{pot}} \tag{46}$$

where ΣC is the total cumulative catch and $n = \text{LYR} - \text{FYR} + 1$.

Aside from catch data, which does not need to be comprehensive, knowledge of a distribution of values for B_{MSY} relative to virgin biomass (B_0) is required. A size-independent estimate of natural mortality M, usually coming from indirect estimates derived by life histories is also needed (i.e., methods detailed in section 2.3.1). DCAC also requires an estimate of the ratio of F_{MSY} to M (c), which is commonly between 0.6-1.0 (MacCall 2009). This value is hard to obtain, and is usually derived from expert opinion.

This approach is better suited for bycatch species whose catch has been monitored for an extended period of time. Also, this method has been shown to be reliable only for species with low mortality rates ($\leq 0.20\ \text{yr}^{-1}$), which are usually slow growing and late maturing, as the depletion correction factor becomes negligible with higher M values. This methodology has the assumption of unbiased catch statistics. It does not assume constant stock abundance; B is explicitly allowed to vary. The requirement of expert opinion to set a ratio of F_{MSY} to M might slightly bias results. The DCAC model assumes that the ecosystem and fishery dynamics do not change over time, which might not be the case with developing fisheries or severely depleted stocks.

Aside from being a methodology that has low data requirements, DCAC allows for easy propagation of uncertainty using Monte Carlo simulation, and thus provides a probability distribution of sustainable yield. DCAC has been used by Pacific Fishery Management Council (PFMC) in the U.S. to set overfishing limits for six species of rockfish (*Sebastes* spp.) and the tope shark *Galeorhinus galeus* (Berkson et al. 2011).The NOAA’s Fisheries Toolbox developed by the National Marine Fisheries Service includes a program for performing DCAC assessments (http://nft.nefsc.noaa.gov/Download.html).

3.5 DEPLETION-BASED STOCK REDUCTION ANALYSIS (DB-SRA)

Depletion-Based Stock Reduction Analysis (DB-SRA, Dick and MacCall 2011) is a recent extension of the DCAC framework, which is incorporated into a stochastic stock reduction analysis (SRA) framework (Walters et al 2006). The DB-SRA incorporates complete stock dynamics, and as such, has slightly higher data requirements than DCAC.

The DB-SRA model requires much more comprehensive catch data than DCAC, which needs to encompass long-term abundances (i.e., before the stock was exploited) in order to have a reliable estimate of B_0. Knowledge of a distribution of values for B_{MSY} relative to B_0 is also required. A size-independent estimate of natural mortality M, usually coming from indirect estimates derived by life histories is also needed (i.e., methods in section 2.3.1). DB-SRA also requires a distribution of values for the ratio F_{MSY}/M, which is commonly between 0.6-1.0 (MacCall 2009). This value is hard to obtain, and is usually derived from expert opinion. A value for age at maturity for the stock is required for the surplus production model that is incorporated into DB-SRA.

Aside from the DCAC model previously explained, DB-SRA includes a two-part production model: one being a standard Pella-Tomlinson-Fletcher (PTF) generalized production model (Fletcher 1978) for high values of B_{MSY}/B_0, while a hybrid Schaefer model based on McAllister et al (2000), for low B_{MSY}/B_0 as the PTF model produces excessive productivity estimates at low biomasses (Fletcher 1978). This does not occur in the hybrid Schaefer model due to its linear rather than negative exponential nature.

The DB-SRA framework used Monte Carlo simulation to assess uncertainty in parameters. When parameters are drawn for the value of B_{MSY}/B_0, which defined as B_{mnpl}:

$$B_{mnpl} = \frac{B_{MSY}}{B_0} \tag{47}$$

its value determines which type of production model is used. If $B_{\mathrm{mnpl}} > 0.5$, the standard Pella-Tomlinson-Fletcher (PTF) generalized production model (Fletcher 1978) is used, and has the form of:

$$P = gm\left(\frac{B_{t-\alpha}}{B_0}\right) - gm\left(\frac{B_{t-\alpha}}{B_0}\right)^n \tag{48}$$

where P is latent annual production, B_0 is virgin biomass, m is MSY, and n is the skewness parameter. Skewness n is calculated by solving:

$$B_{mnpl} = n^{1/(1-n)} \tag{49}$$

g is calculated from:

$$g = \frac{n^{\frac{n}{n-1}}}{n-1} \tag{50}$$

and m is calculated as $m = U_{\mathrm{msy}} * B_{\mathrm{mnpl}} * B_0$, where U_{msy} is the annual exploitation rate:

$$U_{msy} = \left(\frac{F_{msy}}{F_{msy} + M}\right)(1 - e^{-(F_{msy}+M)}) \tag{51}$$

where F_{msy} is calculated by the product between the draws from natural mortality M and the F_{msy}/M ratio ($F_{\mathrm{msy}} = M(F_{\mathrm{msy}}/M)$).

When $B_{\mathrm{mnpl}} < 0.5$, then a modification of the hybrid production model of McAllister et al. (2000) is used, thus the corresponding Schaefer model is:

$$P(B_{t-\alpha} < B_{join}) = B_{t-\alpha}\left(\frac{P(B_{join})}{B_{join}} + c(B_{t-\alpha} - B_{join})\right) \tag{52}$$

where the slope of the Schaefer model (c) is:

$$c = (1-n)gmB_{join}^{n-2}B_0^{-n} \tag{53}$$

with n, g, and m as above. The value for the join-point B_{join} (i.e., the point where the hybrid Schaefer model intersects the PTL model) is set depending on B_{mnpl}:

if $B_{\mathrm{mnpl}} < 0.3$, $B_{\mathrm{join}}/B_0 = 0.5B_{\mathrm{mnpl}}$;

if $0.3 < B_{\mathrm{mnpl}} < 0.5$, $B_{\mathrm{join}}/B_0 = 0.75B_{\mathrm{mnpl}} - 0.075$.

The model, which each parameter draw from the Monte Carlo simulation is then solved for B_0, from which the delay-difference equation is used to estimate time series of abundances:

$$B_t = B_{t-1} + P(B_{t-a}) - C_{t-1} \tag{54}$$

Where C is catch, B_{t} is biomass at time t, and P is latent annual productivity. The initial estimated value of B_0 is then adjusted until the value of B_{T}, (which is the biomass at time T, where T is a specific year with does not have to be the final year in the time series) satisfies the given value of relative depletion level B_{T}/B_0. If successful ($B_{\mathrm{t}} > 0$ for all t), then management quantities can be calculated for the iteration of initial values:

$B_{\mathrm{msy}} = K\ (B_{\mathrm{msy}}/K)$

$F_{\mathrm{msy}} = M\ (F_{\mathrm{msy}}/M)$

MSY = $B_{\mathrm{msy}} * U_{\mathrm{msy}}$

$C_{\mathrm{Fmsy}} = U_{\mathrm{msy}} * B_{\mathrm{t}}$ (equal to overfishing Limit, OFL)

Therefore, when a large number of Monte Carlo simulations have been run, the empirical distributions of these values can be computed. This framework allows for the easy propagation of uncertainty in parameters by drawing them from specified distributions.

The DB-SRA approach accounts for major sources of uncertainty by using distributions rather than point estimates for input parameters. Therefore it provides a more robust analysis than DCAC at the cost of higher data requirements. The performance of DB-SRA has been compared with that of complete stock assessments for data-rich stocks, and this research suggests the models are effective at estimating sustainable yields for data-poor stocks (Dick and MacCall 2011).

3.6 RECOMMENDATIONS

Berkson et al. (2011) recommended the use of DB-SRA when catch data encompasses pre-exploitation levels. In the absence of catch data of such quality, the use of DCAC was suggested. When only recent data is available for a stock that has been fully exploited for the duration of data collection (i.e., stable catch and effort), the natural mortality-based approach is recommended. When no other options are applicable, the scalar approach should be used.

4 OTHER FRAMEWORKS FOR DATA POOR FISHERIES ASSESSMENTS

4.1 PRODUCTIVITY AND SUSCEPTIBILITY ANALYSIS (PSA)

Productivity and Susceptibility Analysis (PSA) is a priority-setting framework in which species of concern are ranked based on two characteristics: their susceptibility to capture and mortality, and their productivity (i.e., their capacity to recover after depletion) (Stobutzki et al. 2001).

Susceptibility is defined by criteria such as catchability, post-handling survival, and range overlap with the fishery. Productivity is defined by criteria such as maximum size, number of eggs produced, and probability of breeding before capture. In one case, a quantitative measure of productivity was used (Simpfendorfer et al. 2008, section 5.4). See Table 3 for an example set of criteria for each characteristic. Each criterion is given a ranking from 1 to 3, with 1 relating to high productivity or low susceptibility (i.e., low risk) and 3 relating to low productivity or high susceptibility (i.e., high risk). Each criterion is given an importance score based on expert opinion, and the total score for each characteristic is the weighted average of that characteristic's associated criteria.

$$S_i = \frac{\sum_{j=1}^{n} w_j R_i}{\sum_{j=1}^{n} w_j} \tag{55}$$

Where S_i is the total susceptibility or productivity ranks for species i, w_j is the weighting for criterion j, R_i is the rank of species i for criterion j, and n is the number of criteria on each axis (Stobutzki et al. 2001). The productivity and susceptibility scores are then plotted on an x-y axis, and the distance to the origin can be used as an index of relative risk. See Figure 2 as an example.

Productivity and Susceptibility Analyses have been widely applied in Australia (Stobutzki et al. 2001; 2002) and the U.S. (Patrick et al. 2009) for data poor situations, and have also been integrated as part of other frameworks, such as Ecological Risk Assessment for the Effects of Fishing, ERAEF (Hobday et al. 2011).

Table 3.Criteria used to assess susceptibility and productivity (recovery) for bycatch species in trawling (redrawn from Stobutzki et al. 2001).

Criteria score	*Weighting*	*Rank*		
		1	*2*	*3*
Susceptibility				
Water column position	3	Demersal or benthic	Benthopelagic	Pelagic
Preferred habitat	3	Soft or muddy sediments or prawn trawl grounds	Soft or muddy sediments but also other habitats (e.g. reefs and estuaries)	Habitats outside prawn trawl grounds
Survival	3	Probability of survival ≤ 33.3%	33.3% < probability of survival ≤ 66.6%	Probability of survival > 66.6%
Range	2	Species range ≤ 3 fishery regions	3 fishery regions < species range ≤ 6 fishery regions	Species range > 6 fishery regions
Day/night catchability	2	Higher catch rate at night	No difference between night and day	Higher catch rate in the day
Diet	2	Known, or are able to feed on commercial prawns	Not known to feed on commercial prawns but feeds on other benthic or demersal organisms	Feeds on pelagic organisms
Depth range	1	Less than 40 m	Not applicable	Deeper than 40 m
Recovery				
Probability of breeding	3	Probability of breeding before capture < 50%	Probability of breeding before capture not significantly different	Probability of breeding before capture > 50%
Maximum size	3	Maximum size < 1066 mm	813 mm < maximum size ≤ 1066	Maximum size < 813 mm
Removal rate	3	Removal rate > 33.3%	33.3% < removal rate ≤ 66.6%	66.6% ≤ removal rate
Reproductive strategy	2	Bear live young or brood young	Guard eggs and/or young	Broadcast spawners
Hermaphroditism	1	Hermaphrodites	Not applicable	Dioecious
Mortality index	1	Mortality index > 3.44	1.88 < mortality index ≤ 3.44	Mortality index ≤ 1.88

PSA does not provide a quantitative estimate of a reference point that can be used as a biological removal target; it is primarily a tool to quickly rate risk in data-poor populations so that further attention may be focused on those species which are under the highest risk. It does require expert opinion in order to assign weighting of each criterion and to score subjective criteria. As such, estimates of removal rates and catchability are highly subjective and prone to bias (Stobutzki et al. 2001). The NOAA's Fisheries Toolbox developed by the National Marine Fisheries Service includes a program for performing PSA assessments (http://nft.nefsc.noaa.gov/Download.html).

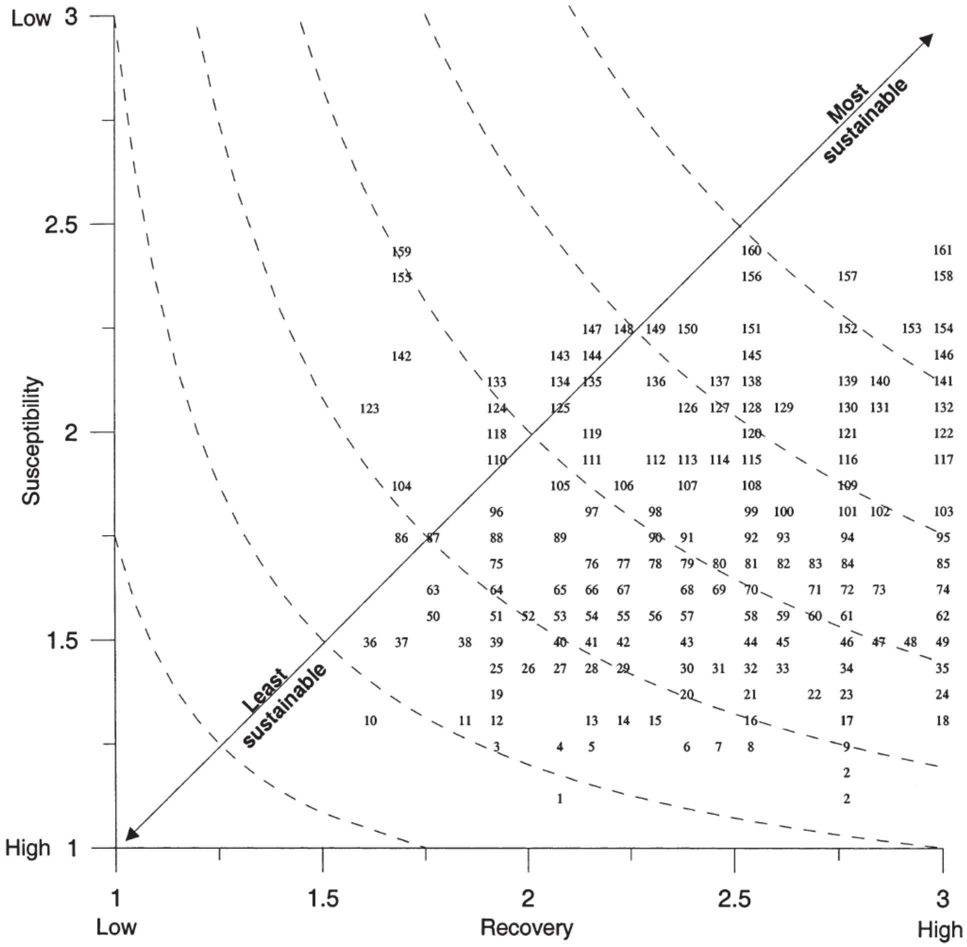

Figure 2.Scatter plot of a Productivity and Susceptibility analysis (PSA) where productivity is ranked in the x-axis and susceptibility in the y-axis. (From Stobutzki et al. 2001).

4.2 SUSTAINABILITY ASSESSMENT FOR FISHING EFFECTS (SAFE)

The Sustainability Assessment for Fishing Effects (SAFE) is a quantitative approach developed by Zhou and Griffiths (2008) which estimates fishing impacts using presence-absence survey data and compares them with life history-based reference points. The SAFE approach is designed for data-poor fisheries and has been used to assess the status of trawl fisheries in northern Australia (Zhou et al 2009).

The first part of this model provides the likelihood of total abundance N_F in the fished ($F = 1$) and unfished ($F = 0$) areas of within a given region. The probability of capturing one or more individuals D is:

$$L(L_F, D|m_i, n_i, A_F, a_i) = \prod_{F=0}^{1} \prod_{\substack{i=1 \\ n_i > 0}}^{C_1} \binom{m_i}{n_i} \left\{ D^{n_i} (1-D)^{m_i - n_i} \left[1 - \left(1 - \frac{a_i}{A_F} \right)^{N_F} \right] \right\} \times \prod_{\substack{i=1 \\ n_i = 0}}^{C_0} \left\{ (1-D)^{m_i} \left[1 - \left(1 - \frac{a_i}{A_F} \right)^{N_F} \right] + \left(1 - \frac{a_i}{A_F} \right)^{N_F} \right\} \tag{56}$$

where i is each surveyed grid, m_i is the number of surveys on grid i, n_i is the number of those surveys a species has been captured in (so $n_\mathrm{i} \leq m_\mathrm{i}$) A_F is the size of area F of the study region, a_i the size of area surveyed in grid i, C_1 the total number of grids where $n_\mathrm{i} > 0$, and C_0 is the total number of grids where $n_\mathrm{i} = 0$. Thus, the parameters N_F and D can be solved by maximizing the likelihood of the equation above (56). When multiple bioregions are surveyed, this analysis is repeated separately for each one to obtain a region-specific value of N_F, or $N_\mathrm{F,R}$. In situations where multiple fishing gears are used, the different capture probabilities for any given species were incorporated using a logistic model:

$$D = \frac{1}{\mathrm{e}^{-(\alpha + \boldsymbol{\beta}\mathbf{M} + \boldsymbol{\gamma}\mathbf{H})} + 1} \tag{57}$$

where vector **M** is the sampling gear type, vector **H** is the area covered by each gear in the gird, and α, vectors $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ are model parameters.

By comparing the relative populations of each species within fished and unfished areas, the proportion of a species' population that could potentially be impacted by fishing across regions in the area of study (P_N), is estimated:

$$P_N = \frac{\sum_{R=1}^{r} N_{R,F=1}}{\sum_{R=1}^{r} \sum_{F=0}^{1} N_{R,F}} \tag{58}$$

where R refers to each one of the r number of regions, and F= 1 and F= 0 refer to the fished and unfished areas within each region, respectively.

After all the previous calculations have been done, the fishing induced mortality rate (u) which is computed as a yearly probability, can be calculated by

$$u = P_N q_N (1 - E) \tag{59}$$

Where q_N is the catch rate of the species with N abundance (i.e., the probability of a fish entering the net), and E is the species-specific probability of escapement, obtained from published values. Thus using equation (4) it can be turned into instantaneous fishing mortality F by $u = 1 - \mathrm{e}^{-F}$.

The second part of the SAFE framework compares the calculated F values with proxies of F_crash. Both methods to obtain a proxy of F_crash explained in section 3.2 (equations 31 and 32) are used, from which the lowest value of F_crash was picked as the comparison point.

The SAFE method does require large amounts of data in the form of survey data, and detailed information on fishing effort and location. However, the method can be applied to any stock from which there are surveys both inside and outside regularly fished grounds, assuming that the stock has similar recruitment and growth trajectories in both areas. An important note is that the proxies used for comparing fishing mortalities have large margins of error, thus findings can be confounded by the quality of these reference points.

4.3 ECOLOGICAL RISK ASSESSMENT FOR THE EFFECTS OF FISHING (ERAEF)

Ecological Risk Assessment for the Effects of Fishing (ERAEF) is a triage framework based on ecosystem-based fisheries management (EBFM) whose hierarchical structure aids in its application in data-poor situations. It accounts for the effects of indirect factors (e.g., habitat destruction, bycatch, ecological interactions) on fish populations. The ERAEF framework assesses them with increasingly more quantitative tools and decreasing uncertainty when specific units in the fishery have been classified as of concern.

The framework consists of four levels of analysis, ranging from mostly qualitative (Scoping) to fully quantitative (Level 3). It assesses the effects of fishing in the following five components: target species; byproduct and bycatch species; threatened, endangered and protected species; habitats; and ecological communities. The hierarchical framework is such that only components assessed as medium or high risk at any given level are assessed in the next level, thus reducing the time and resources used to assess the fishery. The first step in this framework is *Scoping*, which is based primarily on input from stakeholders and expert opinion in order to identify management objectives for each component in the system. After those have been set, Level 1 consists of a “plausible worst case” approach, where for each component the worst case scenario is selected and assessed, thus drastically reducing assessment time. In Level 2, components that were classified as medium or high risk at Level 1 are assessed using proxies for productivity and susceptibility (Productivity and Susceptibility Analysis, PSA) based on methodology by Stobutzki et al. (2001) and described in section 5.1. As previously, only units that score medium or high risk are assessed in Level 3, where a fully quantitative assessment is undertaken using the Sustainability Assessment for Fishing Effects (SAFE) method by Zhou and Griffiths (2008) which is described in section 5.2.

These models can be applied to any taxa. By definition, they assess all the species or stocks involved in a fishery as well as their associated ecological communities. For example, while assessing any given tuna long-line fishery, the framework would also take into account the effects on all potential bycatch species groups, such as sharks, seabirds, and turtles.

As mentioned above, the hierarchical nature of the ERAEF framework allows its implementation even in data poor situations. In such cases, it implements a precautionary approach to identifying and ranking risk by assuming high risk when data are absent or there is not information to determine the contrary (Hobday et al. 2011). The ERAEF methodology has been widely used in fisheries managed by the Australian Government (Hobday et al. 2011).

The main strengths of the ERAEF framework lie in its cost effectiveness, flexibility, and precautionary approach to risk. It is cost effective as low risk units are quickly evaluated with very simple methods, and thus do not require more timely evaluation (and data collection) further in the analysis. The ERAEF framework is customizable to specific fisheries, thus each step can be changed to suit the requirements for meeting the objectives as long as the hierarchy starting from simpler to complex (and more data-hungry) is maintained. The ERAEF framework is explicitly precautionary as it assigns high risk when information is lacking. It is also designed to be biased toward producing false positives (assigning high risk in cases where it is actually low) rather than false negatives.

There are a number of caveats that need to be considered when using the ERAEF framework. Due to its scope, terminology, and the use of multiple levels of assessment, the ERAEF framework might take some time to become familiar with. Another issue is the subjectiveness of the first levels of assessment. Different stakeholders might come up with different risk scores in Level 1 due to its qualitative nature. Thoroughness of identifying all potential activities in Level 1 might seem redundant for some stakeholders as they feel like they might already know that a number of them pose very little risk. Level 2 uses proxies of productivity, rather than productivity estimates, and ignores some current management measures that when considered, might result in different risk scores.

For any given bycatch species, if there are multiple sources and/or fisheries impacting the stock then the ERAEF framework might not be able to identify risk accurately, particularly if they are assessed as low risk in Levels 1 or 2.For example, if risk is assessed as low for a bycatch species for a given fishery, but the species is also part of the bycatch of a number of other fisheries, then the compound effect of all fisheries on the stock might not be assessed accurately using ERAEF. Thus there is a need for integrating assessments across fisheries and components, which is a work in progress (Hobday et al. 2011).

4.4 SIMPFENDORFER ET AL. (2008) ERA FRAMEWORK

Based on the work done by Braccini et al. (2006) and Hobday et al. (2007) on Ecological Risk Assessment (ERA), Simpfendorfer et al. (2008) created a quick framework to assess risk of data-poor shark species which is basically a quantitative version of the PSA. The productivity axis uses the intrinsic rate of increase which can be calculated from the Au and Smith's (1998) equation, matrix projection models, F_{extinct}, or any proxy for F_{crash}. The susceptibility axis was still qualitative, and was ranked in terms of availability (overlap with fishery), encounterability (expert judgment), selectivity (contrasting expected length distributions with observed catchability), and post-capture mortality, if known. In this case, the total risk score was quantified as the Euclidean distance between a fixed point of low risk (i.e., a point with susceptibility score = 0 and an high productivity score) and the position of each species in a plot with productivity and susceptibility in each axis.

For a more holistic comparison aiming at assessing similarities between species, Simpfendorfer et al. (2008) calculated the inflection point of the population growth curve when plotted against population size as a fraction of $B_0(R)$ (Fowler 1988), which is a proxy for the B_{msy}/B_0 ratio. There is an empirical interspecific relationship between R and the product of the intrinsic rate of increase of a population (r) and generation time (T, which in most simple terms is the mid-point between age at first reproduction and maximum age):

$$R = 0.633 - 0.187\log(rT) \tag{60}$$

A third indicator of relative status was obtained by assigning a value from 0 to 1 based on the IUCN Red List Status of each species (Critically Endangered = 1, Endangered = 0.8, Vulnerable = 0.6, Data Deficient = 0.5, Near Threatened = 0.4 and Least Concern = 0.2). For precautionary purposes, Data Deficient species were classified in the mid-range of values. The ERA score, R values, and IUCN Red List Assessment scores just mentioned were combined in a non-metric multidimensional scaling plot (nMDS) in order to further compare the risk status of the species examined and observe any patterns relating to their risk status. As with PSA, this framework only provides a relative comparison of risk between species studied and is susceptible to large uncertainties in the ranking of qualitative assessments. Uncertainties in the estimation of *r* are discussed in previous sections.

4.5 EXTENT OF DECLINE

Another method for assessing relative risk of stocks when only an index of abundance is available is by using the estimated extent of decline, standardized by generation time (Mace and Lande 1991). This method uses the difference is abundance between a standardized time span: three generation time lengths when available (thus maximum age needs to be known), and if not available, a 10 year time period. This methodology is used by the International Union for the Conservation of Nature (IUCN) in their Red List assessments. It allows for rapid comparison of species which have been declining in abundance. Standardizing by generation time allows for comparison across species: longer lived species will take longer to show a proportional decrease than a shorter species with faster turnover rates.

Generally, steeper rates of decline represent greater risk and need for management intervention; hence this approach can be judged according to the reference direction and change in direction (Jennings and Dulvy 2005). Thresholds that have been used to classify increasing levels of concern are available for exploited fishes from IUCN, Committee on the Status of Endangered Wildlife and the American Fisheries Society (Musick 1999, DFO 2007, IUCN 2010) and are increasingly being subject to performance testing (Dulvy et al. 2005, Rice and Legacé 2007, Porszt et al. in press). The relatively low data requirements (index of abundance over a period of time, e.g., CPUE, and maximum age) allows for a simple comparative analysis of species in order to identify those species requiring greatest priority.

4.6 POORFISH

POORFISH is a collaborative effort to create Bayesian belief networks and subsequent stock and biomass dynamic models for data-poor stocks in the European Union. It provides a set of guidelines for assessment and management of data-poor fisheries. Their methodologies are based on well-known stock assessment tools which are parameterized using a probabilistic rather than a frequentist approach. Input probability distributions (known as priors in Bayesian frameworks) are assigned to parameters in the stock assessment. In data-poor situations, probability distributions that contain only limited information can be included.

The POORFISH project did not build any specific tools or models for fisheries management; instead they provided case specific examples of Bayesian implementation in surplus production models, Virtual Population Analyses (VPA), and a range of other decision-making scenarios. The POORFISH project used well-known stock assessment tools and applied them using Bayesian analyses made for each particular scenario studied.

Bayesian approaches are strongly dependent on the belief network that is used as input (priors), thus expert knowledge is require in order to assess the validity and effect of priors on the results. They are however more difficult to implement, and usually need to be tailor made for each assessment, and are suitable for either full stock assessments in which uncertainty is to be considered, or stocks which are just short of having enough data for a complete stock assessment. In the latter case prior distributions can be assigned to those knowledge gaps.

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