## 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 $L_{\max }$

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\begin{equation*}
L_{m}=0.70 L_{\max }+3.29 \tag{1.1}
\end{equation*}
$$

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 $\Delta T$ :
$\Delta L=\frac{\frac{\beta g_{\alpha}-\alpha g_{\beta}}{\left(g_{\alpha}-g_{\beta}\right)-L}}{1-\left(1+\frac{g_{\alpha}-g_{\beta}}{\alpha-\beta}\right)^{\Delta T}}$,
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
$L_{\infty}=\frac{\beta g_{\alpha}-\alpha g_{\beta}}{\left(g_{\alpha}-g_{\beta}\right)} ;$
$k=-\operatorname{Ln}\left(1+\frac{g_{\alpha}-g_{\beta}}{\alpha-\beta}\right)$.

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 $v$ where
$\sigma=v \mu$.

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 $\lambda_{i}=\exp \frac{-0.5\left(\Delta L_{i}-\mu_{i}-m\right)^{2} /\left(\sigma_{i}^{2}+s^{2}\right)}{\left[2 \pi\left(\sigma_{i}^{2}+s^{2}\right)\right]^{0.5}}$

R is the range of observed growth increments $\Delta L_{i}$ 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 $\lambda$.

## 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
$z_{i, 1} \sim \operatorname{Bernoulli}\left(\gamma_{1}\right)$,
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 $\left(z_{i, t}=1\right)$ or by recruitment to the population for a new individual $\left(z_{i, t}=0\right)$ such that
$z_{i, t+1} \mid z_{i, t}, \ldots, z_{i, 1} \sim \operatorname{Bernoulli}\left(z_{i, t} \phi_{i, t}+\gamma_{t+1} \prod_{k=1}^{t}\left(1-z_{i, k}\right)\right)$,
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
$y_{i, t} \mid z_{i, t} \sim \operatorname{Bernoulli}\left(z_{i, t} p_{i, t}\right)$,
where $p$ is the probability of capture. We used a Bayesian analysis and specified uniform priors $\mathrm{U}(0,1)$ 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 $\left(T_{\max }\right)$ and mortality. The equation takes the form
$\operatorname{Ln}(Z)=a+b \operatorname{Ln}\left(T_{\max }\right)$,
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 $T L_{\infty}$ as $T_{\max }=5 \cdot \operatorname{Ln}(2) \cdot k^{-1}$ [61], using the $k$ estimate from equation 2.3.

## References

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