Supporting Information

S1 Appendix  Life history models

Title: Growth and life history variability of the grey reef shark (*Carcharhinus amblyrhynchos*) across its range

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1. Frisk, Miller, and Fogarty (2001) length at maturity

Frisk, Miller, and Fogarty [1] quantified the relationship between body size (total length) and length at maturity and age at maturity for 150 elasmobranch species including requiem sharks. Length at maturity \( L_m \) was significantly related to maximum length \( L_{\text{max}} \)

\[
L_m = 0.70 \, L_{\text{max}} + 3.29.
\]  

(1.1)

The linear relationship between \( L_m \) and \( L_{\text{max}} \) is particularly strong for individuals with \( L_{\text{max}} < 200 \) cm, which includes \( C. \, amblyrhynchos \).

2. Francis (1988) growth model

The Francis [2] formulation of the von Bertalanffy growth function (VBGF) for tag-recapture data describes the expected growth from a fish of initial length \( L \) over some time period \( \Delta T \):

\[
\Delta L = \frac{\beta (\alpha - \beta)}{(\alpha - \beta)^{L}} - \frac{1}{1 - (1 + \frac{\beta}{\alpha - \beta})^{\Delta T}},
\]  

(2.1)

where \( g_\alpha \) and \( g_\beta \) are the mean annual growth increments of a species at reference lengths \( \alpha \) and \( \beta \) (which should be chosen to include a substantial proportion of by the tagging data within their range). We set \( \Delta T = 1 \) and standardized growth to an annual timestep. Parameters \( g_\alpha \) and \( g_\beta \) can be used to estimate the conventional parameters \( L_\infty \) and \( k \) of the VBGF by the equations
\[ L_{\infty} = \frac{\beta g_a - \alpha g_\beta}{(g_a - g_\beta)}, \]  
\[ k = -\ln \left( 1 + \frac{g_a - g_\beta}{a - \beta} \right). \]

The Francis model is flexible in that it allows the addition of additional parameters. Assuming that the growth of a shark of length \( L \) over some time period is normally distributed with mean \( \mu \) and standard deviation \( \sigma \), then growth variability can be described using a single parameter \( \nu \) where

\[ \sigma = \nu \mu. \]

If this mean-variance relationship results in inadequate model fit, then additional parameters can be introduced [2], but this was not necessary for our data. Outliers can also bias growth model parameters, but may represent true values that should not necessarily be discarded. The contamination probability \( p \) can be added to ensure that extreme data points have minimal effect on growth parameters (as long as outliers are somewhat rare). Finally, mean \( m \) and standard deviation \( s \) of measurement error in \( \Delta L \) can be modeled, and the log likelihood function can be rewritten as

\[ \lambda = \sum_{i=1}^{n} \log \left[ (1 - p)\lambda_i + p/R \right], \]

where \( \lambda_i = \exp \left( \frac{-0.5 (\Delta L_i - \mu_i - m)^2 / (\sigma_i^2 + s^2)}{2 \pi (\sigma_i^2 + s^2)^{0.5}} \right) \).
R is the range of observed growth increments $\Delta L_t$ and the likelihood is summed over all observed growth increments. We estimated the model using the `grotag` function with limited memory, bound-constrained BFGS maximization in the `fishmethods` package [3] to find the set of parameters that maximizes $\lambda$.

### 3. Jolly-Seber annual survival ($\phi$)

Royle and Dorazio [4] formulated the Jolly-Seber (JS) for capture-recapture data as a restricted dynamic occupancy model where individuals can be in one of three states: “not yet entered”, “alive”, “dead” [5]. Transitions between these states are determined by the ecological processes entry and survival, which are estimated. We were interested in the probability of annual survival $\phi$, and so we estimated a model with an annual time step where the state of an individual $i$ in the first year is

$$z_{i,1} \sim Bernoulli(\gamma_1),$$  \hspace{1cm} (3.1)

where $\gamma$ is the probability that a “not yet entered” individual enters the population, and $z_{i,t} = 1$ if an individual is “alive” and present, and $z_{i,t} = 0$ if an individual is “dead” or has “not yet entered” the population [5]. Subsequent states of each individual are determined by survival for live individuals already in the population ($z_{i,t} = 1$) or by recruitment to the population for a new individual ($z_{i,t} = 0$) such that

$$z_{i,t+1} | z_{i,t}, ..., z_{i,1} \sim Bernoulli(z_{i,t}\phi_{i,t} + \gamma_{t+1} \prod_{k=1}^{t}(1 - z_{i,k})), \hspace{1cm} (3.2)$$
where $\phi_{i,t}$ is the probability of survival for individual $i$ between year $t$ and $t + 1$. The observation process conditions on the above state process as

$$y_{i,t} \mid z_{i,t} \sim \text{Bernoulli}(z_{i,t}p_{i,t}),$$

(3.3)

where $p$ is the probability of capture. We used a Bayesian analysis and specified uniform priors $U(0,1)$ for all estimated parameters ($\phi, \gamma, p$) to express our ignorance about their values [5]. The model was formulated in the JAGS language with Markov chain Monte Carlo (MCMC) sampling available in the R package rjags [6].

4. Hoenig (1983) total mortality ($Z$)

The Hoenig [7] method of estimating total mortality ($Z$) is parameterized around the observed relationship between longevity ($T_{\text{max}}$) and mortality. The equation takes the form

$$\ln(Z) = a + b \ln(T_{\text{max}}),$$

(4.1)

where $a$ and $b$ are fitted parameters, and $T_{\text{max}}$ is the maximum observed age in the catch. The equation is parameterized separately for teleost fishes ($a = 1.46, b = -1.01$) and cetaceans ($a = 0.941, b = -0.873$), both of which have been used for sharks [8,9]. We assumed that $Z$ was equal to natural mortality $M$ given the absence of fishing at Palmyra. $T_{\text{max}}$ was estimated as the time required to attain >99% of $TL_\infty$ as $T_{\text{max}} = 5 \cdot \ln(2) \cdot k^{-1}$ [61], using the $k$ estimate from equation 2.3.
References

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