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_{max}

$$L_m = 0.70 L_{max} + 3.29. \tag{1.1}$$

The linear relationship between L_m and L_{max} is particularly strong for individuals with $L_{max} < 200$ 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 ΔT :

$$\Delta L = \frac{\frac{\beta g_{\alpha} - \alpha g_{\beta}}{(g_{\alpha} - g_{\beta}) - L}}{1 - \left(1 + \frac{g_{\alpha} - g_{\beta}}{\alpha - \beta}\right)^{\Delta T}},$$
(2.1)

where g_{α} and g_{β} are the mean annual growth increments of a species at reference lengths α and β (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_{α} and g_{β} can be used to estimate the conventional parameters L_{∞} and k of the VBGF by the equations

$$L_{\infty} = \frac{\beta g_{\alpha} - \alpha g_{\beta}}{(g_{\alpha} - g_{\beta})}; \tag{2.2}$$

$$k = -Ln\left(1 + \frac{g_{\alpha} - g_{\beta}}{\alpha - \beta}\right). \tag{2.3}$$

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 μ and standard deviation σ , then growth variability can be described using a single parameter *v* where

$$\sigma = v \,\mu. \tag{2.4}$$

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 ΔL can be modeled, and the log likelihood function can be rewritten as

$$\lambda = \sum_{i=1}^{n} \log[(1-p)\lambda_i + p/R], \qquad (2.5)$$

where
$$\lambda_i = \exp \frac{-0.5(\Delta L_i - \mu_i - m)^2 / (\sigma_i^2 + s^2)}{[2\pi (\sigma_i^2 + s^2)]^{0.5}}$$
 (2.6)

R is the range of observed growth increments ΔL_i 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 λ .

3. Jolly-Seber annual survival (ϕ)

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 ϕ , and so we estimated a model with an annual time step where the state of an individual *i* in the first year is

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

where γ 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

$$z_{i,t+1} \mid z_{i,t}, \dots, z_{i,1} \sim Bernoulli (z_{i,t} \phi_{i,t} + \gamma_{t+1} \prod_{k=1}^{t} (1 - z_{i,k})),$$
(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

$$y_{i,t} \mid z_{i,t} \sim Bernoulli(z_{i,t}p_{i,t}), \tag{3.3}$$

where *p* is the probability of capture. We used a Bayesian analysis and specified uniform priors U(0,1) for all estimated parameters (ϕ , γ , *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_{max}) and mortality. The equation takes the form

$$Ln(Z) = a + b Ln(T_{max}), \tag{4.1}$$

where *a* and *b* are fitted parameters, and T_{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_{max} was estimated as the time required to attain >99% of TL_{∞} as $T_{max} = 5 \cdot \text{Ln}(2) \cdot k^{-1}$ [61], using the *k* estimate from equation 2.3.

References

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