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Seabird risk assessment methods for the Southern Bluefin Tuna surface longline fishery

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The Spatially Explicit Fisheries Risk Assessment (SEFRA) framework has been developed and applied in New Zealand to a variety of mega-fauna that are potentially vulnerable to the effects of fishing, including sea lions, seabirds and dolphins. In the case of seabirds, many of the species caught incidentally by New Zealand vessels are also caught outside of the Exclusive Economic Zone by high seas fisheries, particularly surface longliners fishing for tuna at high latitudes. This has led the SEFRA-seabird framework to be developed in a manner that can include global fishing effort and using global species distribution maps.

The Comission for the Conservation of Southern Bluefin Tuna (CCSBT) is the regional fisheries management organisation responsible for managing southern bluefin tuna surface longline fisheries. In 2019, the SEFRA approach was presented to the CCSBT Working Group on Ecologically Related Species (ERSWG). The current project is an update to that work. It details the SEFRA method used in the most recent application of the framework to CCSBT managed fisheries, which was presented at the Fifteenth Session of the ERSWG in June 2024. Model outputs and results are provided in the CCSBT report from that meeting.

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1. INTRODUCTION

1.1 Spatially Explicit Fisheries Risk Assessment

The Spatially Explicit Fisheries Risk Assessment (SEFRA) framework has been developed and utilised in New Zealand and is now standard procedure for estimating the risk to seabirds from commercial fishing (e.g., Edwards et al. 2023a, Richard et al. 2020, 2017a, Sharp 2019, Richard & Abraham 2015). The approach is designed to accommodate multiple species and fisheries simultaneously, constructing risk profiles as a function of spatial and temporal overlap. Application has been primarily within the New Zealand Exclusive Economic Zone (EEZ), but, since seabirds can migrate widely across the southern hemisphere, a comprehensive assessment of the fisheries risk needs to account for all the fishing effort that may be encountered as they move through international waters. This, as well as the need to inform management outside of the New Zealand EEZ, has motivated application of the method in this wider context (Abraham et al. 2017a,b,c, Ochi et al. 2018, Abraham et al. 2019, Edwards et al. 2023b, CCSBT 2024).

The SEFRA approach is a quasi-spatial model where temporal and spatial overlap of the seabird distribution and fishing effort are used as a covariate with which to predict the captures. Parameterisation of the capture rate per unit of overlap occurs via a fit to fisheries observer capture data, and total captures are then calculated by multiplication of the total overlap (including the unobserved component) with this estimated rate (referred to as the catchability). Deaths are calculated from the predicted captures using a mortality multiplier that accounts for the probability of dead capture and cryptic mortality. Following estimation of the total deaths, the SEFRA approach attempts to quantify the risk using a limit reference point referred to as the Population Sustainability Threshold (PST; Sharp 2019):

$$\text{Risk ratio} = \frac{\text{Deaths}}{\text{PST}} \tag{1a}$$

$$\text{PST} = \frac{1}{2} \cdot \phi \cdot r_{\text{max}} \cdot N \tag{1b}$$

where ϕ is an adjustment used by management to ensure that deaths equal to the PST correspond to a defined population stabilisation or recovery objective; r_{max} is the theoretical unconstrained maximum population growth rate (i.e., under optimal conditions and in the absence of density dependent constraints); and, N is the population size for that species.

If N is the total population size, then it is possible to underestimate the impact of fishing if only a subset of the population is exposed. For the New Zealand context, it was recommended by an independent review that modelling should focus on the adult population only, as there was observed to be a dearth of juvenile captures in domestic fisheries (Lonergan et al. 2017). This decision can also be influenced by data availability, such as the inadequacy of biological and distributional information from immature birds, as well as ambiguity in capture data caused by difficulty in distinguishing maturity stage. For recent domestic applications of SEFRA, N therefore refered to the adult population size (e.g., Edwards et al. 2023a). The southern hemisphere assessment of Edwards et al. (2023b) applied the same assumption, whereas Ochi et al. (2018), for example, assumed that N referred to the total population size.

The PST estimates the total amount of additional death a population can sustain (above natural mortality) whilst still meeting the population recovery goal. However, deaths estimated by SEFRA are typically only a subset of the total anthropogenic mortality. This is most obvious when only a subset of the total fishing effort is being included, but there may also be non-fishery related deaths that are not accounted for. When the deaths estimated by SEFRA correspond to an unknown proportion of total deaths, then comparing those deaths to the PST may be misleading, and not represent a true indication of the prospects for long-term population viability. However, it is still the case that $r_{\max}$ and N are important for determining the relative risk between species: for a given number of deaths a large or productive population can be considered at lower risk, all else being equal. For instances in which the risk ratio cannot be properly calculated, we instead use a relative mortality measure:

$$\text{Relative mortality} = \frac{\text{Deaths}}{r_{\max} \cdot N} \tag{2}$$

where $r_{\max} \cdot N$ is equal to the theoretical maximum growth rate in numbers per year. The relative mortality approach still provides the same relative ranking as that achieved using the PST reference point, because the ϕ term is typically assumed to be the same for all species during comparative assessments.

1.2 Suitability of SEFRA for ecological risk assessment by tRFMOs

The third report of the“Kobe Process” (Kobe III) identified the importance of continued efforts to harmonise tRFMO bycatch and fishing data, and to develop common data confidentiality rules with surrounding protocols on the types of data that can be shared and how it can be used (ICCAT 2011). Although there is currently no formal central repository for data sharing among all tRFMOs, steps made with the WCPFC-IATTC Data Exchange show that there is both a need and a mechanism for this to occur. In addition to the recommendations of Kobe III, the substantial overlap in membership between the various tRFMOs, all requiring routine reporting, incentivises the adoption of standardised reporting as a way of simplifying this requirement for members and cooperating non-members. By ensuring that the requirements of SEFRA fit within the data standards agreed to by the various tRFMOs, and given the common need for ecosystem management reiterated as part of Kobe III, the approach outlined in this document is a method that can be readily applied.

The SEFRA approach for exploring spatial and temporal risk to bycatch species has been applied successfully in the New Zealand context to marine mammals, seabirds and sharks (e.g., MacKenzie et al. 2023, Roberts et al. 2019, Large et al. 2019, Edwards et al. 2023a, Edwards 2023) and when coupled with resulting management actions can be used to manage fisheries risk (e.g., MPI 2021). As such, the approach documented here has been adapted to meet the needs of CCSBT members in exploring risk to seabirds but can be variously adapted to undertake work with other by-catch species.

1.3 Context for the application of SEFRA in the CCSBT

The issue of incidental bycatch of seabirds in southern bluefin tuna (SBT) fisheries was well recognised even at the time of establishment of the Commission for the Conservation of Southern Bluefin Tuna (CCSBT) in 1994. An initial draft of recommendations on reducing this bycatch was developed in 2006 at the 6th meeting of the CCSBT Ecologically Related Species Working Group (ERSWG). In 2008 CCSBT agreed on the need to assess impact on species considered under the ERSWG and in 2018 a resolution to align CCSBT’s ecologically related species (ERS) measures with those of other tuna Regional Fisheries Management Organisations (tRFMOs) was adopted at the 25th Annual Meeting.

At the 13th meeting of the CCSBT ERSWG in 2019, an initial assessment of global seabird bycatch among all tRFMOs through the Areas Beyond National Jurisdiction (ABNJ) Tuna Project was concluded (Abraham et al. 2019). Alongside this assessment, commitments to develop a ERSWG workplan led to the CCSBT Multi-year Seabird Strategy, which was adopted at the 26th Annual Meeting of CCSBT.

A range of actions to be undertaken under each specific objective of the Multi-year Seabird Strategy was developed at the 14th meeting of ERSWG in 2021 and adopted by the 29th Annual meeting of CCSBT, which included an action to "update SEFRA seabird risk assessment," with New Zealand and Japan taking a leading role. This work would also provide a foundation for work across tRFMOs by developing methods suitable for assessing the incidental bycatch of seabird in their respective fisheries.

2. DATA

Data included that which had been collated throughout the course of the current project and as well as previous work for Fisheries New Zealand (Edwards et al. 2023a,b, Peatman et al. 2023, Richard et al. 2020, 2017a,b, Richard & Abraham 2015, 2013). It further includes additional input data submitted directly by Japan and Taiwan, as part of a collaborative update to the intial work of Edwards et al. (2023b) and Abraham et al. (2019, 2017b,c). These data, and the process of collection and review, are presented in accompanying reports (Edwards et al. 2024, CCSBT 2024). Of relevance to description of the methods, we outline some of the terminology used when describing the biological and fisheries data.

2.1 Preparation of the capture data

Biological data are referenced by species code (Table 1). Species are grouped according to shared biological (including behavioural) attributes, and this grouping provides a covariate input for estimation of the catchability. The observed fishery data are presented by fishery group and capture code. Capture codes that are different from the species codes (Table 2) are required because captures are not necessarily recorded at the species level. Rather, captures can be recorded at a lower taxonomic resolution (e.g., the family or genus) and codes are required to represent these lower taxonomic levels. Capture codes can also be grouped. However, these capture groups are not used during the model fit. Rather they are used to construct data summaries that include captures identified to a taxonomic resolution lower than the species level.

When preparing the data for analysis, we acknowledged two sources of error present in the capture data:

1. Incomplete identification: this occurs when a capture is not identified to the species level, but to a lower taxonomic resolution;

2. Incorrect identification: this is when the capture is recorded as something other than what was caught. It can occur at any taxonomic level of recording but is less likely at lower taxonomic resolutions.

In the absence of data pertaining to incorrect identification of birds, some errors of this type were noted during the data preparation process from captures recorded at geographical locations where the species is thought to be absent. However, we did not attempt to include this type of observation error in the model, nor to correct it by removing data. Because the distribution maps were known to contain errors (Edwards et al. 2024) removing captures from regions of zero overlap would have led to underestimation of the catchability. Because the model is fitted to the sum of the overlap (Equation 9), the sum of the overlap was always greater than zero, meaning that it was also not necessary to exclude them. Nevertheless, it was decided to partly compensate for incorrect identification of captures by aggregating captures into lower taxonomic groups. Low resolution capture codes were already present in the data, and we therefore used this approach to account for instances in which incorrect identification was suspected. Specifically, all recorded captures of:

- Northern Buller's albatross (*Thalassarche bulleri platei*) and Southern Buller's albatross (*Thalassarche bulleri bulleri*) were assigned to Buller's albatross (DIB);
- Atlantic yellow-nosed albatross (*Thalassarche chlororhynchos*) and Indian yellow-nosed albatross (*Thalassarche carteri*) were assigned to Yellow-nosed albatrosses (DYN);
- Shy albatross (*Thalassarche cauta*) and New Zealand white-capped albatross (*Thalassarche cauta steadi*) were assigned to Shy-type albatross (DST);
- Gibson's albatross (*Diomedea antipodensis gibsoni*), Antipodean albatross (*Diomedea antipodensis antipodensis*), Wandering albatross (*Diomedea exulans*), Tristan albatross (*Diomedea dabbenena*) and Amsterdam albatross (*Diomedea amsterdamensis*) were assigned to Wandering albatross complex (DWC; Table 2). Captures recorded as being one of the Antipodean albatrosses (*Diomedea antipodensis*) were also assigned to this capture group.

A summary of the capture data, as well as the biological and fishery inputs, is given by Edwards et al. (2024) and CCSBT (2024).

Table 1: Species and species groups used in the southern hemisphere risk assessment model. Species codes are from the FAO-ASFIS species list where possible (https://www.fao.org/fishery/en/species/search). The species group definitions provide a covariate input for estimation of the catchability

Code	Common name	Scientific name	Species group
DIW	Gibson's albatross	*Diomedea antipodensis gibsoni*	Wandering albatross
DQS	Antipodean albatross	*Diomedea antipodensis antipodensis*	Wandering albatross
DIX	Wandering albatross	*Diomedea exulans*	Wandering albatross
DBN	Tristan albatross	*Diomedea dabbenena*	Wandering albatross
DAM	Amsterdam albatross	*Diomedea amsterdamensis*	Wandering albatross
DIP	Southern royal albatross	*Diomedea epomophora*	Royal albatross
DIQ	Northern royal albatross	*Diomedea sanfordi*	Royal albatross
DCR	Atlantic yellow-nosed albatross	*Thalassarche chlororhynchos*	Small albatross
TQH	Indian yellow-nosed albatross	*Thalassarche carteri*	Small albatross
DIM	Black-browed albatross	*Thalassarche melanophris*	Small albatross
TQW	Campbell black-browed albatross	*Thalassarche impavida*	Small albatross
DCU	Shy albatross	*Thalassarche cauta*	Small albatross
TWD	New Zealand white-capped albatross	*Thalassarche cauta steadi*	Small albatross
DKS	Salvin's albatross	*Thalassarche salvini*	Small albatross
DER	Chatham Island albatross	*Thalassarche eremita*	Small albatross
DIC	Grey-headed albatross	*Thalassarche chrysostoma*	Small albatross
DSB	Southern Buller's albatross	*Thalassarche bulleri bulleri*	Small albatross
DNB	Northern Buller's albatross	*Thalassarche bulleri platei*	Small albatross
PHU	Sooty albatross	*Phoebetria fusca*	Sooty albatross
PHE	Light-mantled sooty albatross	*Phoebetria palpebrata*	Sooty albatross
PCI	Grey petrel	*Procellaria cinerea*	Medium petrel
PRK	Black petrel	*Procellaria parkinsoni*	Medium petrel
PCW	Westland petrel	*Procellaria westlandica*	Medium petrel
PRO	White-chinned petrel	*Procellaria aequinoctialis*	Medium petrel
PCN	Spectacled petrel	*Procellaria conspicillata*	Medium petrel

Table 2: Capture codes and groups used in the southern hemisphere risk assessment model. The capture code for the Antipodean albatrosses (*Diomedea antipodensis*) (DGA), is excluded, because all DGA captures were assigned to the DWC capture code as part of the data preparation. The taxonomic resolution is listed, because of it's relevance to the prediction of each capture code by the model. The capture groups are used to summarise and describe the capture data; they are not used as a structural input to the model.

Code	Common name	Scientific name	Resolution	Capture group
DIP	Southern royal albatross	*Diomedea epomophora*	Species	Great albatross
DIQ	Northern royal albatross	*Diomedea sanfordi*	Species	Great albatross
DIM	Black-browed albatross	*Thalassarche melanophris*	Species	Mollymawk
TQW	Campbell black-browed albatross	*Thalassarche impavida*	Species	Mollymawk
DKS	Salvin's albatross	*Thalassarche salvini*	Species	Mollymawk
DER	Chatham Island albatross	*Thalassarche eremita*	Species	Mollymawk
DIC	Grey-headed albatross	*Thalassarche chrysostoma*	Species	Mollymawk
PHU	Sooty albatross	*Phoebetria fusca*	Species	Sooty albatross
PHE	Light-mantled sooty albatross	*Phoebetria palpebrata*	Species	Sooty albatross
PCI	Grey petrel	*Procellaria cinerea*	Species	Medium petrel
PCN	Spectacled petrel	*Procellaria conspicillata*	Species	Medium petrel
DRA	Royal albatrosses	*Diomedea epomophora* and *D. sanfordi*	Complex	Great albatross
DYN	Yellow-nosed albatrosses	*Thalassarche chlororhynchos* and *T. carteri*	Complex	Mollymawk
DST	Shy-type albatross	*Thalassarche cauta* and *T. c. steadi*	Complex	Mollymawk
DBB	Black-browed albatrosses	*Thalassarche melanophris* and *T. impavida*	Complex	Mollymawk
DIB	Buller's albatross	*Thalassarche bulleri bulleri* and *T. bulleri platei*	Complex	Mollymawk
DWC	Wandering albatross complex	*Diomedea exulans, D. dabbenena, D. amsterdamensis, D. antipodensis gibsoni* and *D. a. antipodensis*	Complex	Great albatross
PRZ	Petrel complex	*Procellaria parkinsoni, P. westlandica* and *P. aequinoctialis*	Complex	Medium petrel
DIZ	*Diomedea* spp.	*Diomedea* spp.	Genus	Great albatross
THZ	*Thalassarche* spp.	*Thalassarche* spp.	Genus	Mollymawk
PHZ	*Phoebetria* spp.	*Phoebetria* spp.	Genus	Sooty albatross
PTZ	*Procellaria* spp.	*Procellaria* spp.	Genus	Medium petrel
ALZ	Diomedeidae	Diomedeidae	Family	Unassigned
PRX	Procellariidae	Procellariidae	Family	Unassigned
BLZ	Bird	–	Phyla	Unassigned

2.2 Structural assumptions

To predict captures from overlap the catchability (q) is required. The catchability is usually estimated for a species group rather than a species. This allows the capture records of more abundant species to inform estimation of the catchability for rare and threatened species, which may be similarly vulnerable to fishing but are less frequently caught because of their smaller population size. Species group should preferrably be determined according to feeding behaviour, aggression and willingness to travel large distances to a fishing vessel, all of which will influence the susceptibility to fishing. A catchability coefficient is shared across species within a species group because of an assumption that their vulnerability to fishing is determined by these shared behavioural characteristics.

Recent assessments of risk at the southern hemisphere scale have been designed to cover the 27 Agreement for the Conservation of Albatross and Petrels (ACAP) species (with additional distinction between Antipodean albatross *Diomedea antipodensis antipodensis* and Gibson's albatross *Diomedea antipodensis gibsonii*, and Northen Buller's albatross *Thalassarche bulleri platei* and Southern Buller's albatross *Thalassarche bulleri bulleri*) that inhabit this region (Edwards et al. 2023b, ACAP 2015). These species were assigned to six species groups: wandering albatross, royal albatross, small albatross, sooty albatross, large petrel, and medium petrel. The list of species assessed, along with their species group, is given in Table 1.

Calculating the overlap between fishery group and species group is a critical step in the SEFRA methodology. Considerations for the desired resolution of final results for relevant management purposes and privacy of participating fisheries must be taken into account when defining fisheries groups. In the New Zealand domestic context fishery groups have been defined by method, vessel characteristics and seabird mitigation requirements (Edwards et al. 2023a). For application in tuna Regional Fisheries Management Organizations (tRFMOs), the fleets of individual tRFMO members can each be treated as one fishery fleet, except where there is evidence of clear operational or vessel differences. In the context of the CCSBT, such a distinction could be made for the Japanese joint-venture (JV) operation under New Zealand's flag. This is due to differences in vessel size and operational characteristics between the JV operation and the domestic New Zealand surface longline fleet, as well as the strict management and surveillance requirements under the JV arrangement. For those fisheries groups with no available observed capture data, a proxy value of q can be obtained from a fleet with similar operational characteristics, such as operating area, vessel size, mitigation requirements and gear configuration (described in CCSBT 2024).

3. METHODS

3.1 Seabird population size

Seabird population size data usually indicates the number of breeding pairs per colony. The number of adults per species (s) was therefore calculated from the global sum of the number of breeding pairs and the probability of breeding:

$$N_s^{\text{adults}} = 2 \cdot \frac{N_s^{\text{BP}}}{P_s^{\text{B}}} \tag{3}$$

The number of adults available available to be caught by CCSBT longline fishing fleets during any month of the year was determined from the probability that they are in the southern hemisphere (SH), the probability that they are breeding, and whether they are likely to be attending the nest

Table 3: Glossary of model terms.

Notation	Description
Subscripts	
f	Fishing group
s	Species
z	Species group
k	Capture code
m	Month
x	Spatial location or grid cell
Estimated parameters	
N_s^{BP}	Number of breeding pairs
P_s^{B}	Annual probability of breeding
S_s^{opt}	Annual optimum survivorship
A_s^{curr}	Current age at first breeding
β_0, β_f, $\beta_{z\|f}$	$q_{f,z}$ regression coefficients
γ_0, γ_f, $\gamma_{z\|f}$	$\Psi_{f,z}$ regression coefficients
π_f	Vector of capture assignment probabilities
Derived parameters	
N_s^{adults}	Total number of adults
$N_{s,m}$	Number of adults available to fishing
N_s	$N_{s,m}$ summed across months
$\mathbb{D}_{s,m,x}$	Density of adults available to fishing
$q_{f,z}$	Catchabilty
$\Psi_{f,z}$	Prob. of capture being alive
$C_{f,s}$	Number of captures per species
$C_{f,k}$	Number of captures per capture code
$\kappa_{f,z}$	Mortality multiplier
$D_{f,s}$	Number of deaths per species
Input covariates	
$P_{s,m}^{\mathrm{SH}}$	Probability of an adult being in the southern hemisphere
$P_{s,m}^{\mathrm{nest}}$	Probability of a breeding adult being on the nest
$d_{s,m,x}$	Relative density of adults per square kilometre
$a_{f,m,x}$	Fishing effort
K	Cryptic mortality multiplier
ω	Probability of post-release survivorship
Derived covariates	
$\mathbb{O}_{f,s}$	Density overlap
Observational data	
$C_{f,k}$	Number of observed captures

whilst doing so. The number of available adults per species and month (m) is:

$$N_{s,m} = N_s^{\text{adults}} \cdot (1 - P_s^{\text{B}} \cdot P_{s,m}^{\text{nest}}) \cdot P_{s,m}^{\text{SH}} \tag{4}$$

Outside the breeding season the probability of breeding is zero (i.e., $P_{s,m}^{\text{nest}} = 0$), and all adults in the southern hemisphere are considered available to fishing gear.

The population size $N_{s,m}$ was used for predicting the captures and fitting the model, whereas the total adult population size N_s^{adults} was used for calculation of the relative mortality (Equation 2).

3.2 Spatial overlap

The SEFRA model requires that the individuals available to be caught are represented as a spatial distribution. This spatial distribution is treated as a fixed data input and described using a density term ($d_{s,m,x}$) per species s, grid cell x and month m. Specifically, if $y_{s,m,x}$ is the number of birds in grid cell x, then:

$$d_{s,m,x} = \frac{y_{s,m,x}}{A_x \cdot \sum_x y_{s,m,x}} \tag{5}$$

The value $y_{s,m,x} / \sum_x y_{s,m,x}$ is effectively being treated as the multinomial sampling probability of an individual being in grid cell x during that month. The absolute density, in number of birds per square kilometre, is therefore:

$$\mathbb{D}_{s,m,x} = d_{s,m,x} \cdot N_{s,m} \tag{6}$$

If fishing effort for each fishery group f is allocated to grid cell x, and assuming a uniform distribution of birds and fishing effort within that cell, then we can construct an overlap metric that measures the opportunity for interaction between a bird population and fishing effort:

$$\text{overlap}_{f,s,m,x} = \underbrace{\text{effort}_{f,m,x}}_{a_{f,m,x}} \cdot d_{s,m,x} \tag{7}$$

The overlap provides a measure of the exposure of birds to fishing effort at a particular time and place, relative to the population as a whole. To estimate the catchabiliy, SEFRA uses the density overlap:

$$\underbrace{\text{density overlap}_{f,s}}_{\mathbb{O}_{f,s}} = \sum_{m,x} a_{f,m,x} \cdot \mathbb{D}_{s,m,x} \tag{8}$$

for which we introduce the notation $\mathbb{O}_{f,s}$ and $a_{f,m,x}$ (Table 3; and Sharp 2019). The density overlap is a summation across grid cells and months, per species and fishery, and provides an input to the regression model.

3.3 Fitting the model

3.3.1 Prediction of captures per species

Multiplication of the density overlap with the catchability ($q_{f,z}$) yields the model predicted captures per species and fishing fleet:

$$\underbrace{\text{captures}_{f,s}}_{C_{f,s}} = q_{f,z} \cdot \mathbb{O}_{f,s} \tag{9}$$

The catchability itself is a function of fishery group (f) and species group (z) covariates:

$$\log(q_{f,z}) = \beta_0 + \beta_f + \beta_{z|f} \tag{10}$$

where the fishery group coefficient β_f is centred on the intercept term, with deviations around this intercept constrained to sum to zero. Species group coefficients ($\beta_{z|f}$) were specific to the fishery group and were similarly constrained to sum to zero. This allowed the catchability per species group to deviate from the fishery group effect in a fishery group-specific manner.

Because data were available on the status of captures (i.e., whether captures were alive or dead), we could also estimate the probability of live capture:

$$\operatorname{logit}(\Psi_{f,z}) = \gamma_0 + \gamma_f + \gamma_{z|f} \tag{11}$$

where γ_0 is an intercept term and with coefficients γ_f and $\gamma_{z|f}$ similarly constrained to sum to zero.

3.3.2 Prediction of captures per capture code

Model predicted captures are per species, but to match the observed captures they must be assigned to one or more capture codes, with some of these capture codes representing groups of species. For example, captures of Gibson's albatross (DIW; Table 1) may be recorded using DWC, DIZ, ALZ or BLZ capture codes (Table 2). Whilst, captures of sooty albatross (PHU) may be recorded using PHU, PHZ, ALZ or BLZ capture codes. We are required to map the model predicted captures (per species), onto the observed captures (per capture code) in order to fit the model.

To predict the captures per capture code we introduce the vector of probability terms: π, which are a set of probabilities describing the taxonomic resolution to which a species capture is identified. These probabilities are estimated per fishery group, but the f subscript is ommitted for clarity of presentation:

$$\pi = \{\pi_{\text{species}}, \pi_{\text{complex}}, \pi_{\text{genus}}, \pi_{\text{family}}, \pi_{\text{phyla}}\} \tag{12}$$

The π terms sum to one. For example, a southern royal albatross (DIP) capture will be identified to the species level with probability π_{species} or the genus level with probability π_{genus}. We can also define:

$$\begin{aligned}
\pi^{+}_{\text{species}} &= \pi_{\text{species}} \\
\pi^{+}_{\text{complex}} &= \pi_{\text{species}} + \pi_{\text{complex}} \\
\pi^{+}_{\text{genus}} &= \pi_{\text{species}} + \pi_{\text{complex}} + \pi_{\text{genus}} \\
\pi^{+}_{\text{family}} &= \pi_{\text{species}} + \pi_{\text{complex}} + \pi_{\text{genus}} + \pi_{\text{family}} \\
\pi^{+}_{\text{phyla}} &= \pi_{\text{species}} + \pi_{\text{complex}} + \pi_{\text{genus}} + \pi_{\text{family}} + \pi_{\text{phyla}} = 1
\end{aligned} \tag{13}$$

These are the cumulative probabilities, i.e., the probability of a capture being recorded at that taxonomic resolution or higher, or to "at least" that resolution. For example, π_{complex} gives the probability that a DIP species capture is recorded as a member of the royal albatross species complex (DRA), and π^{+}_{complex} the probability that a DIP capture is recorded as either DIP or DRA. Typically, $\pi_{\text{complex}} < \pi^{+}_{\text{complex}}$, unless the probability of a species capture is zero ($\pi_{\text{species}} = 0$).

The π_{species} term is a single estimated parameter that is being used for multiple species. In reality, because of differences in the ease of identification, each species will likely have a different probability of being identified to the species level. For example, π_{species} may be greater than zero for DIP, but equal to zero for other species that are not recorded to the species level. The same problem will exist at the lower taxonomic resolutions where simple probability terms are used to describe a more complicated process of capture identification. This can in principle be resolved by using a higher resolution of π parameters, and is ulitimately dependent on ability of the data to support the estimation of these parameters.

In general, the cumulative probabilities have the property that:

$$\pi^{+}_{\text{species}} \leq \pi^{+}_{\text{complex}} \leq \pi^{+}_{\text{genus}} \leq \pi^{+}_{\text{family}} \leq \pi^{+}_{\text{phyla}} \tag{14}$$

Using these probabilities we can now predict the observed captures per capture code from the model predicted captures per species. We use the following notation. The observed data are:

- C_k: captures per capture code k;
- C^{+}_{k}: cumulative sum of the captures per capture code k (i.e., the sum of all observed captures to capture code k or a higher taxonomic resolution);

and the model predictions are:

- $\hat{C}_s$: captures per species s;
- $\hat{C}_k$: captures per code k;
- $\hat{C}^{+}_{k}$: cumulative sum of the captures per code k.

The relationship between observations C_k and C^{+}_{k} can be written explicitly using a two-dimensional matrix (also known as a *linear map*). Because of the large number of species in the assessment, which makes it cumbersome to write out in full, we provide an illustration assuming that only DIW, DIQ and PHU are being assessed. In this example, the relationship between the observed captures per capture code (C_k) and the cumulative sum of the observed captures (C^{+}_{k}) is:

$$\begin{bmatrix} C^{+}_{DIW} \\ C^{+}_{DIQ} \\ C^{+}_{PHU} \\ C^{+}_{DWC} \\ C^{+}_{DRA} \\ C^{+}_{DIZ} \\ C^{+}_{PHZ} \\ C^{+}_{ALZ} \\ C^{+}_{BLZ} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \end{bmatrix} \times \begin{bmatrix} C_{DIW} \\ C_{DIQ} \\ C_{PHU} \\ C_{DWC} \\ C_{DRA} \\ C_{DIZ} \\ C_{PHZ} \\ C_{ALZ} \\ C_{BLZ} \end{bmatrix} \tag{15}$$

The relationship between the model predicted species-level captures ($\hat{C}_s$) and the predicted captures per code ($\hat{C}_k$) is:

$$\begin{bmatrix} \hat{C}_{DIW} \\ \hat{C}_{DIQ} \\ \hat{C}_{PHU} \\ \hat{C}_{DWC} \\ \hat{C}_{DRA} \\ \hat{C}_{DIZ} \\ \hat{C}_{PHZ} \\ \hat{C}_{ALZ} \\ \hat{C}_{BLZ} \end{bmatrix} = \begin{bmatrix} \pi_{\text{species}} & 0 & 0 \\ 0 & \pi_{\text{species}} & 0 \\ 0 & 0 & \pi_{\text{species}} \\ \pi_{\text{complex}} & 0 & 0 \\ 0 & \pi_{\text{complex}} & 0 \\ \pi_{\text{genus}} & \pi_{\text{genus}} & 0 \\ 0 & 0 & \pi_{\text{genus}} \\ \pi_{\text{family}} & \pi_{\text{family}} & \pi_{\text{family}} \\ \pi_{\text{phyla}} & \pi_{\text{phyla}} & \pi_{\text{phyla}} \end{bmatrix} \times \begin{bmatrix} \hat{C}_{DIW} \\ \hat{C}_{DIQ} \\ \hat{C}_{PHU} \end{bmatrix} \tag{16}$$

which has the property that $\sum \hat{C}_k = \sum \hat{C}_s$. This property exists because each species-level prediction is partitioned using the probabilites in Equation 12, which sum to one.

One feature of Equation 16 is that it can predict captures even if there are no observations. This is particularly clear for the lower taxonomic resolutions. For example, observations of C_{DIZ} will lead the model to estimate $\pi_{\text{genus}} > 0$, and therefore always predict captures for $\hat{C}_{PHZ}$, even if there are no observations of C_{PHZ} in the data. For this reason the assessment should always be conditioned on species known to be caught, otherwise it will predict captures for additional species not present in the data.

The relationship between model predicted species-level captures ($\hat{C}_s$) and the cumulative sum of model predicted captures ($\hat{C}^+_k$) is:

$$\begin{bmatrix} \hat{C}^+_{DIW} \\ \hat{C}^+_{DIQ} \\ \hat{C}^+_{PHU} \\ \hat{C}^+_{DWC} \\ \hat{C}^+_{DRA} \\ \hat{C}^+_{DIZ} \\ \hat{C}^+_{PHZ} \\ \hat{C}^+_{ALZ} \\ \hat{C}^+_{BLZ} \end{bmatrix} = \begin{bmatrix} \pi^+_{\text{species}} & 0 & 0 \\ 0 & \pi^+_{\text{species}} & 0 \\ 0 & 0 & \pi^+_{\text{species}} \\ \pi^+_{\text{complex}} & 0 & 0 \\ 0 & \pi^+_{\text{complex}} & 0 \\ \pi^+_{\text{genus}} & \pi^+_{\text{genus}} & 0 \\ 0 & 0 & \pi^+_{\text{genus}} \\ \pi^+_{\text{family}} & \pi^+_{\text{family}} & \pi^+_{\text{family}} \\ 1.0 & 1.0 & 1.0 \end{bmatrix} \times \begin{bmatrix} \hat{C}_{DIW} \\ \hat{C}_{DIQ} \\ \hat{C}_{PHU} \end{bmatrix} \tag{17}$$

which has the property that $\hat{C}^+_{BLZ} = \sum \hat{C}_s$. This is useful because it is independent of the estimated π terms. Furthermore, equality of $\hat{C}^+_{BLZ}$ and C^+_{BLZ} ensures that the model is accurately predicting the total number of bird captures.

When diagnosing performance, an important property of the model is that estimates of $\hat{C}_s$ are not independent. If, for example, the number of observed C_{BLZ} increases, then predicted captures for all $\hat{C}_s$ will increase to fit these data. Similarly for other resolutions. In the example being considered here, an increase in observed captures for C_{DIZ} will cause predicted captures of both $\hat{C}_{DIW}$ and $\hat{C}_{DIQ}$ to increase. This property can lead to non-intuitive results, particularly when deciding on which species to include in the assessment. Because species captures can be recorded at a taxonomic resolution that is shared with other species, when adding or removing species from the model the predicted captures for those other species can be affected.

3.3.3 Parameter estimation

Both Equation 16 and Equation 17 describe a relationship between model predictions and observed values, and either of them can be used to construct a likelihood for the model fit. In the current work, Equation 17 was preferred. This was because the cumulative capture data are likely more reliable: real world species-level captures can be recorded at a variety of taxonomic levels, and in general we would expect the sum of the captures to be a more reliable data point than the disaggregated data. In the above example, fitting $\hat{C}_{DIZ}$ to C_{DIZ} is likely more problematic than fitting $\hat{C}^+_{DIZ}$ to C^+_{DIZ}. This is because the reality of DIW and DIQ captures being recorded as C_{DIW}, C_{DIQ}, C_{DWC}, C_{DRA}, or C_{DIZ} will be imperfectly represented by the structural partitions of the π vector; but the cumulative sum of these captures is less likely to be effected by this deficiency. A consequence of the approach is that when calculating the cumulative sum, the data are being pseudo-replicated. However, this should not in itself affect the model fit, only lead us to underestimate the uncertainty, and was considered a necessary approximation for the current work. The model was therefore fitted to the capture data using a Poisson likelihood function conditioned on the cumulative captures:

$$C_k^+ \sim Poisson(\hat{C}_k^+) \tag{18}$$

A Binomial likelihood function, conditioned on the number of captures for which life status was recorded, was used to estimate the probability of a capture being alive ($\Psi_{f,z}$).

Estimated parameters are listed in Table 3. Estimation of the vector of π values allows the model to predict $\hat{C}_k^+$ from $\hat{C}_s$ and π^+ (Equations 13 and 17), as well as $\hat{C}_k$ (Equation 16), with the latter being an optional model diagnostic. Biological parameters N_s^{BP} and P_s^{B} were also estimated, with strongly informed priors, whereas $P_{s,m}^{\mathrm{SH}}$ and $P_{s,m}^{\mathrm{nest}}$ were fixed on input (Edwards et al. 2024). Estimation of N_s^{BP} and P_s^{B} was justified because they are the most important determinants of the number of birds available for capture (Equation 4). The model is able to fit the data by changes in either $q_{f,z}$ or $N_{s,m}$, and by estimating $N_{s,m}$ we can use it as a diagnostic of the model fit. In a correctly specified model, we would not expect N_s^{BP} or P_s^{B} to be updated from their prior values. If this occurs, it can indicate a deficiency in either the data or the structural assumptions, which can then be investigated. Usually it would indicate that $q_{f,z}$ is constrained in a way that prevents it from adequately describing the data, requiring the model to update $N_{s,m}$ instead (for an alternative approach, see Edwards et al. 2023a, where the authors improved model fit by estimating catchability at the species level and preventing the need for model updates to the biological priors). If only minor updates occur, then these are incorporated directly into the relative mortality estimate (Equation 2), ensuring internal consistency of the relative mortality estimate. For the same reasons S_s^{opt} and A_s^{curr} are also estimated, because these are used internally by the model for estimation of $r_{\max}$ (Section 3.4.2). Similar to the other biological paramters, they are provided with informative priors, which we do not expect to be updated. If updates do occur, then this approach allows deficiencies in either the data or the model to be diagnosed, whilst maintaining consistency between the parameters required for calculation of the relative mortality.

All estimation was performed within a Bayesian framework using rstan (R Core Team 2023, Stan Development Team 2023). Predictor coefficients for the catchability (β_f and $\beta_{z|f}$; Equation 10) and live capture (γ_f and $\gamma_{z|f}$; Equation 11) were given standard normal priors, whereas the intercept terms β_0 and γ_0, were given improper (unbounded) prior distributions.

Posterior samples from estimated parameters were inspected visually to ensure convergence of the model, which was typically good. The second most important diagnostic was an assessment of the model fit to the data, for which we compared values of C_k^+ and $\hat{C}_k^+$. The structural partitions of π were evaluated from a comparision of C_k and $\hat{C}_k$. If the structural assumptions are appropriate for the data, then these values should also be similar. Finally, we inspected updates to the biological values, particularly N_s^{BP} and P_s^{B}. If either of these demonstrated strong prior updates then this would indicate model mis-specification.

3.4 Estimating the relative mortality

3.4.1 Prediction of total deaths

During the fitting process we estimate the catchability $q_{f,z}$, which describes the rate of observed capture per unit of density overlap. Using this estimated value we can then predict the total observable captures across all the fishing effort included in the assessment. However, observable captures are only a subset of all the interactions between fishing effort and birds, and from this subset we are required to predict the total number of deaths.

Captures can lead directly to death but will underestimate the total number of deaths because some captures can be cryptic (unobservable even were an observer present). To calculate the number of deaths from the number captures we used a mortality multiplier ($\kappa_{f,z}$). For longline fisheries, we assume that captures that occur during setting invariably cause death by drowning, and can be lost, but that live birds are caught during the haul and are always recorded. To estimate the total number of deaths we therefore need $\kappa_{f,z}$ to account for drowned birds that are lost, and live birds that die post-release.

The probability of a bird being alive at capture ($\Psi_{f,z}$) was estimated as part of the model fit, but for this assessment it was assumed that almost all seabirds that were caught subsequently died (post release survival was given a mean value of $\omega = 0.01$). For birds caught during setting and subsequently lost, it was decided during the second technical workshop in New Zealand to use the surface longline multiplier (K) from the Edwards et al. (2023a) assessment.

The total number of deaths for the surface longline fishery groups was therefore predicted from the model estimated values of $q_{f,z}$ and $\Psi_{f,z}$ using:

$$D_{f,s} = q_{f,z} \cdot \mathbb{O}_{f,s} \cdot \underbrace{(\Psi_{f,z} \cdot (1-\omega) + (1-\Psi_{f,z}) \cdot K)}_{\kappa_{f,z}} \tag{19}$$

All deaths were generated using posterior predictive simulation from a Poisson distribution conditioned on the expected value. The number of total deaths per species is a summation of the deaths across the fishery group:

$$D_s = \sum_f D_{f,s} \tag{20}$$

This was compared with the relative mortality reference point to calculate the relative species-specific risk (Equation 2).

3.4.2 Maximum intrinsic growth, $r_{\max}$

For the relative mortality reference point we are required to estimate a distribution for $r_{\max} = \ln(\lambda)$. This was achieved using allometric theory. Following the approach of Niel & Lebreton (2005), mean generation time is first approximated as:

$$\bar{T} = A + \frac{S}{\lambda - S}$$

Allometric theory defines the optimal generation time such that:

$$T_{[opt]} \cdot \ln(\lambda) = k$$

where $k \approx 1$ is a constant. Therefore under constant fecundity and assumed optimal conditions we can write:

$$\frac{k}{\ln(\lambda)} = A + \frac{S^{opt}}{\lambda - S^{opt}}$$

$$\implies \lambda = \exp\left(k \cdot \left(A + \frac{S^{opt}}{\lambda - S^{opt}}\right)^{-1}\right) \tag{21}$$

which can be solved numerically. This provides the so-called demographic-invariant solution for λ (Niel & Lebreton 2005) that has been used for applications of the SEFRA methodology to date (e.g., Abraham et al. 2017b,c,a, Ochi et al. 2018, Abraham et al. 2019).

To implement this approach, we required information on the optimum survivorship (S_s^{opt}) and the current age at first breeding (A_s^{curr}), with the latter assumed to be indicative of the current environmental conditions. These were treated as estimated parameters within the model, each with strongly informed priors (values and disributions are listed by Edwards et al. 2024). In this way, local minimisation of Equation 21 (i.e., using a root finding algorithm to estimate λ), could be performed for each posterior sample of S_s^{opt}, A_s^{curr}, P_s^B and N_s^{BP}, to calculate the product $r_{\max} \cdot N_s^{\text{adults}}$ as a model output (Equation 3). This was considered preferable to the estimation of $r_{\max}$ outside of the model, however it does make the estimation of the product $r_{\max} \cdot N_s^{\text{adults}}$ susceptible to strong updates of the biological priors, which may be a consequence of model mis-specification. In this instance, estimates of the relative mortality should be treated with caution.

3.4.3 Relative mortality

Using the estimated model parameters, which allow the prediction of deaths, the population size and $r_{\max}$, we were able to calculate the relative mortality per species using Equation 2. Comparing these across species provided an indication of those species most at risk from fishing.

4. RESULTS AND CONCLUSIONS

The model described in this report was applied to data supplied by collaborating members of the CCSBT (Edwards et al. 2024) and presented at the Fifteenth Meeting of the Ecologically Related Species Working Group. Model outputs and diagnostics are provided in the meeting report (CCSBT 2024).

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6. REFERENCES

Abraham, E.; Richard, Y.; Walker, N.; Gibson, W.; Daisuke, O.; Tsuji, S.; Kerwath, S.; Winker, H.; Parsa, M.; Small, C.; Waugh, S. (2017a). Assessment of the risk of surface longline fisheries in the Southern Hemisphere to albatrosses and petrels, for 2016. *Report to the CCSBT ERSWG (CCSBT-ERS/1905/17)*

Abraham, E.R.; Richard, Y.; Walker, N.; Gibson, W.; Daisuke, O.; Tsuji, S.; Kerwath, S.; Winker, H.; Parsa, M.; Small, C.; Waugh, S. (2019). Assessment of the risk of surface longline fisheries in the Southern Hemisphere to albatrosses and petrels, for 2016. *Report to the CCSBT ERSWG (CCSBT-ERS/1905/17)*

Abraham, E.R.; Richard, Y.; Walker, N.; Roux, M.J. (2017b). Assessment of the risk of commercial surface longline fisheries in the southern hemisphere to ACAP seabird species. *Report to the CCSBT ERSWG (CCSBT-ERS/1905/BGD 03)*

Abraham, E.R.; Richard, Y.; Walker, N.; Roux, M.J. (2017c). Assessment of the risk of Southern Hemisphere surface longline fisheries to ACAP species. *Report to the Western and Central Pacific Fisheries Commission Scientific Committee (WCPFC-SC13-2017/EB IP-13)*

ACAP (2015). Albatross and petrel species to which the agreement applies. https://acap.aq/acap-species/307-acap-species-list/file. [Accessed on 4-Aug-2024].

Baker, G.; Candy, S.; Parker, G. (2021). Improving estimates of cryptic mortality for use in seabird risk assessments: loss of seabirds from longline hooks. *New Zealand Aquatic Environment and Biodiversity Report No. 268.* 7 p.

CCSBT (2024). Report of The Fifteenth Meeting of the Ecologically Related Species Working Group, Commission for the Conservation of Southern Bluefin Tuna. 4 – 7 June 2024 Tokyo, Japan. 110 p.

Edwards, C.T.T. (2023). Development of spatial fisheries risk assessment methods for sharks and turtles in New Zealand waters. *New Zealand Aquatic Environment and Biodiversity Report No. 319.* 94 p.

Edwards, C.T.T.; Peatman, T.; Daisuke, O.; Kuo, T.C.; Fischer, J.; Tsuji, S.; Gibson, W. (2024). Seabird risk assessment data inputs for the Southern Bluefin Tuna surface longline fishery. *New Zealand Aquatic Environment and Biodiversity Report No. XXX.*

Edwards, C.T.T.; Peatman, T.; Goad, D.; Webber, D.N. (2023a). Update to the risk assessment for New Zealand seabirds. *New Zealand Aquatic Environment and Biodiversity Report No. 314.*

Edwards, C.T.T.; Peatman, T.; Roberts, J.O.; Devine, J.A.; Hoyle, S.D. (2023b). Updated fisheries risk assessment framework for seabirds in the Southern Hemisphere. *New Zealand Aquatic Environment and Biodiversity Report No. 321.*

ICCAT (2011). Chair's report of the joint third meeting of the tuna regional fisheries management organisations (kobe iii). , International Commission for the Conservation of Atlantic Tunas.

Large, K.; Roberts, J.; Francis, M.; Webber, D. (2019). Spatial assessment of fisheries risk for New Zealand sea lions at the Auckland Islands. *New Zealand Aquatic Environment and Biodiversity Report No. 224.* 85 p.

Lonergan, M.E.; Phillips, R.A.; Thomson, R.B.; Zhou, S. (2017). Independent review of New Zealand's Spatially Explicit Fisheries Risk Assessment approach - 2017. *New Zealand Fisheries Science Review 2017/2* 36 p.

MacKenzie, D.I.; Meyer, S.; Pavanato, H.; Fletcher, D. (2023). Updated spatially explicit fisheries risk assessment for New Zealand marine mammal populations. *New Zealand Aquatic Environment and Biodiversity Report No. 290.* 218 p.

Meyer, S. (2023). Desktop update of estimation of seabird cryptic mortality in trawls, via warp and net captures in the new zealand domestic fleet using standard mitigation. *New Zealand Aquatic Environment and Biodiversity Report No. 322.* 28 p.

MPI, D.. (2021). Hector's and maui dolphin threat management plan 2020. Final report to New Zealand Department of Conservation, New Zealand Department of Conservation Te Papa Atawhai and Fisheries New Zealand Tini a Tangaroa.

Niel, C.; Lebreton, J.D. (2005). Using demographic invariants to detect overharvested bird populations from incomplete data. *Conservation Biology 19* (*3*): 826–835.

Ochi, D.; Abraham, E.; Inoue, Y.; Oshima, K.; Walker, N.; Richard, Y.; Tsuji, S. (2018). Preliminary assessment of the risk of albatrosses by longline fisheries. *Report to the WCPFC Scientific Committee 3rd Regular Session. (WCPFC-SC14-2018/ EB-WP-09 Rev1)*

Peatman, T.; Edwards, C.T.T.; Goad, D.; Webber, D. (2023). Review of biological inputs for the New Zealand Seabird Risk Assessment. *New Zealand Aquatic Environment and Biodiversity Report No. 312.*

R Core Team (2023). R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria

Richard, Y.; Abraham, E.R. (2013). Risk of commercial fisheries to New Zealand seabird populations: Supplementary information. *New Zealand Aquatic Environment and Biodiversity Report No. 109S.*

Richard, Y.; Abraham, E.R. (2015). Assessment of the risk of commercial fisheries to New Zealand seabirds, 2006–07 to 2012–13. *New Zealand Aquatic Environment and Biodiversity Report No. 162.* 85 p.

Richard, Y.; Abraham, E.R.; Berkenbusch, K. (2017a). Assessment of the risk of commercial fisheries to New Zealand seabirds, 2006–07 to 2014–15. *New Zealand Aquatic Environment and Biodiversity Report No. 191.*

Richard, Y.; Abraham, E.R.; Berkenbusch, K. (2017b). Assessment of the risk of commercial fisheries to New Zealand seabirds, 2006–07 to 2014–15: Supplementary information. *New Zealand Aquatic Environment and Biodiversity Report No. 191S.*

Richard, Y.; Abraham, E.R.; Berkenbusch, K. (2020). Assessment of the risk of commercial fisheries to New Zealand seabirds, 2006–07 to 2016–17. *New Zealand Aquatic Environment and Biodiversity Report No. 237.*

Roberts, J.; Webber, D.; Roe, W.; Edwards, C.T.T.; Doonan, I. (2019). Spatial risk assessment of threats to hector's and maui dolphins (*Cephalorhynchus hectori*). *New Zealand Aquatic Environment and Biodiversity Report No. 214.* 168 p.

Sharp, B.R. (2019). Spatially Explicit Fisheries Risk Assessment: A framework for quantifying and managing incidental commercial fisheries impacts on non-target species. Chapter 3, pp. 18–55, *in* Ministry for Primary Industries (2019). *Aquatic Environment and Biodiversity Annual Review 2018*. Compiled by the Fisheries Science Team, Ministry for Primary Industries, Wellington New Zealand. 704 p.

Stan Development Team (2023). RStan: the R interface to Stan. R package version 2.26.22