



Deepwater Catshark (*Apristurus profundorum*)

Supplementary Materials for *Apristurus profundorum* (Date of Assessment: 18th June 2019)

To analyse the *Apristurus profundorum* population trend data, we used a Bayesian state-space tool for trend analysis of abundance indices for IUCN Red List assessment (Just Another Red List Assessment, JARA) (Sherley *et al.* 2020), which builds on the Bayesian state-space tool for averaging relative abundance indices by Winker *et al.* 2018 (Winker *et al.* 2020) and is available open-source on GitHub (www.github.com/henning-winker/JARA). The relative abundance or the population follows an exponential state-space population model of the form: $\mu_{t+1} = \mu_t + r_t$, where μ_t is the logarithm of the expected abundance in year t , and r_t is the normally distributed annual rate of change with mean \bar{r} , the estimable mean rate of change for a population, and process variance σ^2 . We linked the logarithm of the observed relative abundance $I_{t,i}$ for index i (where multiple datasets were available for the same fishery or region) to the expected abundance trend $\log(\hat{I}_t) = \mu_t$, using the observation equation (eqn. 16) from Winker *et al.* (2018). We used a non-informative normal prior for $\bar{r} \sim N(0,1000)$. Priors for the process variance can be either fixed or estimated (see Winker *et al.* 2020 for details). If estimated (default), the priors were $\sigma^2 \sim 1/\text{gamma}(0.001,0.001)$, or approximately uniform on the log scale (e.g. Chaloupka and Balazs 2007). Three Monte Carlo Markov chains were run and initiated by assuming a prior distribution on the initial state centered around the first data point in each abundance time series ($y_{t=1}$), $\mu_1 \sim N(\log(y_1),1000)$. In each chain, between 10,000 and 70,000 iterations were discarded ('burn-in'), and of the remaining 60,000 iterations, 10,000 were selected for posterior inference ('thinning rate' = 6). Thus, posterior distributions were estimated from 30,000 iterations. Analyses were performed using the R Statistical Software v3.6.1 (R Core Team 2018), via the interface from R ('r2jags' library v 0.5-7; Su and Yajima 2015) to JAGS ('Just Another Gibbs Sampler' v4.3.0; Plummer 2003). Convergence was diagnosed using Geweke's diagnostic (Geweke 1992) with thresholds of $p = 0.05$, via the 'coda' library (v0.19-2).

The percentage change $D\%$ was directly calculated from the posteriors of the estimated population time series \hat{I}_t . If the span of \hat{I}_t was longer than 3 x generation length (GL), the percentage change was automatically calculated as the difference between a three-year average around the final observed data point T , and a three-year average around the year corresponding to $T - (3 \times \text{GL})$. The year $T+1$ is always projected to obtain a three-year average around T . We used a three-year average to reduce the influence of short-term fluctuation (Froese *et al.* 2017). If the span of \hat{I} was shorter than $3 \times \text{GL}$, JARA projected forward, by passing the number of desired future years without observations to the model, to attain an \hat{I}_t that spans $3 \times \text{GL} + 2$ years for the calculation of $D\%$. These projections (shown as red dashed lines in the figures below) were based on the posteriors of the estimated decline across all n years in the observed time series: $\bar{r} = \frac{1}{n} \sum_{t=1}^n r_t$. The

projection gives similar results to extrapolating backwards to attain a 3 x GL period and produces a similar result for the D%.

We analysed each time-series, to produce a) a model fit to the observed data (e.g. Figure 1a), b) an annual rate of change (λ) based on the observed data ($\lambda = \exp(\bar{r})$), expressed as a % in e.g. Figure 1b), c) if needed, projected values for each year necessary to extend the time-series to 3 x GL (e.g. Figure 1c), and d) the posterior distribution for the rate of change (%) over 3 x GL (e.g. Figure 1d). Because the posterior distribution comprises an estimated % population change over 3 x GL for each model iteration, these automatically map to the IUCN Red List categories. For example, under criterion A2, an iteration yielding a % population change of +55% would be assigned to the Least Concern category, while iterations giving -82% and -55% would be assigned to Critically Endangered and Endangered, respectively. By assigning the posterior decline from each iteration in this way, it was possible to determine the most likely IUCN Red List category for each time-series separately (Table 1). This probable Category was then used by assessors to inform the species' status while considering other available information that was not included in this analysis (i.e. there is other information beyond timeseries and this JARA analysis that needs to be considered to arrive at a Category, and the final Category may not exactly reflect what JARA suggests).

Table 1. *Apristurus profundorum* – Population change (%) and posterior probabilities for changes falling within the IUCN Red List categories Least Concern (LC), Near Threatened (NT), Vulnerable (VU), Endangered (EN), and Critically Endangered (CR); the “likely status” based on criteria A2–4 is assigned based on the category containing the highest posterior probability, with the exception that NT is also selected where LC obtained the highest probability, but it is < 50%. All probabilistic statements are based on the rate of change over three generation lengths (GL) from projections within JARA. The Global change is based on the rate of change of change over three generation lengths (GL) using all time-series, as index i, at the same time in a same modelisation run (see text for detail).

Region	GL (years)	Data length (years)	Median change	LC	NT	VU	EN	CR	Likely status
Newfoundland and Labrador Shelf, Canada ¹	15	1995-2018	+513.8	100	0	0	0	0	LC

Data sources:

1. *Apristurus profundorum* unpubl. data from Fisheries and Oceans Canada, and NOAA USA, compiled by David W. Kulka.

Newfoundland and Labrador Shelf, Canada: Relative abundance (1995-2018), 2J3K (Canada), Survey index of abundance (mature individuals, Fall season).

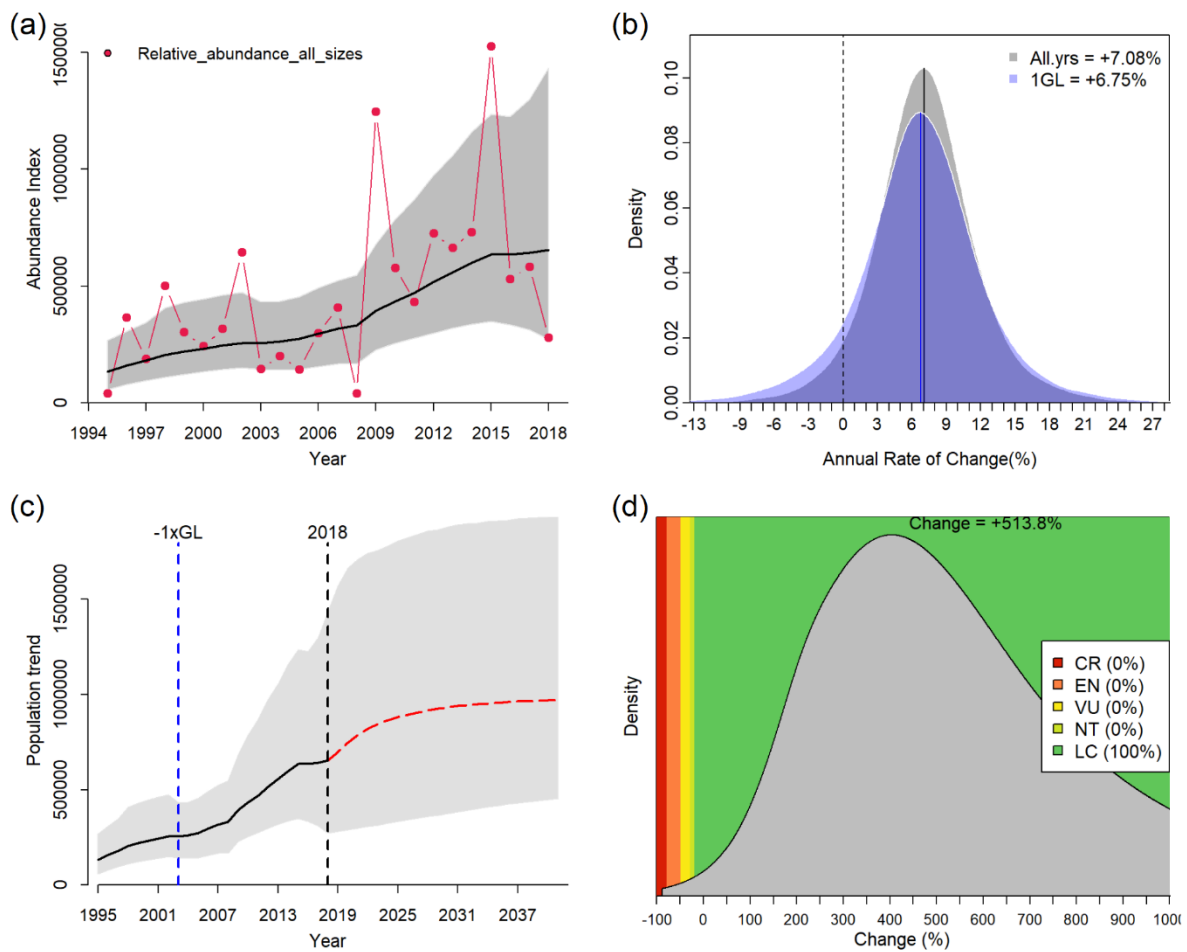


Figure 1. JARA results for *Apristurus profundorum* in the 2J3K (Canada) showing (a) the JARA fit to the observed time-series, (b) the posterior probability for the percentage annual population change calculated from all the observed data (in grey) and from the last 1 generation length of data (in blue), with the mean (solid lines) shown relative to a stable population (% change = 0, black dashed line), (c) the observed (black line) and predicted (red line) population trajectory over three generations (45 years, dashed grey lines), and (d) the median decline over three generation lengths (dashed line) and corresponding probabilities for rates of population decline falling within the IUCN Red List category.

References

- Geweke, J. (1992) Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In: *Bayesian Statistics 4: Proceedings of the Fourth Valencia International Meeting*. (eds J.O. Berger, J.M. Bernardo, A.P. Dawid and A.F.M. Smith). Clarendon Press, Oxford, pp 169–193.
- Plummer, M. (2003) *JAGS: A Program for Analysis of Bayesian Graphical Models using Gibbs Sampling*, (Vol. 124).
- Sherley, R.B., Winker, H., Rigby, C.L., Kyne, P.M., Pollom, R., Pacoureaux, N., Herman, K., Carlson, J.K., Yin, J.S., Kindsvater, H.K., and Dulvy, N.K. (2020) Estimating IUCN Red List population reduction: JARA—A decision-support tool applied to pelagic sharks. *Conservation Letters*, e12688. doi: 10.1111/conl.12688.
- Su, Y.-S. and Yajima, M. (2012) R2jags: A Package for Running jags from R.
- Winker, H., Carvalho, F. and Kapur, M. (2018) JABBA: Just Another Bayesian Biomass Assessment. *Fisheries Research* **204**: 275–288.
- Winker, H., Pacoureaux, N., and Sherley, R. B. (2020) JARA: ‘Just Another Red list Assessment’. *bioRxiv* 672899 doi:10.1101/672899.