Focusing on the front end: A framework for incorporating uncertainty in biological parameters in model ensembles of integrated stock assessments - S1 Appendix

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1. Technical Annex

1.1. Data description

Data representative of the southwest Pacific Ocean (SWPO) swordfish (*Xiphias gladius*) stock were used in Bayesian analyses to develop the multivariate distribution of key biological parameters and relationships that underpinned the model ensemble comparison. These data came from two sources: 1) biological observations of individuals sampled as a part of longline commercial fishing operations in the south Pacific through the Pacific Islands Regional Observer Program (PIRFO), and 2) biological observations of in-

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dividuals collected as a part of scientific research conducted by the Commonwealth Scientific and Industrial Research Organisation (CSIRO) aboard commercial longline vessels operating in the Coral Sea. Data collected as part of the observer program consisted of lower jaw fork length (LJFL cm) and whole weight (WW kg) measurements, as well as sex-determination of the measured individual. For lengths or weights that were not collected as LJFL or WW, respectively, were adjusted according to the standard conversion factors used in Western and Central Pacific Fisheries Commission (WCPFC) stock assessments (SPC-OFP, 2019). Data collected through CSIRO scientific research consisted of age, length, and maturity status by sex (Young and Drake, 2002, 2004). Since CSIRO recorded lengths as eye-orbital fork length (OFL), these measurements were translated to LJFL using the aforementioned conversion factors.

1.2. Bayesian models

Four independent Bayesian analyses using the STAN probabilistic language, implemented in R (v4.0.3) with the *rstan* package (v2.21.2 R Core Team, 2021; STAN Development Team, 2021) were employed to create posterior distributions for the parameters needed to parameterize the growth, spawning potential (the product of female sex-ratio at length and female maturity at length), and length-weight relationships. For each model, 32,000 samples were drawn from 8 separate chains (5,000 samples per chain with 1,000 initial samples discarded as “burn-in”), each with random initial conditions. Default settings were used to setup the Hamiltonian Monte Carlo (HMC) sampling in terms of adapt-delta and tree-depth. Chains were assessed for convergence visually and using the $\hat{R}$ test statistic. All models did not fail convergence tests and appeared well determined on the basis of standard Hamiltonian Monte Carlo diagnostics (e.g., no divergent transitions identified, no maximum tree depth errors, and Bayesian fraction of missing information was not found to be too low).

1.2.1. Length-weight relationship

The relationship between length and weight of fish was modeled using sex-specific power functions. A total of 5,721 individual fish was available and consisted of 2,451 males and 3,270 females. The standard implementation of these models was utilized and consisted of a simple regression on the log scale of weight (w_i) against length (l_i) of each fish i, e.g.,

$$\log(\acute{w_i}) \sim Normal(\log\alpha_{j[i]} + \beta_{j[i]} \times \log(l_i), \sigma) \tag{1}$$

$$w_i = exp(\acute{w_i}) \tag{2}$$

where $\alpha_{j[i]}$ and $\beta_{j[i]}$ are intercept and slope terms specific to the sex j of fish i. Both sexes assumed identical but sex-specific priors for all parameters. Priors were specified to be relatively uninformative with a large CV on the log-scale (0.5). The prior for the regression standard deviation, σ, was $log(\sigma) \sim \text{Normal}(log(0.5), 0.5)$, for the regression intercept parameter α_j $\log(\alpha_j) \sim \text{Normal}(log(10^{-5}), 0.5)$ and for the regression slope parameter $log(\beta_j) \sim \text{Normal}(log(3), 0.5)$. The prior means were taken to be similar to the assumed values for α and β used in the 2017 SWPO swordfish stock assessment (Takeuchi et al., 2017). Linear regression of log-transformed data introduces a bias on the regression intercept parameter α, and we accounted for this by applying a multiplicative correction factor ($e^{\frac{\sigma^2}{2}}$) to our estimates of α_j (Hayes et al., 1995).

For each posterior sample, sex-aggregated parameters $\bar{\alpha}$ and $\bar{\beta}$ were derived. Rather than simply averaging them which would not preserve the correlation structure between parameters, new sex-aggregated parameters were estimated by fitting to the predicted sex-specific weight at length relationship. This was done using non-linear least squares(*nls()* from the *stats* package in R *v*4.0.3):

$$w^* = \bar{\alpha} \times l^{*\bar{\beta}} \tag{3}$$

where w^* was the combined expected sex-specific estimates of weight determined by applying the estimated sex-specific parameters α_j and β_j to a vector of integer lengths l^* from 1 to 300.

1.2.2. Spawning potential

As mentioned, spawning potential at length was determined as the multiplicative combination of female sex-ratio at length and female maturity at length. These relationships were modeled using separate Bayesian models.

The female maturity-at-length relationship was investigated using biological data collected from longline caught swordfish in the Coral Sea (Young and Drake, 2002; Young et al., 2003). A total of 916 individual fish were sampled over the period 1999–2001, consisting of 231 males and 685 females. The lengths of each fish were recorded and histological samples were analyzed to assess the sexual maturity of each fish as outlined in Farley et al. (2016). Only female fish were considered for further analysis.

The resulting dataset consisted of binary data where maturity of fish i, m_i, was determined to be either mature (1) or immature (0). Data were modeled using a modified logistic regression against length l_i. It is occasionally difficult to accurately determine maturity status of some fish, depending on when in the spawning season individuals were sampled. The modifications to the logistic model accommodated errors in determination of maturity (McInturff et al., 2004), either in the form of false positives (designated mature when immature) and false negatives (designated immature when mature). The set of equations for this approach is:

$$m_i \sim \text{Bernoulli}(p_i) \tag{4}$$

$$p_i = \eta\pi_i + (1-\theta)(1-\pi_i) \tag{5}$$

$$\pi_i = \frac{1}{(1+\exp(\phi \times (l_i - \tau)))} \tag{6}$$

where the probability of being mature p_i involves adjustment of the usual function represented by π_i (linear relationship on the logit scale) using the parameters η and θ. These parameters are equivalent to the sensitivity and specificity of the classification problem, respectively. These are given uninformative priors $\text{logit}(\theta) \sim \text{Normal}(0, 1)$, and $\text{logit}(\eta) \sim \text{Normal}(0, 1)$. The parameters ϕ and τ represent the slope and inflection point (e.g., length at 50% maturity; L_{50}) of the maturity relationship, respectively. These parameters were also given uninformative priors $\phi \sim \text{Normal}(0, 5)$ and $\tau \sim \text{Normal}(180, 180)$. The mean value for the prior on τ was informed by prior estimates of L_{50} for this species (Farley et al., 2016).

Female sex-ratio at length data were modeled using a variant of the generalized logistic function. The data comprised all individual fish from PIRFO records south of 5°N through the year 2019, and consisted of 47,506 individual fish. Data were modeled as binary variables s_i, where 0s denoted males (n = 22,089) and and 1s denoted females (n = 25,417). The probability of fish i being female, ρ_i, was modeled as a function of fish length l_i using the following five-parameter model:

$$s_i \sim \text{Bernoulli}(\rho_i) \tag{7}$$

$$\rho_i = \omega + \frac{\lambda - \omega}{(1 + \exp(-\kappa \times (l_i - \delta)))^{\nu}} \tag{8}$$

where ω is the lower asymptote with prior $\text{logit}(\omega) \sim \text{Normal}(0, 0.05)$, λ is the upper asymptote with $\text{logit}(\lambda) \sim \text{Normal}(1, 1)$, κ is the slope of the function with length, with a prior of $\kappa \sim \text{Normal}(0, 0.1)$, δ is a parameter that determines the fish length (cm) at which the inflection point of the function occurs, which had a prior of $\delta \sim \text{Normal}(150, 150)$, and ν which allows asymmetry in the form of the function either side of the inflection point and was given a prior of $\nu \sim \text{Normal}(0, 1)$. All priors were relatively uninformative except for the prior on ω which was very informative (0.5 on logit scale) based on the assumption that sex-ratio at small size (e.g., birth) was 50:50.

The vector of spawning potential(SP^*) was defined for a vector of lengths (l^*) for each posterior sample as:

$$SP^* = \omega + \frac{\lambda - \omega}{(1 + \exp(-\kappa \times (l^* - \delta)))^{\nu}} \times \frac{1}{(1 + \exp(\phi \times (l^* - \tau)))} \tag{9}$$

where l^* was sequence of lengths corresponding to the midpoint of the length composition bins used in the 2017 SWPO stock assessment (Takeuchi et al., 2017). SP^* was normalized to a minimum of 0 and maximum of 1 for each posterior sample.

1.2.3. Growth

Sex-specific growth was modeled using a standard von Bertalanffy function. This model assumed uninformative priors centered on previously estimated values for this species (Farley et al., 2016) and was fit to the CSIRO age and length dataset (Young and Drake, 2004; Farley et al., 2016) where a decimal age was determined from otolith aging(Farley et al., 2020). This data set consisted of 301 individuals, 184 of which were female. The model is given by the following equation:

$$l_i \sim \text{Normal}(L_{\infty,j[i]} \left(1 - \exp\left(-k_{j[i]} \left(a_i - t_{0,j}\right)\right)\right), \sigma_l) \tag{10}$$

where l_i is the length of fish i for a fish at age a (annual), σ_l is the standard deviation of length which has a prior of $log(\sigma_l) \sim \text{Normal}(log(26), 0.5)$. The sex-specific average length of fish at hypothetical infinite ages for sex j $L_{\infty,j}$ had priors $log(L_{\infty,j}) \sim \text{Normal}(\mu_j^{L_\infty}, \sigma_j^{L_\infty})$ where μ^{L_∞} was $log(212)$ and $log(276)$ for males and females respectively, and σ^{L_∞} was 0.5 for both sexes. The sex-specific von Bertalanffy growth coefficient k_j had priors $log(k_{\infty,j}) \sim \text{Normal}(\mu_j^k, \sigma_j^k)$ where μ^k was $log(0.24)$ and $log(0.16)$ for males and females respectively, and σ^k was 0.5 for both sexes. The hypothetical age of a fish when length is 0 $t_{0,j}$ was sex-specific and had priors of $t_{0,j} \sim \text{Normal}(\mu_j^{t_0}, \sigma_j^{t_0})$ where $\mu_j^{t_0}$ was -2.10 and -2.13 for males and female respectively, and $\sigma_j^{t_0}$ was set at 5 for both sexes.

For each posterior sample, sex-aggregated parameters $\bar{L_\infty}$ $\bar{k}$ and $\bar{t_0}$ were derived. Rather than simply averaging the sex-specific parameters, which would not preserve the correlation structure between parameters, new sex-aggregated parameters were estimated by fitting to the predicted sex-specific length at age relationship. This was done using non-linear least squares(*nls()* from the *stats* package in R *v*4.0.3):

$$L^* = \bar{L_\infty} \left(1 - \exp\left(-\bar{k}\left(a^* - \bar{t_0}\right)\right)\right) \tag{11}$$

where L^* was the combined expected sex-specific estimates of length determined by applying the estimated sex-specific parameters $L_{\infty,j}$, k_j, and $t_{0,j}$ to a vector of integer ages a^* from 1 to 20.

1.3. Natural mortality

Recent work (Maunder et al., 2021; *Submitted*) suggests using either a maximum age based ($\frac{5.4}{A_{max}}$; Hamel and Cope, 2021; *Submitted*) or life-history based ($4.118k^{0.73}L_\infty^{-0.33}$ Then et al., 2015) approach for developing an estimate of M for mature individuals (M_{ref}). In this case, M_{ref} was defined as the M at a reference length where the reference length was chosen to be the length at the maximum age (20).

To create a distribution of M_{ref} which corresponded to the parameters from the growth analysis, correlated pairs of L_∞ and k were drawn from the growth model posterior distribution and applied to the life-history approach. Additionally, the coefficients from the life-history approach have their own uncertainty (Then et al., 2015) so a parametric bootstrap was used following the approach from Lopez-Quintero et al. (2017) to draw correlated pairs of parameters for the $\text{Pauly}_{\text{nls-T}}$ relationship in order to incorporate uncertainty in the life-history relationship parameters.

A distribution of age-specific vectors of natural mortality was developed using the Stock Synthesis parameterization (Methot Jr. and Wetzel, 2013) of the Lorenzen Lorenzen (2000) natural mortality curve. This formulation derives age-specific values of natural mortality using the growth curve, and M_{ref}.

1.4. Steepness

Steepness (h) in a stock assessment context is defined over the interval 0.2 – 1 as the ratio of the equilibrium recruitment produced by 20% of the equilibrium unexploited spawning potential to that produced by the equilibrium unexploited spawning potential (Francis, 1992; Harley, 2011). Typically, fisheries data are not very informative about the steepness parameter of the SRR parameters (ISSF, 2011); hence, the steepness parameter was fixed in the assessment. A distribution of steepness was created to account for the limited existing information available for swordfish (Myers et al., 1999). Based on this information, a censored Beta prior was specified in order to restrict the domain to valid values for steepness:

$$h = 0.2 + 0.8 \times x \tag{12}$$

$$x \sim \mathrm{B}(\alpha = 12.878788, \beta = 2.484848) \tag{13}$$

This Beta distribution has a median of 0.88, matching the available scientific information (Myers et al., 1999).

1.5. delta-MVLN approximation for three dimensional joint Kobe-Majuro distribution

Let $x = SB/SB_{MSY}$, $y = F/F_{MSY}$, and $z = SB/SB_{F=0}$ with means (e.g., μ_x), variances (e.g., σ_x^2), and correlations (e.g., ρ_{xy}) that are outputs from MULTIFAN-CL. Both x and y were estimated on a normal scale in MULTIFAN-CL, while z was estimated on the log-scale. In order to sample from a multivariate lognormal (MVLN) distribution the means and variances for x and y were transformed to the log-scale , along with all covariances. A 2^{nd} order Taylor series was used to approximate the log transformed means, variances and covariances following the delta method Fournier et al. (2012). Following the Taylor series approximation, the MVLN distribution for each model was defined by the following equations:

$$\mu\Bigg(ln(x), ln(y), z\Bigg) = \Bigg[ln(\mu_x) - \frac{\sigma_x^2}{2\mu_x^2} \quad ln(\mu_y) - \frac{\sigma_y^2}{2\mu_y^2} \quad \mu_z\Bigg] \tag{14}$$

$$Cov\Bigg(ln(x), ln(y), z\Bigg) = \begin{bmatrix} \frac{\sigma_x^2}{\mu_x^2} + \frac{\sigma_x^4}{4\mu_x^4} & \frac{\rho_{xy}\sigma_x\sigma_y}{\mu_x\mu_y} - \frac{\sigma_x^2\sigma_y^2}{4\mu_x^2\mu_y^2} & \frac{\rho_{xz}\sigma_x\sigma_z}{\mu_x} \\ \frac{\rho_{xy}\sigma_x\sigma_y}{\mu_x\mu_y} - \frac{\sigma_x^2\sigma_y^2}{4\mu_x^2\mu_y^2} & \frac{\sigma_y^2}{\mu_y^2} + \frac{\sigma_y^4}{4\mu_y^4} & \frac{\rho_{yz}\sigma_y\sigma_z}{\mu_y} \\ \frac{\rho_{xz}\sigma_x\sigma_z}{\mu_x} & \frac{\rho_{yz}\sigma_y\sigma_z}{\mu_y} & \sigma_z^2 \end{bmatrix} \tag{15}$$

For each model retained in the ensemble, the estimation uncertainty for the three reference points was approximated by drawing 10,000 samples from the above MVLN distribution. Samples were exponentiated to return them to the normal scale.

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