



Fisheries New Zealand

Tini a Tangaroa

Population effects of commercial fishery and
non-fishery threats on Māui dolphins
(*Cephalorhynchus hectori maui*)

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EXECUTIVE SUMMARY

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- A Bayesian population model was developed for Māui dolphins integrating information from genetic “mark-recapture” observations and a population size time series, also from genetic biopsy.
- Model runs made alternative assumptions of historical threat-specific mortality from direct commercial fishery interactions (set net and trawl) and toxoplasmosis.
- Models estimated a higher median annual non-calf (1+) survival probability for females (0.89) than males (about 0.83), consistent with other assessments using the same data.
- A model run in which non-calf survival was estimated separately in two multi-year blocks estimated that non-calf survival had increased since 2008, a result supported by the mark recapture observations and population size estimates.
- Model projections to the year 2068 estimated a minor effect of alleviating trawl and set net mortalities even when the upper 95% credible interval estimate of annual deaths was assumed (from the spatial fisheries risk model developed for the Threat Management Plan). This effect would be insufficient to stabilise or reverse a declining population trend.
- Model runs alleviating commercial fishery deaths and toxoplasmosis deaths produced increasing or stable population trends, depending on the detection probability of toxoplasmosis deaths relative to predation events.
- The relative detection probability of non-fishery threats is a major uncertainty with respect to this modelling and the Threat Management Plan spatial risk assessment.
- Other known threats to Māui dolphins (e.g. Brucella) for which annual deaths can be estimated could also be assessed using this modelling approach.

1. INTRODUCTION

Fisheries New Zealand and the New Zealand Department of Conservation (DOC) are undertaking a spatially explicit multi-threat risk assessment of threats to Hector's and Māui dolphins, to inform a new Threat Management Plan (TMP) for the species. Under a separate contract to DOC, Dr Jim Roberts has previously produced and described a Bayesian population model for Māui dolphins using NIWA's SeaBird demographic assessment software. This model was fitted to mark-recapture and population size estimates and was reviewed initially at an AEWG meeting on 7 March 2018.

The objectives of this project are to:

1. Re-fit the Māui dolphin population model described above, including historical annual threat-specific deaths arising from both commercial fishery and selected non-fishery threats, consistent with the TMP risk assessment model.
2. In consultation with Fisheries New Zealand and as directed by Fisheries New Zealand scientific working group(s), produce quantitative diagnostics of model fits to mark-recapture and population size estimates.
3. Explore alternate plausible historical impact levels from different threats.
4. Using a base case model and agreed sensitivities, simulate current status and future population recovery trajectories under a range of threat management scenarios identified by Fisheries New Zealand and DOC and/or its scientific working groups, to estimate population trajectories.

2. METHODS

A Bayesian state-space demographic model was developed using NIWA's SeaBird demographic assessment software (e.g. Roberts & Doonan 2016). The likelihood calculation was a generalisation of the Cormack-Jolly-Seber model (Cormack 1964). The model integrated demographic information from genetic "mark-recapture" and population size estimates (e.g. Baker et al. 2016). The model and data are detailed below.

Model partition and parameters

The population model partition was comprised of 12 female classes (see Figure 1): one each for pre-breeder individuals from ages 0 to 9 and a class each for breeders and non-breeders in a respective year. Females were allowed to become breeders from age 4, although the proportion of individuals actually doing so depended on breeding parameter estimates, so could take a small value if supported by the data and priors. Females of age 9 became a breeder or non-breeder at age 10, both of which were assigned as plus groups with no maximum age. There were two male classes for age 0 and age 1, the latter of which was assigned as a plus group (see Figure 1). Māui dolphins were assumed to have low levels of sexual partner fidelity, such that numbers of males at maturation/breeding ages were not required to estimate annual births.

The model time-period was from years 1990 to 2018 and was projected forward 50 years, up to year 2068 with estimates of population size for all classes derived for all projected years.

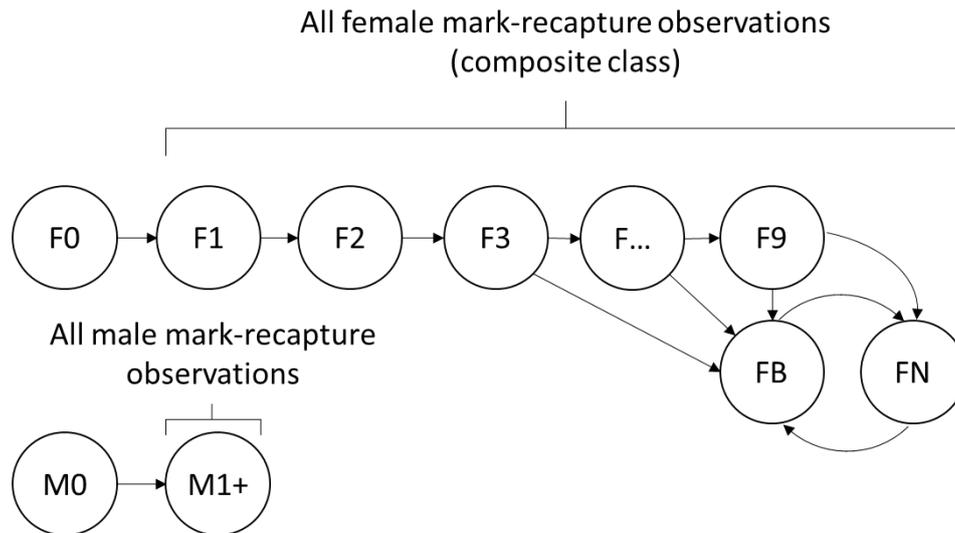


Figure 1: Diagrammatic representation of population model partition and possible transitions between model classes. Class labels denote an individual’s state in a respective model year: sex (“F” = Female or “M” = Male) and demographic stage (age of pre-breeding individuals, from 0-9; or breeding status of individuals that have bred, “B” = Breeder, “N” = Non-breeder). Brackets denote classes for which mark-recapture data were potentially available (i.e., not for calves before their first birthday). Plus groups were assumed for males of class “M1+” (age 1+) and females of classes “FB” and “FN”.

Transitions between classes were governed by demographic rates that gave:

- The annual non-calf survival probability (sex specific—*SurvF* and *SurvM*);
- Annual calf survival probability (*Surv0*, derived from *SurvF*, replicating the approach of Gormley (2009));
- Mean age at first breeding (*a50*),
- Rate of maturation (*k*, fixed at 4); and
- Annual breeding probability (*PrB*).

Normal priors were specified for the estimated reproductive rates *PrB* (mean and c.v. based on estimates from an assessment of Banks Peninsula Hector’s dolphins by Gormley (2009)) and *a50* (mean and c.v. derived from the posterior of “amat” estimated by Edwards et al. (2018)).

A scalar parameter *N1990* gave the population size at age 1+ in year 1990. Also, parameters *Res10* and *Res15* gave the annual resighting probabilities of genetically “marked” individuals in the years 2010 to 2011 and 2015 to 2016, respectively (Table 1).

Table 1: Summary of model parameters.

Parameter label	Description	Prior	Year blocks
<i>N</i> 1990	Non-calf population size in 1990	Uniform prior, bounded at 1 and 1,000	
<i>SurvM</i>	Annual non-calf survival probability of males	Uniform prior, bounded at 0 and 1	1990–2007 and 2008–2018 Model Runs 2.1, 2.2 and 2.3. Single year block for all other model runs.
<i>SurvF</i>	Annual non-calf survival probability of females	Uniform prior, bounded at 0 and 1	1990–2007 and 2008–2018 Model Runs 2.1, 2.2 and 2.3. Single year block for all other model runs.
<i>Surv0</i>	Annual calf survival probability	None; derived as $SurvF * SurvF$	
<i>a</i> 50	Age at 50% first breeding	Normal prior; mean = 7.92; c.v. = 0.025	
<i>k</i>	Rate of maturation	None; value fixed at 4	
<i>PrB</i>	Annual breeding probability	Normal prior; mean = 0.41; c.v. = 0.24	
<i>Res</i> 10	Annual resighting probability of non-calves in 2010 and 2011	Uniform prior, bounded at 0 and 1	2010 to 2011
<i>Res</i> 15	Annual resighting probability of non-calves in 2015 and 2016	Uniform prior, bounded at 0 and 1	2015 to 2016

Demographic observations

All models were fitted to the same set of genetic biopsy derived mark-recapture observations of non-calf (age 1+) individuals (see Baker et al. 2016 for a summary of these data and their collection). A combined mark-recapture time series sample of 57 females and 39 males was used (Figure 2). Genetic “marking” began in 2001, although before 2010 resighting effort was not conducted in a standardised way (i.e. consistent through time), and so, resightings from 2001–2009 have been omitted from the analysis. Resightings of dead individuals were also omitted, since they would have a different resighting probability to live animals in a respective season.

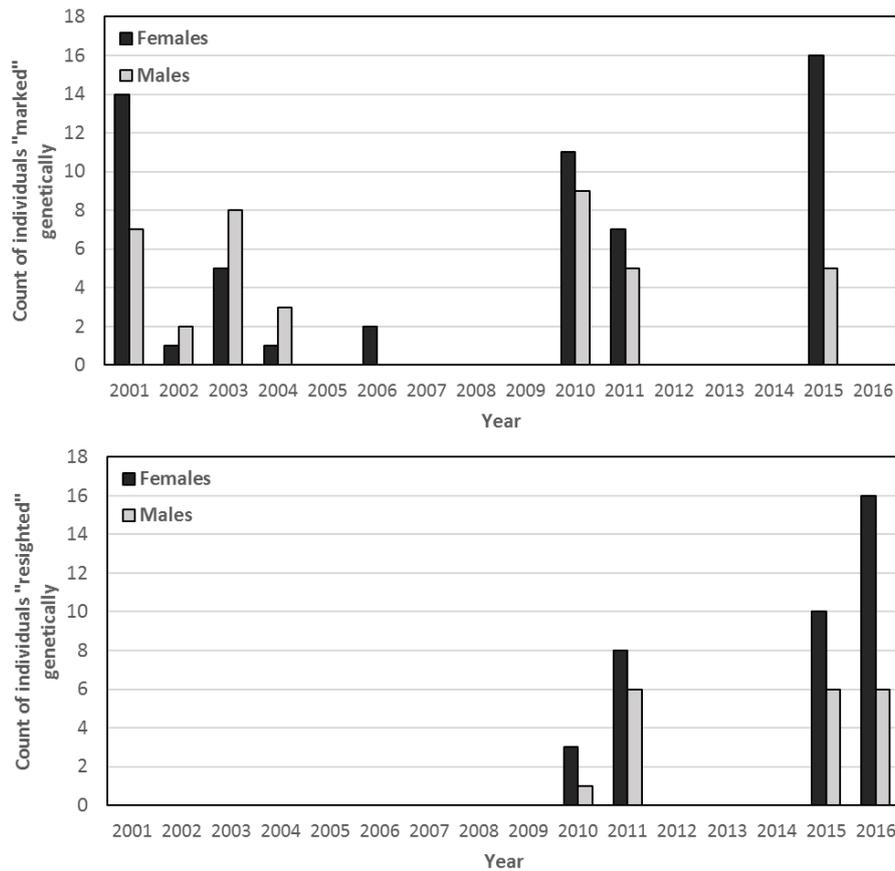


Figure 2: Frequency by year of genetic “marking” of Māui dolphins for which recapture data were fitted by models in this study (top); and frequency by year of recapture for the same sample of individuals (bottom). Note that the lower plot does not include sightings of dead animals or of individuals resighted outside of 2010, 2011, 2015 or 2016.

Models were also fitted to genetic-based population size estimates of non-calves (from Baker et al. 2013; Baker et al. 2016; Hamner et al. 2012). Population size estimates and associated c.v. (derived from confidence limits reported with population size estimates) are shown in Table 2.

Table 2: Non-calf Māui dolphin population size estimate, fit to by all models.

Year	Non-calf population size estimate (assumed c.v.)	Reference
2001	87 (0.2)	Baker et al. (2013)
2002	80 (0.2)	Baker et al. (2013)
2003	74 (0.2)	Baker et al. (2013)
2004	69 (0.3)	Baker et al. (2013)
2006	59 (0.3)	Baker et al. (2013)
2011	55 (0.1)	Hamner et al. (2012)
2016	63 (0.1)	Baker et al. (2016)

Model runs and annual threat-specific deaths

Two groups of models were developed:

1. Assuming a single year block for non-calf survival (i.e. one survival rate estimate each for males and females); and
2. Assuming two multi-year blocks (1990–2007 and 2008–2018) for the survival rate of each sex. This break point was chosen since major fishing area restrictions were implemented in 2008 along the West Coast North Island of New Zealand to protect the resident Māui population

which reduced estimated overlap and annual Māui dolphin deaths after this time (Intermediate spatial risk model outputs presented to July expert panel workshop meeting of project PRO2017-12 by D’Arcy Webber). Also, reliable necropsy information for estimating annual deaths from toxoplasmosis (the non-fishery threat assessed here) were mostly available for the period since 2008 (Roe et al. 2013).

For the first set of model runs (Run IDs 1.1 to 1.5) (Table 3) alternative assumptions were made with respect to historical threat-specific mortality incorporated into population models (i.e. relating to commercial set net and trawl fisheries, or commercial fisheries and toxoplasmosis). Also, sensitivity was assessed with respect to the magnitude of commercial fishery annual deaths (applying the median or upper 95% credible interval) and deaths from toxoplasmosis (assessing sensitivity with respect to the relative detection probability of predation events) (Table 4).

Annual commercial set net and trawl fishery-related deaths were applied based on final Māui dolphin estimates from the spatial risk model developed for the spatial risk assessment of threats to Hector’s and Māui dolphins (Roberts et al. 2019). Since this model assumed constant population size through time, the estimates were rescaled using population size estimates from model Run 1.1, using the estimated population size in a respective year relative to that of 2015–16 as a multiplier.

The second set of model runs (Run IDs 2.1 to 2.3) assumed two adult survival blocks, which produced a different population size trajectory through time, and resulted in a different set of annual threat-specific deaths using the population size scaling method described above, except comparing with model Run 2.1 (Table 4).

Selectivity-at-age with respect to commercial set net and trawl fisheries assumed a double normal functional form and parameters estimated by Davies et al. (2008) (from model run “KRG_2%”, which assumed maximum catchability at age 2; and a maximum annual population growth rate of 4%). With respect to toxoplasmosis deaths, calves were assumed not to be vulnerable, and equal selectivity was assumed for all ages at 1+. Males and females were assumed to be equally vulnerable to commercial fishery and toxoplasmosis deaths.

Table 3: Description of model runs. For all model runs, both MPD and MCMC runs were undertaken.

Run ID	Description
1.1	One non-calf survival year block for each of males and females. No threat mortality.
1.2	As Run 1.1, except incorporating median estimates of commercial fishery capture-related deaths.
1.3	As Run 1.1, except incorporating upper 95% CI estimates of commercial fishery capture-related deaths.
1.4	As Run 1.1, except incorporating median estimates of commercial fishery capture-related deaths and median estimates of toxoplasmosis deaths
1.5	As Run 1.1, except incorporating median estimates of commercial fishery capture-related deaths and median estimates of toxoplasmosis deaths—sensitivity assuming a 10-fold greater detection probability of toxoplasmosis deaths than predation deaths (i.e. assumes lower annual deaths from toxoplasmosis than Run 1.4).
2.1	Two non-calf survival multi-year blocks (1990–2007 and 2008–2018) for each of males and females. No threat mortality.
2.2	As Run 2.1, except incorporating median estimates of commercial fishery capture-related deaths.
2.3	As Run 2.1, except incorporating upper 95% CI estimates of commercial fishery capture-related deaths.

Table 4: Annual deaths of Māui dolphins from commercial fishery-related incidental mortality, toxoplasmosis and predation. Annual death estimates from the Threat Management Plan spatial risk assessment model were adjusted for model estimated changes in population size (Runs 1.1 and 2.1). For 2018, no estimates of annual mortality were available, so 2017 values were used.

Year	Single non-calf survival year block (1990–2018)						Two multi-year non-calf survival blocks (1990–2007 and 2008–2018)			
	Set net median (Runs 1.2, 1.4 & 1.5)	Set net upper (Runs 1.3)	Trawl median (Run 1.2, 1.4 & 1.5)	Trawl upper (Run 1.3)	Toxo-plasmosis (Run 1.4)	Toxo-plasmosis, predation sensitivity (Run 1.5)	Set net median (Run 2.2)	Set net upper (Run 2.3)	Trawl median (Run 2.2)	Trawl upper (Run 2.3)
1990	0.274	0.638	0.028	0.163	2.793	1.594	0.538	1.253	0.056	0.321
1991	0.269	0.628	0.028	0.161	2.748	1.569	0.503	1.173	0.052	0.300
1992	0.265	0.617	0.028	0.158	2.703	1.543	0.471	1.098	0.049	0.281
1993	0.260	0.607	0.027	0.155	2.658	1.517	0.441	1.027	0.046	0.263
1994	0.236	0.551	0.022	0.127	2.613	1.492	0.380	0.887	0.036	0.205
1995	0.267	0.622	0.016	0.089	2.569	1.466	0.408	0.951	0.024	0.137
1996	0.256	0.597	0.020	0.115	2.525	1.441	0.373	0.869	0.029	0.167
1997	0.329	0.767	0.019	0.109	2.481	1.416	0.456	1.062	0.026	0.151
1998	0.285	0.664	0.018	0.101	2.438	1.392	0.375	0.874	0.023	0.132
1999	0.272	0.634	0.023	0.130	2.396	1.368	0.341	0.794	0.028	0.163
2000	0.309	0.721	0.017	0.098	2.354	1.344	0.368	0.858	0.020	0.116
2001	0.289	0.675	0.016	0.090	2.312	1.320	0.328	0.764	0.018	0.102
2002	0.319	0.743	0.015	0.084	2.271	1.297	0.343	0.800	0.016	0.090
2003	0.260	0.607	0.010	0.058	2.231	1.274	0.266	0.621	0.010	0.060
2004	0.230	0.535	0.011	0.062	2.192	1.251	0.224	0.521	0.010	0.060
2005	0.226	0.526	0.010	0.056	2.153	1.229	0.209	0.487	0.009	0.052
2006	0.206	0.481	0.008	0.043	2.114	1.207	0.181	0.423	0.007	0.038
2007	0.218	0.508	0.007	0.041	2.077	1.185	0.182	0.425	0.006	0.034
2008	0.193	0.449	0.007	0.038	2.040	1.164	0.153	0.357	0.005	0.030
2009	0.178	0.414	0.006	0.036	2.003	1.144	0.147	0.342	0.005	0.030
2010	0.148	0.345	0.006	0.034	1.967	1.123	0.127	0.296	0.005	0.029
2011	0.151	0.353	0.005	0.027	1.932	1.103	0.135	0.314	0.004	0.024
2012	0.153	0.356	0.009	0.050	1.897	1.083	0.141	0.329	0.008	0.046
2013	0.122	0.284	0.009	0.050	1.863	1.064	0.117	0.273	0.008	0.049
2014	0.136	0.317	0.007	0.041	1.830	1.045	0.136	0.317	0.007	0.041
2015	0.107	0.250	0.006	0.035	1.797	1.026	0.112	0.260	0.006	0.036
2016	0.074	0.172	0.006	0.034	1.765	1.008	0.080	0.186	0.006	0.036
2017	0.069	0.160	0.005	0.031	1.765	1.008	0.069	0.160	0.005	0.031
2018	0.069	0.160	0.005	0.031	1.765	1.008	0.069	0.160	0.005	0.031

MCMC runs

MCMC model runs were undertaken for all models described in Table 3. MCMC chains were continued for 2 million iterations, taking samples every 1,000 iterations, to give a total of 2,000 samples for each model run. No burn in period was specified, as all model traces indicated good mixing of all estimated parameters from the start of the chain.

Population projections

SeaBird was used to undertake population projections from year 2019 to 2068 (50 years into the future), using MCMC parameter estimates. Model Runs 2.1 to 2.3 used the 2008–2018 estimate of non-calf survival for males and females (*SurvM* and *SurvF*).

The population growth rate of non-calves (λ) was derived from population projections, calculated in the terminal year (λ_{2068}). In addition, population status (with respect to non-calves) in 2068 relative to 2018 (N2068 (%N2018)) was calculated from projected population size. For all model runs, threat-specific mortality was assumed to be zero in all future years, i.e. projections for model Runs 1.2 to 1.5 and 2.2 to 2.3 estimated the population trajectory when fully alleviating mortalities arising from a specific threat. Population projections from model Runs 1.1 and 2.1, which did not specifically incorporate threat specific mortalities (i.e. non-calf survival was not adjusted for threat-specific deaths), essentially assumed a continuation of recent demographic rates (as no threats were alleviated).

3. RESULTS

MPD model runs

Model fits were good to both population size estimates of non-calves (Figure 3) and to mark recapture observations (Figure 4). With respect to the population size fits (Figure 3), a V-shaped trend in residuals was obtained indicating that a change in demographic rates may have occurred during this time.

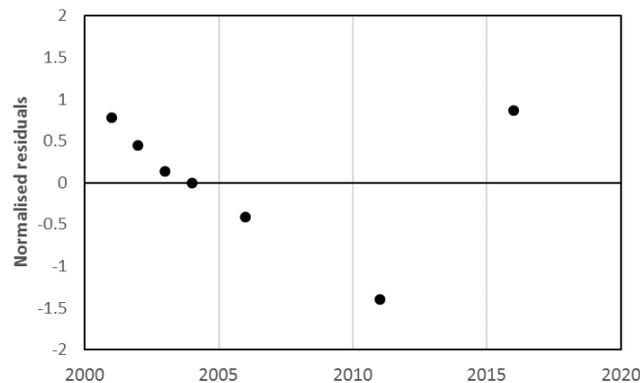


Figure 3: Normalised residuals of model Run 1.1 (one survival, no threats) fit to census estimates.

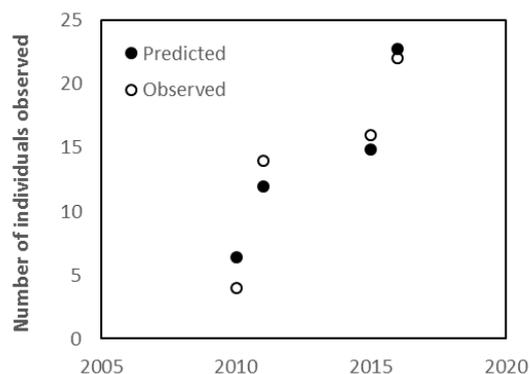


Figure 4: Number of genetically marked dolphins seen in each recapture year and numbers predicted seen by model Run 1.1 (one survival, no threats).

Model Run 1.1 (single non-calf survival year block) produced non-calf survival estimates of 0.89 for females and 0.84 for males (Table 5). This was consistent with estimates of an individual-based modelling assessment by Cooke et al. (2018) using the same mark-recapture observations, which estimated an annual non-calf survival probability of 0.88 and obtained better fits when allowing sex-specific non-calf survival rate.

Model Run 2.1 (which had two non-calf survival year-blocks) estimated an increase in the non-calf survival rate of females ($SurvF = 0.85$ from 1990–2007 and 0.93 from 2008–2018) and males ($SurvM = 0.81$ from 1990–2007 and 0.86 from 2008–2018) (Table 5). Likelihood profiles of $SurvF$ for the two year-blocks indicated that the both the mark-recapture and census data were consistent with this increase in $SurvF$ through time (Figure 5).

The posteriors of breeding rate parameters (PrB , the annual breeding probability; and $a50$, the average age at first breeding) were essentially the same as the priors (comparing Table 5 with Table 1). The mark-recapture observations provided no information with respect to annual breeding probability. However, the time series of population size estimates (Table 2) will have provided some information on annual breeding rate, in conjunction with survival-at-age from the mark recapture data and population size. The likelihood profile of $SurvF$ (annual survival probability of non-calf females) for model Run 1.1, indicated that the prior on PrB (Normal prior; mean = 0.41 ; c.v. = 0.24) was influential, although broadly consistent with information from the population size time series and mark-recapture observation (Figure 5, top).

Neither the mark-recapture observations nor population size estimates provide any information with respect to demographic rates prior to 2000. Hence the estimate of $N1990$ (non-calf numbers in 1990) will be extrapolated from demographic information from the post-2000s period. The higher $N1990$ estimate obtained from model Run 2.1 (180 compared with 93 from model Run 1.1, Table 5) resulted from the low non-calf male and female survival estimates from the 1990 to 2007 year block (i.e. the lower the survival estimate from this period, the higher the population size in 1990 must be in order to fit to population size estimates in the 2000s).

Table 5: Summary of point estimates for both model runs not incorporating threat specific annual deaths.

Parameter	Run 1.1	Run 2.1
$N1990$	93	180
$SurvM$	0.84	0.81 (1990–2007) 0.86 (2008–2018)
$SurvF$	0.89	0.85 (1990–2007) 0.93 (2008–2018)
$a50$	7.92	7.92
PrB	0.39	0.40
$Res10$	0.39	0.41
$Res15$	0.57	0.52

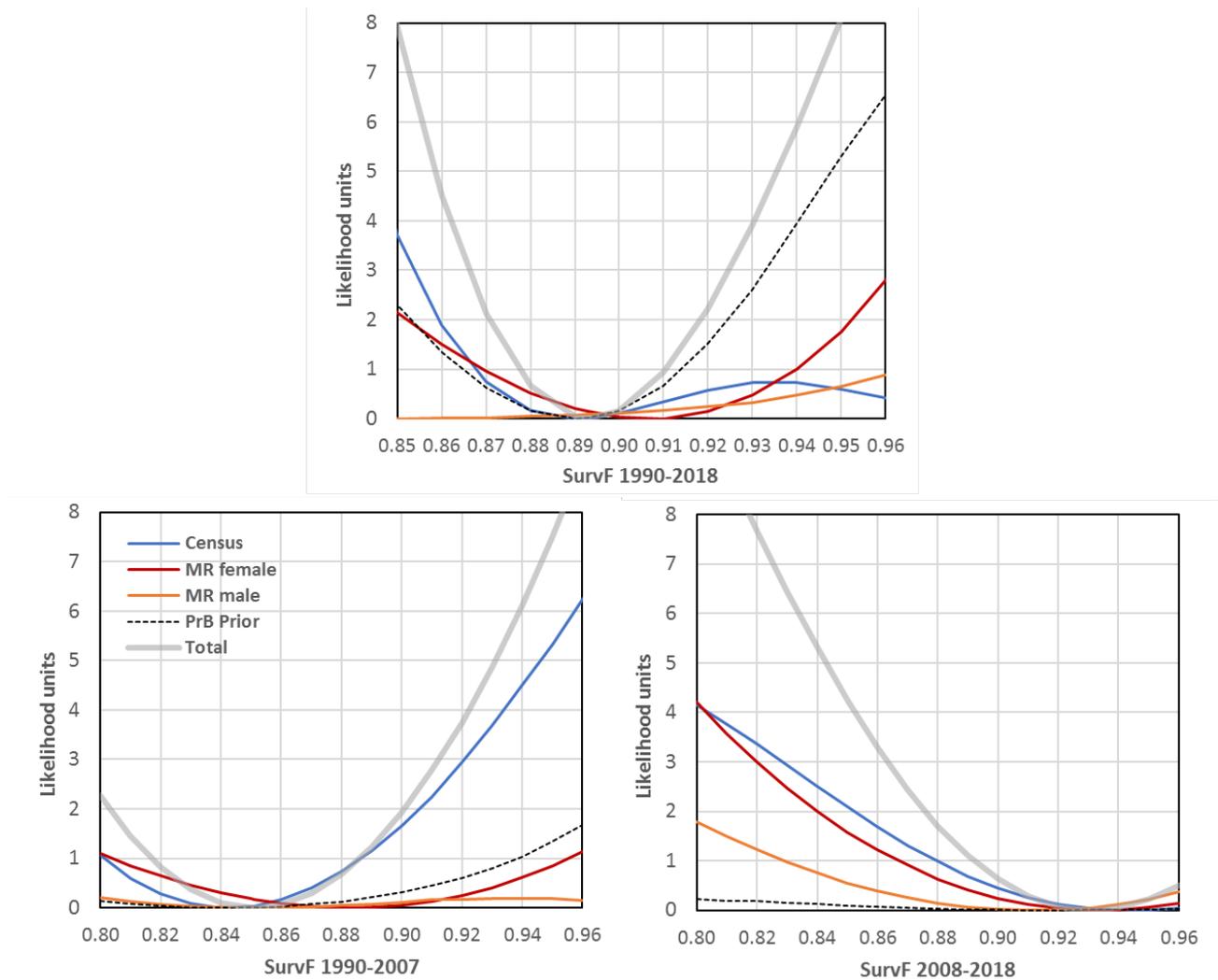


Figure 5: Likelihood profile of observations and an influential prior given alternative values of female non-calf annual survival probability. Top—Model Run 1.1 single survival year block; bottom—Model Run 2.1, two survival year blocks (1990–2007 and 2008–2018). Legend labels denote observations (“Census” = census estimates; “MR female” = female mark recapture observations; “MR male” = male mark recapture observations; “PrB prior” = prior on annual breeding probability; “Total” = combined negative log likelihood contribution of all observations and priors).

MCMC model runs

MCMC diagnostic plots are shown for model Run 1.1 and Run 2.1 (both model runs with no threat-specific annual mortality specified). The trace plots indicate good mixing for all estimated model parameters (Figure 6 and Figure 7). There was also no evidence of drift in the posterior, comparing the first, second and third portions of the chain for each parameter (Figure 8 and Figure 9). Diagnostics indicate comparable model performance for the other model runs (not shown here).

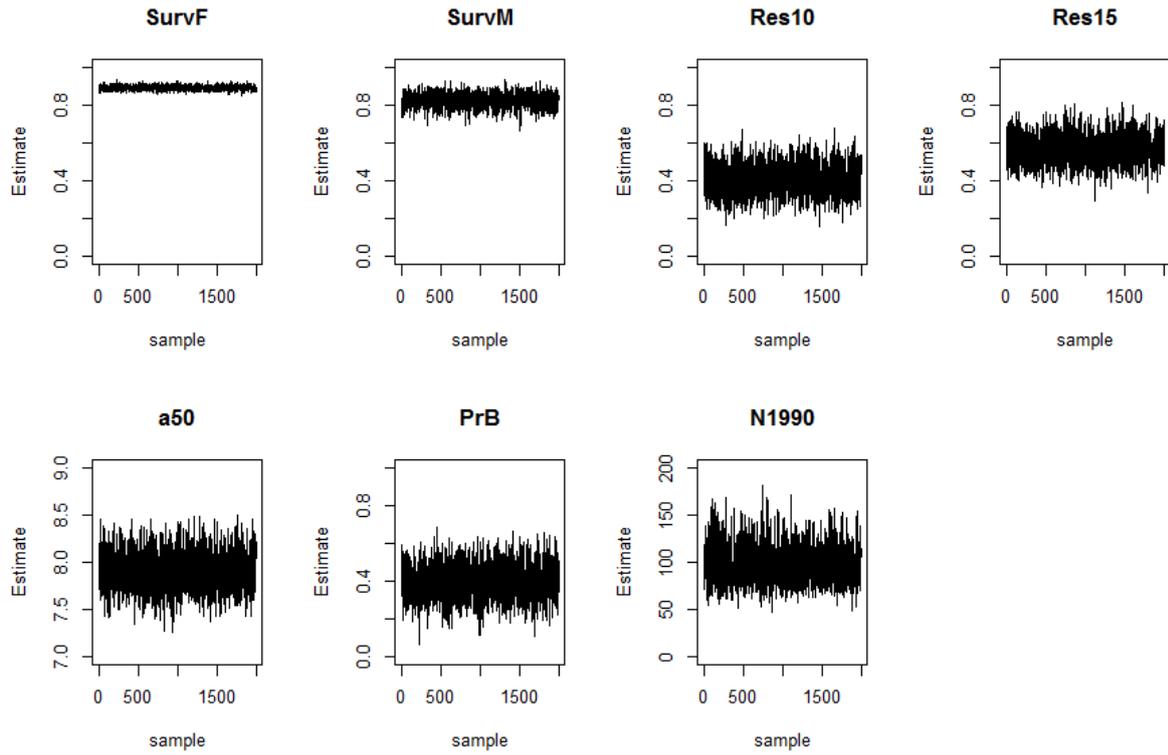


Figure 6: MCMC traces for all parameters estimated by model Run 1.1. See Table 1 for a description of each parameter.

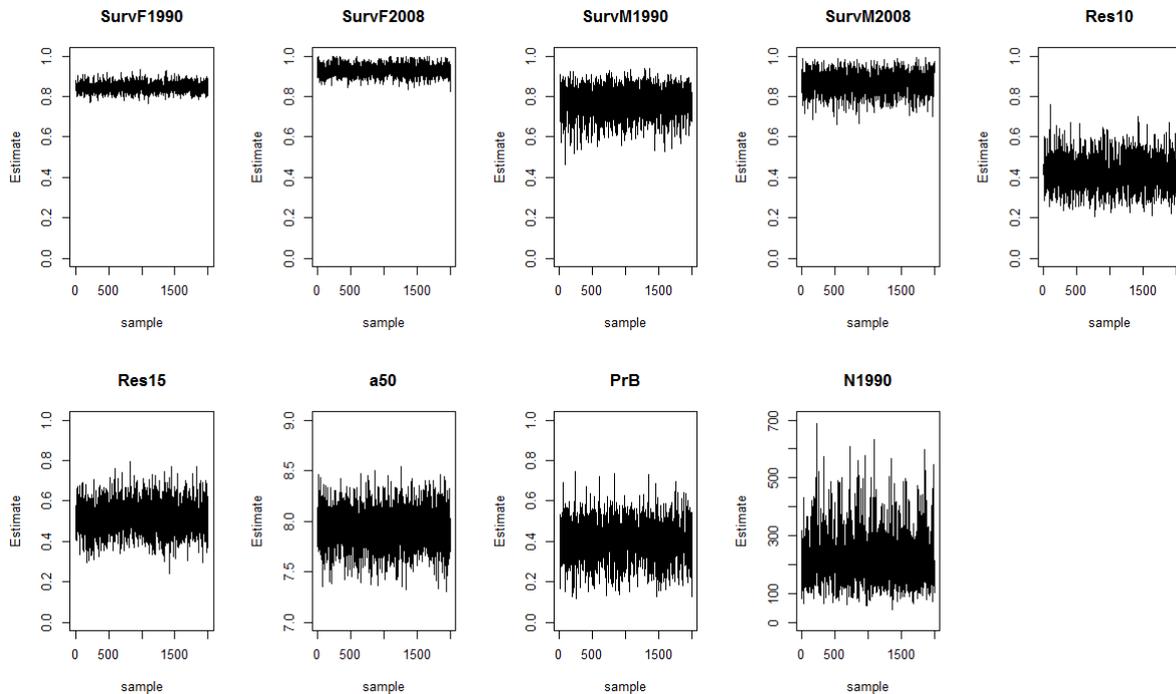


Figure 7: MCMC traces for all parameters estimated by model Run 2.1. See Table 1 for a description of each parameter.

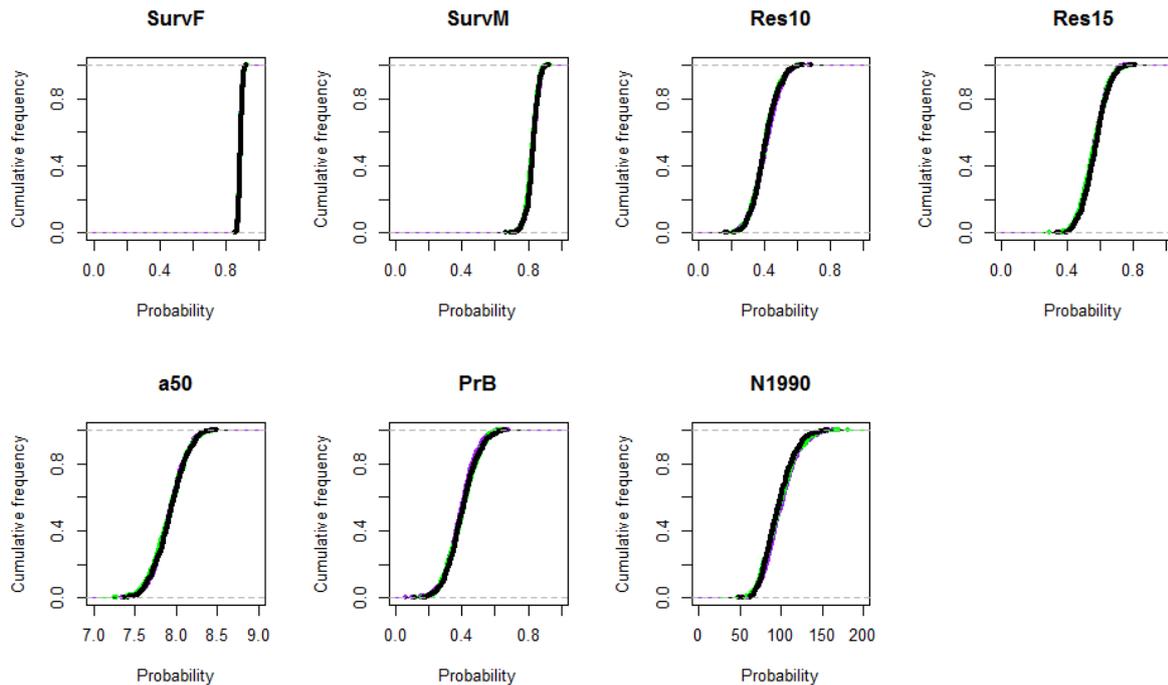


Figure 8: Cumulative frequency plots for all parameters estimated by model Run 1.1. The three thirds of the MCMC chain are in different colours and may be obscured where they agree well.

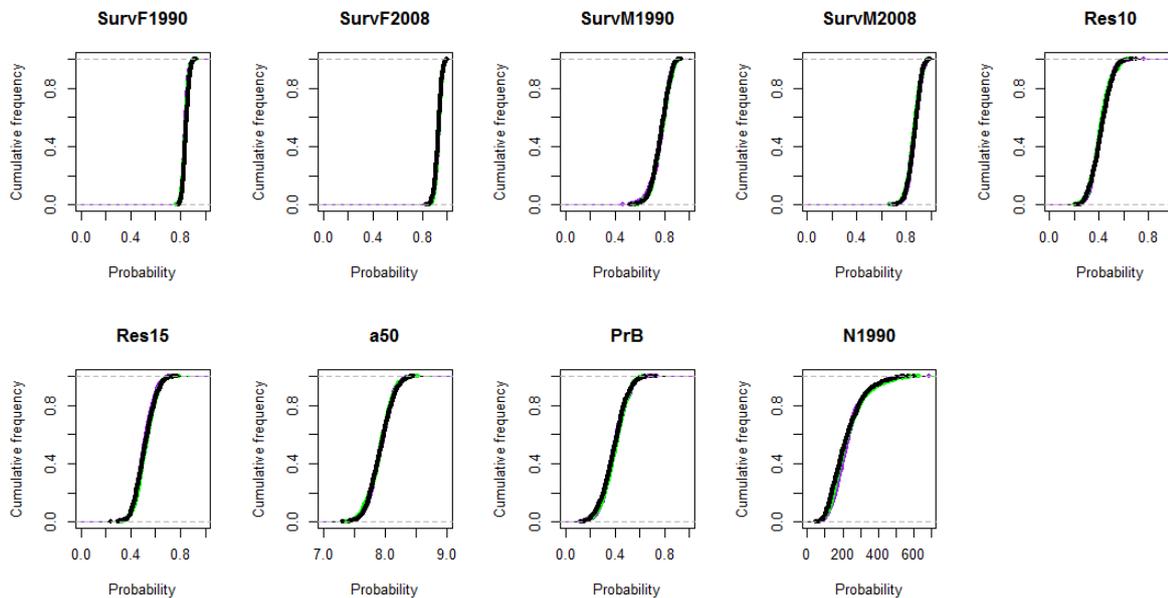


Figure 9: Cumulative frequency plots for all parameters estimated by model Run 2.1. The three thirds of the MCMC chain are in different colours and may be obscured where they agree well.

Median MCMC estimates of all model parameters agreed closely with point estimates (comparing Table 6 and Table 7 with Table 5). With respect to model runs with a single non-calf survival year block (Runs 1.1. to 1.5, for alternative threat-specific annual death scenarios), MCMC parameter estimates were near-identical for all model runs, except that runs incorporating toxoplasmosis mortality estimates (1.4, assuming an equal detection probability of predation deaths and other non-fishery related deaths; and 1.5, assuming a 10-fold reduction in relative detection probability of predation deaths) produced slightly

increased estimates of *SurvF* (0.92, 95% CI = 0.90–0.95; and 0.91, 95% CI = 0.89–0.93, respectively) relative to model Run 1.1 (not incorporating threat specific mortality) (*SurvF* = 0.89, 95% CI = 0.87–0.92), or model runs including set net and trawl mortalities (Run 1.2 and 1.3). Similar between-model differences were obtained with respect to male survival (*SurvM*) (Table 6).

Table 6: MCMC parameter estimates for all model runs with one non-calf survival year block (median estimates and 95% CI in parentheses). Runs 1.2 – 1.5 refer to models in which the lethal threats listed in the run description have been alleviated (i.e. threat impacts are reduced to zero in projected future population trajectories).

Parameter	MCMC median estimates (95% CI)				
	Run 1.1 No threat alleviated	Run 1.2 Median fisheries impact alleviated	Run 1.3 High fisheries impact alleviated	Run 1.4 Median fishery & toxoplasmosis impacts alleviated	Run 1.5 Median fishery & Toxoplasmosis impact alleviated; (predation detection sensitivity)
<i>N</i> 1990	95 (66–143)	97 (65–146)	97 (68–144)	94 (69–131)	95 (68–135)
<i>SurvM</i>	0.83 (0.75–0.89)	0.83 (0.76–0.90)	0.83 (0.76–0.90)	0.86 (0.77–0.93)	0.85 (0.77–0.92)
<i>SurvF</i>	0.89 (0.87–0.92)	0.89 (0.87–0.92)	0.90 (0.88–0.92)	0.92 (0.90–0.95)	0.91 (0.89–0.93)
<i>a</i> 50	7.93 (7.53–8.31)	7.92 (7.51–8.30)	7.93 (7.54–8.31)	7.93 (7.54–8.29)	7.92 (7.51–8.29)
<i>PrB</i>	0.40 (0.23–0.58)	0.39 (0.23–0.58)	0.39 (0.22–0.58)	0.40 (0.22–0.58)	0.40 (0.21–0.57)
<i>Res</i> 10	0.40 (0.25–0.57)	0.40 (0.26–0.56)	0.40 (0.27–0.55)	0.41 (0.26–0.56)	0.40 (0.26–0.58)
<i>Res</i> 15	0.57 (0.42–0.71)	0.57 (0.43–0.72)	0.57 (0.42–0.72)	0.57 (0.43–0.72)	0.57 (0.41–0.72)

Table 7: MCMC parameter estimates for all model runs with two non-calf survival year blocks (median estimates and 95% CI in parentheses).

Parameter	MCMC median estimates (95% CI)		
	Run 2.1 Two survivals, no threats alleviated	Run 2.2 Two survivals, median fisheries impact alleviated	Run 2.3 Two survivals, high fisheries impact alleviated
<i>N</i> 1990	211 (93–479)	203 (95–458)	204 (91–424)
<i>SurvM</i> 1990	0.78 (0.62–0.89)	0.78 (0.63–0.90)	0.79 (0.63–0.90)
<i>SurvM</i> 2008	0.87 (0.76–0.96)	0.87 (0.75–0.96)	0.87 (0.76–0.96)
<i>SurvF</i> 1990	0.84 (0.80–0.89)	0.85 (0.80–0.90)	0.85 (0.81–0.90)
<i>SurvF</i> 2008	0.93 (0.88–0.98)	0.93 (0.88–0.98)	0.93 (0.88–0.98)
<i>a</i> 50	7.93 (7.55–8.31)	7.93 (7.55–8.29)	7.93 (7.54–8.31)
<i>PrB</i>	0.40 (0.21–0.58)	0.40 (0.22–0.59)	0.40 (0.23–0.59)
<i>Res</i> 10	0.42 (0.28–0.59)	0.42 (0.28–0.58)	0.42 (0.26–0.58)
<i>Res</i> 15	0.51 (0.37–0.67)	0.51 (0.37–0.67)	0.52 (0.37–0.66)

Model projections

Depending on whether one or two non-calf survival multi-year blocks were estimated, population projections using MCMC samples produced either a declining (one year block for each of *SurvF* and *SurvM*) or an increasing population trajectory in future years (two multi-year blocks, sampling from the 2008–2018 estimate). Regardless of the assumption of temporal non-calf survival, uncertainty is high with respect to future population trajectory and population status, with overlapping credible intervals when comparing most model runs (Table 8, Figure 10 and Figure 11). Run 1.1, which did not

incorporate threat-specific annual deaths (projections assume a continuation of recent demographic rates) estimated a population growth rate in 2068 (λ_{2068}) of 0.980 (95% CI = 0.962–0.998).

The likely effects of different threat management options were investigated in model runs 1.2 to 1.5 and 2.2 to 2.3 by progressively alleviating one or more lethal threats in turn. In these model runs, ‘alleviating’ a threat means that from the 2019 year, the impact of that threat was set to zero in future projections, and the effect of the threat was then evaluated by comparing the zero-future-impact trajectory with the trajectory in which the projected impact level was unchanged.

In models with a single non-calf survival block, population trajectories in model runs in which set net and trawl mortalities were alleviated (run 1.2) were only slightly different from trajectories in which commercial fisheries threats remained unchanged (run 1.1); both of these runs estimated ongoing population decline. When assuming commercial fisheries impacts equal to the upper 95% credible interval of annual deaths from the spatial risk assessment model (Run 1.3; $\lambda_{2068} = 0.987$; 95% CI = 0.967–1.004), the model estimated a slightly higher median estimate of λ_{2068} when this impact was alleviated.

Of the model runs assuming a single non-calf survival year block, only model Run 1.4 (alleviating median commercial fishery deaths and toxoplasmosis impacts, and assuming that predation and non-predation deaths have equal detection probability) resulted in an increasing population size ($\lambda_{2068} = 1.014$; 95% CI = 0.993–1.035) (Table 8).

Model Run 1.5 was a sensitivity run designed to test the effects of assuming equal detection probability for all non-fishery deaths including predation. This model run assumed a 10-fold lower detection probability of predation deaths, resulting in a higher estimated proportion of non-fisheries deaths attributable to predation and a correspondingly lower proportion attributed to toxoplasmosis. Consequently, alleviating this (reduced) toxoplasmosis mortality had a correspondingly smaller effect on population trajectory and estimated stable population size ($\lambda_{2068} = 0.998$; 95% CI = 0.982–1.017) relative to run 1.4.

Table 8: Projected population growth rate (λ_{2068}) and population status (N 2068 (%N 2018)) of Māui dolphins with alternative assumptions of historical threat-specific annual deaths. The effect of alleviating a specific threat is obtained by comparing model Runs 1.2 to 1.5 with 1.1 and Runs 2.2 to 2.3 with 2.1.

Run	Population growth rate (λ_{2068})	Population status N 2068 (%N 2018)
1.1	0.980 (0.962–0.998)	36 (14–91)
1.2	0.982 (0.963–1.002)	41 (15–113)
1.3	0.987 (0.967–1.004)	51 (18–124)
1.4	1.014 (0.993–1.035)	192 (68–544)
1.5	0.998 (0.982–1.017)	91 (40–226)
2.1	1.025 (0.968–1.086)	353 (21–5 785)
2.2	1.026 (0.969–1.084)	362 (24–5 395)
2.3	1.028 (0.973–1.087)	408 (30–6 086)

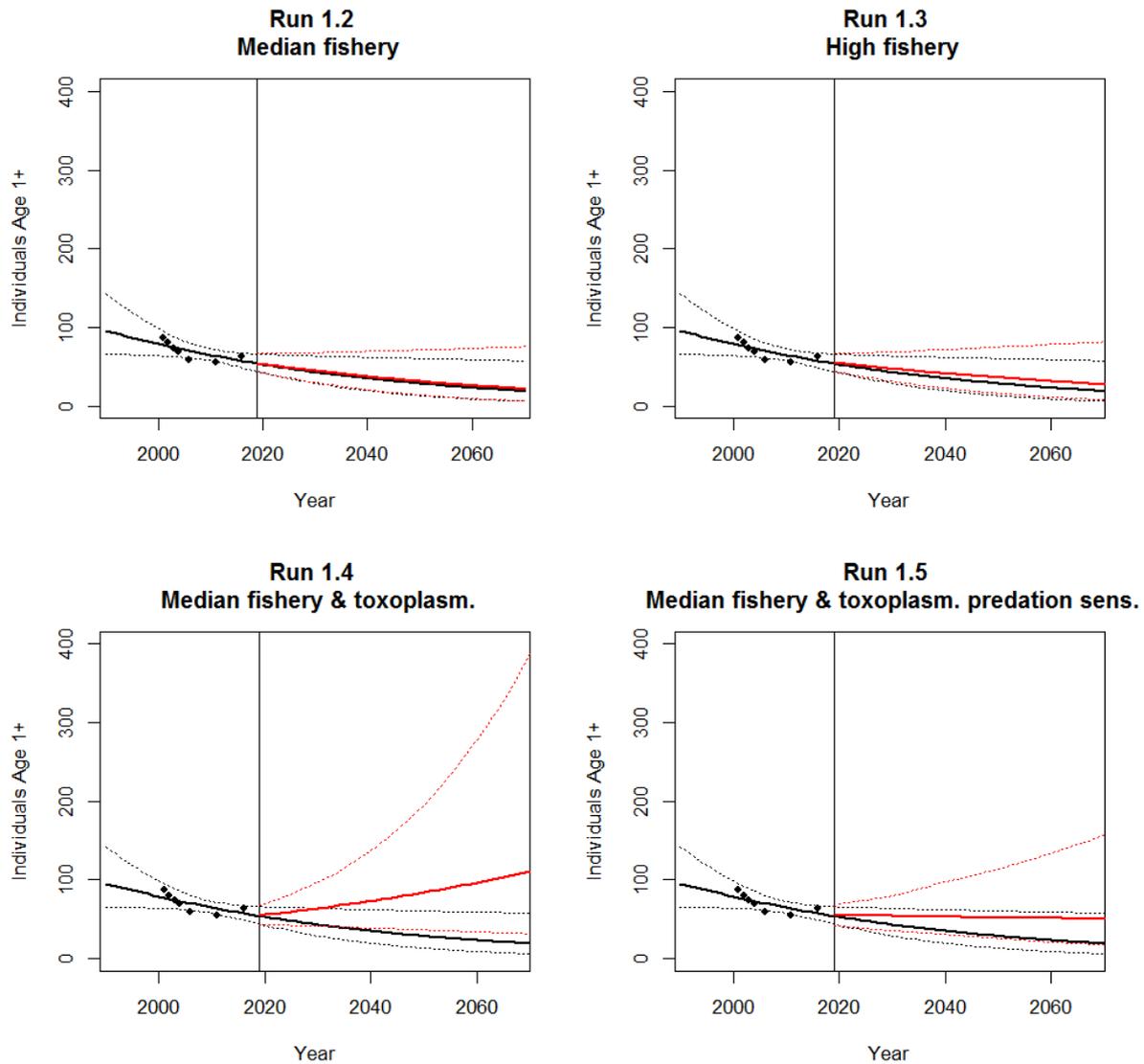


Figure 10: Māui dolphin population projections with alternative assumptions with respect to alleviating threat-specific annual deaths. Current year (2019) highlighted by vertical line. To the left of this line: black lines are the median and 95% CI of MCMC estimates of non-calf population trajectory; and census estimates (black points). To the right of the vertical line: black lines are median and the 95% CI of projected population trajectory for model Run 1.1 (essentially a continuation of recent demographic rates). Projections alleviating threat-specific mortality are shown in red: Run 1.2, alleviating median estimates of annual set net and trawl deaths (top-left); Run 1.3, alleviating upper 95% estimates of annual set net and trawl deaths (top-right); Run 1.4, alleviating median commercial fishery deaths and toxoplasmosis, assuming equal detection probability of non-fishery causes of death (bottom-right); and Run 1.5, alleviating median commercial fishery deaths toxoplasmosis, assuming 10-fold decrease in detection probability of predation mortality. For all trajectories, the three lines represent median and 95% CI of MCMC estimates.

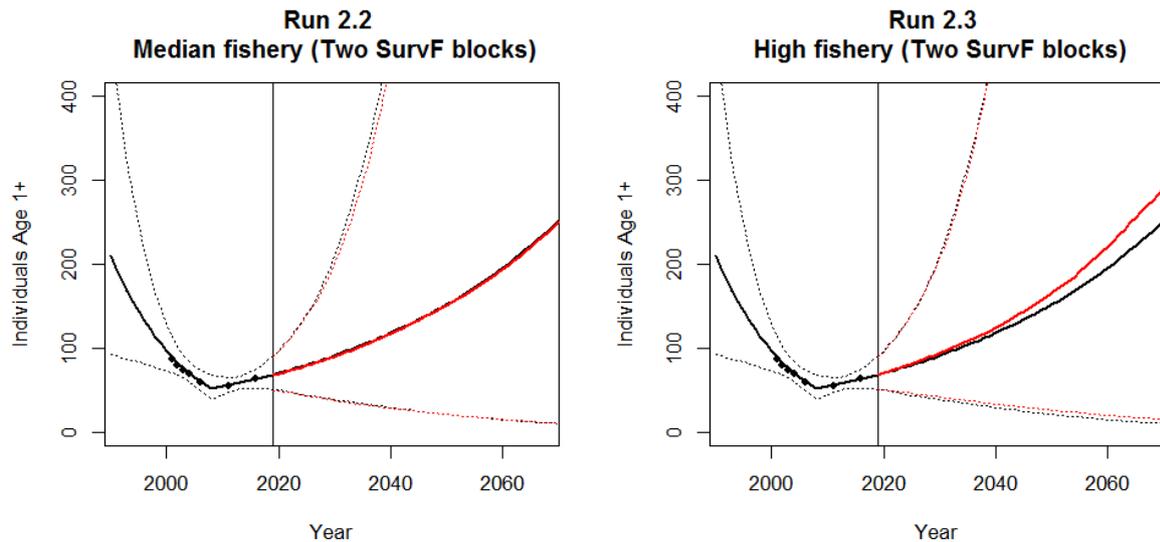


Figure 11: As Figure 10, except model runs apply two separate non-calf survival year blocks (1990–2007 and 2008–2018). Run 2.1 (in black), shows projections with continuation of recent demographic rates. Projections alleviating threat-specific mortality are shown in red: Run 2.2, alleviating median estimates of annual set net and trawl deaths (left); Run 2.3 alleviating the upper 95% CI estimates of annual set net and trawl deaths (right). Note change in y-axis extent relative to Figure 10.

4. CONCLUSIONS

A Bayesian Māui dolphin population model was developed integrating information from genetic “mark-recapture” and a population size time series. Model runs made alternative assumptions of historical threat-specific mortality from direct commercial fishery interactions (set net and trawl) and toxoplasmosis. These models indicated a higher annual non-calf (age 1+) survival probability for females (median about 0.89) than males (median about 0.83) (see Table 6 and Table 7), though uncertainty associated with these estimates was high. An individual-based model assessment using the same data (Cooke et al. 2018) also found evidence for different survival of males and females. Both assessments assumed a closed population and an equal resighting probability of males and females (i.e. there is no emigration or change in the sightability of a demographic through time). However, the assumption of a closed population will, in this case, produce a precautionary (pessimistic) outcome since individuals not seen again will contribute to a reduction in the survival and population growth rates obtained.

Model runs assuming two non-calf survival year blocks estimated increased non-calf survival since 2008, though with a high level of uncertainty (Table 7) and this was supported by both the mark recapture observations and population size estimates fitted to by the models (Figure 5). Note that since both datasets were derived from genetic biopsy information they cannot be regarded as fully independent. However, an earlier run of the assessment model found no difference in parameter estimates when using photo-ID of Māui dolphins.

Cooke et al. (2018) undertook a sensitivity with a 50% reduction in human-induced mortality rate, which produced a similar degree of fit to a model with consistent mortality rate through time. However, their assessment did not fit to census population size estimates, as the assessment reported on here did, so these outputs are not inconsistent.

The direction of the population trajectory depended on whether one non-calf survival year block (decreasing trajectory; e.g. model run 1.1, $\lambda_{2068} = 0.980$, 95% CI = 0.962–0.998) or two multi-year blocks were assumed (increasing trajectory; e.g. model Run 2.1, $\lambda_{2068} = 1.025$, 95 % CI = 0.968–

1.086). These population trajectories are consistent with those of Cooke et al. (2018), who estimated a 2–3% annual reduction in population size for models *without* a year trend in annual survival (consistent with 98.0% from model run 1.1) and 0.2% annual decline (effectively stable) for a model run *with* a year trend in survival.

Model projections to the year 2068 estimated a minor population effect (with greatly overlapping posteriors; Table 8) of alleviating trawl and set net mortalities when commercial fisheries impact were assumed to be at the high end of the estimated range, i.e. applying the upper 95% estimate of annual deaths from the spatial risk model developed for the Threat Management Plan (Runs 1.3 and 2.3). However, this would be insufficient to stabilise or reverse a declining population trend. This is consistent with the outputs of the Threat Management Plan spatial risk model, which estimated risk ratios for commercial set net (0.28; 95% CI = 0.00–1.23) and inshore trawl (0.00; 95% CI = 0.00–0.30), i.e., below levels that would compromise their recovery to 90% of unimpacted status (Roberts et al. 2019).

The model run alleviating commercial fishery and toxoplasmosis deaths when assuming an equal detection probability of predation and other non-fishery causes of death (Run 1.4) produced an increasing population trend. However, when predation deaths were assumed to have a 10-fold lower detection probability (Run 1.5), the implication is that a higher proportion of animals are dying from predation, and a correspondingly lower proportion are dying from toxoplasmosis; in this case, alleviating commercial fishery and toxoplasmosis deaths led to a stable (but not growing) population size. For this scenario (Run 1.5), the assumed combined deaths for commercial fishing and toxoplasmosis declined from 1.9 annual deaths in 1990 to 1.1 annual deaths in 2018, due to the estimated decrease in population size; Table 4). With respect to the spatial risk assessment, the corresponding risk ratio estimated for toxoplasmosis mortality was 4.01 (95% CI = 1.47–10.47), i.e. highly likely to be sufficient to prevent population recovery to 90% of unimpacted status (Roberts et al. 2019). The risk ratio obtained for toxoplasmosis mortality and the population effects of alleviating this threat are both highly sensitive to the assumption of relative detection probability of different non-fishery threats.

The modelling assumed an equal vulnerability of males and females to toxoplasmosis, although seven out of the nine Hector's and Māui dolphins that died from toxoplasmosis were females, including six that were sexually mature (Roberts et al. 2019). If the models had assumed a greater vulnerability of females to toxoplasmosis mortality, this would have implied that the population level impact of toxoplasmosis is higher than has been estimated here.

The existing model could be used to assess the population effects of alleviating other known non-fishery threats to Maui dolphins (e.g. *Brucella* (Buckle et al. 2017)), for which annual deaths estimates are available. Future modelling assessments of the Māui dolphin population would benefit from additional information with respect to demographic parameters influencing reproductive rates. In the current assessment, estimates for Hector's dolphin were used, although these are likely to have different population status with respect to carrying capacity, and appear to have very different social group dynamics (Oremus et al. 2012). Future research to assess breeding rate, age at first breeding and longevity would be particularly beneficial. In addition, continued collection of photo-ID based observations would provide additional information for estimating demographic rates, independent of genetic-based information.

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