Assessing the Population-level Impacts of North Pacific Loggerhead and Western Pacific Leatherback Turtle Interactions in the Hawaii-based Shallow-set Longline Fishery

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Summer L. Martin[1], Zachary Siders[2], Tomoharu Eguchi[3], Brian Langseth[1], Annie Yau[3], Jason Baker[1], Robert Ahrens[2], and T. Todd Jones[1]

[1] Pacific Islands Fisheries Science Center

   National Marine Fisheries Service
   1845 Wasp Boulevard
   Honolulu, HI 96818

[2] Fisheries and Aquatic Sciences Program
   University of Florida, Institute of Food and Agricultural Sciences
   P.O. Box 110180
   Gainesville, Florida 32611

[3] Southwest Fisheries Science Center
   National Marine Fisheries Service
   8901 La Jolla Shores Drive
   La Jolla, CA 92037

U.S. Department of Commerce
Wilbur L. Ross, Jr., Secretary

National Oceanic and Atmospheric Administration
Neil A. Jacobs, Ph.D., Acting NOAA Administrator

National Marine Fisheries Service
Chris Oliver, Assistant Administrator for Fisheries

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Executive Summary

This population assessment is for the North Pacific (NP) loggerhead turtle (*Caretta caretta*) Distinct Population Segment (DPS) and the western Pacific (WP) leatherback turtle (*Dermochelys coriacea*) nesting population, with the sole purpose of evaluating the population-level impacts of a single U.S. commercial fishery, the Hawaii-based shallow-set longline (SSLL) fishery on these two populations. Both populations are listed as Endangered under the Endangered Species Act (ESA), NP loggerheads as a DPS and WP leatherbacks as a global species. This assessment was performed in a Bayesian framework with four main components: nesting data imputation (leatherbacks only), nesting trend analysis, population viability analysis (PVA), and incorporation of direct SSLL fishery take into the PVA (i.e., adding a "take model" component). Conducting PVAs under scenarios with and without future takes by the SSLL fishery allowed for evaluation of the impact of the fishery on the population status (e.g., abundance relative to pre-determined thresholds) and trends for the two populations. Trends and abundance for nesting females were estimated using a Bayesian state-space model (Boyd et al. 2017) with exponential population growth as the underlying process. Time series data used in the model originated from long-term nesting beach monitoring programs in Japan (loggerheads) and Indonesia (leatherbacks). The loggerhead data from Japan were provided as annual nest counts from three index beaches (Maehama, Inakahama, and Yotsusehama) from 1985 to 2015. The leatherback data came from two index beaches in Indonesia (Jamursba Medi and Wermon) from 2001 to 2017. The leatherback data set contained months with no monitoring effort; thus, we developed a model to impute the missing data in order to produce a time series of annual nest counts. The imputation model was autoregressive with a lag of one month (AR1 model) where the relationship between the numbers of nests in two months was modeled by the Fourier series.

This assessment indicated an increasing trend for NP loggerheads (2.3% annually; 95% CI: −11.1% to 15.6%) and a declining trend for the WP leatherbacks (−6.1% annually; 95% CI: −23.8% to 12.2%). For loggerheads, current abundance was estimated at 4541 total nesters (95% CI: 4074–5063) for the three index beaches in Japan which represent approximately 52% of all nesting individuals. For leatherbacks, current abundance for the two index beaches in Indonesia, which represent approximately 75% of all nesting individuals, was estimated from the median and 95% confidence limits of the imputed nest counts. Estimates of total nesters were as follows: 790 (95% CI: 666–942) using the median for nest counts, 515 (95% CI: 425–634) using the lower 95% limit, and 1224 (95% CI: 1052–1425), using the upper 95% limit. It is important to note that these population growth rates better reflect long-term annual trends in the number of nesters rather than true population growth rates for the following reasons: (i) the model relies exclusively on nest count data, which we assume provide an index of Annual Nester abundance, (ii) nesters represent only a small portion of the total population that also includes adult males and immature turtles of both sexes, and (iii) assuming that the growth rate for nesters represents the growth rate for the whole population would also assume a stable age distribution, and we have no data to confirm this for either population.

The PVA was developed to generate specific results to meet the needs outlined by the Pacific Islands Regional Office (PIRO) in a 2018 request, specifically: (1) mean and median times until each species declines to 50%, 25%, and 12.5% of current abundance estimates, (2) probability of each species reaching those thresholds in 5, 10, 25, 50, and 100-year time intervals with associated 95% confidence intervals, and (3) estimates of the species' mean log growth rate

(with variance and 95% confidence intervals) and finite rate of increase (lambda; with variance and 95% confidence intervals). PVAs projections out 100 years in the future suggested a 100% chance of leatherbacks falling below 50% of their current abundance, with a mean of 13 years to reach that threshold, and a 33% chance of loggerheads falling below the 50% abundance threshold, with a mean of 25 years to reach that threshold. At 10 years in the future, the chance of falling below the 50% abundance threshold was 40% for leatherbacks and 8% for loggerheads.

The take model component was developed to assess the population impacts of direct interactions between SSLL fishery gear (i.e., longline hooks) and turtles from the specified populations. A direct interaction can result in the immediate death of a turtle, or the turtle may be released alive, with or without trailing gear. For turtles released alive, PIRO assigns post-interaction mortality percentages (i.e., percent chance of death after release) by following the rubric outlined in Ryder et al. (2006). The rubric includes an injury category and a release condition that, when combined, provide a probability of mortality for each turtle (0 to 1, with 1 being dead). Thus, "take" in the model is equivalent to a probability of mortality resulting from interaction with the fishery. However, other possible forms of take (e.g., oil spills) are not considered here. Additionally, the model does not explicitly address sub-lethal effects potentially experienced by turtles released with injuries or trailing gear (e.g., reduced fitness, growth, or fecundity). We are not aware of any data quantifying sub-lethal effects to support inclusion of such effects into the model.

The primary challenge of incorporating take into the analysis is in converting the anticipated future take of each species, which is comprised of various lengths, ages, stages (i.e., juvenile or adult), and sexes, to adult nester equivalents (ANE). This step is necessary, as it converts the future take into nester equivalents, which are the only index of abundance available. Distributions were generated for life history parameters of each species using the best scientific information available. An ANE was then calculated for each individual of the anticipated take for future years using draws from several parameters in the calculation: length and post-interaction mortality based on historical incidental take data, back-calculated age with years until maturity based on a von Bertalanffy growth model, juvenile survival rate, sex, and a remigration interval.

Take was applied in two different ways: (1) adding in the historical interactions from the SSLL fishery back to the populations, and (2) removing the predicted takes from the PVA projections. There were no discernible changes to the probabilities of falling below abundance thresholds (50%, 25%, and 12.5% of current abundance) when comparing the "no take" and "take" scenarios for the future. The one exception was that for leatherbacks, where the difference between the "no take" and "take" scenarios became apparent after 2060 and the projection suggested the population would go extinct roughly 5 years sooner in the "take" scenario than in the "no take" scenario (around 2110 vs. 2115). However, in the 10-year future timeframe, which is perhaps more biologically realistic to use for impact assessments, there was no discernible difference between the "no take" and "take" projection scenarios for either species. This finding suggests that continued operation of the SSLL fishery would not negatively impact the NP loggerhead or WP leatherback populations in terms of changing their projected population growth trends or nesting female abundances. The turtles are largely released alive by this fishery, which employs 100% observer coverage, circle hooks, and finfish bait as bycatch mitigation measures. The number of interactions in the SSLL fishery is relatively low compared to other

sources of bycatch in the Pacific (Lewison et al. 2004), and the current findings suggest the fishery is not a major driver of population trends for the western Pacific leatherback or North Pacific loggerhead.

Introduction

Background

The Hawaii-based shallow-set longline (SSLL) fishery has historically interacted with four marine turtle species, including the North Pacific (NP) loggerhead (*Caretta caretta*) Distinct Population Segment (DPS), the western Pacific (WP) leatherback (*Dermochelys coriacea*) population, the eastern and western Pacific olive ridley (*Lepidochelys olivacea*) populations, and several green (*Chelonia mydas*) turtle DPSs. As a result of historically high interactions (i.e., incidental takes) with loggerhead and leatherback turtles (prior to the year 2000), the fishery is currently subject to closure for the remainder of the calendar year when the number of interactions with either species reaches pre-determined numbers (i.e., hard caps). In 2019, the fishery was shut down on March 27 for exceeding the annual loggerhead turtle cap of 17 interactions, reduced from a hard cap of 34 in previous years.

In 2018, the Pacific Islands Regional Office (PIRO) requested an assessment of status and trends for the North Pacific loggerhead and western Pacific leatherback populations that are impacted by the SSLL fishery to support its pending Biological Opinion ("the BiOp") on the continued operation of the SSLL fishery. PIFSC assembled a team of marine turtle ecologists and fisheries scientists from PIFSC and SWFSC ("the Team") to respond to the request. The Team conducted an extensive review of previous modeling efforts used to evaluate fishery impacts on loggerhead and leatherback turtles in the SSLL fishery, and determined an optimal modeling approach to estimate trends and conduct population viability analyses given the data available for the impacted populations. See Appendix I for the Team's review and justification of the selected approach, which was tailored to answer PIRO's specific requests for the following information: (1) mean and median times until each species declines to 50%, 25%, and 12.5% of current abundance estimates, (2) probability of each species reaching those thresholds in 5, 10, 25, 50, and 100-year time intervals with associated 95% confidence intervals, and (3) estimates of the species' mean log growth rate (with variance and 95% confidence intervals) and finite rate of increase (lambda; with variance and 95% confidence intervals).

The Team completed its analysis and submitted it to external reviewers with technical expertise in population modeling in August 2018, also providing a copy to PIRO at that time. The Team made some improvements to the analysis implementing feedback received from the reviews and submitted a final version to PIRO in early October 2018. The Team presented the modeling approach and results to the Western Pacific Regional Fisheries Management Council's ("the Council") Scientific and Statistical Committee (SSC), which accepted and approved the approach and assessment. Members of the SSC commented that incidental take could be readily added within the framework assembled by the Team.

In accordance with comments from external reviewers and the SSC, the Team moved forward with the development of a statistical model addressing effects of historical take (2004 to present) on population trends and projections, and potential impacts from anticipated future take levels by the SSLL fishery. As noted by the Council's SSC members, the original trend and population viability analyses produced by the Team could be modified to include incidental take so that results can be compared for "no take" and "take" scenarios for past and future years. In doing so, there are a number of modeling decisions to be made. PIFSC reassembled the Team (with some

personnel changes) in June 2019 to complete the modeling effort and prepare for another external review, this time with the focus on the integration of take into the model. PIRO also completed its BiOp in June 2019.

The "take model" described herein is an analytical tool which was developed to assess the population impacts of a specific type of take by the fishery—namely, the direct interactions between fishing gear (i.e., longline hooks or line) and turtles from the specified populations. A direct interaction can result in the immediate death of a turtle, or the turtle may be released alive, with or without trailing gear. For turtles released alive, PIRO assigns post-interaction mortality percentages (i.e., percent chance of death after release) by following the rubric outlined in Ryder et al. (2006). The rubric includes an injury category and a release condition that, when combined, provide the estimated probability of mortality for each turtle (0 to 1, with 1 being dead). Thus, "take" as defined in the model is equivalent to a probability of mortality resulting from interaction with the fishery. However, other possible forms of take (e.g., oil spills, collision, or noise) are not considered here.

The take model does not explicitly address sub-lethal effects potentially experienced by turtles released with injuries or trailing gear (e.g., reduced fitness, growth, or fecundity). We are not aware of any data quantifying sub-lethal effects to support inclusion of such effects into the model; Ryder et al. (2006) noted that while there was some evidence of sub-lethal effects on foraging behavior, no data were available to quantify the impacts on fecundity. Furthermore, the mortality coefficients in Ryder et al. (2006) were estimates agreed upon by a panel of experts (including marine turtle biologists and veterinarians). They are likely conservative for the species (i.e., the experts likely did not underestimate the impacts of gear interactions on the turtles) but the accuracy of the estimates is unknown. Adding sub-lethal impacts into the mortality estimates would likely place them within the range of the original estimates, which do not have uncertainties specified. For example, expert suggestions for the appropriate mortality rate for high risk injuries ranged from 40 to 70%, with a cluster of responses in the 40–50% range (Ryder et al. 2006). Finally, every turtle released alive receives a post-interaction mortality probability greater than zero in Ryder et al. (2006), with 5% chance of death as the minimum for hooked turtles and with a 1% minimum for entanglement only. This inherently reduces the impact of those turtles by reducing their fecundity in the model by the same amount.

North Pacific Loggerhead Turtles

The North Pacific loggerhead population ("NP loggerheads") is recognized as a distinct population segment and listed as Endangered under the Endangered Species Act (ESA). NP loggerheads nest exclusively in Japan, in three regions or management units (MUs): Mainland Japan, Yakushima, and Okinawa. After the turtles emerge as hatchlings on their natal beaches in Japan, they spend their developmental years (i.e., >20 years until sexual maturity (Tomaszewicz et al. 2015)) foraging in the North Pacific, with the oceanic central North Pacific and neritic zones off Baja California and California identified as two key developmental areas (Kobayashi et al. 2008; Polovina et al. 2006; Polovina et al. 2000). Once mature, they forage in oceanic or neritic waters closer to Japan in between breeding seasons (Hatase et al. 2002; Hatase et al. 2010), with adult females returning to nest, on average, every 3.3 years (mean "remigration interval") and laying 4.6 nests per season (mean "clutch frequency") (see Hatase et al. 2013). Similar to most marine turtle populations worldwide, the only available monitoring data that are

suitable for assessing population status and trends are nest count data. The Sea Turtle Association of Japan (STAJ) provided annual nest count data for our use in this assessment, with the data coming exclusively from three beaches in Yakushima: Inakahama (1986–2015), Maehama (1989–2015), and Yotsusehama (1999–2015). The three beaches comprise an estimated 52% (Matsuzawa, Sea Turtle Association of Japan, pers. comm.) of annual nesting for the population. We consider these data to be the best scientific information available and use them as an index of abundance for NP loggerheads.

Western Pacific Leatherback Turtles

The western Pacific leatherback population ("WP leatherbacks") is currently listed as Endangered as part of a single global population of leatherback turtles. While it is not currently recognized as a distinct population segment under the ESA, it is genetically and ecologically different from other populations and is treated as such for management purposes related to the SSLL fishery. Nesting for this population occurs in the Indo-Pacific region, primarily in Indonesia, Papua New Guinea, and Solomon Islands, and to a lesser extent in Vanuatu. The WP leatherbacks are wide-ranging and undergo long migrations between nesting grounds and foraging areas. There are at least three important foraging regions for the WP leatherbacks, including pelagic areas of the Northeast Pacific (NEP; off the coasts of California, Oregon, and Washington), the North Pacific Transition Zone (NPTZ), and the South China Sea (Benson et al. 2011). The SSLL fishery is only known to interact with those foraging in the NEP and NPTZ. Females mature after 16.1 years (mean age at maturity) (Jones et al. 2011), and those from NEP and NPTZ foraging areas return to nest, on average, every 3.1 years (mean remigration interval, which was derived from Lontoh (2014)), laying 5.5 nests per season (mean clutch frequency) (Tapilatu et al. 2013). The only monitoring data that are suitable for trend analysis are nest counts from two beaches in the Bird's Head Peninsula of Papua Barat, Indonesia. Our Indonesian colleagues provided monthly nest count data for those beaches, Jamursba Medi (2001–2017) and Wermon (2006–2017), for our use in this assessment. However, due to the presence of gaps in the monthly data, we had to impute missing values to estimate annual nest counts prior to our trend analysis. While there is a single peak in nesting activity during the summer at Jamursba Medi, there are both summer and winter peaks in nesting at Wermon. The two beaches comprise approximately 75% (NOAA Fisheries and USFWS Leatherback Turtle Status Review, in Review) of nesting for the population. We consider these data to be the best scientific information available and use them as an index of abundance for WP leatherbacks.

Methods

Data

The analyses in this report are based on nest count data originating from long-term monitoring programs in Japan (loggerheads) and Indonesia (leatherbacks) as stated previously. Raw nest count data were made available by international colleagues for this analysis (Figure 1). The loggerhead data from Japan were provided as annual nest counts from three index beaches (Maehama, Inakahama, and Yotsusehama) from 1985 to 2015. The leatherback data came from two index beaches in Indonesia (Jamursba Medi and Wermon) from 2001 to 2017. The leatherback dataset contained months with no monitoring effort; thus, we developed a model to impute the missing data in order to produce a time series of annual nest counts (see **Monthly Nest Count Imputations for Leatherback Turtles**).
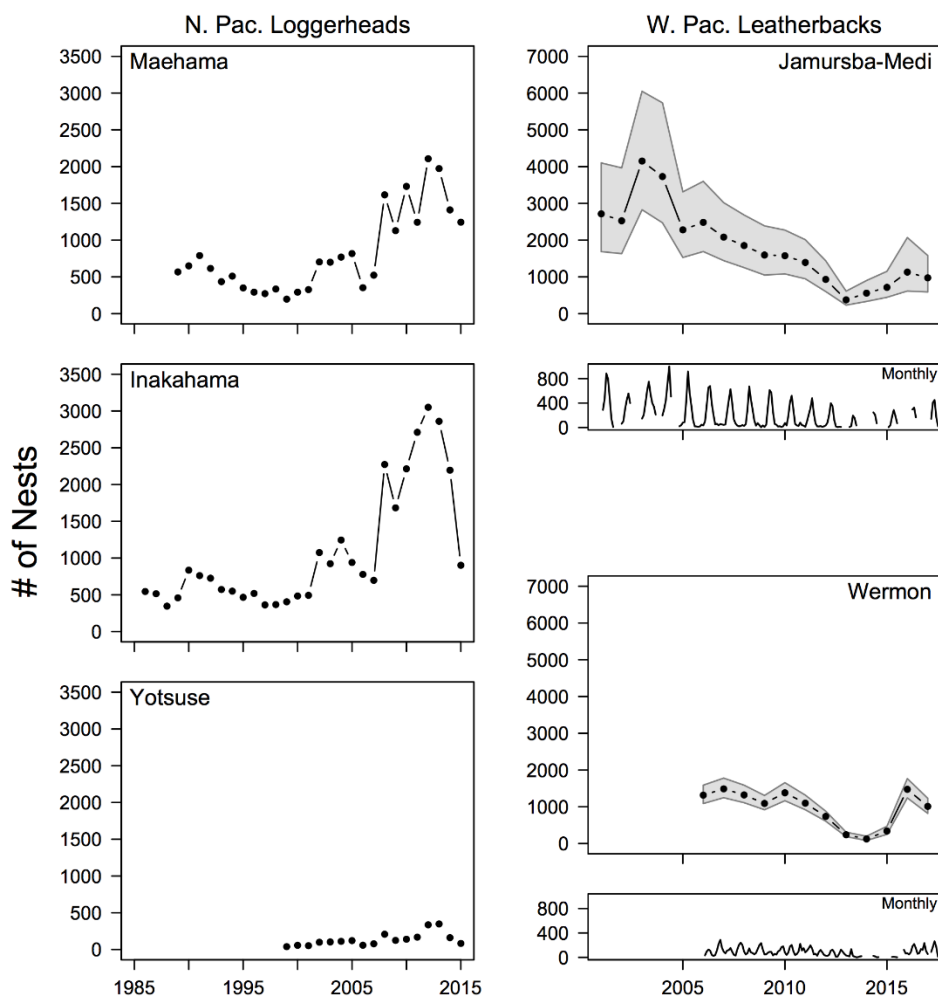
Figure 1. Raw nest count data available for this analysis. For North Pacific loggerhead turtles, annual nest count data came from three beaches in Japan (Maehama, Inakahama, and Yotsusehama) from 1985 to 2015. For western Pacific leatherback turtles, monthly nest count data came from two beaches in Indonesia (Jamursba Medi and Wermon) from 2001 to 2017. Annual counts for leatherbacks were imputed within this analysis (see Section 2.3); estimates are shown as median annual counts (points) with 95% credible intervals (gray shading).

Modeling Overview

Nest counts for both species were converted into the number of females nesting each year ("Annual Nesters") using their respective clutch frequencies (see Appendix II). Trend analysis was conducted in a population modeling framework to allow for extraction of population growth rates and annual abundance estimates, which were used to perform a population viability analysis (PVA) for each population. The anticipated take level (ATL) for each population (McCracken 2018) was incorporated into the PVA model to allow for a quantitative comparison of future scenarios with and without incidental fishery take; the mean annual ATL was 10 for leatherbacks and 15.6 for loggerheads (see *Predicting Anticipated Take Levels (ATLs): Turtle Interactions in Future Years*). The modeling framework is shown in Figure 2, with details on each step of the modeling process outlined in the sections below. Full R code for all aspects of the modeling is provided in Appendix III.

Figure 2. Overview of the modeling framework used to assess population trends and viability for North Pacific loggerhead and western Pacific leatherback turtles, as well as the impact of incidental takes by the Hawaii-based shallow-set longline fishery on the two populations. (A) Data imputations for monthly nest counts for leatherback turtles nesting in Indonesia. (B) Trend analysis of nest count data to estimate population growth rates and current abundance. (C) Population viability analysis including future projections of population size and assessment of the impacts of anticipated take levels on the projections; $\lambda = e^r$, where r is the instantaneous population growth rate (i.e., long-term annual trend), and λ ("lambda") is the finite rate of increase for the population.

Monthly Nest Count Imputations for Leatherback Turtles

To impute missing monthly nest counts in the leatherback data from Indonesia, we used a Bayesian hierarchical model. In the model, the natural logarithm ("natural log") of monthly counts at a nesting beach was modeled as an auto-regressive model (Eq. 1):

$$u_{t,m} = s_{t,m} + X_{t-1,m-1}$$

Eq. 1

where $u_{t,m}$ is the mean of the natural log of the true (unobserved) number of nests at time (t) of month (m), $s_{t,m}$ is the "slope" parameter at time t, which is defined by month (m = 1 to 12), and $X_{t-1,m}$ is the natural log of the true nest count at time t − 1. The time index starts at the first month of the time series and increases monthly, whereas the month index (m) corresponds to sequential months within each nesting season (i.e., months 1 through 12). The nesting season starts in April (m = 1) and ends in March (m = 12) of the next calendar year. For example, the mean of the number of nests during July of the fourth season would be indexed as $u_{43,4}$ (43rd time step and fourth month of the season).

The state-space (i.e., biological process of interest, which in this case is the natural log of the true number of nests ($X_{t,m}$) laid per month on a beach, either Jamursba Medi or Wermon) is modeled with a normal distribution with the mean ($u_{t,m}$) and standard deviation (σ_x), which was assumed to be constant over time (Eq. 2).

$$X_{t,m} \sim N(u_{t,m}, \sigma_X)$$

Eq. 2

Given the state-space process for the natural log of the true number of nests ($X_{t,m}$), observations ($y_{t,m}$) (i.e., monthly nest counts recorded on either beach in natural log space) are modeled with another normal distribution with standard deviation (σ_y), which also was assumed to be constant over time (Eq. 3).

$$y_{t,m} \sim N(X_{t,m}, \sigma_y)$$

Eq. 3

The slope ($s_{t,m}$) parameters are modeled with the discrete Fourier series by acknowledging the periodicity of nesting (Eq. 4). For Jamursba Medi, we used a 12-month period to capture the single summer peak in nesting, whereas for Wermon we used 6 months to capture the summer and winter peaks (Figure 5).

$$s_{t,m} = \beta_1 * cos\left(2\pi\left(\frac{m}{period}\right)\right) + \beta_2 * sin\left(2\pi\left(\frac{m}{period}\right)\right)$$

Eq. 4

The two coefficients (β_1 and β_2) were estimated from the data.

Annual number of nests for each season (April through March; X_T) were then computed (Eq. 5) as the sum of estimated true monthly log numbers of nests ($X_{t,m}$) which were derived from imputed log observed nest counts ($y_{t,m}$).

$$X_T = \sum_{m=1}^{12} \exp (X_{,m})$$

<div align="right">Eq. 5</div>

where $X_{,m}$ indicates all t values from m = 1 to m = 12.

Prior distributions for the parameters were not flat but with large uncertainties in the natural-log space. Normal distributions with mean = 0 and variance = 1 were used for the two parameters for the Fourier discrete function (β_1, β_2), whereas gamma distributions with the shape parameter = 2, and rate parameter = 0.5 were used for the standard deviation parameters for the process (σ_X) and observation (σ_y) models.

The posterior distributions for ($X_{t,m}$) were used to determine the number of total nesters. The medians of the posterior distributions were used as point estimates, whereas lower and upper 95% confidence limits were used to incorporate the estimated uncertainty in the imputed numbers of nests. The model (Eq. 2) was fit to the two data sets from leatherback nesting beaches (Jamursba Medi and Wermon) using JAGS (v. 4.3.0; (Plummer 2003; 2017)) through the jagsUI package (Kellner 2018) in R (v. 3.5.3; R Development Core Team (2018).

Trend Analysis and Population Viability Analysis

Estimating Historical Trends and Current Nester Abundance

Population growth rates were estimated using a stochastic density-independent exponential growth model (Eq. 6–Eq. 8) applied to nest count data (Boyd et al. 2017; Holmes et al. 2007) as follows:

$$N_j = N_{j-1}e^r$$

<div align="right">Eq. 6</div>

where N_j is the number of Annual Nesters in year j, r is the instantaneous population growth rate (i.e., long-term annual trend), and $e^r = \lambda$ (i.e., "lambda," the finite rate of increase for the population).

This model is commonly used for long-lived, slow-growing, late-maturing species such as sea turtles whose populations have been depleted to relatively low levels. The assumption of density-independence could be evaluated in a future assessment by running a density-dependent model (e.g., Gompertz model), which would allow for the population reaching a carrying capacity at some point in the future. This is only potentially relevant for increasing populations. The data inputs to the model were time series of Annual Nesters (i.e., the number of females arriving on a beach each year to nest), which were derived from observed nest counts by simply dividing nests by mean clutch frequency (4.6 for loggerheads and 5.5 for leatherbacks, Appendix II). This static conversion from nests to nesters had no bearing on the estimation process, but put the results into management-relevant terms (i.e., nester abundance). The number of Annual Nesters summed across the number of years of one remigration interval (e.g., 3.3 years for loggerheads) yields a snapshot of the Total Nesters in the population.

It is important to note that the population growth rates estimated here are better interpreted as a long-term annual trends in the number of nesters rather than true population growth rates for the

following reasons: (i) the model relies exclusively on nest count data, which we assume provide an index of Annual Nester abundance, (ii) nesters represent only a small portion of the total population that also includes adult males and immature turtles of both sexes, and (iii) assuming that the growth rate for nesters represents the growth rate for the whole population would also assume a stable age distribution, and we have no data to confirm this for either population. The exponential growth equation (Eq. 6) was transformed into natural log space (Eq. 7) and solved for the population growth rate (Eq. 8):

$$ln(N_j) = ln(N_{j-1}) + r$$

Eq. 7

$$r = ln(N_j) - ln(N_{j-1})$$

Eq. 8

Following Boyd et al. (2017) and the methods outlined in their Appendix S1, we constructed a Bayesian state-space model (BSSM, Figure 3) from the natural log version of the exponential population growth equation (Eq. 7). The BSSM framework allows for estimation of both process variation (i.e., environmental and demographic variability that leads to additional changes in the number of Annual Nesters from year to year) and observation uncertainty (i.e., imperfect data collection), and provides parameter estimates with probability distributions (i.e., posterior distributions) which are useful for conveying uncertainty in management applications. Model inputs were the time series of Annual Nesters as described above.
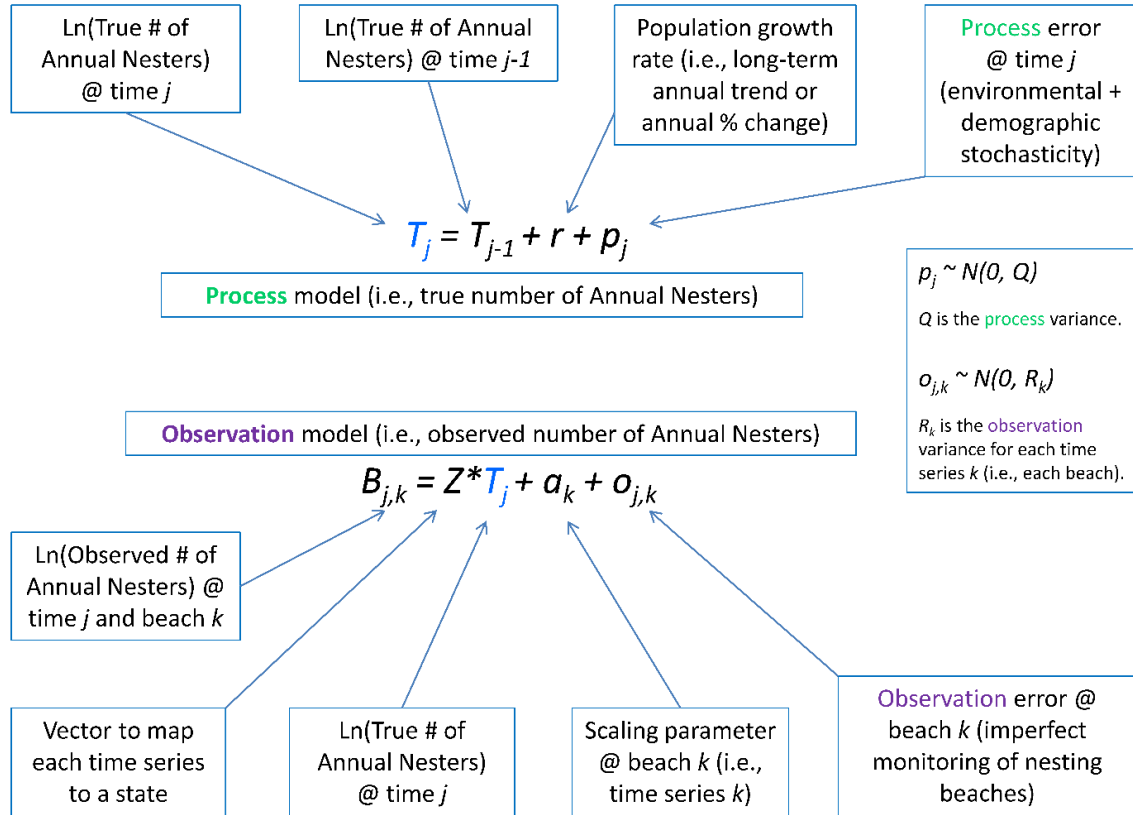
Figure 3. Schematic illustration of Bayesian state-space model based on stochastic density-independent exponential population growth. There are two major components: a process model describing the true number females nesting each year and an observation model relating the observed count data to the true number of nesting females. Three parameters are estimated: (1) r, the instantaneous population growth rate, (2) Q, process error variance, and (3) R, observation error variance. The model also provides a predicted count (number of nesting females) with a probability distribution for each year of observed data. The predicted value for the final year of observed data is then used as a starting point for future projections.

Adapting the methods in Boyd et al. (2017), the process equation of the BSSM model is written in discrete-time and log-space:

$$T_j = T_{j-1} + r + p_j \qquad \text{where } p_j \sim N(0, Q) \qquad \text{(process equation)} \qquad \text{Eq. 9}$$

where T_j is the natural log of the true (unobserved) number of Annual Nesters in year (j), r is the instantaneous population growth rate (i.e., long-term annual population trend), p_j is the process error at year (j), and Q is the variance of the state process (time invariant). The true state variable, T_j, is not directly measured for the NP loggerheads or WP leatherbacks. Instead, nest counts are observed on multiple beaches for each population, and the resulting time series come with various forms of observation uncertainty (i.e., missed nests or falsely identified nests). The relationship between the observed data and the corresponding true number of Annual Nesters is defined by a second equation:

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$$B_j = T_j + o_j \qquad \text{where } o_j \sim N(0, R) \quad \text{(observation equation)} \qquad \text{Eq. 10}$$

where B_j is the natural log of the observed Annual Nesters, o_j is the observation error at year (j), and R is the variance of the observation process (time invariant).

This basic model can be expanded to accommodate multiple state vectors, representing several populations and multiple time series (Hinrichsen and Holmes 2009):

$$T_j = T_{j-1} + r + p_j \qquad \text{where } p_j \sim MVN(0, Q_j) \quad \text{(process equation)} \qquad \text{Eq. 11}$$

$$B_j = \mathbf{Z} * T_j + a + o_j \qquad \text{where } o_j \sim MVN(0, R_j) \quad \text{(observation equation)} \quad \text{Eq. 12}$$

where Q_j is the process variance-covariance matrix, R_j is the observation variance-covariance matrix, $\mathbf{Z}$ is a matrix that maps the set of time series to the set of state vectors, and a is a vector of scaling parameters (Boyd et al. 2017). In the multivariate setting, the number of underlying population states (corresponding to the number of populations) may vary from 1, …, I, where I is the number of time series (Boyd et al. 2017). For both NP loggerheads and WP leatherbacks, we defined the model to have only one population (one state vector) with multiple time series of observations (i.e., multiple beaches), as this structure best represented the known population dynamics which include exchange of individuals and genetic similarity across the studied beaches. We assumed the observation error for each beach to be independent. These decisions simplified the distributions for the process and observation errors to normal distributions (rather than multivariate normal distributions as shown in Eq. 11 and Eq. 12). The annotated model code (in JAGS format) is provided in Figure 4.

```
# Original code provided by C. Boyd from Boyd et al. 2017 and adapted slightly here with input from C. Boyd
# This model structure is specific to the case of a single population that has a single growth rate (denoted r here)
# and a single process variance (denoted Q here).
# This structure was determined by the NOAA team to be the most biologically relevant (vs. multiple r and/or Q)
# For NP loggerheads, there are 3 time series of nesters (each derived from nest counts on separate beaches)
# and these time series represent 3 observations of the same "true state" variable of interest,
# which is the number of females that nest each year ("annual nesters")
# For WP leatherbacks, there are 2 time series of nesters from the 2 primary nesting beaches
# T = true state; number of nesters per year in NATURAL LOG SPACE
# B = observed state; number of nesters per year in NATURAL LOG SPACE
# nesters per year (Annual Nesters) is derived as observed nest counts divided by mean clutch frequency

model
{
  A[1] <- 0;      # A is scaling factor for each time series (nesting beach), set first beach to 0
  for(j in 2:n.timeseries) {A[j] ~ dnorm(a_mean,1/(a_sd^2));} # set priors, A for each subsequent time series

  r ~ dnorm(u_mean,1/(u_sd^2));      # set prior, r is population growth rate in exponential growth equation
  tauQ ~ dgamma(q_alpha,q_beta);   # set prior, Q is process variance, tauQ is used to derive precision
  Q <- 1/tauQ;                      # define tauQ as precision (1/variance) - model requires this format

  T0 ~ dnorm(t0_mean, 1/(t0_sd^2)); # set prior, T0 is initial state (total # of annual nesters)
  predT[1] <- T0 + r;               # define predicted nesters at year 1 as predT[1] = T0 plus growth rate r
  T[1] <- predT[1];                 # define true state (# of nesters) at year 1 as T[1] = predT[1]

  for(k in 1:n.timeseries) {             # for each time series (annual nesters from a single beach)
    tauR[k] ~ dgamma(r_alpha,r_beta);  # set prior, R is observation variance, tauR is precision
    R[k] <- 1/tauR[k];                  # define tauR as precision (1/variance)
    predB[k,1] <- Z[k,1] * T[1] + A[k];    # define first value of predB (predicted OBSERVED annual nesters)
                      # Z (matrix) maps time series to the state vectors (1 state vector in this case)
    B[k,1] ~ dnorm(predB[k,1], tauR[k]);}   # set prior for first value of B (OBSERVED annual nesters)

  for(j in 2:n.yrs) {                    # for each year of observed data beyond year 1...
    predT[j] <- T[j-1] + r;             # define predicted nesters for a year as previous year plus growth rate
    T[j] ~ dnorm(predT[j],tauQ);        # set prior, T is true state (annual nesters)

    for(k in 1:n.timeseries) {          # for each time series...
      predB[k,j] <- Z[k,1] * T[j] + A[k]; # define predB (predicted OBSERVED annual nesters) for time series & year
                      # Z (matrix) maps time series to the state vectors (1 state vector in this case)
                      # A is vector of scaling parameters (first one is 0, see code at top)
      B[k,j] ~ dnorm(predB[k,j], tauR[k]);}  # set prior, B is OBSERVED annual nesters for time series & year
  }
}
```

Figure 4. Bayesian state-space model code used in the analysis of historical trends for North Pacific loggerheads and western Pacific leatherbacks (JAGS code for use in R). Full code for all aspects of the modeling described in this report is included in Appendix III.

Posterior distributions of the model parameters were numerically derived using Markov chain Monte Carlo (MCMC) simulation in JAGS (Plummer 2003, 2017) in R (R Development Core Team 2018) with 'coda' and 'jagsUI' packages. The MCMC simulations were based on 10,000 samples of 2 chains, where every other sample was retained to reduce the auto-correlation among samples (thinning). The first 1000 samples of each chain were discarded as a burn-in sample. The burn-in sample is used for finding the central part of joint posterior distribution and is not helpful for making inference of the parameters (Gelman et al. 2013). The estimation process was conducted on the data set for each species separately (i.e., the three time series of Annual Nesters for loggerhead turtles and two time series for leatherback turtles for a total of two models, one per species). Prior distributions are described in Table 1. Convergence of MCMC sampling was determined via examination of trace plots, effective sample sizes, Geweke statistics (Geweke 1992), and Gelman and Rubin statistics.

Table 1. Prior distributions for the Bayesian state-space model historical population trend analysis.

Parameter	Prior distribution	Interpretation
r	Normal($0, \sigma^2$), $\sigma = 0.5$	instantaneous population growth rate (i.e., long-term annual trend)
Q	Inv-Gamma(0.01, 0.01)	inverse of Q, process error variance (precision)
T_0	Normal($B_{1,1}, \sigma^2$), $\sigma = 10$	initial true state of ln (Annual Nesters) at time $j = 0$; ($B_{k,1}$) is the first observed data point from Jamursba Medi for leatherbacks and Inakahama for loggerheads (the beaches with the earliest year of data)
R_k	Inv-Gamma(0.01, 0.01)	inverse of R_k, observation error variance (precision) for the kth time series
a_k	Normal($0, \sigma^2$), $\sigma = 4$	scaling parameter for the kth time series; a_1 is set to 0

From the model outputs, we were most interested in the posterior distributions for r, the annual population growth rate (i.e., long-term annual trend); Q, the process variance; and T_{final}, the estimated true log Annual Nesters for the final year of observed data (see Figure 3). We used the joint posterior distribution for these parameters to project forward 100 years into the future (details below). We also used the posterior distributions of Annual Nesters for the final four years of data (2012–2015 for loggerheads; 2014–2017 for leatherbacks) to estimate Current Abundance:

$$N_{current} = \frac{RI * (e^{T_{final}} + e^{T_{final-1}} + e^{T_{final-2}} + e^{T_{final-3}})}{4}$$

Eq. 13

where RI is the remigration interval for the population and N_{final} is the median Annual Nesters estimated for the final year of data (i.e., 2017 for leatherbacks and 2015 for loggerheads), $N_{final-1}$ is for the second to final year of data, and so on. This estimate serves as a snapshot of Total Reproductive Females in the population and assumes no mortality of adult females during the RI period.

Future Projections

After the historical trend model was run and the parameters estimated, Population Viability Analysis (PVA) projections were conducted using a simulation approach with 10,000 runs for each species. Each projection was initialized in its starting year with a paired draw from the MCMC samples for Annual Nesters ($N_0 = N_{final}$), instantaneous population growth rate (r), and process error variance (Q) from the final data year of the historical trend analysis (2015 for loggerheads; 2017 for leatherbacks). For each subsequent year in the projection, a new growth rate and a new process error variance were drawn as pairs from the MCMC samples (i.e., the joint posterior distribution), making the projections dynamic to reflect inter-annual variation in the observed data as well as the biology of the species. Pulling paired draws from the MCMC samples constrained the values of the parameters to realistic combinations, thereby keeping the uncertainty in the projections reasonable. For each year, the number of Annual Nesters was calculated according to the exponential growth equation but with the addition of a process error (Eq. 11; see model diagram in Figure 3). If the number of Annual Nesters dropped below zero in a given year, the population was considered to be extirpated and was set at zero for all remaining years of the simulation. Each projection was simulated for 100 years (2016–2116 for loggerheads; 2018–2118 for leatherbacks). The projections were completed in R (R Development Core Team 2018) using the 'coda' and 'jagsUI' packages (Kellner 2018; Plummer 2017).

Evaluating Projections against Abundance Thresholds

The probability of falling below 50%, 25%, and 12.5% of the current population size (i.e., Annual Nesters on the beaches studied, N_0) was calculated at 5, 10, 25, 50, and 100-year time steps by summing the number of projections below the thresholds at a given time step and dividing by the total number of projections (10,000). For the 100-year time step and for simulation runs that fell below a given population threshold, the mean, median, and 95% confidence limits of number of years to reach the threshold were calculated.

Incorporating Fishery Interactions into the Model

In principle, incorporating the SSLL incidental take of loggerheads and leatherbacks into the PVA projections is simple. During the calculation of the number of females in the next time step (i.e., season), N_{j+1}, the number of females in the current time step, N_j, is reduced by the incidental take in the current time step, F_j, then multiplied by the finite population growth rate, λ (i.e., e^r) (Eq. 14).

$$N_{j+1} = \left(N_j - F_j \right) * e^r$$

Eq. 14

Ultimately, the challenge is converting the incidental take of a given species that is comprised of various lengths, ages, stages (i.e., juvenile or adult), and sexes to adult nester equivalents (ANE).

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To do so, life history parameters of each species were collated, compared, and used to generate a distribution of each parameter (Appendix II).

Predicting Anticipated Take Levels (ATLs): Turtle Interactions in Future Years

The first step in the take model is generating the number and characteristics of the anticipated turtles that will be taken in each year. The number of turtles is referred to as the annual anticipated take level (ATL; i.e., the number of turtles the fishery anticipates taking in each future year). Each year's ATL was drawn from a Conway-Maxwell Poisson distribution (CMP), a two parameter version of the Poisson distribution that includes a scale parameter (ν) (Eq. 15).

$$ATL_j \sim \sum_{s=1}^{3} CMP\left(\mu_{s,j}, \nu_{s,j}\right)$$

Eq. 15

where $\mu_{s,j}$ is the mean of the CMP distribution, and s is one of three within-year segments which are summed to produce the annual ATL (McCracken 2018). The estimation of the CMP distribution's parameters was broken into three time periods per year: (1) January 1 – March 20; (2) March 21 – November 18; and (3) November 20 – December 31 (McCracken 2018). For NP Loggerheads, the year 2011 was excluded from the estimation of the parameter estimates and time blocks 2 and 3 were combined. For WP Leatherbacks, CMP parameters were estimated for each time block. In the take model, the CMP parameters were used to draw an ATL for each time block and then summed (Eq. 15 above) to result in an annual ATL. The inclusion of ν allows for the variance of the distribution to not equal the mean, μ, which an assumption of a standard Poisson distribution. Thus, the number of turtles taken by the fishery in a given year can be over or under-dispersed relative to a Poisson distribution when using the CMP distribution.

A critical assumption to the estimation of the ATL per McCracken (2018) is that the conditions generating the historical take levels were constant (e.g., the fishery effort, closures, population size). This is obviously not true and results in the estimation of future ATLs to be independent of changes in the generating processes. McCracken (2018) discusses these assumptions and the impacts of the short time series of historic takes in estimating the ATL. However, as the ATL estimates provided by McCracken (2018) represent the best available science, we use them herein.

Take Demographics

Lengths and Fishery Mortality
In summary, each individual of the anticipated take received a length and fishery mortality from a bivariate normal distribution, a back-calculated age with years until maturity based on a von Bertalanffy growth model, juvenile survival rate, sex, and a remigration interval.

For each individual in the annual ATL, demographic characteristics were computed. Based on the historical incidental take, a bivariate normal distribution was used to generate lengths (in logarithmic space) and assigned fishery mortality (in logit space) (Eq. 16).

$$\begin{pmatrix} log\ (L_k) \\ logit(D_k) \end{pmatrix} \sim MVN \begin{pmatrix} \theta_{L,j} \\ \theta_D \end{pmatrix}, \Sigma$$

Eq. 16

$$\theta_{L,j} = \alpha_0 + \alpha_1 F_j$$

Eq. 17

$$\Sigma = \begin{bmatrix} \sigma_L^2 & \rho_{L,D}\sigma_L\sigma_D \\ \rho_{L,D}\sigma_L\sigma_D & \sigma_D^2 \end{bmatrix}$$

Eq. 18

Where $\theta_{L,j}$ is a linear function (Eq. 17) of the annual incidental take, F_j, with intercept, α_0, and slope, α_1, and Σ is the variance-covariance matrix (Eq. 18) with variances, σ_L^2 and σ_D^2, for the log lengths and logit fishery mortality with a correlation of $\rho_{L,D}$. This formulation allows for the log lengths ($log\ (L_k)$) and logit assigned fishery mortality ($logit(D_k)$) to have correlated draws. The parameters of the multivariate normal distribution (α_0, α_1, σ_L, σ_D, and $\rho_{L,D}$) were solved for in a Bayesian framework using STAN via RStan (Stan Development Team 2018) with 7,500 simulations per chain (5,000 as burn-in and 2,500 retained) with 4 chains. We used weakly informative prior distributions for all parameters (Gelman et al. 2017); normal prior distributions with mean 0 and standard deviation of 2 for α_0, α_1, half-normal with mean 0 and a standard deviation of 2 for σ_L and σ_D, and for $\rho_{L,D}$ which had a prior distribution of $\frac{\rho_{L,D}+1}{2} \sim Beta(2,2)$. All MCMC simulations converged with $\hat{R} < 1.1$ for all parameters (Gelman and Rubin 1992).

Age and Stage
From the lengths of all historically taken loggerheads (n = 197) and leatherbacks (n = 105), a von Bertalanffy growth model (VBGM) was used to calculate the expected length at age across the range of lengths for each species. The predicted age at length of each individual, A_k, was determined by using the minimum length of the VBGM predicted lengths and lengths of turtles that were anticipated to be taken in the fishery. Using the VBGM for each species, the age at maturity, A_{mat}, was assumed as the age corresponding to a length of 97.5% of L_∞, the asymptotic maximum length. Using the best scientific information available, this was 16.1 years for leatherbacks (Jones et al. 2011) and 26.5 years for loggerheads (See Appendix IV for the loggerhead VBGM methods).

Turtles in the anticipated take with ages less than A_{mat} or lengths less than 97.5% of L_∞ were considered immature. The years until maturity for all immature turtles was calculated as $Y_k = A_{mat} - A_k$, where A_k indicates the age of the kth individual.

Remigration Interval, Juvenile Survival, and Sex
We ran both deterministic and stochastic versions of the take model. In deterministic runs, each individual in the anticipated take was assigned the mean remigration interval (RI) (3.06 for leatherbacks, 3.30 for loggerheads) and the mean juvenile survival (φ_J) (0.81 for leatherbacks, 0.80 for loggerheads). In stochastic runs, each individual's remigration interval was drawn from a CMP distribution for leatherbacks ($\mu = 3.06, \nu = 2.36$) and a truncated normal distribution for loggerheads ($\mu = 3.3, \sigma = 2.30$) greater than 0 (derived from Lontoh et al. 2014; Hatase et al. 2013). The CMP parameters for the leatherback remigration interval were solved for by fitting a CMP distribution to known remigration intervals of leatherbacks from the North Pacific Transition Zone and the Northeast Pacific reported in Lontoh (2014) using the compoisson

package in R (Dunn 2012). In stochastic runs, the juvenile survival was drawn from a normal distribution ($\mu = 0.81, \sigma = 0.030$, for leatherbacks; $\mu = 0.80, \sigma = 0.031$, for loggerheads). The sex of each animal was drawn from a Bernoulli distribution with the probability of being female equal to 0.73 in leatherbacks and 0.65 in loggerheads (Benson et al. 2011; Snover 2008). During stochastic runs, the probability of being female was used to draw the expected sex of each animal from a Bernoulli distribution. See Appendix II for parameter sources.

Adult Nester Equivalent (ANE) calculation
To calculate the ANE for each individual (k) in the anticipated take, adults were given ANEs of 1 and juvenile ANEs were calculated by projecting the juvenile survival over the number of years to maturity and dividing by the remigration interval (Eq. 19).

$$ANE_k = \frac{\varphi_J^{Y_k}}{RI}$$

Eq. 19

The division by the remigration interval was necessary to account for the population viability analysis projections being made in terms of annual nesting females (i.e., the number of females nesting in a given year).

For deterministic and stochastic runs, the stochastic nature of sex ratio and fishery mortality (derived from the historical take and assigned mortality) were applied to adjust the individual ANE. In the latter, the probability of an individual taken by the fishery dying was used with a Bernoulli distribution to simulate whether an individual died. Thus, the ANE of the kth individual was computed such that when the individual was a juvenile, female ($Sex = 1$) and ended up dying ($Discard = 1$), the ANE was defined as Eq. 19, whereas when the individual was adult and either male ($Sex = 0$) or ends up alive ($Discard = 0$) the ANE equals 0 (Eq. 20).

$$ANE_{realized,k} = \begin{cases} \frac{\varphi_J^{Y_k}}{RI}, Stage = J \\ 1 \times Sex \times Discard, Stage = A \end{cases}$$

Eq. 20

Historical ANE Imputation
To account for the historical impact of the SSLL on the respective population growth rates, the ANE of the historical incidental take was calculated in a deterministic fashion for all turtles encountered. Similar to the anticipated take in the PVA projections, each turtle's length was used to generate a likely age, stage, and years until maturity. For juveniles, the number of years until maturity was rounded to the nearest year. Adults were assumed to be nesting the year of their interaction with the SSLL fishery. To calculate the cumulative impact of the incidental take of each turtle, the projected nesting years were calculated as the following:

$$Y_{nest,k} = \begin{cases} Y_F + Y_k, y = 1 \\ Y_{nest,k} - 1 + RI, y > 1 \end{cases}$$

Eq. 21

where Y_F is the year the incidental take occurred, Y_k is the years to maturity, and RI is the remigration interval, which was assumed to be 3 years (rounded from 3.06 for leatherbacks and 3.3 for loggerheads). Thus, a juvenile caught in 2005 with 2 years to maturity would first nest in

2007, then again in 2010, then again in 2013, then again in 2016, and so on (see Figure 10). For the purpose of computing the historical take, nesting years between 2004 and 2017 for leatherbacks and 2004 and 2015 for loggerheads were used. However, the survival probability between each nesting year had to be accounted for so that the assumed initial ANE was adjusted as the following:

$$ANE_{k,j} = \begin{cases} \varphi_J^{Nest_1} \times PF \times D_k, y = 1 \\ \varphi_A^{RI}, y > 1 \end{cases}$$

Eq. 22

where φ_J and φ_A are the juvenile and adult survival rates (0.81 and 0.89 for leatherbacks; and 0.80 and 0.90 for loggerheads, respectively), PF is the proportion of females, and D is the assigned fishery mortality. The result is that adult females have an ANE of 1 in the first year (as $Nest_1 = 0$) and the ANE of juvenile females is adjusted for the years until maturity (as $Nest_1 = Y_k$). For all subsequent nesting years, all turtles are adult and assumed a discounted ANE for their years between nesting ($Y_{nest,k} = RI$). When summed across turtles, it equals the expected ANE determined for a given year (Eq. 23). The historical ANEs for each species are shown in Figure 11.

$$ANE_{realized,j} = \sum_{k=1}^{n} ANE_{realized,k,j}$$

Eq. 23

Take Calculation

After converting all individuals to ANEs, Eq. 14 is modified to:

$$N_{j+1} = \left(N_j - ANE_{realized,j}\right) * e^r$$

Eq. 24

where the Take, F_j, from Equation 14 is substituted out for the summation of the individual ANEs in a given year. To account for the process variance, Q, from the trend analysis, the above equation (Eq. 24) was modified to draw N_{j+1} from a normal distribution:

$$N_{j+1} = N\left(\left(N_j - ANE_{realized,j}\right) * e^r, Q\right)$$

Eq. 25

This modified population growth model, which now incorporates take as ANEs, is then used as the basis for the same 100-year PVA projection process described above to produce future scenarios with take.

Modeling Assumptions

The analyses conducted herein required a number of assumptions. We summarize the most important assumptions here to provide context for interpretation of the analyses and results. This list is not exhaustive of all technical assumptions made within the models.

Imputation:
1. The true number of nests per month is distributed normally, where the monthly means can be modeled with a discrete Fourier series with a fixed annual frequency. In other words, the number of peaks within a year is constant over the years. The variance around the means is assumed constant over the years.
2. We used an autoregressive model with a lag of one month (AR1 model) where the relationship between the numbers of nests in two months is modeled by the Fourier series. We assume this model sufficiently captures the cyclical nature of nesting throughout the year.

Trend:
1. The proportion of total nests observed on a given beach is constant through time.
2. The time series of observed number of annual nesters are representative of the populations, as are the population growth rates observed for nesters. Note that index beaches are typically identified for long-term monitoring because they represent the population well.
3. The clutch frequency is constant through time.
4. The population growth rate is density-independent for each species (i.e., no carrying capacity or Allee effects in the timeframe considered).
5. The population growth rate is the same across the different beaches for each species (i.e., there is a single biological process resulting in a single trend).
6. The process and observation variances are estimable (with so few beaches, the prior has a lot of influence).
7. The index beaches in both Japan and Indonesia were observed with constant effort or were effort-corrected by the data collectors prior to being provided to PIFSC to form the time series used in these analyses.
8. The remigration interval is constant through time.

Projections:
1. The population will face the same threats in the future as it did in the past. The PVA applies the population growth rate from the past, which was influenced by some particular magnitude of threats, to the future trajectory of the population. It does not account for the impacts of new or increasing threats, such as the loss of nesting habitat from climate change.

Take model:
1. The anticipated take level (ATL) is constant through time and independent of fishery effort. This assumption was made by McCracken (2018) when generating the ATLs for the fishery.
2. The distribution of turtles' sizes and post-interaction mortalities in the past is representative of what will be encountered in the future. We make this assumption when we use the fisheries observer data to inform characteristics of future turtles taken by the fishery, and do so because these are the best available data for the task.
3. The life history parameters are indicative of the populations of interest and are estimated accurately. Specifically, A_{mat} (age at maturity) is 0.975 of L_{inf} (asymptotic length; average length of mature females).
4. Turtles will nest immediately once they reach maturity.

Conservation Implications

We made a number of decisions in the analyses that were inherently conservative for the turtle species in question (i.e., likely inflated the mortality relative to the true). We highlight those here to provide context for interpretation:

1. We applied the entire anticipated take for the fishery in future years to the index beaches for which we had data; however, those index beaches represent only 52% and 75% of the nesting populations for loggerheads and leatherbacks, respectively. Assessing the impact of the entire take on the index beach populations rather than the full populations is conservative for the species.

2. The Bayesian trend analysis accounts for the parameter uncertainty by incorporating estimated uncertainty of demographic parameters. Consequently, we found large uncertainty around the estimated population growth rate (r), which resulted in greater or lesser chance of recovering than what was found from a frequentist approach. This finding provides an accurate assessment of the projected population given what we know about the population.

3. The anticipated take level is biased high (the CMP distribution tends to draw ATLs that are higher than the take levels observed in previous years).

4. In calculating Adult Nester Equivalents (ANEs) in our historical analysis of fishery impacts (see **Historical ANE Imputation**), we assume that nesters would have repeatedly returned to nest at a constant remigration interval with an annual probability of survival equal to 0.89 for leatherbacks and 0.90 for loggerheads. However, for loggerheads, Japanese colleagues have indicated that nesters have a relatively low probability of being observed nesting in future years after their initial sighting (approximately 0.30), suggesting potentially high threats in the marine environment. If this is true, then the ANE values in our historical analysis (see **Historical ANE Imputation**) are inflated compared to the true ANE values (i.e., we added back loggerhead nesters to the population when in reality they had a low chance of surviving to the next nesting season).

Results

Monthly Nest Count Imputations for Leatherback Turtles

The distributions of nests across months for both index beaches in Indonesia are shown in Figure 5. The main nesting season in Jamursba Medi is from May through September with peak nesting in June/July. Wermon has a similar summer nesting peak with another winter nesting season peaking in December/January.
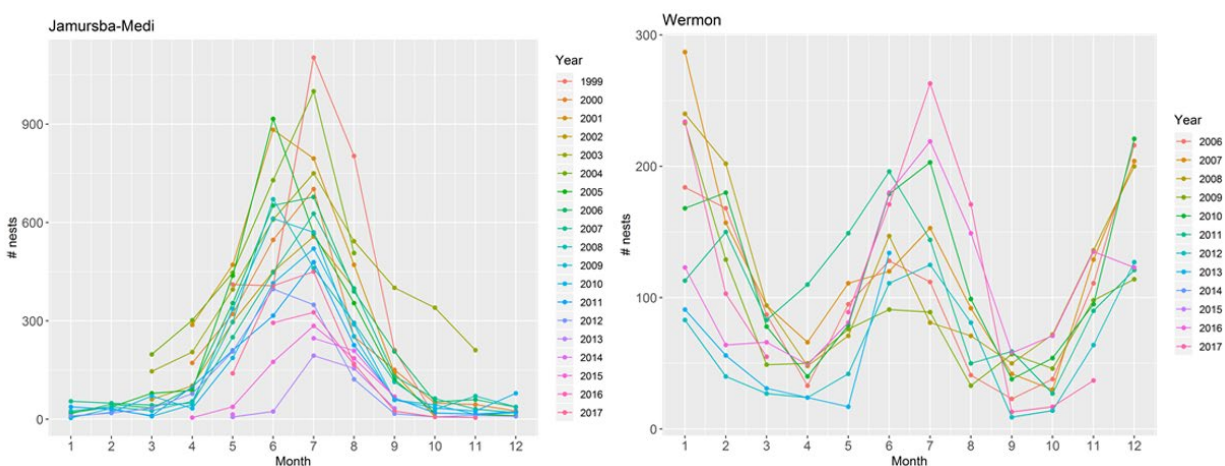
Figure 5. Monthly nest counts at Jamursba-Medi and Wermon showing the bimodal pattern for Wermon.

The observed and imputed nest count data are shown in Figure 6 for leatherback turtles (note – loggerhead nest count data was provided to NOAA as annual counts). The data for this analysis came from the two leatherback index nesting beaches in Indonesia (Jamursba-Medi and Wermon). Observed monthly leatherback nest counts are depicted as red dots, imputed monthly nest counts are depicted as blue dots, and annual (from imputed data) numbers of nests are depicted as black dots with 95% credible interval shading. The median imputed nests ranged from 380 to 4150 and 127 to 1489 annually for Jamursba Medi and Wermon, respectively. The annual imputed data time-series shown in Figure 6 with uncertainty were used for the long-term trends and current abundance estimates.
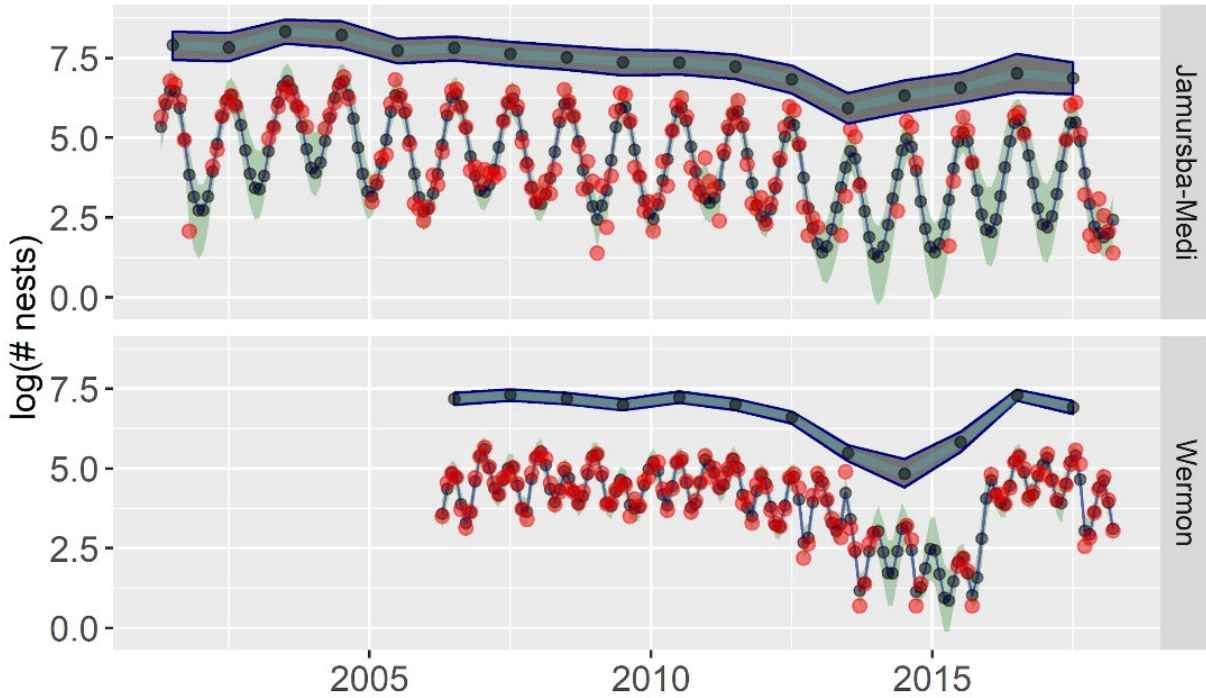
Figure 6. Leatherback monthly nest count imputations in natural log space.

Long-term Trend and Current Abundance

North Pacific Loggerheads

The Bayesian state-space model suggests the loggerhead population (based on annual nesters) is increasing at 2.3% per year ($r = 0.023$) (see Figure 7). Figure 7 depicts the trend for the three loggerhead nesting beaches of Inakahama, Maehama, and Yotsusehama, Japan. The median long-term trend is depicted as a black line with 95% credible interval shading (gray). The observed data (Annual Nesters) are black dots; the model-predicted Annual Nesters (median values) are red dots. Distributions are shown around the modeled number of Annual Nesters in the starting year (blue) and final year (purple).
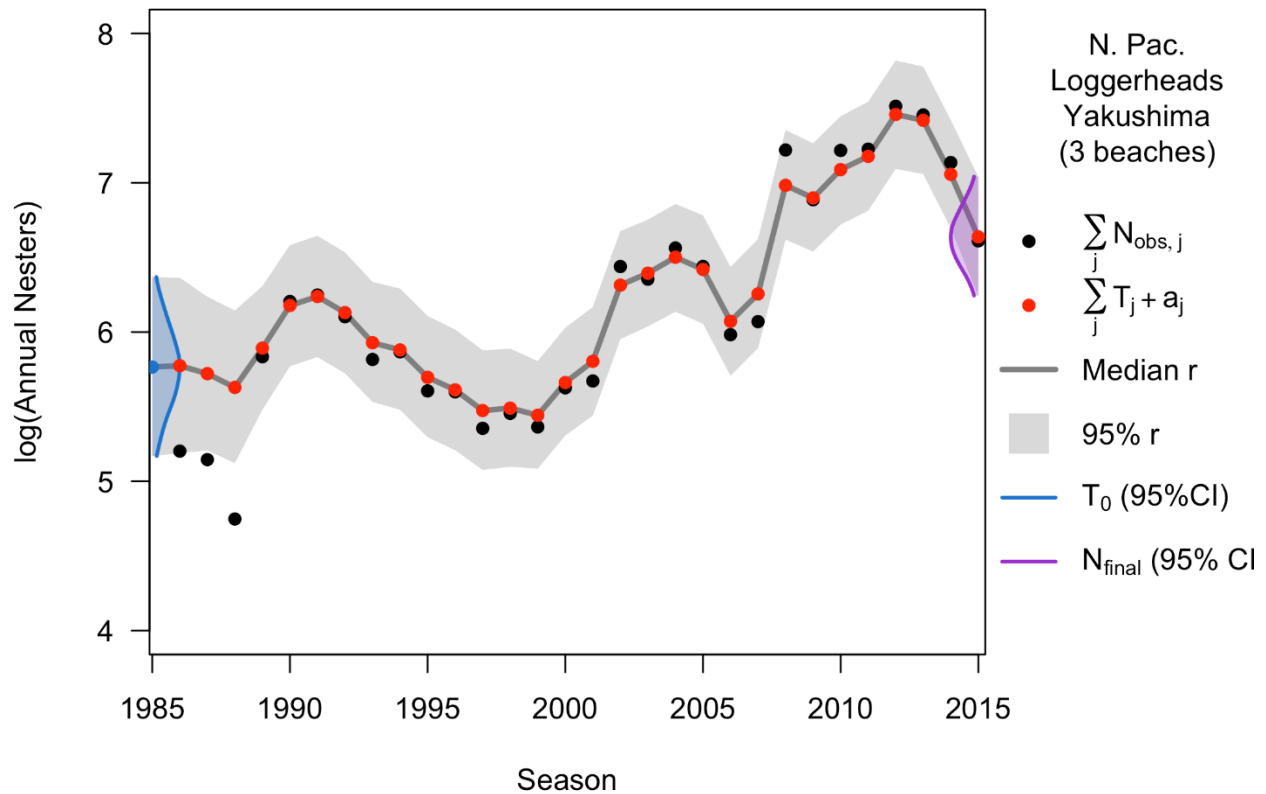
Figure 7. Model fit from trend analysis for North Pacific loggerheads nesting in Japan (Inakahama, Maehama, and Yotsusehama beaches). Notation: $N_{obs,j}$ is Annual Nesters observed in year j (derived from raw nest counts using mean clutch frequency); T_j is ln(Annual Nesters) in year j, the true population state; a_j is the scaling factor for a specific beach (time series); r is the instantaneous population growth rate; T_0 is the initial population state in year j = 0; N_{final}, the number of Annual Nesters in the final year of data, which is also the starting point for the PVA projections.

The joint posterior distributions of *r* (population growth rate), *Q* (process error variance), and N_0 (Annual Nesters in 2015, $N_0 = N_{final}$) from the trend analysis are shown in Figure 8. The joint distributions show the relationship between population growth rate and abundance of Annual Nesters. These joint distributions form the basis of the PVA projections, as drawing parameter values from the joint posterior distribution constrains them to realistic combinations, thereby keeping the uncertainty in the projections reasonable (see *PVA Projections for North Pacific Loggerhead Turtles*).
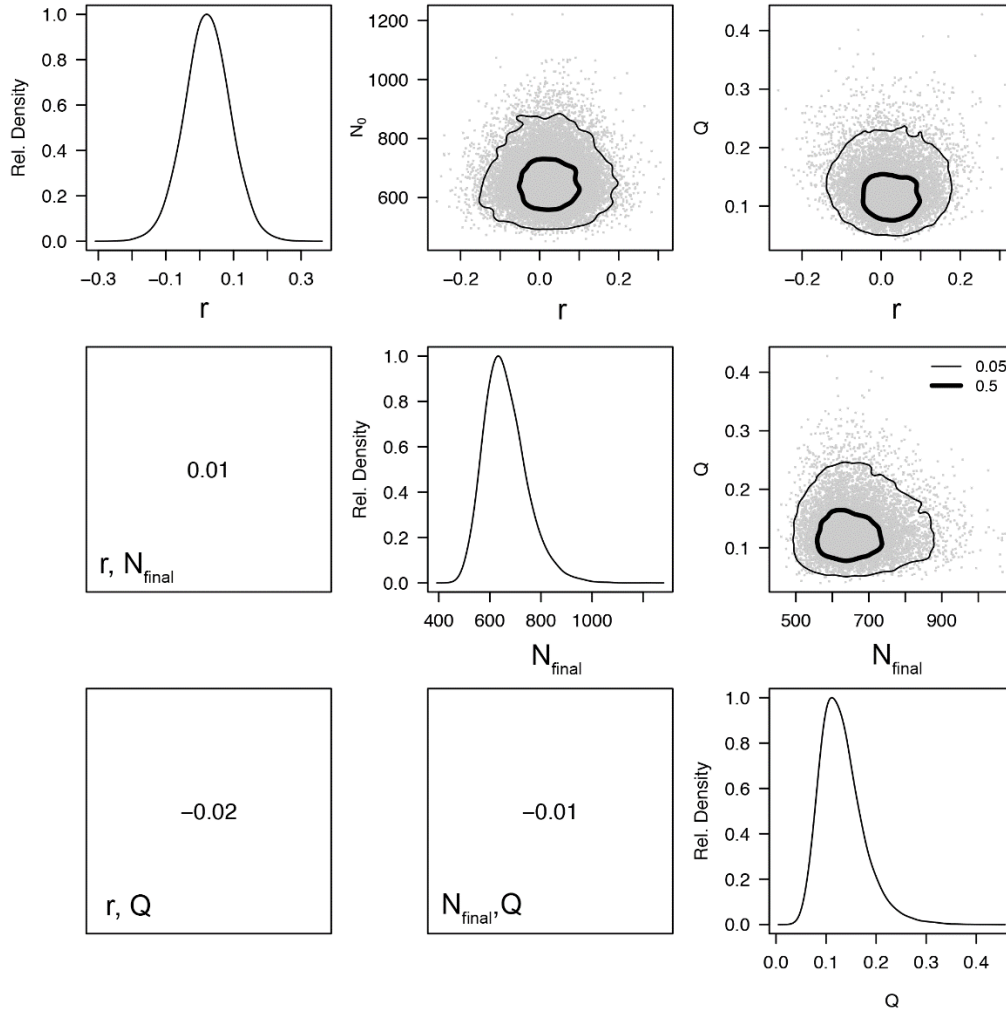
Figure 8. Joint posterior distributions of r (instantaneous population growth rate), Q (process error variance), and N_0 (Annual Nesters in 2015, N_{final}) from the trend analysis for North Pacific loggerheads.

Along with the estimates of the population growth rate (inferred from the number of nests) an estimate of current female abundance for the portion of North Pacific loggerheads nesting on the three monitoring beaches for which data were available (Inakahama, Maehama, and Yotsusehama) was produced (Table 2). The estimates were derived from the trend analysis and serve as the best available index of current abundance. N_{final}, $N_{final-1}$, $N_{final-2}$, $N_{final-3}$ are the number of Annual Nesters in years 2015, 2014, 2013, and 2012, respectively. Total Nesters ($\sum_{j=final-3}^{final} N_j$) was calculated as a snapshot of current abundance as of 2015 using the estimates from the final 4 years as described in Eq. 13.

Table 2. Estimated number of nesting females for the portion of North Pacific loggerheads nesting on the three monitoring beaches for which data were available (Inakahama, Maehama, and Yotsusehama). The three beaches comprise approximately 52% of total nesting for the population. L95% = the lower 95% credible limit and U95% = the upper 95% credible limit.

	L95%	Median	U95%
$N_{final-3}$	1529	1851	2236
$N_{final-2}$	1461	1778	2153
$N_{final-1}$	977	1202	1449
N_{final}	529	651	858
$\sum_{j=final-3}^{final} N_j$	4074	4541	5063

Western Pacific Leatherbacks

The Bayesian state-space model suggests the leatherback population (based on annual nesters) is decreasing at 6.1% per year ($r = -0.061$) (see Figure 9). Figure 9 depicts the modeled trend for the two leatherback nesting beaches of Jamursba Medi and Wermon, Indonesia. The median long-term trend is depicted as a black line with 95% credible interval shading (gray). The observed data (Annual Nesters) are black dots; the model-predicted Annual Nesters (median values) are red dots. Distributions are shown around the modeled number of Annual Nesters in the starting year (blue) and final year (purple).
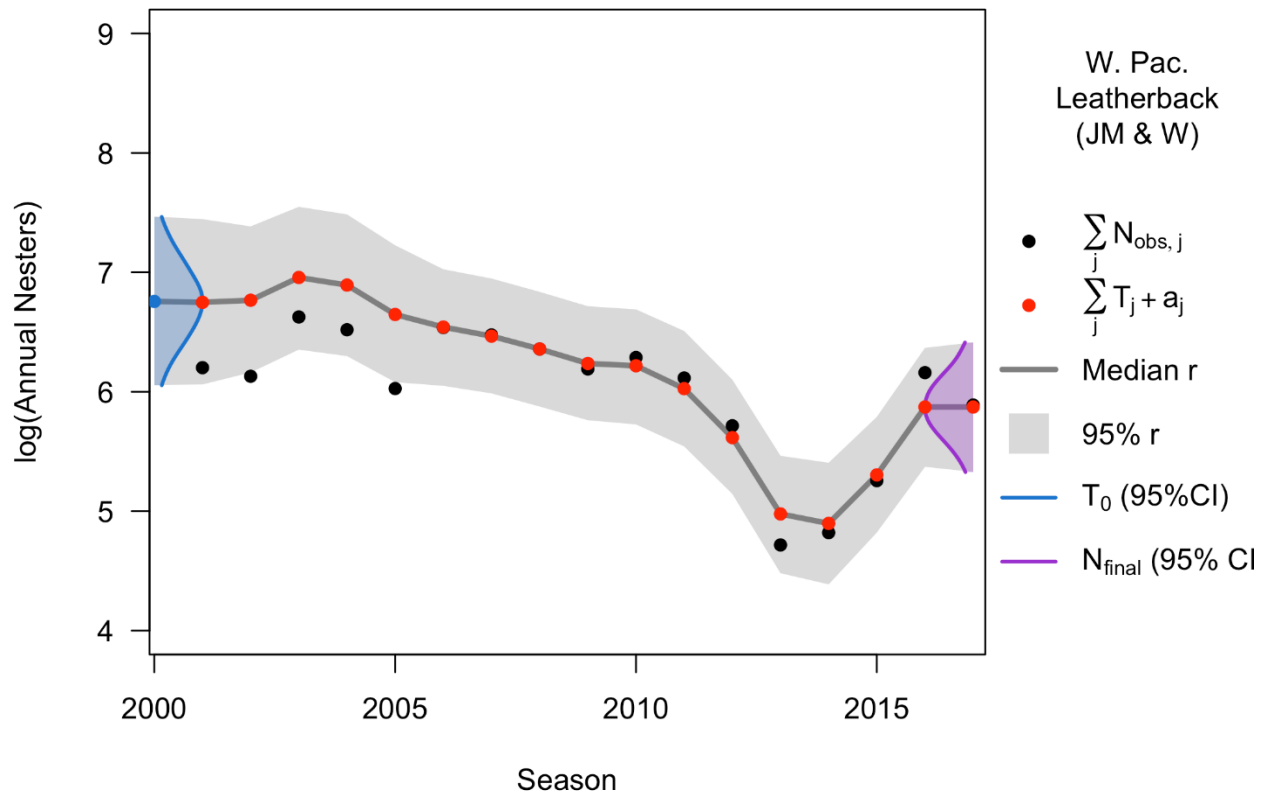
Figure 9. Model fit from trend analysis for western Pacific leatherbacks nesting in Indonesia (Jamursba Medi and Wermon beaches). Notation: $N_{obs,j}$ is Annual Nesters observed in year j (derived from raw nest counts using mean clutch frequency); T_j is ln(Annual Nesters) in year j, the true population state (T_j); a_j is the scaling factor for a specific beach (time series); r, the instantaneous population growth rate; T_0 is the initial population state in year j = 0; N_{final}, the number of Annual Nesters in the final year of data, which is also the starting point for the PVA projections.

The joint posterior distributions of *r* (long-term growth rate), *Q* (process error variance), and *N₀* (Annual Nesters in 2017) from the trend analysis are shown in Figure 10. The joint distributions show the relationship with population growth rate and abundance of annual nesters.
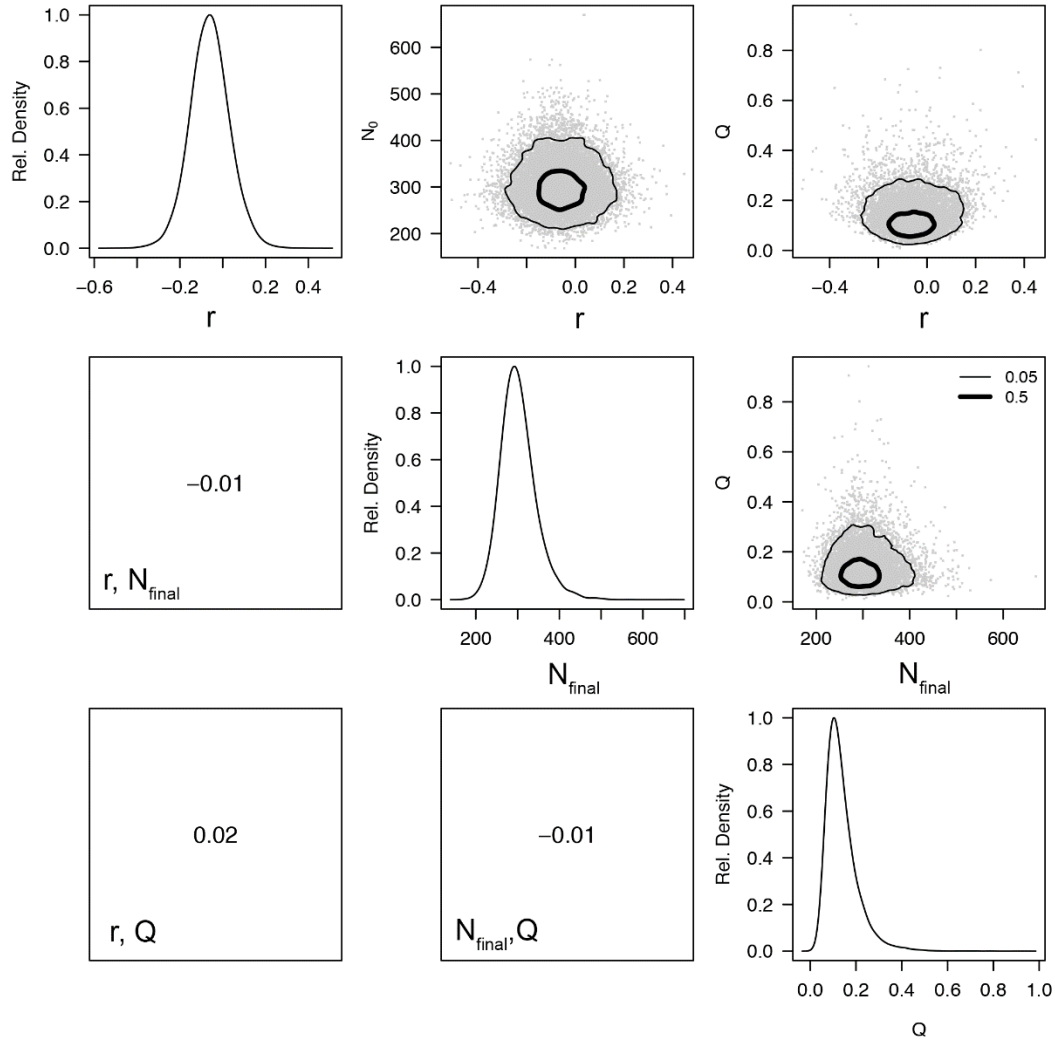
Figure 10. Joint posterior distributions of r (long-term growth rate), Q (process error variance), and N_{final} (Annual Nesters in 2017) from the trend analysis for western Pacific leatherbacks.

Along with the estimates of the population growth rate (inferred from the number of nests) an estimate of current female abundance for the portion of western Pacific leatherbacks nesting on the two monitoring beaches for which data were available (Jamursba Medi and Wermon) was produced (Table 3). The two beaches comprise approximately 75% of total nesting for the population (National Marine Fisheries Service and U.S. Fish and Wildlife Service *In review*). The estimates are derived from the trend analysis and serve as the best available index of current abundance. N_{final}, $N_{final-1}$, $N_{final-2}$, $N_{final-3}$ are the number of Annual Nesters in years 2017, 2016, 2015, and 2014, respectively. Total Nesters ($\sum_{j=final-3}^{final} N_j$) was calculated as a snapshot of current abundance as of 2017 using the estimates from the final four years as described in Figure 13.

Table 3. Estimated number of nesting females for the portion of western Pacific leatherbacks nesting on the two monitoring beaches for which data were available (Jamursba Medi and Wermon). The two beaches comprise approximately 75% of total nesting for the population. L95% = lower 95% credible limit and U95% = upper 95% credible limit. Median, Low, and High correspond to the median and lower and upper limits of estimated number of nests from the imputation process.

	Median			Low			High		
	L95%	Median	U95%	L95%	Median	U95%	L95%	Median	U95%
$N_{final-3}$	118	162	211	79	109	147	169	238	302
$N_{final-2}$	166	217	280	111	148	195	250	323	409
$N_{final-1}$	256	340	445	156	209	281	425	565	727
N_{final}	237	309	417	153	204	281	371	469	628
$\sum_{j=final-3}^{final} N_j$	666	790	942	425	515	634	1052	1224	1425

Incorporating Fishery Interactions into the Model

Historical Take

An example demonstrating how historical take is added back into the population as part of a retrospective analysis is shown in Figure 11. The analysis produces a population trend that excludes the observed (100% observer coverage) historical SSLL fishery turtle interactions. In this example the projected ANE for a single leatherback turtle caught in 2005 with a 137.2 cm SCL, an estimated age of 14.22 years, 1.88 years from maturity, and an assigned stage of juvenile would be an ANE = 0.66. As the turtle was caught in 2005 with 1.88 years to maturity, the ANE for this turtle would be added back into the Adult Nester population in 2007 (P_j^2; shown in orange in Figure 11). The ANE does not account for the sex ratio and assigned post-interaction mortality (0.3), when accounting for sex ratio and the assigned post-interaction mortality, the expected realized ANE in the first year of nesting is 0.14 ($P_j^2 * PF * D_i$ shown in black in Figure 11).
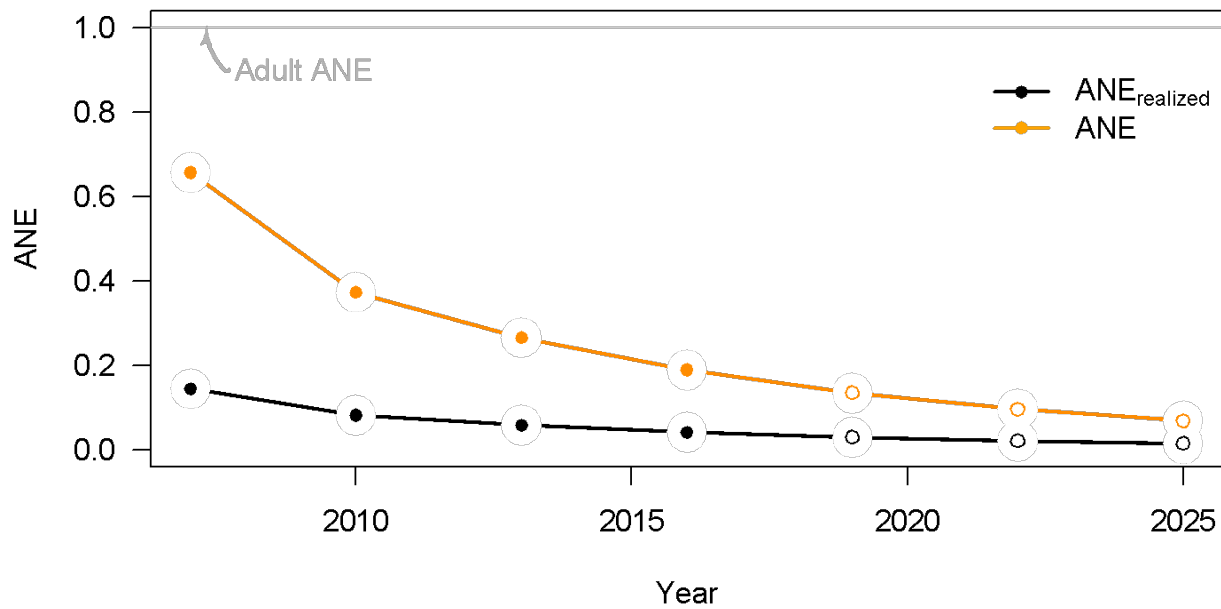
Figure 11. An example demonstrating how historical take is added back into the population as part of a retrospective analysis of the population trend that excludes historical SSLL fishery turtle interactions. The orange line depicts the ANE when accounting for carapace length, estimated age, time to maturity, and stage based survival rates. The black line depicts the ANE when including the assigned fishing mortality and sex-ratio. Ultimately the analysis converts fisheries interactions into adult nesters (the modeled data of the PVA). Solid circles indicate years in which the ANE would be added back to the population (between 2004 and 2017). Open circles occur in years beyond the data.

The cumulative historical take ANE for each year is expressed as ($\sum_{k=1}^{n} ANE_{realized,k,j}$). In any year the take of adult females from that year and any carryover ANE from previous years are summed. In Figure 12, the realized ANE for leatherbacks (dark blue) and loggerheads (brown) is depicted. The realized ANE is higher in leatherbacks than loggerheads as 36% of incidental takes are adults in leatherbacks versus 8% are adults in loggerheads.
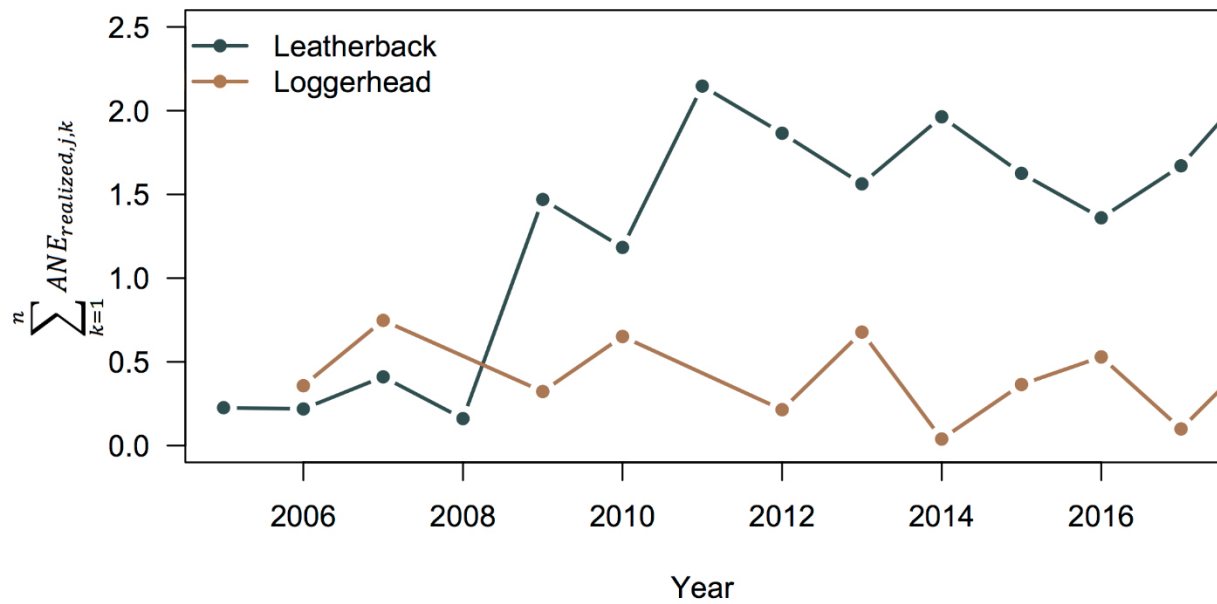
Figure 12. The historical ANE for each year for each species (leatherbacks in dark blue; loggerheads in brown). The cumulative historical take ANE for each year is expressed as ($\sum_{k=1}^{n} ANE_{realized,k,j}$).

North Pacific Loggerhead Turtles

There was no discernible difference between the median and posterior distribution of r (population growth rate) for North Pacific loggerheads under historical "no take" and "take" scenarios (see Figure 13 and Table 4). The growth rate estimation was conducted on either N_j, the number of Annual Nesters in year j, or $N_j - F$, Annual Nesters minus historical take. The "no take" scenario removes the population impacts of historical interactions in the SSLL fishery. The distributions are perfectly overlapping, indicating the population growth rate did not change when the turtles taken by the fishery were added back in to the population prior to analyzing the trend.
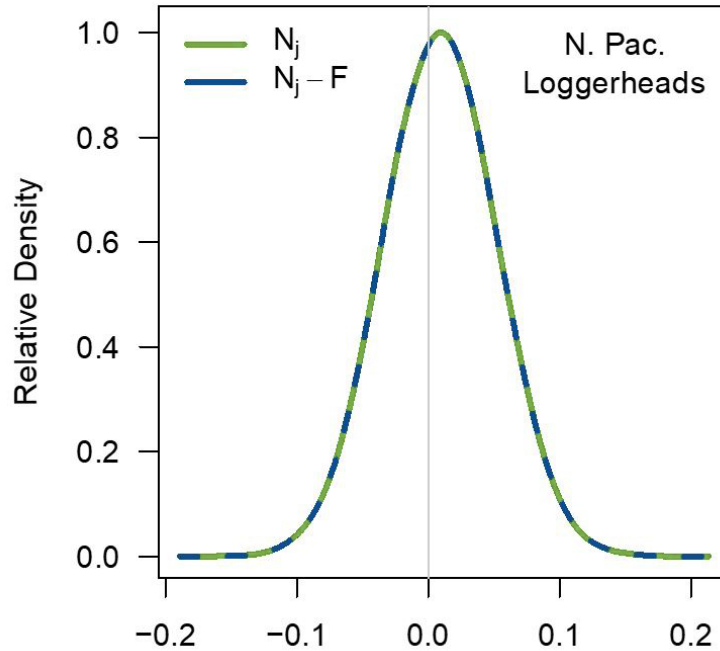
Figure 13. Posterior distribution of r (population growth rate) for North Pacific loggerheads under historical "no take" (N$_j$) and "take" (N$_j$–F) scenarios.

A complete summary of the long-term annual trend (i.e., population growth rate) for North Pacific loggerheads under "no take" and "take" scenarios over the period of available nest monitoring data (1985–2015), including log population trend (r) and λ with the mean ($\underline{x}$), median ($\tilde{x}$), variance (σ_x), lower 95% (L95%) and upper 95% (U95%) of the statistic, is found in Table 4. The "no take" scenario removes the population impacts of historical interactions in the Hawaii-based SSLL fishery. Both scenarios suggest a growth rate of 2.3% per year in the number of females nesting annually. The estimates are based on the available data from three beaches in Japan (Inakahama, Maehama, and Yotsusehama) that comprise approximately 52% of total nesting.

Table 4. Summary of the long-term trend (i.e., population growth rate) for North Pacific loggerheads under "no take" and "take" scenarios over the period of available nest monitoring data (1985–2015).

	No Take	Take
r	0.023	0.023
$\tilde{r}$	0.023	0.023
σ_r	0.005	0.005
$r_{L95\%}$	−0.11	−0.111
$r_{U95\%}$	0.156	0.156
λ	1.026	1.026
$\tilde{\lambda}$	1.023	1.023
σ_λ	0.005	0.005
$\lambda_{L95\%}$	0.895	0.895
$\lambda_{U95\%}$	1.169	1.169

Western Pacific Leatherback Turtles

There was no discernible difference between the median and posterior distribution of U (long-term growth rate) for western Pacific leatherbacks under historical "no take" and "take" scenarios (see Figure 14 and Table 5). The growth rate estimation was conducted on either N_j, the number of Annual Nesters in year j, or $N_j - F$, Annual Nesters minus Take. The "no take" scenario removes the population impacts of historical interactions in the SSLL fishery. The distributions are completely overlapping, indicating the population growth rate did not change when the turtles taken by the fishery were added back in to the population prior to analyzing the trend.
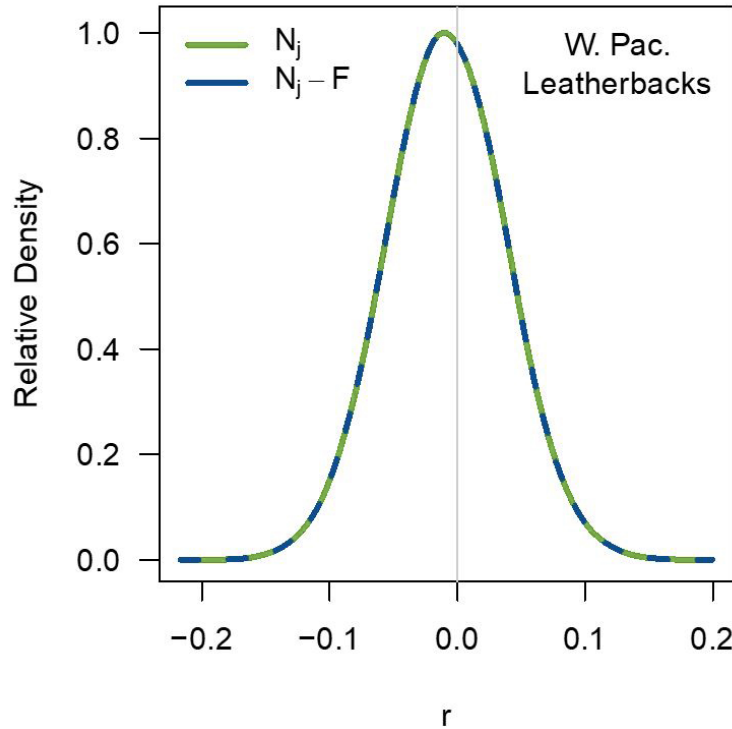
Figure 14. Posterior distribution of r (population growth rate) for western Pacific leatherbacks under historical "no take" (N_j) and "take" (N_j–F) scenarios.

A complete summary of the long-term trend (i.e., population growth rate) for western Pacific leatherbacks under "no take" and "take" scenarios over the period of available nest monitoring data (2001–2017), including log population trend (r) and λ with the mean ($\underline{x}$), median ($\tilde{x}$), variance (σ_x), lower 95% (L95%) and upper 95% (U95%) of the statistic, is found in Table 4. The estimates are based on the available data from two beaches in Indonesia (Jamursba Medi and Wermon) that comprise approximately 75% of total nesting. The "no take" scenario removes the population impacts of historical interactions in the Hawaii-based shallow-set longline fishery. Three estimates are provided (Median, Low, and High), corresponding with three different scenarios from the imputed monthly count estimates (median, lower 95%, and upper 95% from the imputed nest counts). Results suggest a declining trend, with median trend estimates of −6.1% per year (−5.6% to −6.4%) in the number of females nesting annually. All scenarios (take and no take) suggest a declining growth rate of 6.1% (median) per year in the number of females nesting annually. The estimates are based on the available data from two beaches in Indonesia (Jamursba Medi and Wermon) that comprise approximately 75% of total nesting.

Table 5. Summary of the long-term annual trend (i.e., population growth rate) for western Pacific leatherbacks under "no take" and "take" scenarios over the period of available nest monitoring data (2001–2017). Results include log population trend (r) and λ with the mean ($\underline{x}$), median ($\tilde{x}$), variance (σ_x), lower 95% (L95%) and upper 95% (U95%) of the statistic.

	Median		Low		High	
	No Take	Take	No Take	Take	No Take	Take
$\underline{r}$	−0.06	−0.06	−0.063	−0.063	−0.055	−0.055
$\tilde{r}$	−0.061	−0.061	−0.064	−0.064	−0.056	−0.056
σ_r	0.008	0.008	0.008	0.009	0.009	0.009
$r_{L95\%}$	−0.238	−0.24	−0.243	−0.245	−0.236	−0.237
$r_{U95\%}$	0.122	0.123	0.121	0.123	0.131	0.132
$\underline{\lambda}$	0.946	0.945	0.943	0.943	0.951	0.951
$\tilde{\lambda}$	0.941	0.941	0.938	0.938	0.946	0.946
σ_λ	0.007	0.008	0.008	0.008	0.008	0.008
$\lambda_{L95\%}$	0.788	0.787	0.785	0.783	0.79	0.789
$\lambda_{U95\%}$	1.13	1.131	1.128	1.13	1.14	1.141

Population Viability Analysis (PVA) with Take and without Take

Assigned lengths and mortality for predicted interactions

For leatherbacks, the median correlation between length and assigned post-interaction mortality parameters was −0.04 and, for loggerheads, the median correlation between parameters was 0.15. The former correlation indicates a very weak negative correlation between length and assigned fishery mortality and, the latter correlation, indicates a weak positive correlation between length and fishery mortality. For leatherbacks, α_0 was 141 cm SCL and α_1 was 0.00003 and, for loggerheads, α_0 was 63 cm SCL and α_1 was −0.006. The former slope indicates no significant effect of the number of incidental takes on the expected lengths and, the latter, indicates a slight negative effect of the number of incidental takes on the expected length (i.e., the mean length decreases as a function of increasing take). The mean assigned post-interaction mortality, μ_D, (in probability space) was 0.19 for leatherbacks and 0.10 for loggerheads. The posterior distributions of all bivariate normal parameters for the take demographics are in Figure 15; the median of all parameters were used for drawing lengths and assigned fishery mortality.
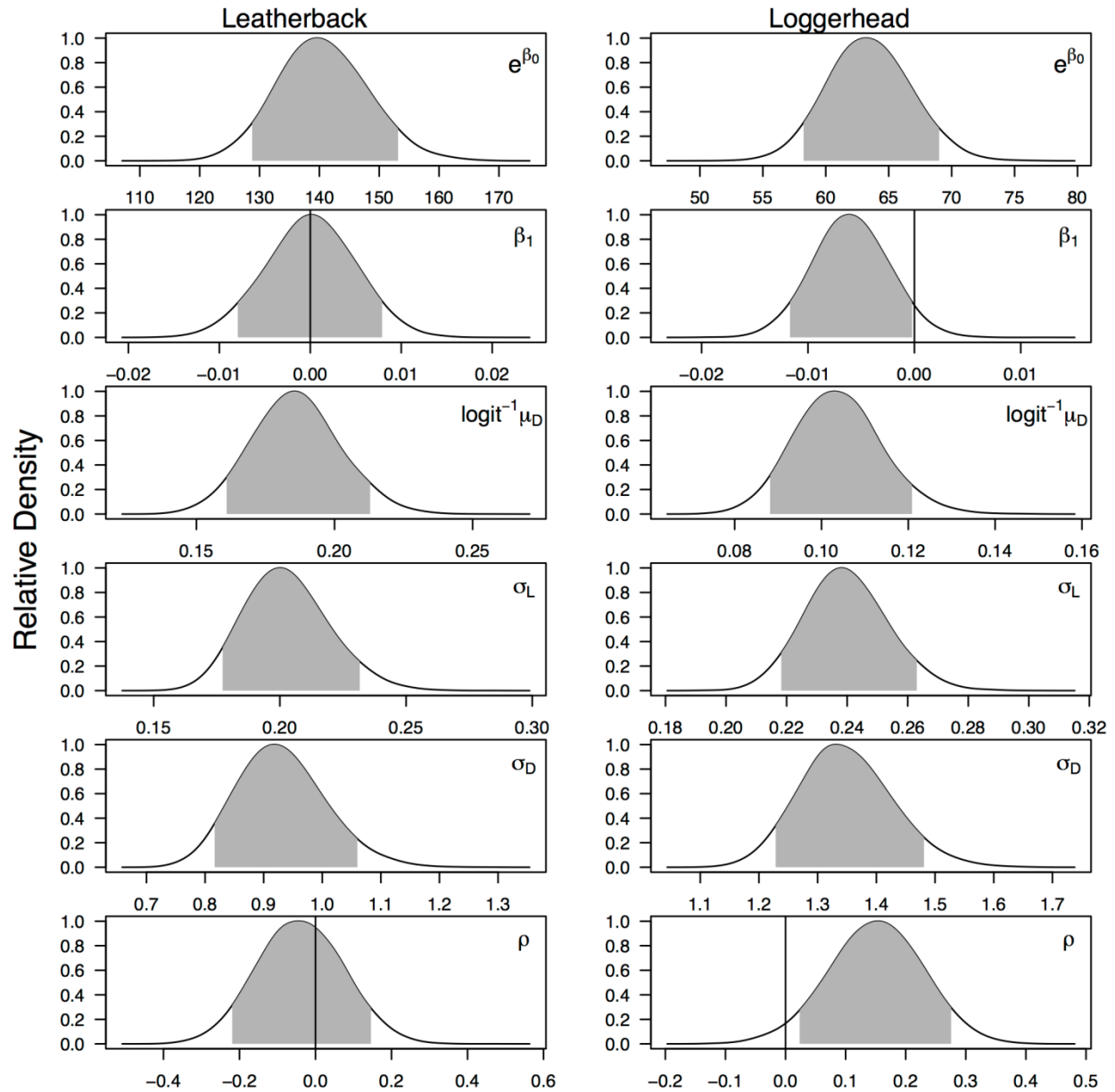
Figure 15. Posterior distributions of parameters (y-axes are relative densities) used in the multivariate normal distribution to generate lengths and assigned fishery mortality for each individual in the annual anticipated take. The intercept ($\beta_0 = \alpha_0$) and slope ($\beta_1 = \alpha_1$) were used to model the mean log lengths as a function of the take. For visualization, the intercept has been exponentiated to the anti-log scale in cm of SCL. The remaining parameters are the mean logit assigned fishery mortality (using an inverse logit transform; $\text{logit}^{-1} \mu_D$), the standard deviations of log lengths (σ_L), and logit fishery mortality (σ_D), and the correlation between the log lengths and the logit discard mortality(ρ).

PVA Projections for North Pacific Loggerhead Turtles

Projections out to 100 years for loggerheads reflect the 2.3% annual growth rate estimated from the 1985–2015 data (Figure 16). There is no discernible difference between the deterministic and stochastic models (top vs. bottom panel in Figure 16). There is also no discernible difference between the "no take" and "take" scenarios for the future, shown by the completely overlapping medians and shaded credible envelopes in Figure 16 (note – natural log scale is used for the 100 year projections to facilitate visual detection of differences between the two scenarios) and the difference plot in Figure 17 centered on zero.
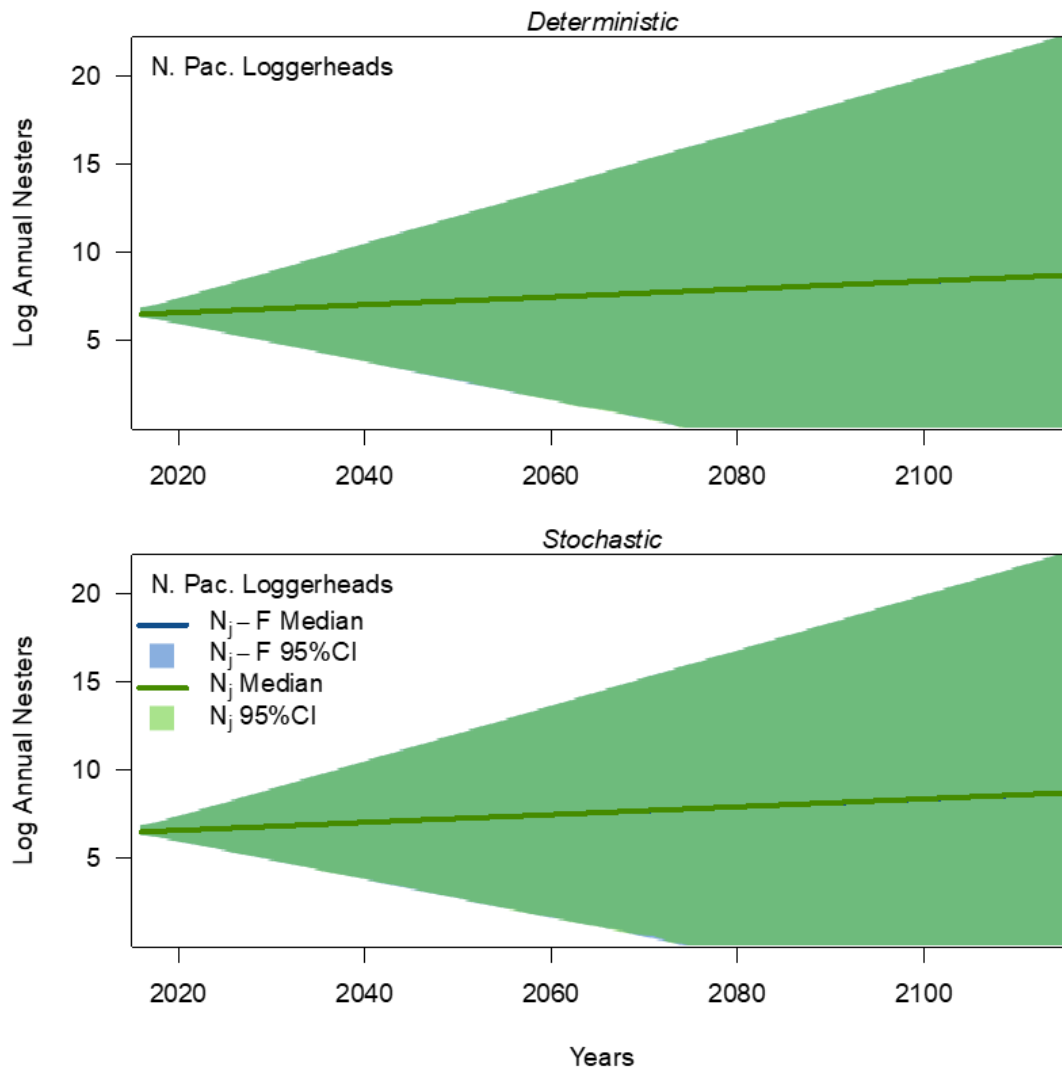
Figure 16. One-hundred-year projections of Annual Nesters (vertical axis is in natural log units) for North Pacific loggerheads under future scenarios including take (N_j – F) and no take (N_j). Projections begin a year after the final year of available data (2015) and end 100 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel.

35

Deterministic

N. Pac. Loggerheads

Stochastic

N. Pac. Loggerheads

— $N_j - (N_j - F)$ Median

◼ $N_j - (N_j - F)$ 95%CI

Years
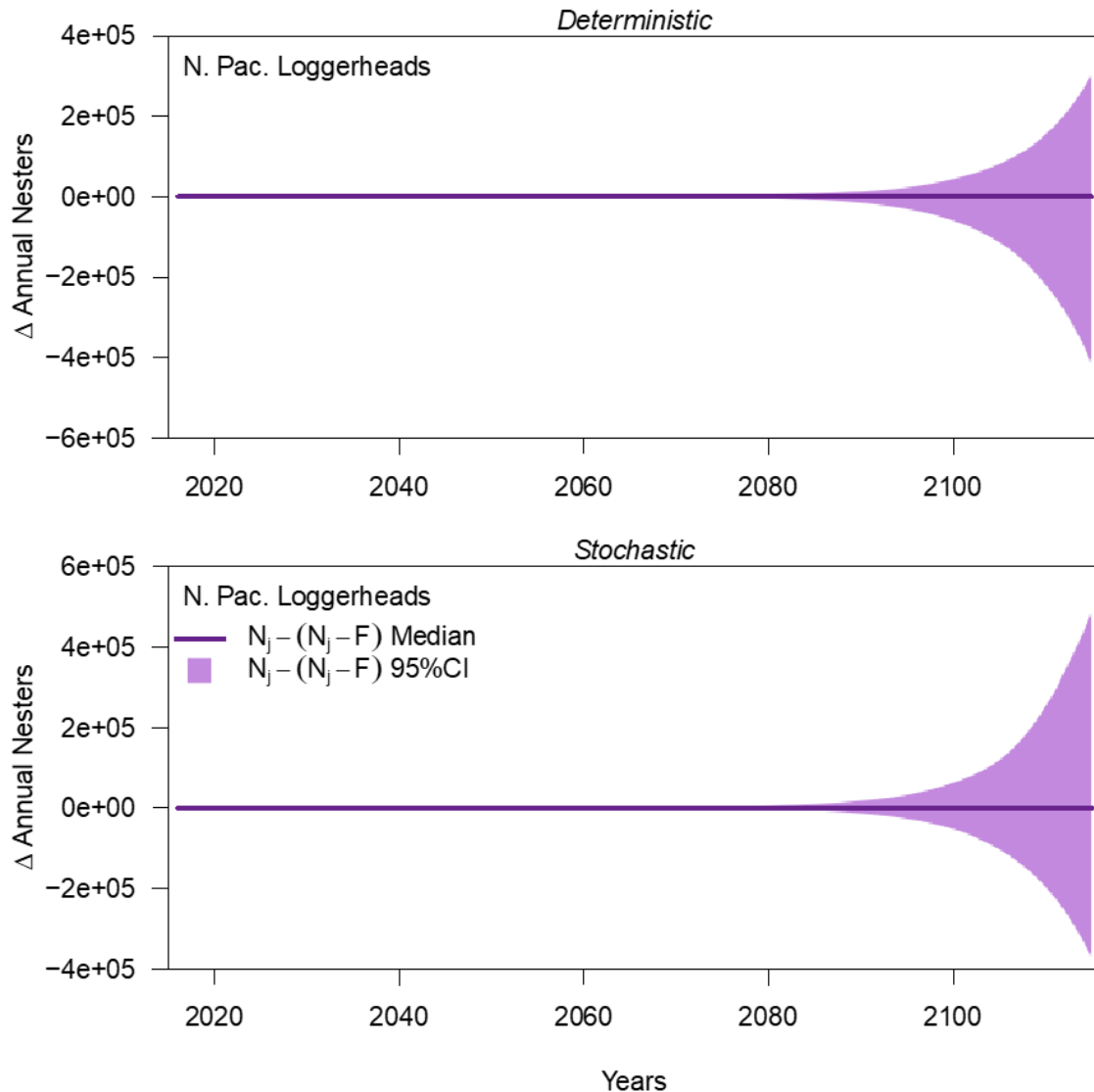
Figure 17. Difference plots of 100-year projections of Annual Nesters for North Pacific loggerheads under future scenarios including take ($N_j - F$) and no take (N_j). Projections begin a year after the final year of available data (2015) and end 100 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel.

Projections out to 10 years into the future are more relevant biologically for management purposes than to 100 years given the estimated uncertainty in the population parameters. Specifically, the effects of the environmental or anthropogenic drivers on the population would be lagged; therefore, we think the first 10 years is largely based on the previously observed trend but after that we do not have sufficient information to account for uncertainty of the drivers that affect the populations. For loggerheads, there was again no discernible difference between the deterministic and stochastic versions of the model or between the "no take" and "take" scenarios (Figure 18 and Figure 19) (note – to provide a sense of the actual magnitude change in Annual Nesters over the shorter time frame, we do not use the natural log scale here).
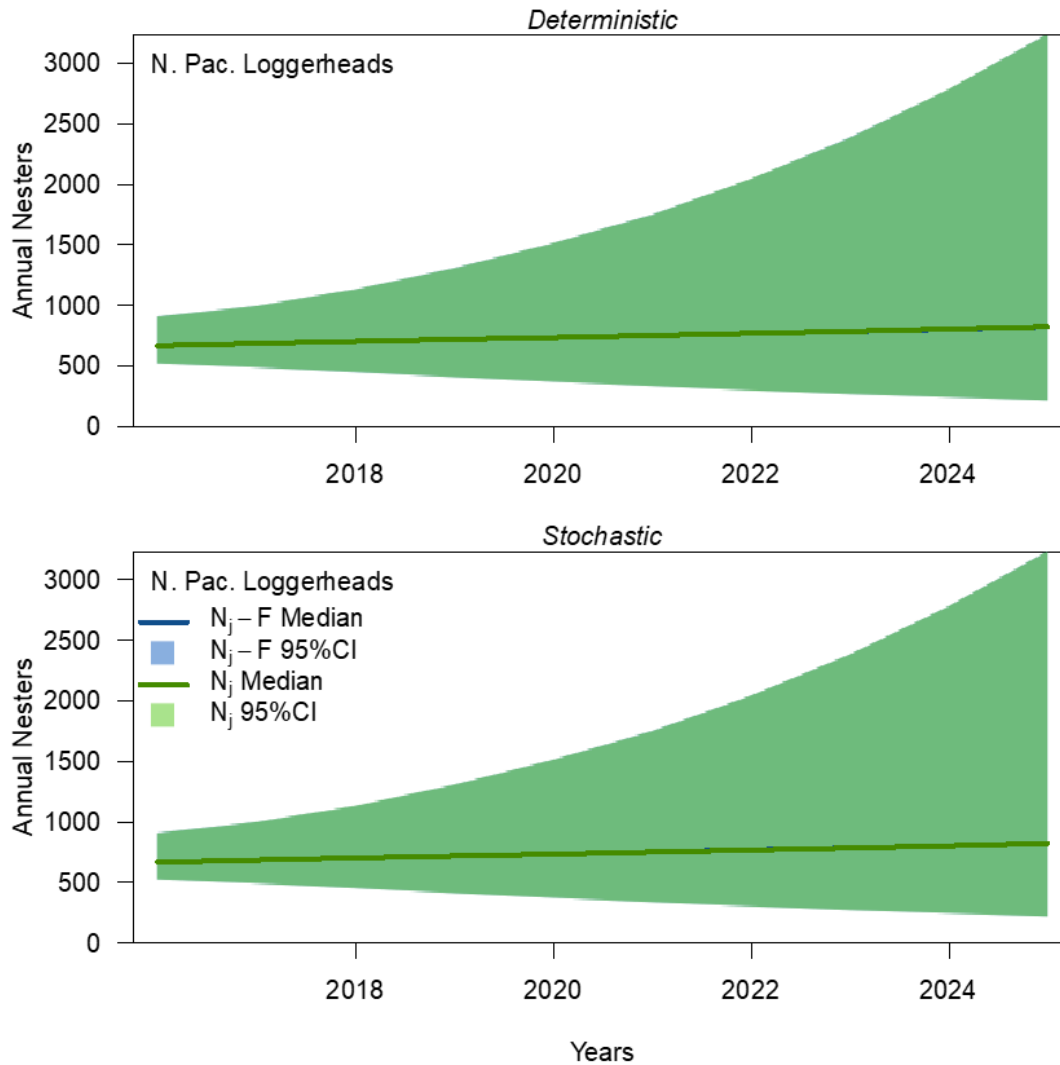
Figure 18. Ten-year projections of Annual Nesters for North Pacific loggerheads under future scenarios including take (N_j – F) and no take (N_j). Projections begin a year after the final year of available data (2015) and end 10 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel. Note the almost exact overlay of trend and uncertainty envelope.
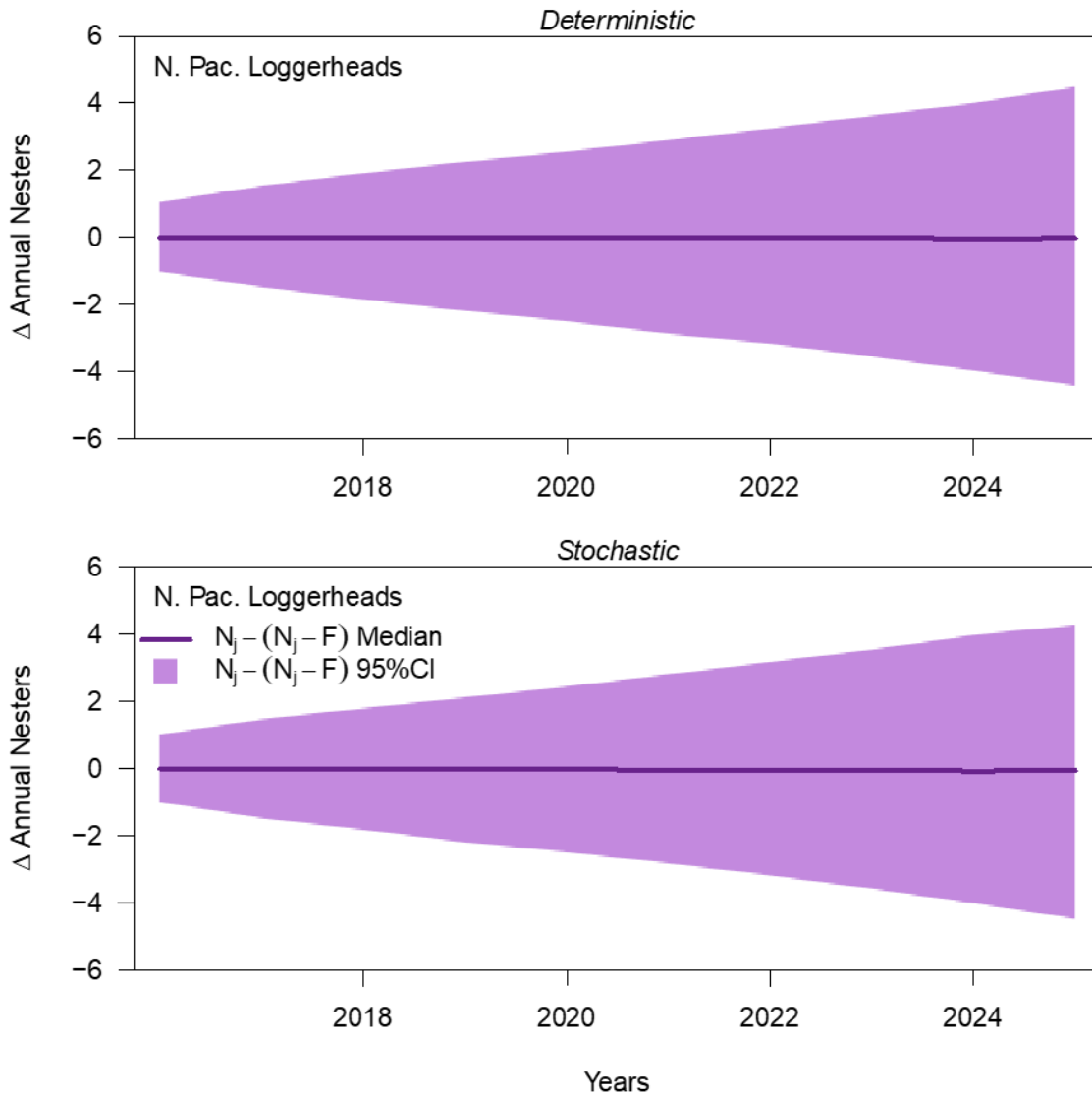
Figure 19. Difference plots of 10-year projections of Annual Nesters for North Pacific loggerheads under future scenarios including take ($N_j - F$) and no take (N_j). Projections begin a year after the final year of available data (2015) and end 10 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel. Note the almost exact overlay of trend and uncertainty envelope.

For loggerheads, 33% of the simulation runs projected that Annual Nesters would fall below 50% of current Annual Nesters within 25 years (95% CI: 5–82 years), while 67% of runs ended with Annual Nesters above that threshold (Table 6). The chances of falling below the lower abundance thresholds (25% and 12.5% of current abundance) were smaller (28% and 25%, respectively) and took longer (37 and 45 years, respectively). There was no discernible difference in the probabilities of falling below any of the thresholds (50%, 25%, and 12.5% of current abundance) between the "no take" and "take" scenarios (Table 6).

Table 6. For North Pacific loggerheads, the probability of the population being above or below ($p > \theta$ or $p < \theta$, respectively) abundance thresholds (50%, 25%, 12.5% of current Annual Nesters) within the 100-year simulation time frame, and the number of years (mean, median, & 95% credible interval [CI]) to reach each threshold for all runs that fall below them. Results are from the stochastic model, both with and without take, and with historical ANEs added back into the population; results from the deterministic model were not notably different. Δ(NT-T) shows the difference between the take and no take projection scenarios.

		$p > \theta$	$p < \theta$	Mean yr	Median yr	L95% yr	U95% yr
50%	No Take	0.67	0.33	25.2	18	5	82
	Take	0.67	0.33	25.2	18	5	82
	Δ(NT-T)	0	0	0.0	0	0	0
25%	No Take	0.72	0.28	37.4	31	10	92
	Take	0.72	0.28	37.4	31	10	92
	Δ(NT-T)	0	0	0.0	0	0	0
12.5%	No Take	0.75	0.25	45.2	41	14	94
	Take	0.75	0.25	45.2	41	14	94
	Δ(NT-T)	0	0	0	0	0	0

The probability of the loggerhead nesting population falling below the abundance thresholds within time frames shorter than 100 years ranged from 0 (for all thresholds at 5 years) to 0.29 (for the 50% threshold at 50 years) (Table 7). For each abundance threshold, the difference between the "no take" and "take" scenarios was non-existent to negligible for the median and 95% CI probability estimates (Table 7).

Table 7. For North Pacific loggerheads, probability (median with 95% credible intervals [CI]) of the population reaching abundance thresholds at 5, 10, 25, 50, and 100 years from final data year (2015). Results are from the stochastic version of the take model with historical takes accounted for by adding the ANEs back into the population. Scenarios with and without take are provided, with Δ(NT-T) showing the difference between the two scenarios. * indicates a difference attributable to simulation rounding error.

		5 yr	10 yr	25 yr	50 yr	100 yr
50%	No Take	0.01	0.08	0.21	0.29	0.33
	Take	0.01	0.08	0.22	0.29	0.33
	Δ*(NT-T)*	0.00	0.00	−0.01*	0	0
50%-L95	No Take	0.01	0.08	0.21	0.28	0.32
	Take	0.01	0.08	0.21	0.28	0.32
	Δ*(NT-T)*	0	0	0	0	0
50%-U95	No Take	0.01	0.08	0.22	0.29	0.33
	Take	0.01	0.08	0.22	0.29	0.33
	Δ*(NT-T)*	0	0	0	0	0
25%	No Take	0	0.01	0.11	0.21	0.29
	Take	0	0.01	0.11	0.22	0.29
	Δ*(NT-T)*	0	0	0	−0.01*	0
25%-L95	No Take	0	0.01	0.11	0.21	0.28
	Take	0	0.01	0.11	0.21	0.28
	Δ*(NT-T)*	0	0	0	0	0
25%-U95	No Take	0	0.01	0.12	0.22	0.29
	Take	0	0.01	0.12	0.22	0.29
	Δ*(NT-T)*	0	0	0	0	0
12.5%	No Take	0	0	0.05	0.16	0.25
	Take	0	0	0.05	0.16	0.25
	Δ*(NT-T)*	0	0	0	0	0
12.5%-L95	No Take	0	0	0.05	0.15	0.24
	Take	0	0	0.05	0.16	0.24
	Δ*(NT-T)*	0	0	0	−0.01*	0
12.5%-U95	No Take	0	0	0.06	0.16	0.25
	Take	0	0	0.06	0.16	0.25
	Δ*(NT-T)*	0	0	0	0	0

PVA Projections for Western Pacific Leatherback Turtles

Projections out to 100 years for leatherbacks reflect the −6.1% annual decline estimated from the 2001–2017 data (Figure 20). The difference between the deterministic and stochastic models is negligible (top vs. bottom panel in Figure 20). There is a subtle yet discernible difference between the "no take" and "take" scenarios, shown by the diverging medians and shaded credible envelopes in Figure 20 (note – natural log scale is used for the 100 year projections to emphasize the differences between the two scenarios) and the slight divergence from zero in later years on the difference plot in Figure 21. The difference slowly becomes apparent after 2060 and suggests the population would go extinct roughly 5 years sooner than in the "no take" scenario (around 2110 vs. 2115).
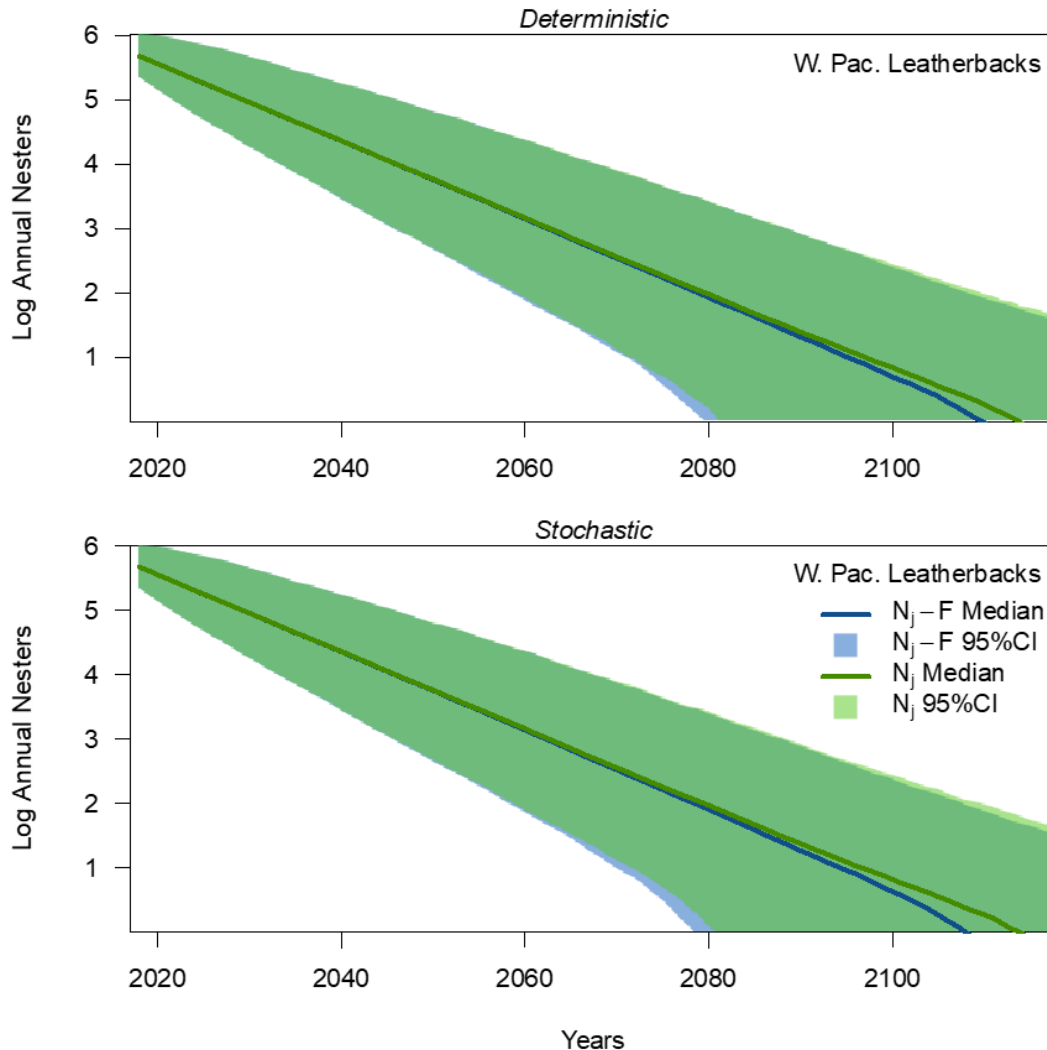
Figure 20. 100-year projections of Annual Nesters (vertical axis is in natural log units) for western Pacific leatherbacks under future scenarios including take (N_j − F) and no take (N_j). Projections begin a year after the final year of available data (2017) and end 100 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel.
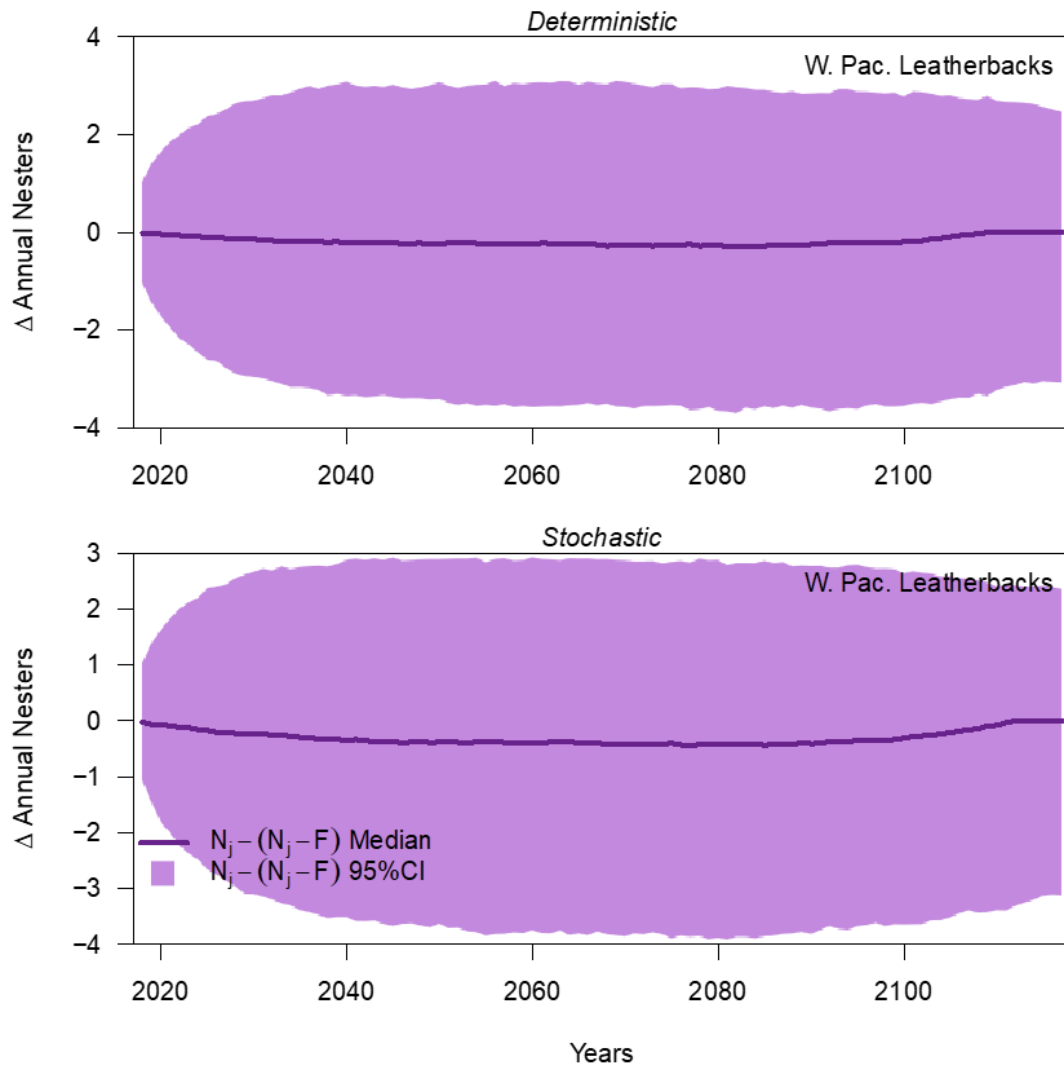
Figure 21. Difference plots of 100-year projections of Annual Nesters (vertical axis is in natural log units) for western Pacific leatherbacks under future scenarios including take ($N_j - F$) and no take (N_j). Projections begin a year after the final year of available data (2017) and end 100 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel.

Projections out to 10 years into the future are more relevant biologically for management purposes than to 100 years given the estimated uncertainty in the population parameters. Specifically, the effects of the environmental or anthropogenic drivers on the population would be lagged; therefore, we think the first 10 years is largely based on the previously observed trend but after that we do not have sufficient information to account for uncertainty of the drivers that affect the populations. For leatherbacks, there is no discernible difference between the deterministic and stochastic versions of the model when looking out only 10 years. Importantly, the difference seen between the "no take" and "take" scenarios in the 100-year projection is not seen in the 10-year projection (Figure 22 and Figure 23) (note – to provide a sense of the actual magnitude change in Annual Nesters over the shorter time frame, we do not use the natural log scale here).
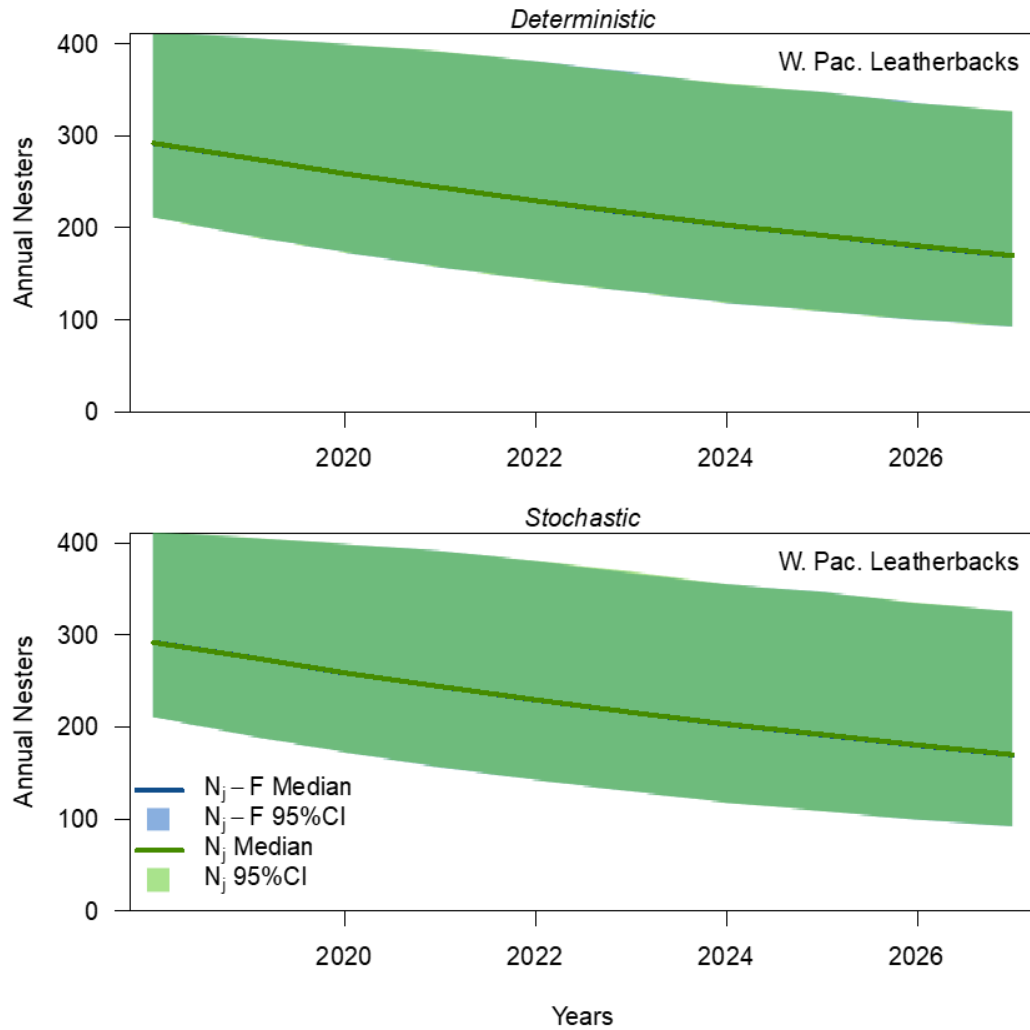
Figure 22. 10-year projections of Annual Nesters for North Pacific loggerheads under future scenarios including take ($N_j - F$) and no take (N_j). Projections begin a year after the final year of available data (2017) and end 10 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel.
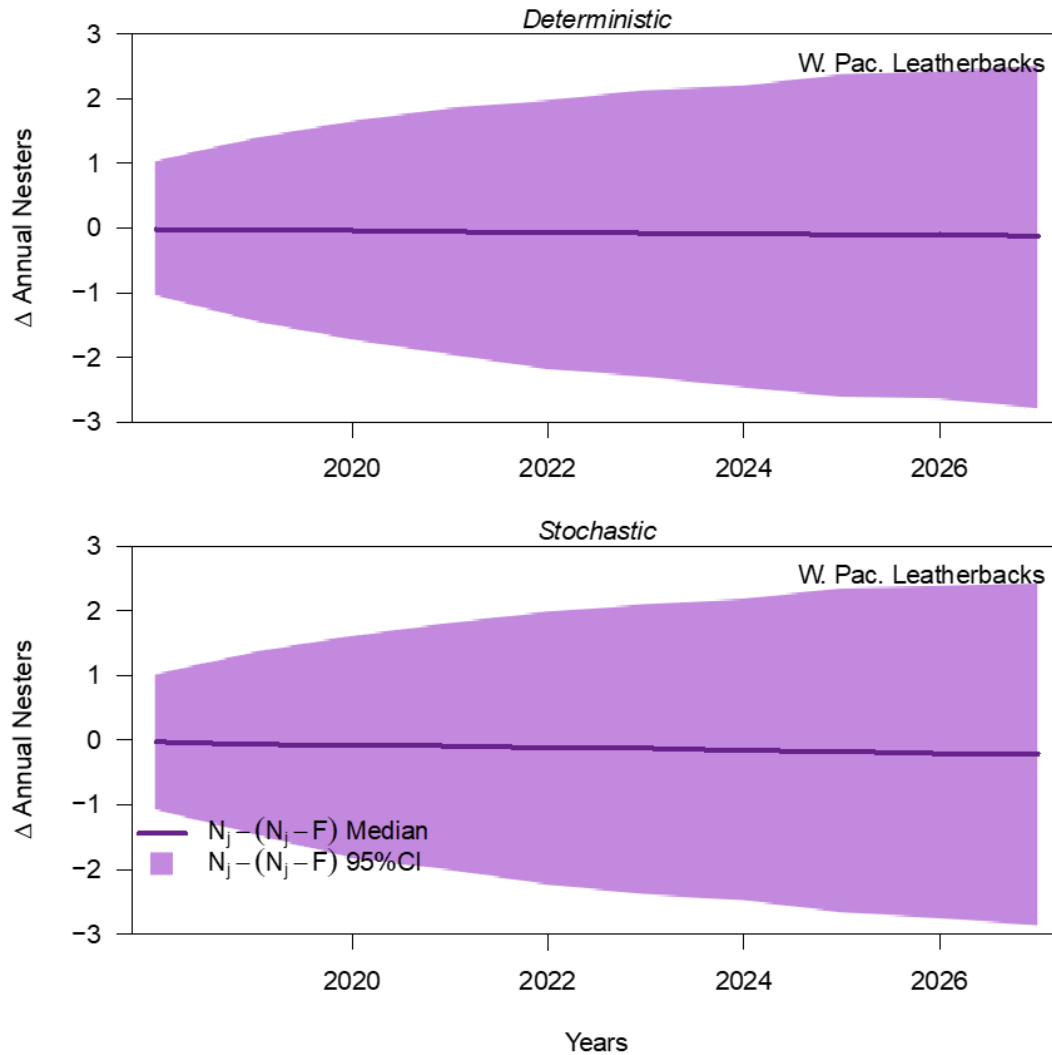
Figure 23. Difference plots for 10-year projections of Annual Nesters for North Pacific loggerheads under future scenarios including take ($N_j – F$) and no take (N_j). Projections begin a year after the final year of available data (2017) and end 10 years later. Top panel shows results from a fully deterministic version of the take model in which the parameters are set at point estimates rather than pulled from distributions as they are in the stochastic version in the bottom panel.

For leatherbacks, 100% of the simulation runs projected that Annual Nesters would fall below 50% of current Annual Nesters within 13 years (95% CI: 5–26 years) (Table 8). The chances of falling below the lower abundance thresholds (25% and 12.5% of current abundance) were smaller (24% and 36%, respectively) and it took longer to reach them (23 and 35 years, respectively). Comparing the "no take" and "take" scenarios, there was no discernible difference in the probability of falling below the 50% abundance threshold, but there was a slight difference of 1 year for the 25% threshold (in the U95% estimate) and the 12.5% threshold (median estimate) (Table 8).

Table 8. For western Pacific leatherbacks, the probability of the population being above or below (*p* > θ or *p* < θ, respectively) abundance thresholds (50%, 25%, 12.5% of current Annual Nesters) within the 100-year simulation time frame, and the number of years (mean, median, & 95% credible interval [CI]) to reach each threshold for all runs that fall below them. Results are from the stochastic model, both with and without take, and with historical ANEs added back into the population; results from the deterministic model were not notably different. Δ(NT-T) shows the difference between the take and no take projection scenarios. Results are based on the median imputed monthly count values.

		$p > \theta$	$p < \theta$	Mean yr	Median yr	L95% yr	U95% yr
50%	No Take	0	1	12.7	12	5	26
	Take	0	1	12.7	12	5	26
	Δ*(NT-T)*	0	0	0	0	0	0
25%	No Take	0	1	24.2	23	13	42
	Take	0	1	24.1	23	13	41
	Δ*(NT-T)*	0	0	0.1	0	0	1
12.50%	No Take	0	1	35.7	35	21	56
	Take	0	1	35.5	34	21	56
	Δ*(NT-T)*	0	0	0.2	1	0	0

The probability of the leatherback nesting population falling below the abundance thresholds within time frames shorter than 100 years ranged from 0 (for 25% and 12.5% thresholds at 5–10 years) to 100% (for the 25% and 50% thresholds at 50 years) (Table 9). For each abundance threshold, the difference between the "no take" and "take" scenarios was non-existent to negligible for the median and 95% CI probability estimates (Table 9).

Table 9. For western Pacific leatherbacks, probability (median with 95% credible intervals [CI]) of the population reaching abundance thresholds at 5, 10, 25, 50, and 100 years from final data year (2017). Results are from the stochastic version of the take model with historical takes accounted for by adding the ANEs back into the population. Scenarios with and without take are provided, with ∆(NT-T) showing the difference between the two scenarios. * indicates a difference attributable to simulation rounding error.

		5 yr	10 yr	25 yr	50 yr	100 yr
50%	No Take	0.03	0.40	0.97	1	1
	Take	0.03	0.40	0.97	1	1
	∆*(NT-T)*	0	0	0	0	0
50%-L95	No Take	0.03	0.39	0.97	1	1
	Take	0.03	0.39	0.97	1	1
	∆(NT-T)	0	0	0	0	0
50%-U95	No Take	0.03	0.40	0.97	1	1
	Take	0.03	0.40	0.97	1	1
	∆(NT-T)	0	0	0	0	0
25%	No Take	0	0	0.63	1	1
	Take	0	0	0.64	1	1
	∆(NT-T)	0	0	−0.01*	0	0
25%-L95	No Take	0	0	0.63	1	1
	Take	0	0	0.63	1	1
	∆(NT-T)	0	0	0	0	0
25%-U95	No Take	0	0	0.64	1	1
	Take	0	0	0.64	1	1
	∆(NT-T)	0	0	0	0	0
12.5%	No Take	0	0	0.11	0.94	1
	Take	0	0	0.11	0.94	1
	∆(NT-T)	0	0	0	0	0
12.5%-L95	No Take	0	0	0.10	0.94	1
	Take	0	0	0.11	0.94	1
	∆(NT-T)	0	0	−0.01*	0	0
12.5%-U95	No Take	0	0	0.11	0.94	1
	Take	0	0	0.11	0.94	1
	∆(NT-T)	0	0	0	0	0

Discussion

The purpose of this analysis was to estimate long-term trends, conduct population viability analyses, and assess the population impacts of continued operation of the SSLL fishery on the western Pacific leatherback and North Pacific loggerhead populations. Time series of nest count data from Indonesia (leatherbacks, 2001–2017) and Japan (loggerheads, 1985–2015) formed the basis of this analysis, and missing data was imputed for leatherbacks prior to the trend analysis. A Bayesian state-space population growth model indicated a declining trend for leatherbacks (−6.1% annually; 95% CI: −5.6% to −6.4%) and an increasing trend for loggerheads (2.3% annually; 95% CI: −11.1% to 15.6%). For loggerheads, current abundance was estimated at 4541 (95% CI: 4074–5063) Total Nesters for the three index beaches in Japan which represent 52% of all nesting. For leatherbacks, there were three estimates of current abundance for the two index beaches in Indonesia which represent 75% of all nesting: (1) from median imputed nest counts, 790 Total Nesters (95% CI: 666–942), (2), from lower 95% imputed nest counts, 515 Total Nesters (95% CI: 425–634), and (3) from upper 95% imputed nest counts, 1224 (95% CI: 1052–1425). The trend was also analyzed with historical impacts from the SSLL fishery removed (i.e., by adding back ANEs to the population); however, there was no difference between the trends for the "no take" and "take" scenarios for either species for the past. Population viability analyses projecting the trends 100 years into the future suggested a 100% chance of leatherbacks falling below 50% of their current abundance, with a mean of 13 years to reach that threshold; loggerheads had a 33% chance of falling below the 50% abundance threshold, with a mean of 25 years to reach that threshold. At 10 years in the future, the chance of falling below the 50% abundance threshold was 40% for leatherbacks and 8% for loggerheads. There were almost no changes to the probabilities of falling below abundance thresholds (50%, 25%, and 12.5% of current abundance) when comparing the "no take" and "take" scenarios for the future. The one exception was that for leatherbacks, the difference between the "no take" and "take" scenarios became apparent after 2060 and the projection suggested the population would go extinct roughly 5 years sooner in the "take" scenario than in the "no take" scenario (around 2110 vs. 2115). However, in the 10-year future time frame, which is perhaps more biologically relevant to use for impact assessments, there was no discernible difference between the "no take" and "take" projection scenarios for either species.

Acknowledgements

Literature Cited

Benson SR, Eguchi T, Foley DG, Forney KA, Bailey H, Hitipeuw C, Samber BP, Tapilatu RF, Rei V, Ramohia P. 2011. Large-scale movements and high-use areas of western pacific leatherback turtles, Dermochelys coriacea. Ecosphere. 2(7):1-27.

Boyd C, DeMaster DP, Waples RS, Ward EJ, Taylor BL. 2017. Consistent extinction risk assessment under the US Endangered Species Act. Conservation Letters. 10(3):328-336.

Dunn J. 2012. Compoisson: Conway–maxwell–poisson distribution. R package version 03.

Gelman A, Rubin DB. 1992. Inference from iterative simulation using multiple sequences. Statistical science. 7(4):457-472.

Gelman A, Simpson D, Betancourt M. 2017. The prior can often only be understood in the context of the likelihood. Entropy. 19(10):555.

Geweke J. 1992. Evaluating the accuracy of sampling-based approaches to the calculations of posterior moments. Bayesian statistics. 4:641-649.

Hatase H, Goto K, Sato K, Bando T, Matsuzawa Y, Sakamoto W. 2002. Using annual body size fluctuations to explore potential causes for the decline in a nesting population of the loggerhead turtle *Caretta caretta* at Senri Beach, Japan. Marine Ecology Progress Series. 245:299-304.

Hatase H, Omuta K, Tsukamoto K. 2010. Oceanic residents, neritic migrants: A possible mechanism underlying foraging dichotomy in adult female loggerhead turtles (*Caretta caretta*). Marine biology. 157(6):1337-1342.

Hatase H, Omuta K, Tsukamoto K. 2013. A mechanism that maintains alternative life histories in a loggerhead sea turtle population. Ecology. 94(11):2583-2594.

Hinrichsen R, Holmes EE. 2009. Using multivariate state-space models to study spatial structure and dynamics. Spatial Ecology.145-166.

Holmes EE, Sabo JL, Viscido SV, Fagan WF. 2007. A statistical approach to quasi-extinction forecasting. Ecology Letters. 10(12):1182-1198.

Jones TT, Hastings MD, Bostrom BL, Pauly D, Jones DR. 2011. Growth of captive leatherback turtles, dermochelys coriacea, with inferences on growth in the wild: Implications for population decline and recovery. Journal of Experimental Marine Biology and Ecology. 399(1):84-92.

Kellner K. 2018. Jagsui: A wrapper around 'rjags' to streamline 'jags' analyses. R package version 1.5.0. https://CRAN.R-project.org/package=jagsUI.

Kobayashi DR, Polovina JJ, Parker DM, Kamezaki N, Cheng I-J, Uchida I, Dutton PH, Balazs GH. 2008. Pelagic habitat characterization of loggerhead sea turtles, caretta caretta, in the

north pacific ocean (1997–2006): Insights from satellite tag tracking and remotely sensed data. Journal of Experimental Marine Biology and Ecology. 356(1-2):96-114.

Lewison RL, Freeman SA, Crowder LB. 2004. Quantifying the effects of fisheries on threatened species: The impact of pelagic longlines on loggerhead and leatherback sea turtles. Ecology letters. 7(3):221-231.

Lontoh DN. 2014. Variation in tissue stable isotopes, body size, and reproduction of western Pacific leatherback turtles. Master's Thesis, San José State University.

McCracken ML. 2018. Hawaii permitted shallow-set longline fishery estimated anticipated take level for Endangered Species Act listed species. In: NOAA Fisheries Pacific Islands Science Center, editor. Honolulu, HI USA.

National Marine Fisheries Service and U.S. Fish and Wildlife Service. In review. Endangered Species Act status review of the leatherback turtle (*Dermochelys coriacea*). Report to the National Marine Fisheries Service Office of Protected Resources and US Fish and Wildlife Service. p. 342.

Plummer M. 2003. Jags: A program for analysis of bayesian graphical models using Gibbs sampling. Proceedings of the 3rd international workshop on distributed statistical computing. Vienna, Austria.

Plummer M. 2017. Jags version 4.3.0 user manual. http://mcmc-jagssourceforgenet/.

Polovina J, Uchida I, Balazs G, Howell EA, Parker D, Dutton P. 2006. The kuroshio extension bifurcation region: A pelagic hotspot for juvenile loggerhead sea turtles. Deep Sea Research Part II: Topical Studies in Oceanography. 53(3-4):326-339.

Polovina JJ, Kobayashi DR, Parker DM, Seki MP, Balazs GH. 2000. Turtles on the edge: Movement of loggerhead turtles (caretta caretta) along oceanic fronts, spanning longline fishing grounds in the central north pacific, 1997–1998. Fisheries Oceanography. 9(1):71-82.

R Development Core Team. 2018. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing.

Ryder CE, Conant TA, Schroeder BA. 2006. Report of the workshop on marine turtle longline post-interaction mortality. NOAA Technical Memorandum NMFS-OPR. 29.

Snover ML. 2008. Assessment of the population-level impacts of potential increases in marine turtle interactions resulting from a Hawaii longline association proposal to expand the Hawaii-based shallow-set fishery. National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Pacific Islands Fisheries Science Center, Marine Turtle Assessment Program.

Stan Development Team. 2018. Rstan: The R interface to Stan. R package version 2.17.3.

Tapilatu RF, Dutton PH, Tiwari M, Wibbels T, Ferdinandus HV, Iwanggin WG, Nugroho BH. 2013. Long-term decline of the western pacific leatherback, dermochelys coriacea: A globally important sea turtle population. Ecosphere. 4(2):1-15.

Tomaszewicz CNT, Seminoff JA, Avens L, Goshe LR, Peckham SH, Rguez-Baron JM, Bickerman K, Kurle CM. 2015. Age and residency duration of loggerhead turtles at a north Pacific bycatch hotspot using skeletochronology. Biological conservation. 186:134-142.

Appendix I: PIFSC October 5, 2018 Response to PIRO September 7, 2018 Memorandum

Note: *PIRO Memorandum text in blue italicized text.* PIFSC responses in black text.

The subject memorandum:

MEMORANDUM FOR: *Dr. T. Todd Jones, Marine Turtle Program,*
NMFS Pacific Islands Fisheries Science Center

FROM: *Ann M. Garrett*
Assistant Regional Administrator, Protected Resources Division
NMFS Pacific Islands Regional Office

SUBJECT: *Review of draft response to PRD's request for information to support ESA section 7 consultation on the effects of Hawaii-based longline fisheries on ESA listed species*

Background from memo:

"On April 6, 2018, PIRO's Protected Resources Division sent a request for information through Michael Tosatto, PIRO Regional Administrator, in support of ESA section 7 consultation on the effects of Hawaii-based longline fisheries on ESA-listed species. I received your draft word document on August 19 and additional supporting files on August 21. We have completed our review of your submitted materials and ask that you make the following modifications to your assessment documents:"

Below we provide portions or sections of the memorandum (*blue italicized text*) and then provide our answers in black.

Comments and PIFSC Response:

1. *Specifically, identify the number of demographically-independent units (populations, subpopulations, demes, etc.) that comprise each "species" (that is, the entity that has been listed as endangered) and estimate the status of these demographic units over time using the metrics and thresholds described in the terms of reference. That is, the assessment should address the structure and performance of the two species as they have been listed, the sub-populations that comprise these species, the populations that comprise the various sub-populations, and the demes that comprise those sub-populations.*

The original memo dated April 6th, 2018 from Michael Tosatto (PIRO 2018) did not ask for the above. PIFSC provided what was requested in paragraph two of the original memo, using the best available nesting abundance time series data: (1) population trends, which are a measure of the "current population status", for leatherbacks (western Pacific nesting population) and loggerheads (North Pacific DPS), (2) estimates for the mean and median time until each population declines to 50%, 25%, and 12.5% of current abundance estimates, and (3) estimated probabilities of each population reaching those thresholds in 5, 10, 25, 50, and 100-year time

intervals with associated 95% confidence intervals. We are not aware of a NMFS or other document or body of work that recognizes demographically-independent units for leatherbacks or loggerheads below the level at which they are currently listed under ESA or IUCN http://www.iucnredlist.org/details/46967817/0 (North Pacific Loggerhead DPS and the western Pacific leatherback [see Wallace et al. (2010a)]). Nor are we aware of data series that would allow modeling of such units. The above request is of the scope of a Status Review Team (SRT) and currently, there is a SRT for leatherbacks that includes representatives from PIRO and PIFSC. Status reviews often take a year or more to complete and a request of that nature is outside the scope of what PIFSC can provide in the allotted time frame. We will not be providing any further analyses or sub analyses of the populations in questions. We provide further responses below in the detailed points:

- *For the leatherback sea turtle, the Western Pacific "sub-population" is represented by the sub-populations (nests) at Papua as well as Papua New Guinea, Solomon Islands, and Vanuatu. The assessment should address demographic performance of each of these nesting aggregations to provide insight into the probable status and trend of this sub-populations. This would include an assessment of the boreal summer nesters and boreal winter nesters, and the role of males.*

The comment contains three separate issues, (i) that the western Pacific population of leatherback turtles has nesting sites outside of the 'index' nesting beaches of Jamursba Medi and Wermon, (ii) that there is a summer versus winter phenomenon of nesting within the 'index' beaches, and (iii) the model does not address males. We will respond to each in turn:

(i) For the western Pacific leatherback nesting population, the only data sufficient for time series analysis come from Jamursba Medi and Wermon beaches in West Papua, Indonesia. To our knowledge, data series from Papua New Guinea, Solomon Islands, and Vanuatu sufficient for population modeling do not exist. The purpose of the 'index' beaches of Jamursba Medi and Wermon is that they allow focused effort to produce reliable time series.

(ii) The western Pacific population of leatherbacks turtles includes the nesting beaches of Indonesia (e.g., Jamursba Medi, Wermon), Papua New Guinea, Solomon Islands, and Vanuatu (non-inclusive of all leatherback nesting). Nesting turtles from this region show a bimodal nesting pattern with peaks in the Northern Hemisphere winter and summer. The evolutionary and environmental drivers are not understood; however, limited satellite tracking data (n=126) from the beaches of Indonesia and foraging areas off of California suggest that there may be divergences in the foraging areas used by summer versus winter nesters (Benson et al. 2011). The genetic analyses conducted on samples from the beaches of Indonesia do not suggest the summer or winter nesters differ genetically and the role of males and recruitment of hatchlings to the summer versus winter phenomenon is further unknown. For the two beaches where we have time series data of abundance (i.e., Jamursba Medi and Wermon) the summer nesters largely drive the signal. Jamursba Medi has the most consistent nesting observation effort and its nesters are primarily summer nesters. Wermon has a stronger bimodal pattern, however, with summer and winter nesting in roughly equal proportions. We have performed the analyses on summer versus winter nesters for both beaches combined (Jamursba Medi and Wermon) and for each beach independently. We are happy to provide these analyses. However, our team of 6 scientists discussed this at length and recommends using the single combined trend that accounts for all nesters on both beaches that has already been provided to PIRO. There is

inadequate knowledge to date as to whether females will nest in different seasons or if late or early nests within seasons will have hatchlings swept into different areas. Based on the uncertainty in splitting the nesting data and the strong signal from the summer nesters we suggest that the best scientific information available (BSIA) is to model the beaches (i.e., Jamursba Medi, Wermon) as a single population with projection.

(iii) We will address the male issue here, and this will be our response for the several instances in which the issue is raised in the comments. The index of population abundance we have is nesting females and it is most appropriate to fit to nesting trends and generate future projections. We do not have quantitative information on sex-ratio or how sex-ratio will change in the future projections. Sex-ratio for the purposes of the requested modeling would be static; therefore, to add males into our projections we would simply multiply the model-estimated number of nesting females by the sex ratio (if the ratio is 50:50 then multiply model estimates of nesting females by 2 to get total male and female estimates). This would not change the trajectories, growth rates, or probabilities of reduction thresholds calculated for nesting females only.

Little is known about male sea turtles for any species or population. Leatherback sea turtles are largely oceanic-pelagic in their distribution throughout ontogeny (Bolten 2003) with observations of pelagic foraging in some select nearshore (neritic) areas (e.g, Benson et al. (2011)). Loggerhead turtles in the North Pacific have an extended oceanic-pelagic phase (Briscoe et al. 2016b) returning to breeding grounds in Japan once approaching sexual maturity. To assess marine turtle population trends, time series of abundance data are required and the only available time series of abundance data come from nesting observations. The leatherback and loggerhead populations do not bask and because of their oceanic-pelagic nature in-water observations and captures are very limited. Furthermore, leatherback turtles are generally not boarded and loggerhead turtles are released alive when incidentally caught in the Hawaii-based shallow set longline fishery providing no data on the sex of the bycaught turtles (juvenile and sub-adult turtles do not display sexual dimorphism). Curtis et al. (2015) included males in their model of leatherback turtles, however, they used data on 37 juvenile to adult turtles caught off California from 2000 to 2007 (Benson et al. 2011) which represented a point estimate that was then applied throughout their model. The generated sex ratio was from a small sample size, an isolated region of the known leatherback distribution, and averaged proportion female from different life-stages. We found the point estimate from limited captures would arbitrarily increase uncertainty and would be less defensible than projecting nesting females from a nest abundance time series. While there are some studies of hatchling sex-ratio for marine turtle populations, it is not known how hatchling sex-ratios propagate through a population into breeding or operational sex-ratios. We recommend that the best approach is to model Annual Females derived from annual nests and to not include a metric/parameter for males.

- *For the North Pacific loggerhead sea turtle, the assessment should address the demographic structure and performance of each population, which are represented by the regional management units identified by {Matsuzawa, 2016 #7} as (a) the Ryukyu unit, (b) Yakushima Island unit, and (c) the mainland unit. Smaller nesting aggregations would represent sub-populations. These, and the role of males, also should be addressed.*

The Matsuzawa et al. (2016) study includes 12 beaches throughout Japan; however, there are no time series of nesting data for most of these beaches to our knowledge. There are 36 beaches listed for the IUCN Redlist <http://www.iucnredlist.org/details/83652278/0> assessment

of the North Pacific Loggerhead and the genetic diversity and fluidity between these nesting beaches is unknown. For these reasons an assessment of the potential management units within the North Pacific DPS is not possible. Furthermore, the only available time series data available and permissible for our use are from three nesting beaches in Yakushima, Japan. The three beaches including their proportion of total nesting are Inakahama (29%), Maehama (20%), and Yotsusehama (3%), which together comprise approximately 52% of loggerhead nesting in Japan; these data were used in our analyses.

2. Describe the criteria used to review the modeling options and discard modeling options.
3. Describe the alternative state-space models available and considered.
4. Clearly articulate the model used, why it was selected, the variables considered in the model, and the initial setting for those variables, and any population models underlying the statespace model (the Leslie life history model). Include alternative scenarios that were considered or actually modeled, and explain why those alternatives were not selected.
5. Clearly list the assumptions made for modeling, such as assumptions of density independence. Explain why those assumptions were advisable or necessary, and the consequences of the assumptions if they later prove to be incorrect.

Our responses to points 2-4 and 6 are in the "Modeling Approach" section below.

6. Clearly identify the data used to drive the model including any transformation and corrections applied to those data before they were used.

For North Pacific loggerhead turtles, available raw data were time series of Annual Nest Counts from three nesting beaches in Yakushima, Japan – Inakahama (1986-2015), Maehama (1989-2015), and Yotsusehama (1999-2015). These beaches represent approximately 52% of loggerhead turtle nesting for this population. These are the official datasets provided by Japanese colleagues and permissible for our use; they are the best scientific data available for this analysis. For trend estimation, we input the data as Annual Female Counts, which were simply Annual Nest Counts divided by a clutch frequency of 3 nests per female (Conant et al. 2009).

For western Pacific leatherback turtles, available raw data were time series of Monthly Nest Counts from two nesting beaches in West Papua, Indonesia – Jamursba Medi (2001-2017) and Wermon (2006-2017, except 2013-2015). These beaches represent approximately 85% of leatherback nesting for this population. These datasets were provided by Indonesian colleagues (via collaborators at Southwest Fisheries Science Center) and are permissible for our use; they are the best scientific data available for this analysis. Although there were count data for Jamursba Medi for 1999-2000, we chose not to include them, as they did not fit with the current regime of standardized monitoring which includes particular attention to protecting nests and enhancing the nesting habitat (see WPRFMC (2004)). The Monthly Nest Count time series had some missing data due to low or no monitoring effort in some months. To impute missing data, we conducted an auto-regressive time series analysis with one year of lag using a Bayesian state-space model with two variances and two slope parameters in the state model. The two variances corresponded to high and low counts, whereas the two slope parameters corresponded to increasing and decreasing phases of nest counts. After imputing missing data, the Monthly Nest Counts were summed into Annual Nest Counts. Wermon beach did not have sufficient data for 2013-2015, so no imputed data were used for those years. For trend

estimation, we input the data as Annual Female Counts, which were simply Annual Nest Counts divided by a clutch frequency of 5.5 nests per female (Tapilatu et al. 2013).

See subsection "7. Modeling Decisions" in the "Modeling Approach" section below for further details on data transformations from raw Annual Nest Counts.

Modeling Approach

1. Overview

On April 6, 2018 PIRO requested that PIFSC provide model-based estimates of specific parameters pertaining to marine turtle populations in support of the current Biological Opinion for the Hawaii-based shallow-set longline fishery (PIRO 2018). The requested parameter estimates of interest included projected mean and median time to reach specific fractions of current abundance, the probability of reaching those fractions of current abundance at specific future time points, and estimates of projected population growth rates with associated uncertainty. In response, PIFSC convened a team of PIFSC and SWFSC scientists (the "Team") with expertise in population assessments, quantitative modeling, and marine turtle biology to determine the best approach given the specific questions asked in the memo, the current knowledge of the specific turtle populations in question, and the data available to PIFSC for analysis and public dissemination. The Team consisted of Drs. T. Todd Jones, Summer Martin, Tomo Eguchi, Annie Yau, Brian Langseth, and Jason Baker. In a series of meetings from April through June, the Team tackled three major tasks: (1) review the modeling methods employed in previous Biological Opinions for the fishery (specifically, climate-based models, diffusion approximation models, and stochastic exponential growth models), (2) review the demographic models for loggerhead and leatherback turtles produced by Dr. Milani Chaloupka in 2002 for NMFS to explore fishery impacts, and (3) determine the best approach forward to provide the information PIRO requested given data limitations and expert knowledge about the populations impacted by the fishery. The population models in (1) and (2) differ in their complexity (e.g., number of parameters), structure (e.g., which life stages are included), and the amount of specific biological data (e.g., growth and death rates for all life stages vs. annual nest counts and clutch frequencies) required as inputs, and consequently also vary in the number of assumptions to be applied. Not all of the models described above can be used to conduct a population viability analysis (PVA), in other words not all of the models described in (1) and (2) would yield estimates of the parameters requested by PIRO.

This document outlines the key discussion points raised by the PIFSC/SWFSC Team as it accomplished tasks (1) - (3) above. The discussion below provides support for the decisions made by the Team. In summary, the Team unanimously decided the following:

1. The climate-based approach employed by Van Houtan (2011) is inappropriate for fulfilling PIRO's requests. Among other reasons for this conclusion, this approach does not provide estimates of population growth rate requested by PIRO.
2. The diffusion-approximation PVA is an appropriate analytical method (Snover 2008), but it does not deliver results with probability-based uncertainty.
3. Non-climate-based stochastic exponential growth models (based on nest count data), paired with a numerical approximation PVA (Van Houtan 2011), could be used to provide the information PIRO requested, though improvements to this modeling

approach could be warranted to better capture and propagate uncertainty into future estimates.

4. The complex demographic models developed by Dr. Chaloupka (Chaloupka 2002b, a) are useful as heuristic tools to explore the sensitivity of population trajectories to various biological parameters (e.g., survival rates for various life stages or remigration intervals), but they are inappropriate for the task at hand due to a lack of population-specific data to inform input parameter estimates (and their uncertainty).

5. Given PIRO's request and the available data, the best approach is to use annual nest counts as an index of abundance, estimate a long-term population growth rate over the period of data collection, estimate an index of current abundance, project the estimated trend forward using the estimated population growth rate, and evaluate the probability of the projections falling below specified thresholds (percentages of the index of current abundance) at specified points in the future.

6. There are various ways to estimate the long-term population growth rate (e.g., log-linear regression of the nest counts over time, fitting a distribution to interannual log differences in nest counts, and state-space population models). Several were explored and similar results were achieved.

7. The most robust approach to completely fulfill PIRO's request given the available data is to use a Bayesian state-space PVA using nest count time series as inputs, which accounts for both environmental variability and observation error in estimating the long-term trend and produces final results with probabilities to characterize uncertainty.

2. Climate-based models by Van Houtan

The 2012 Biological Opinion for the Hawaii-based shallow-set longline fishery (NMFS 2012) included a climate-based approach which estimated future trajectories of North Pacific loggerhead and western Pacific leatherback turtle populations and assessed potential impacts to those populations from the fishery. This approach was described in an internal PIFSC report by Van Houtan (2011) but the methods were based on a previous study by Van Houtan and Halley (2011). In short, Van Houtan and Halley (2011) correlated nesting activity of loggerhead turtles at Japanese beaches to a lagged oceanographic index (Pacific Decadal Oscillation) and sea surface temperature (SST) at 8-28° N and 120-128° E during the November-January before the nesting season. The latter has been found to correlate with the number of nesters in Japan previously (Chaloupka et al. 2008). Van Houtan (2011) applied the same approach to loggerhead turtles and modified it for leatherback turtles using PDO and an upwelling index from the California Current. The Team raised a number of concerns about this approach and the appropriateness of using it to answer the current PIRO request. Specific issues with the approach are detailed below within broader categories of concerns about: (1) the inability of the method to produce the outputs requested by PIRO, (2) the general modeling framework, (3) biological aspects of the models, given the Team's knowledge of the species and populations in question, (4) climate aspects of the models, and (5) lack of reproducibility of the models.

Inability to meet PIRO's request

These particular climate-based models cannot fulfill PIRO's requests. PIRO asked for an evaluation of the risks of falling below specified abundance thresholds (50%, 25%, and 12.5% of current abundance estimates) at 5, 10, 25, 50, and 100 year time frames. These climate-based

models can only project up to one lag into the future (22 years for leatherbacks and 25 years for loggerheads). This is due to the structure of the models, which includes a climate-based age at first reproduction determined by a correlation with climate index lagged by 22 to 25 years. The climate index used (Pacific Decadal Oscillation, PDO) cannot be predicted, thus the model can only predict 22-25 years beyond the most recent measurements of PDO. Additionally, the models do not generate estimates of long-term population growth rate parameters ('r' or 'lambda') and their associated uncertainty (i.e., 95% confidence intervals), as PIRO requested. Further, the models do not employ a straightforward estimated index of abundance (e.g., Annual Nests or Annual Females). Instead, the modeled response variable is a standardized anomaly of the natural log of nest counts. There is no apparent way to convert this standardized log-anomaly to abundance in order to calculate probabilities of the population falling below the various abundance thresholds as PIRO requested. Based on these concerns alone, the climate-based approach was deemed inadequate for answering PIRO's current questions. The Team also discussed several additional concerns about the models, which are described below.

General modeling framework

There were a number of concerns about the general modeling framework and its application to fishery management decisions. At its core, the approach transforms auto-correlated time series (e.g., nesting activity and environmental/oceanographic indices) using opaque methods, and fits a single time lag using generalized linear models (GLMs) to match environmental patterns to those of nesting females and hatch year turtles. For loggerheads, the model considers only two environmental indices (Pacific Decadal Oscillation, PDO, and sea surface temperature, SST); for leatherbacks, it considers PDO and California Current Upwelling (CCU). For both species, the model only considers effects of these environmental indices on two life stages: nesting females and hatch year turtles. The selection of the lag was not based on biology or *a priori* hypotheses, rather multiple lags were tested until one was significantly correlated with the data and that one was chosen as the solution. Subsequently, it was purported to match the age at first reproduction. Regarding the data transformations, the nesting activity was defined as the normalized natural-log transformed annual nest counts, with a justification that this was "consistent with the observed pattern of variability of wild populations" but the citations referenced as support did not involve transformed data. It was therefore unclear how Van Houtan and Halley (2011) normalized nest counts. The Team assumed that data were standardized by subtracting the sample mean from data and dividing by the sample standard deviation, resulting in a mean of zero and standard deviation of one. However, the trend in data, if any, was lost through this transformation. Correlations with environmental variability (oceanographic indices) were computed for anomalies; positive or negative values from the sample mean.

This climate-based approach is not based on population dynamics theory, but rather on a lag correlation index. It is not surprising to find correlations between two auto-correlated time series (in this case environmental indices and wildlife patterns) when the data are somehow transformed and multiple lags are tested until one is statistically significant; if you try enough different time series and lags, you will eventually find a statistically significant correlation. The Team questioned some elements of this modeling approach: (1) why use a model based only on fitted correlations rather than a population dynamics model incorporating relevant climate variables?, and (2) why were only GLMs fitted, when generalized additive models (GAMs) could have also been used to explore non-linear relationships between climate and nesting activity? The Team considered dubious the claim that climate change is driving population change based only on fitted lagged correlations that do not demonstrate causality. In general, the Team

concluded that this approach requires many poorly-supported assumptions and that it was not appropriate to use such models to determine turtle population status and trends in the context of questions asked by PIRO for management.

Biology of the species

Several concerns arose in the Team's discussions about how these particular climate-based models treated various aspects of the biology of loggerhead and leatherback turtle populations. First, only two life stages were considered to be influenced by oceanographic conditions in these models. The first was the hatch year stage. Collectively, the world's scientific experts on marine turtles know very little about this stage due to the difficulties in studying these small, highly mobile animals at sea, far from coastlines. Empirical data for this stage are extremely limited, which limits our understanding of their survival rates and how they are actually influenced by oceanographic factors. The models considered SST and PDO as causing changes in the annual survivorship of the first year turtles, but there are no data to support this assumption. There is high natural variability in survival rates of juveniles in their entire 20-30 year life stage and the probability of surviving to maturity is extremely low (1 in 1,000 to 1 in 10,000 hatchlings), but we do not know how or when specific drivers (e.g., predation, environmental variation, or anthropogenic mortality) influence these rates. Additionally, Van Houtan and Halley (2011) and Van Houtan (2011) assume juvenile loggerheads move into the northwestern part of the Pacific (Figures 1 and 4, respectively). However, recent studies have shown that juvenile loggerheads distribute more widely throughout the North Pacific (Kobayashi et al. 2008, Kobayashi et al. 2011, Allen et al. 2013, Briscoe et al. 2016a, Briscoe et al. 2016b), and thus may be impacted differently than this climate-based model suggests. Van Houtan (2011) also assumes juvenile leatherbacks move into the southwestern part of the North Pacific in a geographically distinct area from the loggerheads and thus the effect of PDO on leatherbacks is opposite its effect on loggerheads. However, an active dispersal simulation model by Gaspar and Lalire (2017) suggests that leatherbacks from Indonesia (Jamursba Medi beach) move into the same areas as loggerheads within the first 1-5 years of life (20 - 40° N in the western North Pacific). A dispersal model simulation of loggerhead hatchlings from Japan by Okuyama et al. (2011) further demonstrates this geographic overlap. These dispersal models suggest effects of PDO on loggerheads and leatherbacks that are the opposite of those specified in the climate-based approach by Van Houtan (2011).

The other life stage influenced by climate in the models is that of nesting females, for which the most empirical data exists. Oceanographic effects might influence adults by impacting resource availability during foraging periods, which can subsequently impact their remigration intervals, but that doesn't necessarily affect abundance over time (climate-induced resource limitation leading to adult mortality would be an extreme scenario). The model completely relies on the fitted lag as a fixed age of sexual maturity (25 and 22 years for loggerheads and leatherbacks, respectively). However, it is well known that individual growth rates and age at sexual maturity vary among individuals of these populations, especially as they are known to use many different foraging areas throughout a vast ocean basin. Also problematic is that the lag used is only associated with neophytes, females that are nesting for the first time. However, turtles nesting each year are made up of both neophytes and remigrants. Data on the proportion of neophytes each year would be required to properly adjust the annual nest counts to reflect neophyte counts and remigrant counts.

The climate-based approach used by Van Houtan and Halley (2011) and Van Houtan (2011) conclude that demographic factors, e.g., survivorship and birth rates, are not important to the

oscillation of loggerhead nesting. Van Houtan and Halley (2011) claimed that "… changes in loggerhead nesting over at least the last several decades are strongly correlated with ocean oscillations." They further claimed that "… climate forcing seems to dominate population dynamics." They do not mention incidental mortality in fisheries, which has been implicated in the decline of marine turtle populations globally (Lewison et al. 2004a, Lewison et al. 2004b, Wallace et al. 2010b). For North Pacific loggerheads, there have been reports of mass mortality events along the juvenile foraging ground along the Pacific coast of Baja Peninsula, Mexico in connection with gillnet fisheries (e.g., Peckham et al. 2007, Peckham et al. 2008, Koch et al. 2013). These deaths (demographic events) may have played a large a role in the abundance of loggerhead turtles in the North Pacific; however, the documentation supporting the climate-based models makes no mention of any of these papers. Instead it suggests that the historical declines observed for both North Pacific loggerheads and Jamursba Medi leatherbacks is explained by the environmental drivers in the models (Van Houtan 2011), rather than fisheries bycatch or harvesting of nesting females and eggs, which are known to have been high over the period of decline. Further, if we accept the conclusions of these authors that the future nesting female anomaly can be predicted by using PDO and SST within a particular region, then how do we convert this standardized log-anomaly to abundance itself? The procedure for doing this is not clear.

Finally, now that time has passed since the climate-based approach was developed, it seems that the models' projections were not realized. The projections were essentially in the opposite direction of the long-term trends observed for both the loggerhead (observed positive trend since the 1990s) and leatherback (observed negative trend since 2001) populations. If we examine shorter-term model predictions from their start in 2010 to the most recent year of available data, we find the following. For loggerheads, the model predicts a decline for 2010-2016, but the observed data increased over 2010-2013 and decreased over 2013-2016, suggesting the predicted pattern of oscillations was wrong for half of the time period. For leatherbacks (Jamursba Medi), the model predicts an increase over 2010-2013, a decrease over 2013-2015, an increase over 2015-2016, and a decrease over 2016-2017; the observed data decreased over 2010-2013, increased over 2013-2016, and decreased 2016-2017, suggesting the model predicted the opposite pattern of what really happened for the majority of the time period.

Climate aspects of the models

The Team identified several issues specific to the climate aspects of the climate-based approach produced by Van Houtan. A climate-based approach to modeling population trends such as the one in question should include a population dynamics model and carefully consider the population's spatial structure, the climate index selected, the choice of time lag, the influence of the climatic effect on the life stages in question (e.g., hatchlings and nesters), and the forecasted climate. The Team was not satisfied with the treatment of these aspects in the Van Houtan models, which included a fair number of assumptions.

The climate variables included in the models came from IPCC climate models (e.g., scenario A2 for SST), but there were a number of concerns in the way they were used. First, the IPCC models were not developed for short-term projections, but in this case were indeed used for short-term projections (22-25 years). Additionally, the uncertainty of climate predictions was not incorporated into Van Houtan's model projections, which may have underestimated the uncertainty in the nest count predictions by an unknown but possibly large amount. The nest count prediction figures in Van Houtan and Halley (2011) and Van Houtan (2011) appear to

grossly underestimate the uncertainty because of this omission. Without this environmental variability, the climate-based approach is deterministic in nature with less stochasticity than the non-climate-based PVA models produced by Van Houtan (2011) -- this is not ideal for management decision-making purposes. Ultimately, including climate into a PVA model may add more uncertainty because climate predictions are also uncertain, and there are many different impacts on the different life-stages of the population, most of which were not accounted for in the Van Houtan approach.

One finding in this climate-based approach was that, by subtracting 25 years from the PDO index, the authors could somewhat match the lagged PDO values and model predictions of the nest count anomalies in Japan. However, as noted above, we have to be careful in how we interpret these results, as the response variable in this analysis was the standardized anomaly of the log nest counts. It appears that PDO was also standardized, even though it was not stated as such in Van Houtan and Halley (2011).

Lack of reproducibility of the models

There were several issues regarding reproducibility of the climate-based models which created some difficulty in evaluating them or interpreting their results. As noted above, the method for transforming nest count data into anomalies was unclear, as was the standardization of the PDO index. The data for the analyses were not made available (e.g., eight time series for Japan), nor were the methods clear enough to reproduce the results. Also, in the Van Houtan and Halley (2011) analysis, they removed two data points because the numbers were less than 20 nests, which skewed the normalization process. The Team questioned whether this removal would introduce bias in some way, as certainly these counts were as important as any other count in the data. Data points should not be omitted simply because they are low or high. Further, the authors did not provide estimated parameter values for any of these models, nor model selection results (i.e., delta AIC values for each dataset). Consequently, it was not possible to replicate these results.

3. Demographic models by Chaloupka

In reviewing potential modeling approaches for answering PIRO's questions, the Team discussed the possibility of using stage-based demographic models, and in particular, those previously developed by Dr. Milani Chaloupka for Pacific loggerhead and leatherback turtle populations. A natural starting point for discussions was a review of the models themselves, previous Biological Opinions, and external technical reviews of the models. An excerpt from the 2002 Biological Opinion for the Hawaii-based shallow set longline fishery (pg. 162 in NMFS (2002)) summarizes the models and NMFS's conclusion about the applicability of the models for management purposes:

"In early 2002, Dr. Milani Chaloupka developed a series of simulation models that were designed to help us overcome the limits in our knowledge of the population ecology of sea turtles in the Pacific Ocean (Chaloupka 2002a, b, Chaloupka 2002c). These models use differential equations (running in Berkeley Madonna software) to simulate time-varying demographic processes that can be subject to environmental and demographic stochasticity; the models were designed to allow managers and other interested parties to quickly consider the effects of small changes in some variables on a population's trajectory over time. After carefully reviewing these models, NMFS concluded that, without much more information on the biology and ecology of sea turtles in the Pacific Ocean, it would be inappropriate to use the

models as the basis for biological opinions or other, specific management purposes. In particular, comprehensive models like the ones developed by Dr. Chaloupka require detailed information on the biology and ecology of sea turtles and the environmental relationships that, as we discussed in the preceding paragraphs, is not available for sea turtles in the Pacific Ocean. Using this kind of model under those circumstances would give the appearance of numerical precision without the reality of it (Burgman et al. 1993, Reed et al. 1998, Cortés 1999, Morris and Doak 2002)."

After review of the models (Chaloupka 2002a, b), the previous external CIE reviews (CEFAS 2002, NMFS 2004, CEFAS 2009), and extensive discussions, the Team concluded that even though 16 years has passed, the decision by NMFS not to use such models for biological opinions or management purposes was still prudent from a scientific perspective. Detailed information on the biology North Pacific loggerhead and Western Pacific leatherback turtle populations is still lacking, and there are too many unknown demographic parameters across all life stages to employ such a demographic model with any confidence that it reflects reality. Following is a summary of the Team's concerns with using demographic models, specifically those previously developed by Dr. Chaloupka, to answer PIRO's questions in support of the current Biological Opinion. In brief, the issues raised are related to: (1) lack of population-specific data to inform a complex model with a high number of parameters, (2) biological or ecological aspects of the models, (3) lack of uncertainty included in the models, (4) sensitivity of the model to certain data-poor biological parameters, and (5) appropriateness of the method to fulfill PIRO's request.

Complex model with a large number of biological parameters

The demographic models by Dr. Chaloupka employ a complex sex- and age- structured Leslie-matrix approach to characterizing population dynamics. This approach requires a user to provide estimates for a large number of biological parameters (e.g., somatic growth rates, survival rate, and reproductive values) for each specific ageclass (e.g., eggs, hatchlings, neonates, juveniles, subadults, potential adult breeders, post-breeders). In the absence of population-specific empirical data to inform these parameters, estimates may be borrowed from similar populations from the same or different ocean. Due to a paucity of the required demographic data on North Pacific loggerheads and western Pacific leatherbacks, Chaloupka borrowed estimates from other populations or species. For example, for the North Pacific loggerhead model, many demographic parameters were based on the southwestern Pacific "stock" and other populations. A statistical model based on the southwestern Pacific loggerhead turtles should not be used as a management tool for the northwestern Pacific stock, or vice versa, as these two stocks are genetically distinct (Bowen 2003) and experience different environmental and ecological drivers, including anthropogenic threats.

In addition to inputting parameters from other populations, the parameters then had to be "tuned" (i.e., a process of adjusting values and evaluating model outcomes) to force the population into a stable age distribution. Recognizing the limitations of the data inputs, Chaloupka noted that the models were heuristic tools intended to improve our understanding of the population dynamics for the data-poor populations in question, and that the models are not applicable for robust management decisions. He also noted that the limited data available for both the North Pacific loggerhead and western Pacific leatherback abundance "precludes any robust fitting procedures and quantitative model validation" (Chaloupka 2002a, b). Overall, it was not clear which biological values were borrowed from which other populations, and which were tuned. The Team agreed that given the best available data on both populations which

generally lacked biological age- or sex-structured estimates, the elaborate, complicated simulation models developed by Chaloupka were not appropriate for evaluating the specific management questions.

Biological or ecological aspects of the models

The Team discussed some biological/ecological aspects of the models. While we have slightly more data now in 2018 than in 2002 when the models were created, we are still not in a place where we can build age- or size-structured models. For example, we do have some juvenile loggerhead abundance estimates at two foraging grounds (Southern California and Baja) based upon aerial estimates, but we don't know the proportion of the population that goes to these areas. The new information adds to our understanding of spatial patterns, but we cannot incorporate it into a stage-based demographic model. To implement stage-based demographic models would require better population-specific estimates of growth and survival rates and reproductive outputs for all life stages (at a minimum). As noted above, the biological complexity of the models without adequate data to support that complexity was concerning. Thus, the Team agreed that the best way forward was to use a simpler approach that only relies primarily on the data available (annual nest counts at different beaches) and not on scarce data from other populations.

The Chaloupka models assume density-dependence in the models for both loggerheads and leatherbacks. This decision was questioned by the Team due to the low population sizes of the long-lived, slow-growing, late-maturing species being modeled. Density-dependence generally occurs at high population levels in so-called K-selected species, and there is no empirical evidence of density-dependence in turtles at low population sizes (either higher population growth rates or Allee effects reducing the probability of finding a mate; Hays (2004)). Mating in sea turtles occurs offshore from nesting beaches, with individuals typically returning to their natal beach or nearby beaches. This location-specific breeding behavior may play a role in preventing Allee effects at small population sizes, allowing turtle populations to recover at exponential rates. Thus, including density-dependence in the models requires the user to provide even more parameters to specify the functional form of the relationships, but there are no population-specific data to inform this process.

Lack of uncertainty in the models

The Team noted the demographic models lacked uncertainty for the various parameters included in the models. The models used point estimates for many parameters without including or explaining the variability or uncertainty surrounding those estimates. Some parameters were determined by tuning the model, but it was not clear which parameters were tuned, to what extent they were tuned, and whether it was appropriate to do so. Without considering uncertainty of the estimated demographic parameters used in the models, the simulation analyses end up conveying falsely precise results. Since the models do not propagate uncertainty through to the results, there is no way to use the models to obtain uncertainty estimates (i.e., the output is not an estimate with a distribution). There is stochasticity in the models, but for each simulation run, the output is still just a single point estimate result. The Team would not recommend using such results as a management tool because the probable errors from the simulations are hidden.

It was not surprising, however, that parameter uncertainty was not included in the models. We currently do not know the uncertainty for the number of nesting females, which is the easiest

aspect of turtle populations to study. For other important nesting demographic parameters, we do not have robust estimates (with uncertainty) of how often they nest (3-5 years?), how many clutches each female lays in a season (3-6?), how long will each female survives (i.e., will she be observed nesting one or ten more times?), the hatching success on different beaches, or the emergence rate for nests. Beyond nesting ecology, the models include life-history stage parameters such as growth rates and stage-based mortality, and we understand these parameters far less than we do the nesting ecology parameters.

Sensitivity of the models to data-poor biological parameters

The models results were most sensitive to annual variation in the proportion of females that breed, the maximum number of clutches laid per season by a female, and the pelagic and benthic ageclass survival probabilities. The Team noted that any modeling approach chosen for addressing PIRO's requests should carefully consider all input parameter estimates and associated uncertainty. Unfortunately, the very parameters Chaloupka found his models were most sensitive to are ones that we know very little about. Therefore using a model that is very sensitive to to them is not a defensible approach for informing management decisions.

Lack of transparency

The Team noted transparency issues with the complex nature of the demographic models developed by Chaloupka. It was difficult to determine what was really driving the outcomes of the models. There was no clear accounting of which biological parameters were obtained from the population in question versus borrowed from other populations. It was difficult to follow some of the documentation in order to reproduce the models. Based on the high number of parameters that a user would have to tweak to produce a stable outcome, it did not appear to be a stable model.

Appropriateness of the demographic models to fulfill PIRO's request

While it is possible to apply Chaloupka's stage-based demographic models (or others like them) to answer PIRO's requests, the Team agreed that it was not a good approach based on the reasons described above. Given that the model is stochastic, and that an estimate of population abundance is available, one could use the models to determine how long it takes for the population to reach percentages of the current abundance, with uncertainty estimates. Thus at face value, these models could be used. However, these models were designed for model tuning and testing, not for management use. The Team agrees with the many CIE reviewer comments along the same lines, one of which stated, "We certainly can't approve use of the model beyond heuristic exploration" (Dan Goodman in NMFS (2004)).

4. Diffusion approximation method by Snover

The Team discussed a diffusion approximation method for estimating extinction risk in turtle populations which was described in a PIFSC internal report by Snover (2008) and included in the 2008 Biological Opinion for the Hawaii-based shallow set longline fishery (NMFS 2008). This approach was based on peer-reviewed research conducted by Snover and Heppell (2009), which built upon previously established diffusion approximation methods for estimating quasi-extinction risks (Dennis et al. 1991, Holmes 2001, Holmes and Fagan 2002, Morris and Doak 2002). This method uses time series of abundances (i.e., annual nest counts) to estimate two key parameters using simple linear regression (Dennis et al. 1991, Snover and Heppell 2009):

mean population growth rate and its variance. These parameters are then used to estimate PVA risk metrics, including mean time to extinction and probabilities of declining to a preset threshold (quasi-extinction) (Dennis et al. 1991, Snover and Heppell 2009). This approach is a count-based PVA based on a model for exponential growth in a randomly varying environment (Morris and Doak 2002, Snover 2008), with $N_{t+1} = N_t e^{rt}$, where N is the population size, t is time and r is the population growth rate. The variance of the log population growth rate accounts for environmental and demographic stochasticity and observation error (Snover 2008).

This approach certainly has merits and was recognized by the Team as a possible starting point for providing answers to PIRO's request. Compared to a complex stage-based demographic model, this approach allows one to more easily see what is driving the outcome. It is a frequentist method that has solid underpinnings in the scientific literature, and it offers perhaps more realistic projections than the other approaches discussed (i.e., climate-based approach and stage-based demographic models). The parametric bootstrap approach used to compute the susceptibility to quasi-extinction (proportion of bootstrap replicates that indicate a >90% chance of dropping below a pre-defined quasi-extinction threshold) and the decision rules used to categorize a population as being "at risk" of falling below a threshold would need to be modified to address PIRO's specific requests of estimating the probability of falling below specific thresholds. In contrast to numerical approximation methods, this analytical approach includes explicit mathematical equations, which can be computationally efficient.

There were concerns about the modeling framework that could influence the results. First, as the available data are annual nest counts, the model would actually be estimating some fraction of the population over time (rather than the total population) since most females do not return to nest every year. Snover addressed this by applying a run-sum (i.e., adding a few years of data together to capture a cohort of nesting females). Snover (2008) used a run-sum of three years, which was based on a remigration interval, but CIE reviewers (CEFAS 2009) suggested that sensitivity analyses be performed on this decision to use a three year run-sum. The Team noted that the run-sum addresses the remigration interval issue, but does not account for variation in survey effort. However, the question of whether it is best to use run-sums is not specific to Snover's approach, but arises for any method using annual nest count data. A question arose as to how many years of data should be included in the analysis. Snover and Heppell (2009) indicated that the model was most accurate with >20 years of data. However, using a longer time series would downweight the importance of the data in recent years, which is more likely reflective of the current dynamics and trend. These decisions about remigration interval and time series length impact the resulting population growth rate and its variance, which, in this approach, contains the survey observation error, environmental variation, and demographic variation all wrapped into one term. In general, the Team agreed with the CIE reviews that this approach was valid, but that: (1) more sensitivity analyses could be performed (especially for the extension of the approach that incorporates fisheries take), (2) propagating uncertainty through to the results would be an improvement, such that outputs are point estimates with distributions, and (3) a Bayesian approach could provide a better framework for dealing with some of the drawbacks of the frequentist diffusion approximation approach, especially if managers are interested in probabilities of the population falling below thresholds.

5. Empirically-derived stochastic exponential growth model by Van Houtan

In support of the 2012 Biological Opinion for the Hawaii-based shallow-set longline fishery, Van Houtan employed a modeling approach he called a "classical approach to population viability" or an "empirically-derived stochastic exponential growth (SEG) model" (Van Houtan 2011). This

approach was similar to Snover's diffusion approximation (DA) application in many ways: (1) it was based on a stochastic exponential growth model to describe observed population changes, (2) it used annual nest count data (natural log transformed) from Jamursba Medi, Indonesia for leatherbacks and from Japan for loggerheads, (3) it employed a run-sum method of annual counts based on a remigration interval, and (4) it converted nest counts to nesting females using clutch frequency. However, Van Houtan's approach differed from Snover's in how it estimated the population growth rate, r, and generated future projections. Rather than use the DA methods, he estimated r by fitting a normal distribution to the interannual differences in log nest counts and then made projections using Monte Carlo methods to randomly select r from the fitted distribution for thousands of simulation runs (each run having a constant r across future years). The Team discussed this approach and the claims made by Van Houtan (2011) in his explanation of the method and its caveats.

Van Houtan (2011) stated that both the DA model and his empirically-derived SEG model make two assumptions: "(i) demographic forces are the primary factor driving population dynamics, and (ii) that the factors that regulate population dynamics remain constant through time". He stated that "neither of these assumptions may be warranted, however" and cited his publication (Van Houtan and Halley 2011) that includes the climate-based models described above. The Team found the first two statements inaccurate, and noted that the purpose of the third statement is seemingly to highlight his preference for the climate-based models presented in the same report, which presumably do not make the same assumptions. First, population dynamics are always affected by demographic forces. The only way a population can change its size is through demographic events - births, deaths, emigrations and immigrations. So the first stated assumption is not an assumption, it is fact. For his second claim, i.e., the factors that regulate population dynamics remain constant over time, there is no such assumption. The factors that affected the population in the past will *continue to* affect the population in the future – but this is not equivalent to "constant over time." In fact, this approach selects different r values from a fitted normal distribution around the mean and variance of the population growth rate which are estimated from observed changes in abundance. Consequently, the distribution of past growth rates is assumed to be operative in the future. It might be reasonably expected that the particular factors that influenced past observed rates will operate similarly in the future, but that is not strictly speaking an assumption of this modeling approach. Van Houtan also fails to point out that another very important assumption made was that r follows a normal distribution.

In explaining why he chose the empirically-derived SEG method over the DA method, Van Houtan states that Kendall (2009) showed that "diffusion approximation systematically overestimates extinction risk, especially for species with life history patterns like sea turtles." However, examining Kendall's paper, as well as Snover and Heppell (2009), reveals more nuance. For example, Snover and Heppell's approach is not the same as the plain DA approach, which was the subject of investigation by Kendall (2009). Snover and Heppell (2009) looked at how a new metric (susceptibility to quasi-extinction or SQT) would perform based on the DA approach. Through simulations, they satisfied themselves (and the reviewers) that the new metric is indeed useful in determining a population's status – even for a species with non-continuous breeding. Further, Kendall (2009) reported that "… for many populations/species the bias was quite small, especially when the overall risk was high. In those populations for which I could calculate confidence intervals of extinction risk, the bias was never more than 20% of the width of the 95% confidence interval, suggesting that bias is a relatively minor component of the estimation error." Also, Kendall stated that "In two of the policy applications that I examined, the impact of the bias was modest. The relative risk of populations was sometimes misranked, but only if the risk difference between them was small. In such cases the choice of which population to protect will likely be driven by factors such as feasibility and cost." Thus, the bias associated

with the DA approach may not be a major issue and Snover's approach takes into account the possible bias. Consequently, the statement by Van Houtan that the DA approach was not appropriate is unfounded.

The Team agreed that the empirically-derived SEG model could be used to address PIRO's requests, but that adjustments should be made to the method. First, Van Houtan assumed that the population growth rate of each simulation run for the future projection was constant over time, which may not reflect interannual variation in the observed data. This could be adjusted by instead randomly drawing from the estimated distribution for r in each future year. This would capture the variability in the long-term population trend, which is simply the integration of each interannual trend, effectively an overall average of interannual trend values. There is variation in the estimate of a long-term trend inherently, due to many factors (e.g., data accuracy, population response to variability in environment). The data show this in that they do not produce a straight line throughout the time period of observation; they fluctuate. Drawing a new trend each future year matches this reality: interannual variability but on the average the same long term pattern. Further, this approach suffers from many of the same modeling decisions as Snover's DA approach (i.e., run-sum based on a fixed remigration interval, projection time frame into future based on generation time, constant growth rate each run), so many of the criticisms of the Snover model from the CIE reviews also exist here but could be improved upon. However, the Team recognizes that adding uncertainty to biological parameters such as remigration intervals, clutch frequencies, and age at maturity is difficult when data don't exist to inform the parameters, and that the result may simply be to increase the uncertainty surrounding the modeled future trends. Finally, the Team noted that theoretically, the empirically-derived SEG (numerical approximation approach) and the DA (analytical approach) should produce similar population growth rates and projected trends.

6. Selecting a modeling approach to estimate long-term trends and conduct a Population Viability Analysis to answer PIRO's request

The Team acknowledged that there are many approaches to estimating a long-term population trend, and various modeling decisions to make within any given approach. After deciding that neither the climate-based approach from the previous Biological Opinion nor the complex stage-based demographic models developed by Milani Chaloupka (or similar models that would require an abundance of biological parameter data) were appropriate for the current task, the Team moved on to select an appropriate method for estimating long-term trends which would then inform a count-based Population Viability Analysis (PVA). The Team considered and experimented with a few commonly used estimation approaches, including: (1) log-linear regression of count data, (2) fitting a distribution to interannual log differences in count data, (3) Bayesian state-space models. All of these approaches include a stochastic exponential growth model at their core, rely exclusively on nesting time series data as model inputs, and have been previously used on marine turtle populations. In fact, the first approach was employed as part of the diffusion approximation models implemented by Snover (2008), the second approach was employed by Van Houtan (2011) in his empirically-derived stochastic exponential growth models, and the third approach was applied by Boyd et al. (2017) in examining extinction risk of several Endangered Species Act listed populations. Following is a summary of the Team's discussions and conclusions about the three approaches and the decision to pursue a Bayesian state-space model as the most robust method for addressing PIRO's request (PIRO 2018).

The primary goal for all of the approaches is to estimate a long-term trend, which is the population growth rate parameter, r, in the stochastic exponential growth equation $N_{t+1} = N_t e^{rt}$,

where N is the population size and t is time. It is important to note, however, that the best available data are annual nest counts, which only represent a portion of the mature females in the population because females do not return to nest every year. Annual nest counts therefore provide an index for the only segment of the population (mature females) that we can sufficiently track through time. No data are available to provide an index of abundance for other age classes. Due to this data limitation, the estimated r does not actually represent the true population growth rate for the population of interest (e.g., North Pacific loggerhead turtles). Even if the data were annual number of females rather than nests, we probably still could not assume a stable age distribution (an assumption that would be required for the growth rate to represent the entire population) due to a lack of data on other age classes. Further, given the observed variability in year-to-year nest counts, our estimates of r will have large uncertainty around them. There is no way around this problem unless we set some limits on r through a prior distribution or cut-off values. The consequence of this reality is that any sort of future projections of nest counts will have large uncertainty in them. Therefore, how the models deal with the variability in the data and characterize uncertainty is an important consideration.

There were a few key issues associated with the log-linear regression and interannual log difference approaches that made them suboptimal approaches compared to a Bayesian state-space model. First, neither method separates the possible sources of variation in the annual nest count data. Those sources include (1) observation error (imperfect data collection, with the possibility that some nests are missed, misidentified, or misrecorded, and/or that sampling methods change somewhat between years or observers), and (2) process error, which is comprised of both environmental stochasticity (e.g., variability in food and habitat resources) and demographic stochasticity (chance events of individual mortality and reproduction that influence population growth rates). As a result, both methods are relatively sensitive to errors in count data and changes to sampling methodology between years. This is most extreme in the interannual log differences approach, as it is specifically focused on the difference between each consecutive pair of years, which can vary because of more than just changes in abundance. Instead of separating those sources of variation, both methods wrap them into the variance associated with the mean long-term trend, resulting in trend estimates with high uncertainty that are subsequently propagated through to future projections with high uncertainty. Thus, the two methods fall short in their ability to adequately capture the long-term trend. The log-linear regression under-captures the full degree of interannual variability in the data, while the interannual log differences method over-captures it. Finally, the results are packaged as point estimates with 95% confidence intervals rather than probability distributions. Monte Carlo simulation methods can then be used to create multiple projection runs, and we can calculate the proportion of runs falling below an abundance threshold in place of estimating probabilities, as requested by PIRO. However, this workaround would be improved by starting with probability distributions for the parameters being used to generate future projections.

A Bayesian state-space model that is based on stochastic exponential population growth addresses the shortcomings of the other two methods outlined above. Specifically, Bayesian methods are designed to produce posterior probability distributions for estimated parameters based on data, and these distributions can be directly used to generate future projections. This provides PIRO with results that are based on probabilities. Additionally, the "state-space" aspect of the model allows specification of both a biological process model and an observation model, which allows the sources of variability in the annual nest count data to be parsed out and estimated separately. Consequently, the estimate for the long-term trend parameter is better isolated from noise in the data, and the variance surrounding its mean more accurately captures the variation in the trend itself without being conflated with data collection errors and natural variability (environmental and demographic). The Team identified the Bayesian state-space

modeling methods used by Boyd et al. (2017) as fully capable of producing specific count-based PVA results requested by PIRO. The approach is robust, has been tested on turtle populations, and is simply a Bayesian adaptation of multivariate autoregressive state space (MARSS) models used for analysis of ecological time series; the MARSS package in R uses maximum likelihood estimation rather than Bayesian estimation (Holmes et al. 2012, R Development Core Team 2012, Holmes et al. 2014, Boyd et al. 2017).

7. Modeling decisions

Data transformations

The best available data are annual nest counts from Japan for North Pacific loggerheads and from Indonesia (Jamursba Medi and Wermon beaches) for western Pacific leatherbacks. For the trend estimation, we converted annual nest counts to annual female counts using a fixed clutch frequency based on best available data (3 nests per female for loggerheads (Conant et al. 2009) and 5.5 nests per female for leatherbacks (Tapilatu et al. 2013)). This conversion to annual females scaled the results but did not substantively change the trend. The Team considered using a running-sum ("run-sum") approach to add nesting females across three years (based on assumed remigration interval), but found this extra transformation of the data to be unnecessary, as it only further changes an index of abundance. Also, there were a few missing years in the Wermon beach data, which would prevent computing a run-sum across some years. Further, there was precedent to estimate the trend using annual nesting females rather than run-sum totals of nesting females, as demonstrated by Boyd et al. (2017). The natural log transformation of annual female counts is a standard choice when working within an exponential growth model, and appears in all the modeling approaches discussed in this document.

Current abundance estimates

PIRO's memo requested a comparison of future projections to current abundance estimates (PIRO 2018). Current abundance estimates do not exist for either population in question. Therefore, as an index of current abundance, we calculated a run-sum total using the model estimates for the final three years of data (e.g., 2015-2017 for leatherbacks); three years reflects the best available data on remigration interval for both loggerheads and leatherbacks, which we assume provides a snapshot of the total abundance of nesting females. Specifically, we pulled the estimated number of annual females for each of the last three years from an individual MCMC run, and summed those to produce an estimated index of total reproductive females in the population.

Future projections including dynamic growth rate

The long-term trend (i.e., growth rate, *r*, for the annual females index) estimated for the data time series is used to generate future projections through a simulation procedure. Each simulation run begins with three components: (1) a starting point for annual females -- this is the estimated number of annual females for the final year, as described above, (2) a value of *r* drawn from a normal distribution centered around the mean and standard deviation derived from the posterior estimates, and (3) a value of *Q*, process error variance, drawn from a lognormal distribution centered around the mean and standard deviation derived from its posterior estimates. For all subsequent years in a simulation run, a constant versus dynamic approach was considered for the long-term population growth rate value. In the constant approach, a

single *r* and *Q* value are drawn from their distributions and those values are used for every subsequent year up to 100 years. In the dynamic approach, a new value of *r* and Q are drawn from their respective distributions for each future year up to 100 years. In test scenarios, using a constant value across years produced much higher uncertainty around the future projections than using a dynamic trend. Because the raw data are annual nest counts rather than a more comprehensive index of the population, and because females do not nest every year, we do observe high and low values in consecutive years. The Team therefore decided to use the dynamic approach, as it better represented the interannual oscillations observed in the annual count data and produced more ecologically realistic projections over a 100 year time scale.

Probabilities of falling below abundance thresholds

PIRO requested estimates of the time (number of years) it will take for the impacted loggerhead and leatherback populations to decline to specified abundance thresholds, as well as estimates of the probability that each population will reach those thresholds at specified points in the future (PIRO 2018). To fulfill this request, we generated 10,000 simulated projections for 100 years in the future for each population (see above). The projections were made in units of annual females, consistent with our use of annual females for estimating the long-term trend; this decision was also made by Boyd et al. (2017). However, as PIRO's request defined the thresholds in terms of "current abundance estimates" (50%, 25%, and 12.5% of current abundance estimates), we calculated run-sums from the future projections (again using 3 years based on assumed remigration intervals) and compared them to the run-sum estimates of current abundance for the final data years as described above. As noted previously, the 3-year run-sum provides an estimated snapshot of total reproductive females in the population, which is our best estimate for an index of abundance, based on the available data. To estimate the probability of falling below each threshold, we computed the proportion of simulation runs falling below (and remaining below) each threshold. For those runs falling below a threshold, we computed the time in number of years it took to reach the threshold (mean, median, 95% credible intervals).

METHODS

Modeling the long-term trend

Our approach to estimate the long-term population trend, i.e., population growth rate, is based on a stochastic density-independent exponential growth model, which we implement within a Bayesian state-space modeling framework, following Boyd et al. (2017). Estimation of the Bayesian state-space model was completed in JAGS (Plummer 2003), and projections (see below) were completed in R (R Development Core Team 2012) using the 'coda' and 'jagsUI' packages (Plummer et al. 2006, Kellner 2015). This type of model is commonly used for long-lived, slow-growing, late-maturing species such as sea turtles whose populations have been depleted to relatively low levels. The framework allows for estimation of both process variation (i.e., environmental and demographic variability) and observation uncertainty (i.e., imperfect data collection), and provides parameter estimates with probability distributions. The only inputs to the model are time series of nest count data, which we assume are an index of abundance for reproductive females in the population. The basic exponential growth equation underlying this approach is outlined below, and the model structure is described in Figure 1.

Exponential growth equation:

$N_{t+dt} = N_t * exp(r*dt)$

N_t = population size (number of individuals) at time t

dt = delta t, or difference in time (unit = years)

r = population growth rate, or log growth rate (i.e., long-term trend)

$\exp(r)$ = λ or "lambda", the finite rate of increase

Log-transformed equation & solved for growth rate:

$log(N_{t+dt}) = log(N_t) + r*dt$

$r = [log(N_{t+dt}) - log(N_t)]/dt$

From the model outputs, we were most interested in the posterior distributions estimated for r, the population growth rate or long-term trend; Q, the process error variance; and N_{final}, the predicted nesting female count for the final year of observed data (see Figure 1). We used these three posterior distributions to project forward 100 years into the future (details below). The parameter distributions were estimated through a Bayesian model fitting process in which the program employs a Markov Chain Monte Carlo simulation to fit the model parameters to each set of data separately (i.e., the three time series of Annual Females for loggerhead turtles and two time series for leatherback turtles for a total of 2 models, 1 per species). Models were checked for suitable performance using the following diagnostic tools: examination of trace plots, effective sample sizes, Geweke statistics, Gelman statistics, and Deviance Information Criterion.

Future projections

Future projections were generated using a simulation approach with 10,000 runs for each model. Each run began with a draw from each of three model-estimated distributions: the nesting female count in the final observed year, N_{final}; the growth rate, r; and the process error variance, Q. For each future year, new values of r and Q were drawn, making the projected growth rate and process error variance dynamic and best reflecting interannual variation in the observed data as well as the biology of the species. For each run, the number of nesting females for each future year was calculated according to the exponential growth equation but with the addition of a process error (see model diagram below). In addition, a Current Abundance Estimate was generated for each projection run by summing the last 3 estimated count values (N_{final}, $N_{final-1}$, and $N_{final-2}$) from the same MCMC run as where the N_{final} value was drawn for the projection. The three year running sum was based on assuming a three year remigration interval (applicable to both loggerheads and leatherbacks), with the assumption that summing all females that nest during that period provides a snapshot of Total Reproductive Females in the population.
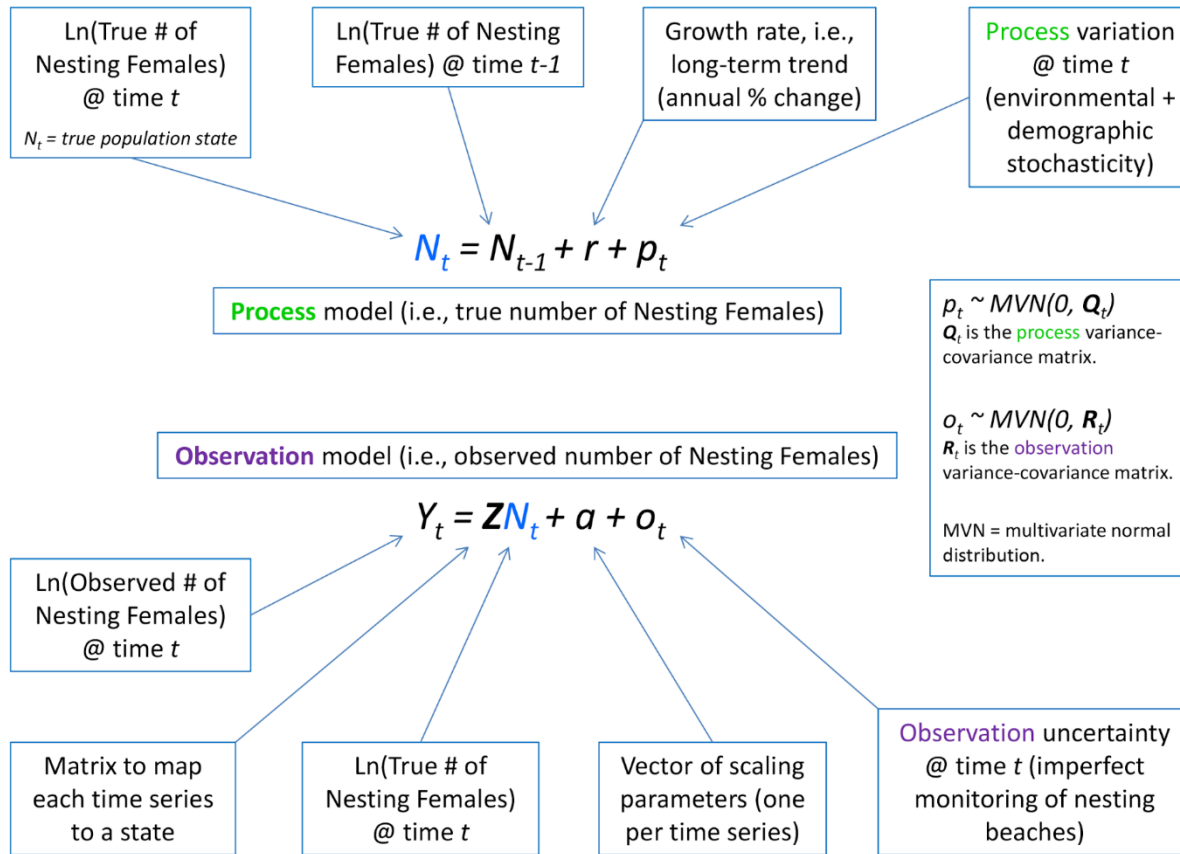
Figure 1. *Schematic illustration of Bayesian state-space model based on stochastic density-independent exponential population growth. There are two major components: a process model describing the true number females nesting each year and an observation model relating the observed count data to the true number of nesting females. Three parameters are estimated: (1) r, the long-term trend, i.e., population growth rate, (2) Q, process error variance, and (3) R, observation error variance. The model also provides a predicted count (number of nesting females) with a probability distribution for each year of observed data. The predicted value for the final year of observed data is then used as a starting point for future projections.*

Evaluating projections against abundance thresholds

We calculated 3-year running sums from the Annual Female projections to create an index of Total Reproductive Females. This allowed us to compare the projections to the Current Abundance Estimates calculated above. To do so, we computed the proportion of runs for which the projected Total Reproductive Females fell below (and remained below) PIRO's specified thresholds (50%, 25%, and 12.5% of Current Abundance) by 100 years in the future. For the set of runs ending below a threshold, we calculated the mean, median, and 95% credible interval for the number of years until the population fell below the threshold. We also calculated the probability of the projected Total Reproductive Females falling below each threshold at 5, 10, 25, 50, and 100 years in the future.

MODEL RESULTS SUMMARY

North Pacific Loggerhead Turtles

1. Data: Annual Female Counts (raw Annual Nest Counts divided by clutch frequency of 3 nests per female; (Conant et al. 2009)). We use annual counts instead of a running sum to minimize assumptions about remigration interval. Raw data are comprised of time series from three nesting beaches in Yakushima, Japan – Inakahama (1986-2015), Maehama (1989-2015), and Yotsusehama (1999-2015). These beaches represent approximately 52% of loggerhead turtle nesting in Japan. These are the best available data and were provided by Japanese colleagues. The data are shown below as the natural log of annual nesting females; this is how they were input to the model.

2. Model Fit: fit population growth rate, 'r', using Bayesian state-space model approach based on density-independent stochastic exponential population growth as in Boyd et al. (2017). Other model approaches were considered; however, the Bayesian state-space approach incorporates uncertainty better and partitions that uncertainty into both process and observation error components. The predicted model median (blue line) with 95% credible intervals (gray shading) are overlaid on data points (black dots) for each time series, scaled appropriately by the model-estimated scaling parameters.

3. Current abundance estimate: use model-estimated Annual Female distributions for 2013-2015 to estimate an <u>index</u> of current Total Reproductive Female abundance; this is computed as a 3-year run sum (3 year remigration interval; (Conant et al. 2009)). The estimated distributions for 2013-2015 Annual Females and the summed Total Reproductive Females estimate are summarized in the table below.

Observed data year	Median	Lower 95% CI	Upper 95% CI
Final Data Yr -2	1777	1465	2165
Final Data Yr -1	1203	984	1448
Final Data Yr -0	652	527	855
Sums=CurAbundEst	3632	2976	4468

4. Projections: start with a value drawn from the posterior distribution of Annual Females for 2015; use dynamic 'r' (draw new 'r' each future year within a simulation run) and dynamic process error variance, 'Q,' to add natural variability. The figure below shows the 10,000 model projection runs for 100 years into the future from the final data year (2015). Model projections are of Annual Females in natural log space.
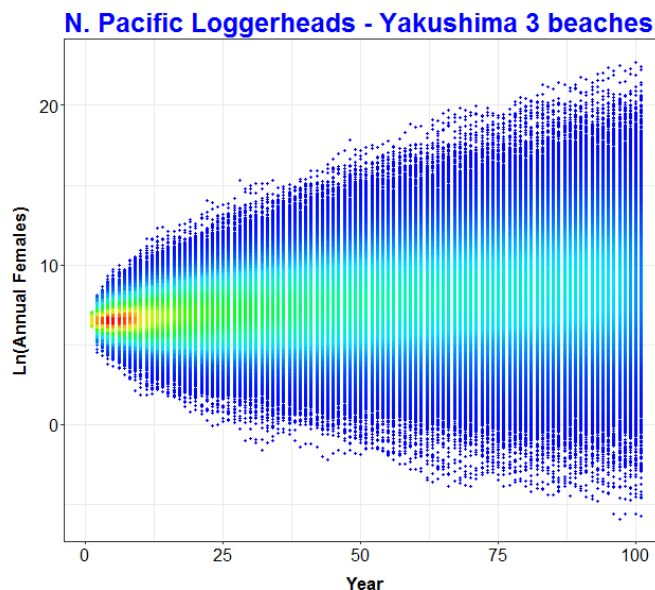
N. Pacific Loggerheads - Yakushima 3 beaches

5. Abundance thresholds: each future projection (n = 10,000 simulation runs) of Total Reproductive Females (3 year running sum of projected Annual Females) is compared to the specified fraction (50%, 25%, or 12.5%) of its specific starting estimate for current Total Reproductive Females.

Loggerhead Table 1: Probability of the population reaching abundance thresholds within the 100 year projection period, and time in years (mean, median, & 95% credible interval [CI]) to reach the threshold for all runs that fall below the threshold.

Threshold	Probability of staying above threshold	Probability of falling below threshold	Years to reach threshold (Mean)	Years (Median)	Years (lower 95% CI)	Years (upper 95% CI)
50% abundance	75%	25%	49	50	2	99
25% abundance	80%	20%	56	59	3	99
12.5% abundance	85%	15%	62	68	7	99

Loggerhead Table 2: Probability (with 95% credible intervals [CI]) of the population reaching abundance thresholds at 5, 10, 25, 50, and 100 years from final data year (2015).

Abundance Threshold	yr 5	yr 10	yr 25	yr 50	yr 100
50%	13%	14%	16%	18%	25%
lower 95% CI	12%	13%	15%	17%	25%
upper 95% CI	13%	15%	16%	18%	26%
25%	3%	6%	9%	12%	20%
lower 95% CI	3%	6%	9%	12%	19%
upper 95% CI	4%	7%	10%	13%	20%
12.5%	0%	2%	5%	8%	15%
lower 95% CI	0%	2%	5%	8%	14%
upper 95% CI	0%	2%	6%	9%	16%

6. Population growth rates: Bayesian model estimates provide an index of population growth using the best available index of population abundance derived from nest count data. Estimating true population growth rates would require additional data or assumptions about the population age distribution. Rates reflect the long-term trend estimated using the Annual Female Count data described above. For r, if values are positive then growth is positive; if values are negative then growth is negative. For λ lambda, if values are greater than 1 then growth is positive; if values are less than 1 then growth is negative.

> **Log growth rate of population (r):**
> > mean: 0.024
> > median: 0.024
> > variance: 0.005
> > 95% CI: -0.108 to 0.156
>
> **Finite rate of increase (λ):**
> > mean: 1.024
> > median: 1.024
> > 95% CI: 0.897 to 1.168

<u>Western Pacific Leatherback Turtles</u>

1. Data: Annual Female Counts (raw Annual Nest Counts divided by clutch frequency of 5.5 nests per female; (Tapilatu et al. 2013)). We use annual counts instead of a running sum to minimize assumptions about remigration interval. Raw data are comprised of time series from two nesting beaches in Bird's Head, West Papua, Indonesia – Jamursba Medi (2001-2017) and Wermon (2006-2017, except 2013-2015). These beaches represent approximately 85% of nesting for the western Pacific leatherback population. These are the best available data and were provided by Indonesian colleagues. The data are shown below as the natural log of annual nesting females; this is how they were input to the model.

2. Model Fit: fit population growth rate, 'r', using Bayesian state-space model approach based on density-independent stochastic exponential population growth as in Boyd et al. (2017). Other model approaches were considered; however, the Bayesian state-space approach incorporates uncertainty better and partitions that uncertainty into both process and observation error components. The predicted model median (blue line) with 95% credible intervals (gray shading) are overlaid on data points (black dots) for each time series, scaled appropriately by the model-estimated scaling parameters.

Jamursba Medi Leatherback Turtles / Wermon Leatherback Turtles

3. Current abundance estimate: use model-estimated Annual Female distributions for 2015-2017 to estimate an index of current Total Reproductive Female abundance; this is computed as a 3-year run sum (3 year assumed remigration interval). The estimated distributions for 2015-2017 Annual Females and the summed Total Reproductive Females estimate are summarized in the table below.

Observed data year	Median	Lower 95% CI	Upper 95% CI
Final Data Yr -2	340	275	433
Final Data Yr -1	439	350	552
Final Data Yr -0	401	324	495
Sums=CurAbundEst	1180	949	1479

4. Projections: start with a value drawn from the posterior distribution of Annual Females for 2017; use dynamic 'r' (draw new 'r' each future year within a simulation run) and dynamic process error variance, 'Q,' to add natural variability. The figure below shows the 10,000 model projection runs for 100 years into the future from the final data year (2017). Model projections are of Annual Females in natural log space.
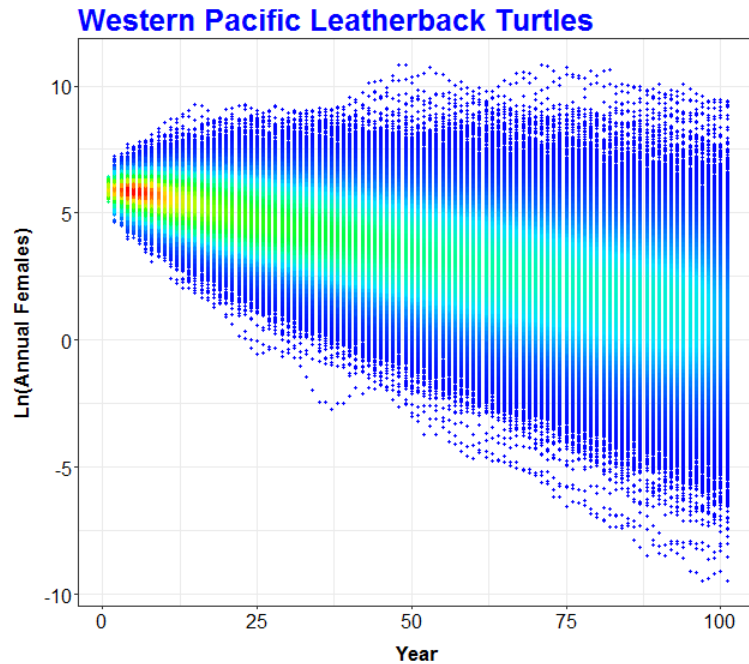
Western Pacific Leatherback Turtles

5. Abundance thresholds: each future projection (n = 10,000 simulation runs) of Total Reproductive Females (3 year running sum of projected Annual Females) is compared to the specified fraction (50%, 25%, or 12.5%) of its specific starting estimate for current Total Reproductive Females.

Leatherback Table 1: Probability of the population reaching abundance thresholds within the 100 year projection period, and time in years (mean, median, & 95% credible interval [CI]) to reach the threshold for all runs that fall below the threshold.

Threshold	Probability of staying above threshold	Probability of falling below threshold	Years to reach threshold (Mean)	Years (Median)	Years (lower 95% CI)	Years (upper 95% CI)
50% abundance	2%	98%	26	18	3	86
25% abundance	5%	95%	37	31	7	91
12.5% abundance	9%	91%	46	43	13	95

Leatherback Table 2: Probability (with 95% credible intervals [CI]) of the population reaching abundance thresholds at 5, 10, 25, 50, and 100 years from final data year (2017).

Abundance Threshold	yr 5	yr 10	yr 25	yr 50	yr 100
50%	12%	36%	68%	87%	98%
lower 95% CI	11%	35%	67%	87%	97%
upper 95% CI	13%	36%	69%	88%	98%
25%	0%	8%	45%	76%	95%
lower 95% CI	0%	7%	44%	75%	95%
upper 95% CI	1%	8%	46%	76%	96%
12.5%	0%	1%	22%	61%	91%
lower 95% CI	0%	1%	21%	60%	90%
upper 95% CI	0%	1%	23%	62%	91%

6. Population growth rates: Bayesian model estimates provide an index of population growth using the best available index of population abundance derived from nest count data. Estimating true population growth rates would require additional data or assumptions about the population age distribution. Rates reflect the long-term trend estimated using the Annual Female Count data described above. For *r*, if values are positive then growth is positive; if values are negative then growth is negative. For λ lambda, if values are greater than 1 then growth is positive; if values are less than 1 then growth is negative.

Log growth rate of population (r):
      mean: -0.053
      median: -0.053

      variance: 0.003

      95% CI: -0.164 to 0.059

Finite rate of increase (λ):
      mean: 0.949

      median: 0.948

      95% CI: 0.849 to 1.061

REFERENCES

Allen, C. D., G. E. Lemons, T. Eguchi, R. A. LeRoux, C. C. Fahy, P. H. Dutton, S. H. Peckham, and J. A. Seminoff. 2013. Stable isotope analysis reveals migratory origin of loggerhead turtles in the Southern California Bight. Marine Ecology Progress Series **472**:275-285.

Benson, S. R., T. Eguchi, D. G. Foley, K. A. Forney, H. Bailey, C. Hitipeuw, B. P. Samber, R. F. Tapilatu, V. Rei, and P. Ramohia. 2011. Large-scale movements and high-use areas of western Pacific leatherback turtles, Dermochelys coriacea. Ecosphere **2**:1-27.

Bolten, A. B. 2003. Variation in sea turtle life history patterns: neritic vs. oceanic developmental stages. The biology of sea turtles **2**:243-257.

Bowen, B. 2003. What is a loggerhead turtle? The genetic perspective. Loggerhead sea turtles. Smithsonian Institution Press, Washington, DC:7-27.

Boyd, C., D. P. DeMaster, R. S. Waples, E. J. Ward, and B. L. Taylor. 2017. Consistent extinction risk assessment under the US Endangered Species Act. Conservation Letters **10**:328-336.

Briscoe, D., D. Parker, G. Balazs, M. Kurita, T. Saito, H. Okamoto, M. Rice, J. Polovina, and L. Crowder. 2016a. Active dispersal in loggerhead sea turtles (Caretta caretta) during the 'lost years'. Proc. R. Soc. B **283**:20160690.

Briscoe, D., D. Parker, S. Bograd, E. Hazen, K. Scales, G. Balazs, M. Kurita, T. Saito, H. Okamoto, and M. Rice. 2016b. Multi-year tracking reveals extensive pelagic phase of juvenile loggerhead sea turtles in the North Pacific. Movement ecology **4**:23.

Burgman, M. A., S. Ferson, and H. R. Akçakaya. 1993. Risk assessment in conservation biology. Springer Science & Business Media.

CEFAS. 2002. Review of three simulation models for sea turtle biology and management in the Pacific.*in* Independent System for Peer Review, editor. The Centre for Environment, Fisheries & Aquaculture Science, University of Miami, Miami, FL.

CEFAS. 2009. Review of Impacts of Potential Increases in Hawaii Shallow-set Swordfish Longline Effort on Sea Turtle Populations.*in* Center for Independent Experts Independent System for Peer Review, editor. The Centre for Environment, Fisheries & Aquaculture Science, University of Miami, Miami, FL.

Chaloupka, M. 2002a. Development of a Stochastic Metapopulation Model for the Western Pacific Leatherback Sea Turtle Stock: Background Material and Model Documentation. National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Honolulu, Hawaii.

Chaloupka, M. 2002b. Development of a Stochastic Population Model for the Northwestern Pacific Loggerhead Sea Turtle Stock: Background Material and Model Documentation. National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Honolulu, Hawaii.

Chaloupka, M. 2002c. Stochastic simulation modelling of southern Great Barrier Reef green turtle population dynamics. Ecological modelling **148**:79-109.

Chaloupka, M., N. Kamezaki, and C. Limpus. 2008. Is climate change affecting the population dynamics of the endangered Pacific loggerhead sea turtle? Journal of Experimental Marine Biology and Ecology **356**:136-143.

Conant, T. A., P. H. Dutton, T. Eguchi, S. P. Epperly, C. C. Fahy, M. H. Godfrey, S. L. MacPherson, E. E. Possardt, B. A. Schroeder, and J. A. Seminoff. 2009. Loggerhead sea turtle (Caretta caretta) 2009 status review under the US Endangered Species Act. Report of the loggerhead biological review Team to the National Marine Fisheries Service **222**:5-2.

Cortés, E. 1999. A stochastic stage-based population model of the sandbar shark in the western North Atlantic. Pages 115-136 *in* American Fisheries Society Symposium.

Curtis, K. A., J. E. Moore, and S. R. Benson. 2015. Estimating limit reference points for western Pacific leatherback turtles (Dermochelys coriacea) in the US west coast EEZ. PloS one **10**:e0136452.

Dennis, B., P. L. Munholland, and J. M. Scott. 1991. Estimation of growth and extinction parameters for endangered species. Ecological monographs **61**:115-143.

Gaspar, P., and M. Lalire. 2017. A model for simulating the active dispersal of juvenile sea turtles with a case study on western Pacific leatherback turtles. PloS one **12**:e0181595.

Hays, G. C. 2004. Good news for sea turtles. Trends in Ecology & Evolution **19**:349-351.

Holmes, E., E. Ward, and M. Scheuerell. 2014. Analysis of multivariate time-series using the MARSS package. NOAA Fisheries, Northwest Fisheries Science Center **2725**:98112.

Holmes, E. E. 2001. Estimating risks in declining populations with poor data. Proceedings of the National Academy of Sciences **98**:5072-5077.

Holmes, E. E., and W. F. Fagan. 2002. Validating population viability analysis for corrupted data sets. Ecology **83**:2379-2386.

Holmes, E. E., E. J. Ward, and K. Wills. 2012. MARSS: Multivariate Autoregressive State-space Models for Analyzing Time-series Data. R journal **4**.

Kellner, K. 2015. jagsUI: A Wrapper Around'rjags' to Streamline'JAGS'Analyses. R package version 1.3. 7.

Kendall, B. E. 2009. The diffusion approximation overestimates the extinction risk for count-based PVA. Conservation Letters **2**:216-225.

Kobayashi, D. R., I.-J. Cheng, D. M. Parker, J. J. Polovina, N. Kamezaki, and G. H. Balazs. 2011. Loggerhead turtle (Caretta caretta) movement off the coast of Taiwan: characterization of a hotspot in the East China Sea and investigation of mesoscale eddies. ICES Journal of Marine Science **68**:707-718.

Kobayashi, D. R., J. J. Polovina, D. M. Parker, N. Kamezaki, I.-J. Cheng, I. Uchida, P. H. Dutton, and G. H. Balazs. 2008. Pelagic habitat characterization of loggerhead sea turtles, Caretta caretta, in the North Pacific Ocean (1997–2006): insights from satellite tag tracking and remotely sensed data. Journal of Experimental Marine Biology and Ecology **356**:96-114.

Koch, V., H. Peckham, A. Mancini, and T. Eguchi. 2013. Estimating at-sea mortality of marine turtles from stranding frequencies and drifter experiments. PloS one **8**:e56776.

Lewison, R. L., L. B. Crowder, A. J. Read, and S. A. Freeman. 2004a. Understanding impacts of fisheries bycatch on marine megafauna. Trends in Ecology & Evolution **19**:598-604.

Lewison, R. L., S. A. Freeman, and L. B. Crowder. 2004b. Quantifying the effects of fisheries on threatened species: the impact of pelagic longlines on loggerhead and leatherback sea turtles. Ecology letters **7**:221-231.

Matsuzawa, Y., N. Kamezaki, T. Ishihara, K. Omuta, H. Takeshita, K. Goto, T. Arata, H. Honda, K. Kameda, and Y. Kashima. 2016. Fine-scale genetic population structure of loggerhead turtles in the Northwest Pacific. Endangered Species Research **30**:83-93.

Morris, W. F., and D. F. Doak. 2002. Quantitative conservation biology. Sinauer, Sunderland, Massachusetts, USA.

NMFS. 2002. Biological Opinion on Authorization of Pelagic Fisheries under the Fishery Management Plan for Pelagic Fisheries of the Western Pacific Region. National Marine Fisheries Service, Pacific Islands Region, Protected Resources Division, Honolulu, HI.

NMFS. 2004. Summary Report of "Workshop on the Use of Population Models in Conservation of Sea Turtles" meeting held May 6-7, 2003 at the National Marine Fisheries Service PIFSC (Pacific Islands Fishery Science Center), Honolulu, Hawaii. National Marine Fisheries Service, PIFSC, Honolulu, Hawaii.

NMFS. 2008. Biological Opinion on Management Modifications for the Hawaii-based Shallow-set Longline Swordfish Fishery - Implementation of Amendment 18 to the Fishery Management Plan for Pelagic Fisheries of the Western Pacific Region. National Marine Fisheries Service, Pacific Islands Region, Protected Resources Division, Honolulu, HI.

NMFS. 2012. Biological Opinion on Continued Operation of the Hawaii-based Shallow-set Longline Swordfish Fishery - under Amendment 18 to the Fishery Management Plan for Pelagic Fisheries of the Western Pacific Region. National Marine Fisheries Service, Pacific Islands Region, Protected Resources Division, Honolulu, HI.

Okuyama, J., T. Kitagawa, K. Zenimoto, S. Kimura, N. Arai, Y. Sasai, and H. Sasaki. 2011. Trans-Pacific dispersal of loggerhead turtle hatchlings inferred from numerical simulation modeling. Marine biology **158**:2055-2063.

Peckham, S. H., D. M. Diaz, A. Walli, G. Ruiz, L. B. Crowder, and W. J. Nichols. 2007. Small-scale fisheries bycatch jeopardizes endangered Pacific loggerhead turtles. PloS one **2**:e1041.

Peckham, S. H., D. Maldonado-Diaz, V. Koch, A. Mancini, A. Gaos, M. T. Tinker, and W. J. Nichols. 2008. High mortality of loggerhead turtles due to bycatch, human consumption and strandings at Baja California Sur, Mexico, 2003 to 2007. Endangered Species Research **5**:171-183.

PIRO. 2018. Memorandum: Request for information in support of ESA section 7 consultation on the effects of Hawaii-based longline fisheries on ESA-listed species. Pacific Islands Regional Office, Honolulu, HI.

Plummer, M. 2003. JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling.*in* Proceedings of the 3rd international workshop on distributed statistical computing. Vienna, Austria.

Plummer, M., N. Best, K. Cowles, and K. Vines. 2006. CODA: convergence diagnosis and output analysis for MCMC. R news **6**:7-11.

R Development Core Team. 2012. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

Reed, J. M., D. D. Murphy, and P. F. Brussard. 1998. Efficacy of population viability analysis. Wildlife Society Bulletin (1973-2006) **26**:244-251.

Snover, M. L. 2008. Assessment of the population-level impacts of potential increases in marine turtle interactions resulting from a Hawaii Longline Association proposal to expand the Hawaii-based shallow-set fishery. National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Pacific Islands Fisheries Science Center, Marine Turtle Assessment Program.

Snover, M. L., and S. S. Heppell. 2009. Application of diffusion approximation for risk assessments of sea turtle populations. Ecological Applications **19**:774-785.

Tapilatu, R. F., P. H. Dutton, M. Tiwari, T. Wibbels, H. V. Ferdinandus, W. G. Iwanggin, and B. H. Nugroho. 2013. Long-term decline of the western Pacific leatherback, Dermochelys coriacea: a globally important sea turtle population. Ecosphere **4**:1-15.

Van Houtan, K. 2011. Assessing the impact of fishery actions to marine turtle populations in the North Pacific using classical and climate-based models. NOAA Fisheries, Pacific Islands Science Center, IR-11-024, Honolulu, HI USA.

Van Houtan, K. S., and J. M. Halley. 2011. Long-term climate forcing in loggerhead sea turtle nesting. PloS one **6**:e19043.

Wallace, B. P., A. D. DiMatteo, B. J. Hurley, E. M. Finkbeiner, A. B. Bolten, M. Y. Chaloupka, B. J. Hutchinson, F. A. Abreu-Grobois, D. Amorocho, and K. A. Bjorndal. 2010a. Regional management units for marine turtles: a novel framework for prioritizing conservation and research across multiple scales. PloS one **5**:e15465.

Wallace, B. P., R. L. Lewison, S. L. McDonald, R. K. McDonald, C. Y. Kot, S. Kelez, R. K. Bjorkland, E. M. Finkbeiner, and L. B. Crowder. 2010b. Global patterns of marine turtle bycatch. Conservation Letters **3**:131-142.

WPRFMC. 2004. Western Pacific Regional Fisheries Management Council Sea Turtle
    Workshop Proceedings.

Appendix II: Parameter Estimates and Sources

Sp	Param	Description	Estimate	SE	Low	Upp	Pop	Source	Justification/Notes
Dc	Linf	VBGF: average size of nesting females (SCL in cm)	142.7	1.64			Mix	Jones et al. (2011) *JEMB*	best available growth model, both globally and for W. Pacific specifically
Dc	k	VBGF: Brody growth coefficient in VBGF	0.2262	0.021			Mix	Jones et al. (2011) *JEMB*	best available growth model, both globally and for W. Pacific specifically
Dc	t0	VBGF: hypothetical age animals would be length = 0	-0.17	0.07			Mix	Jones et al. (2011) *JEMB*	best available growth model, both globally and for W. Pacific specifically
Dc	Amat	VBGF: age at maturity (97.5% of Linf in VBGF)	16.1				Mix	Jones et al. (2011) *JEMB*	best available growth model, both globally and for W. Pacific specifically (Age at maturity confirmed recently with skeletochronology by L. Avens et al. (2020) in *Marine Biology*)
Dc	SCL_slo	slope: SCL conversion to CCL	1.04					Tucker & Frazer (1991) *Herpetologica*	best available but didn't end up needing, as no CCL measurements for Dc
Dc	SCL_int	intercept: SCL conversion to CCL	2.04					Tucker & Fraser (1991) *Herpetologica*	best available but didn't end up needing, as no CCL measurements for Dc
Dc	CF	clutch frequency = # of nests laid by a female in a season	5.5	SD 1.6	3	10	W. Pac	Tapilatu et al. (2013) *Ecosphere*	most recent estimate of clutch frequency
Dc	CS	clutch size = # of eggs laid in one nest	77.9	2.35			W. Pac	Tapilatu & Tiwari (2007) *Copeia*	most recent estimate of clutch size using direct count observations

Sp	Param	Description	Estimate	SE	Low	Upp	Pop	Source	Justification/Notes
Dc	RI	remigration interval = # of years between nesting years	3.06				W. Pac	derived from Lontoh (2014) master's thesis	most recent estimate; specific to CNP foraging area; estimated Poisson scale parameter was 2.36
Dc	Pj	survival of juveniles (probability from one age to next)	0.81	0.03			WP	Jones et al. (2012) *PLoS One*	best available; based on population growth model calculating natural mortality based on known age at maturity
Dc	Pa	survival of adults (probability from one age to next)	0.893	0.013			CB	Dutton et al. (2005) *Biol Cons*	Jones et al. (2012) was too low due to conflating fisheries & natural mortality; thus, use Dutton et al. (2005) estimate as best available for a growing population at the time so probably a better estimate of what Pa actually is
Dc	PF	proportion female = sex ratio	0.73					Benson et al. (2011) *Ecosphere*	Using Benson et al 2011 (Ecosphere) 27:10 female:male (27 females and 10 males captured/sat-tagged) as best (only) available estimate even though CA foragers different foraging stock and size ranges that are not necessarily representative of Dc taken in SSLL
Cc	CCL_slo	slope: CCL conversion to SCL	0.9084					SM model of Zug (1995)	best available SCL/CCL measurements data for CNP & specific sizes that interact w/ SSLL

Sp	Param	Description	Estimate	SE	Low	Upp	Pop	Source	Justification/Notes
Cc	CCL_int	intercept: CCL conversion to SCL	0.0303					SM model of Zug (1995)	best available SCL/CCL measurements data for CNP & specific sizes that interact w/ SSLL
Cc	Pj	survival of juveniles (probability from one age to next)	0.8	0.031	0.74	0.86	Mix	Snover (2008) PIFSC IR-08-010; Conant et al. (2009)	these two papers are best available and generally accepted survival rates for the parameter; Conant et al. (2009) had mortality rates estimated from population model; Snover (2008) range includes Conant et al. (2009)
Cc	Pa	survival of adults (probability from one age to next)	0.895	0.028	0.84	0.95	Mix	Snover (2008) PIFSC IR-08-010; Conant et al (2009)	best available and generally accepted survival rates for the parameter
Cc	PF	proportion female = sex ratio	0.65				Mix	Snover (2008) PIFSC IR-08-010; Conant et al. (2009)	best available and generally accepted sex ratio and consistent with expert consensus for this population given lack of empirical data; Conant et al. (2009) had mortality rates estimated from population model; Snover (2008) range includes Conant et al. (2009)
Cc	CF	clutch frequency = # of nests laid by a female in a season	4.6	SD 1.1			NP	Hatase et al. (2013) *Ecology*	most recent available; study based on Yakushima nesters which is the driver of NP pop (52% for 3 beaches in our analysis)

Sp	Param	Description	Estimate	SE	Low	Upp	Pop	Source	Justification/Notes
Cc	CS	clutch size = # of eggs laid in one nest	122	SD 18.4	83.5	148	NP	Hatase et al. (2013) *Ecology*	most recent available; study based on Yakushima nesters which is the driver of NP pop (52% for 3 beaches in our analysis)
Cc	RI	remigration interval = # of years in between nesting years	3.3	2.3	1	10	NP	Hatase et al. (2013) *Ecology*	most recent available; study based on Yakushima nesters which is the driver of NP pop (52% for three beaches in our analysis)
Cc	Linf	VBGF: average size of nesting females (SCL in cm)	86.9				NP	ZS model from data in Turner-Tomaszewicz (2015) *Biol Cons*	best available data used to construct VBGF model
Cc	k	VBGF: Brody growth coefficient in VBGF	0.09				NP	ZS model from data in Turner-Tomaszewicz (2015) *Biol Cons*	best available data used to construct VBGF model
Cc	t0	VBGF: hypothetical age animals would be length = 0	-2.467				NP	ZS model from data in Turner-Tomaszewicz (2015) *Biol Cons*	best available data used to construct VBGF model
Cc	Amat	Zach generate. VBGF: age at maturity. # of ages as a juvenile (to get to Amat)	37.9				NP	ZS model of Loggerhead growth; Zug (1995) data, Turner-Tomascewiz (2015) *Biol Cons* data, & Hatase et al. (2002) *STAJ* nesters data	Using 85 cm ± 4.5 cm (SD) as average nesting SCL length (Linf) from Hatase et al. (2002) *MEPS*
Cc	Linf_L0	VBGF: average size of nesting females (SCL in cm)	80.4474				NP	ZS model from data in Turner-Tomaszewicz (2015) *Biol Cons*	best available data used to construct VBGF model

Sp	Param	Description	Estimate	SE	Low	Upp	Pop	Source	Justification/Notes
Cc	k_L0	VBGF: Brody growth coefficient in VBGF	0.1396				NP	ZS model from data in Turner-Tomaszewicz (2015) *Biol Cons*	best available data used to construct VBGF model
Cc	L0	VBGF: length at birth (hatching)	4.7363				NP	ZS model from data in Turner-Tomaszewicz (2015) *Biol Cons*	best available data used to construct VBGF model
Cc	Amat	VBGF: age at maturity. # of ages as a juvenile (to reach Amat)	26.4951				NP	ZS model of Loggerhead growth; Zug (1995) data, Turner-Tomascewiz (2015) *Biol Cons* data, & Hatase et al. (2002) STAJ nesters data	Using 85 cm ± 4.5 cm (SD) as average nesting SCL length (Linf) from Hatase et al. (2002) *MEPS*

Sp = species
Param = parameter
SE = standard error (except where SD is indicated for standard deviation)
Low = lower value if a range is known
Upp = upper value if a range is known
Pop = population of leatherback turtles
Dc = Dermochelys coriacea (leatherback sea turtle)
Cc = Caretta caretta (loggerhead sea turtle)
Pop "Mix" = mixed population of leatherback turtles; not only western Pacific nesting population
Pop "CB" = Caribbean nesting population of leatherback turtles
Pop "W. Pac" = western Pacific nesting population of leatherback turtles
Pop "N. Pac" = portion of western Pacific nesting population of leatherback turtles found
        foraging in the North Pacific
CNP = Central North Pacific foraging area used by western Pacific leatherback turtles
ZS = Zach Siders (coauthor on this report; produced loggerhead growth model used herein)
VBGF = von Bertalanffy growth function
CCL = curved carapace length
SCL = straight carapace length

References

Avens L, Goshe LR, Zug GR, Balazs GH, Benson SR, Harris H. 2020. Regional comparison of leatherback sea turtle maturation attributes and reproductive longevity. Marine Biology. 167(1):4.

Benson SR, Eguchi T, Foley DG, Forney KA, Bailey H, Hitipeuw C, Samber BP, Tapilatu RF, Rei V, Ramohia P. 2011. Large-scale movements and high-use areas of western Pacific leatherback turtles, Dermochelys coriacea. Ecosphere. 2(7):1-27.

Conant TA, Dutton PH, Eguchi T, Epperly SP, Fahy CC, Godfrey MH, MacPherson SL, Possardt EE, Schroeder BA, Seminoff JA. 2009. Loggerhead sea turtle (Caretta caretta) 2009 status review under the US Endangered Species Act. Report of the loggerhead biological review Team to the National Marine Fisheries Service. 222:5-2.

Dutton DL, Dutton PH, Chaloupka M, Boulon RH. 2005. Increase of a Caribbean leatherback turtle Dermochelys coriacea nesting population linked to long-term nest protection. Biol Cons. 126(2):186-194.

Hatase H, Goto K, Sato K, Bando T, Matsuzawa Y, Sakamoto W. 2002. Using annual body size fluctuations to explore potential causes for the decline in a nesting population of the loggerhead turtle Caretta caretta at Senri Beach, Japan. Mar Ecol Prog S. 245:299-304.

Hatase H, Omuta K, Tsukamoto K. 2013. A mechanism that maintains alternative life histories in a loggerhead sea turtle population. Ecol. 94(11):2583-2594.

Jones TT, Bostrom BL, Hastings MD, Van Houtan KS, Pauly D, Jones DR. 2012. Resource requirements of the Pacific leatherback turtle population. PLoS One. 7(10).

Jones TT, Hastings MD, Bostrom BL, Pauly D, Jones DR. 2011. Growth of captive leatherback turtles, Dermochelys coriacea, with inferences on growth in the wild: Implications for population decline and recovery. J Exper Mar Biol Ecol. 399(1):84-92.

Lontoh DN. 2014. Variation in tissue stable isotopes, body size, and reproduction of western pacific leatherback turtles. Master's Thesis, San José State University.

Snover ML. 2008. Assessment of the population-level impacts of potential increases in marine turtle interactions resulting from a Hawaii longline association proposal to expand the Hawaii-based shallow-set fishery. National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Pacific Islands Fisheries Science Center, Marine Turtle Assessment Program.

Tapilatu RF, Dutton PH, Tiwari M, Wibbels T, Ferdinandus HV, Iwanggin WG, Nugroho BH. 2013. Long-term decline of the western pacific leatherback, dermochelys coriacea: A globally important sea turtle population. Ecosphere. 4(2):1-15.

Tapilatu RF, Tiwari M. 2007. Leatherback turtle, Dermochelys coriacea, hatching success at Jamursba-medi and Wermon beaches in Papua, Indonesia. Chelonian Conservation and Biology. 6(1):154-158.

Tomaszewicz CNT, Seminoff JA, Avens L, Goshe LR, Peckham SH, Rguez-Baron JM, Bickerman K, Kurle CM. 2015. Age and residency duration of loggerhead turtles at a north pacific bycatch hotspot using skeletochronology. Biological conservation. 186:134-142.

Tucker AD, Frazer NB. 1991. Reproductive variation in leatherback turtles, Dermochelys coriacea, at Culebra National Wildlife Refuge, Puerto Rico. Herpetologica.115-124.

Zug GR, Balazs GH, Wetherall JA. 1995. Growth in juvenile loggerhead seaturtles (Caretta caretta) in the north Pacific pelagic habitat. Copeia. 1995(2):484-487.

Appendix III: R Code

A.   Integrated Take Model Code

```
#@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
#@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
#
#       PIFSC Hawaiian SSLL Sea Turtle Take Model
#
#@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
#@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
# Date Initialized: August 3, 2019
# Compiler: Zach Siders
# Authors: Tomo Eguchi, Summer Martin, Zach Siders, T. Todd Jones


###----------------------------------------------------
#               Initialization
###----------------------------------------------------
        #devtools::install_github( "James-Thorson/Conway-Maxwell-Poisson" )
        library(CMP)
        library(compoisson)
        library(mvtnorm)
        library(truncnorm)
        library(doParallel)  #Foreach Parallel Adaptor
        library(foreach)     #Provides foreach looping construct
        library(abind)
        library(jagsUI)
        library(coda)
        library(tidyverse) #must be loaded after compoisson due to masking of MASS::select
        library(loo)
        library(rstan)
        rstan_options(auto_write = TRUE)
        options(mc.cores = parallel::detectCores())
```

```
main.folder <- "/Volumes/HDD/Users/Zach/Documents/Projects/NOAA_BioOp_Take_LH_LB/Models/Integrated/"

#####
#####
redo <- FALSE #FLAG TO RERUN ALL PREVIOUS OPS
#####
#####

data.path <- paste0(main.folder,"Data/")
imput.path <- paste0(main.folder,"Imputation/")
trend.path <- paste0(main.folder,"Trend/")
table.path <- paste0(main.folder,"Output/Tables/")
fig.path <- paste0(main.folder,"Output/Figures/")
sim.path <- paste0(main.folder,"Output/Simulations/")

if(!dir.exists(data.path)) dir.create(data.path)
if(!dir.exists(imput.path)) dir.create(imput.path)
if(!dir.exists(trend.path)) dir.create(trend.path)
if(!dir.exists(paste0(main.folder,"Output"))) dir.create(paste0(main.folder,"Output"))
if(!dir.exists(table.path)) dir.create(table.path)
if(!dir.exists(fig.path)) dir.create(fig.path)
if(!dir.exists(sim.path)) dir.create(sim.path)

source(paste0(main.folder,"take_helper_Fn.R"))

###----------------------------------------------------------------
#      LOGGERHEAD GROWTH (led by Zach Siders)
###----------------------------------------------------------------
#Collaborators: Rob Ahrens, Nicholas Ducharme-Barth, T. Todd Jones, Summer Martin, Calandra N. Turner Tomaszewicz

check.prerun <- file.exists(paste0(data.path,"VBGM_HMC_sims.Rdata"))
if(!check.prerun | redo){
```

```
CC.growth <- read.csv(paste0(data.path, 'NPCc CCL at est age.csv'))

#Hatchling size (Nishimura 1967)
CC.hatchling <- read.csv(paste0(data.path, "Nishimura_1967_Hatchling.csv"))

hatchling_size <- mean(CC.hatchling$Length_cm)
hatchling_sd <- sd(CC.hatchling$Length_cm)

CC.nester <- read.csv(paste0(data.path,"Hatase_2002_Nesters.csv"))

gen_nester <- unlist(apply(CC.nester, 1, function(x) {rnorm(x[3], x[1], x[2])}))
nester_size <- mean(gen_nester)/10
nester_sd <- sd(gen_nester)/10

CC.growth.stan.dat <- list(n_obs = nrow(CC.growth),
        age = CC.growth$Est_Age+0.001,
        l = CC.growth$CCL,
        seq_ages = seq(0, max(CC.growth$Est_Age), by=0.1),
        nseq = length(seq(0, max(CC.growth$Est_Age), by=0.1)),
        nester_size = nester_size,
        nester_sd = nester_sd,
        n_hatchlings = nrow(CC.hatchling),
        hatchling_size = CC.hatchling$Length_cm)

CC.growth.stan.fit.l0 <- stan(model_code=vbgm_stan_l0_ln,
        data = CC.growth.stan.dat,
        init = init.vbgm.l0,
        warmup = 5000,
        iter = 7500)

CC.growth.stan.sims.l0 <- rstan::extract(CC.growth.stan.fit.l0)
```

```
                CC.VBGF <- with(CC.growth.stan.sims.l0, list(model="Lknot", Linf = median(Linf), K = median(K), Lknot =
median(Lknot), Amat=median(Amat)))

                save(CC.growth.stan.sims.l0, file=paste0(data.path,"VBGM_HMC_sims.Rdata"))
        }else{
                load(file=paste0(data.path,"VBGM_HMC_sims.Rdata"))
                CC.VBGF <- with(CC.growth.stan.sims.l0, list(model="Lknot", Linf = median(Linf), K = median(K), Lknot =
median(Lknot), Amat=median(Amat)))
        }
###-----------------------------------------------------
#               IMPUTATION (led by Tomo Eguchi)
###-----------------------------------------------------
        check.prerun <- file.exists(paste0(imput.path, "N_imput.Rdata"))
        if(!check.prerun | redo){
                ###-------------------------------------------------
                #               Process Raw Observations of Nests (DC)
                ###-------------------------------------------------

                        period.JM <- 12
                        period.W <- 6
                        maxN <- 10000

                        all.years <- 2001:2017
                        idx <- 1:length(all.years)

                        year.begin.JM <- 2001
                        year.end <- 2017
                        data.jags.JM <- data.extract(location = "JM",
                                        year.begin = year.begin.JM,
                                        year.end = year.end,
                                        file.path = data.path)

                        JM.keep <- 2001:2017
```

```r
idx.JM <- idx[all.years %in% JM.keep]
n.keep.JM <- length(idx.JM)
dt.JM <- idx.JM[2:length(idx.JM)] - idx.JM[1:(length(idx.JM)-1)]


year.begin.W <- 2006
data.jags.W <- data.extract(location = "W",
                    year.begin = year.begin.W,
                    year.end = year.end,
                     file.path = data.path)
W.keep <- c(2006, 2007, 2008, 2009, 2010, 2011, 2012, 2016, 2017)
idx.W <- idx[all.years %in% W.keep]
n.keep.W <- length(idx.W)
dt.W <- idx.W[2:length(idx.W)] - idx.W[1:(length(idx.W)-1)]


#Combine datasets for analysis
# JM has more data than W, so we need to pad W data
y.W <- rbind(array(data = NA,
              dim = c(nrow(data.jags.JM$jags.data2$y) - nrow(data.jags.W$jags.data2$y),
                   ncol(data.jags.JM$jags.data2$y))),
          data.jags.W$jags.data2$y)

y <- cbind(as.vector(t(data.jags.JM$jags.data2$y)), as.vector(t(y.W)))
y.raw <- as.data.frame(apply(y,2,exp))
colnames(y.raw) <- c("JM","W")
y.raw$year.frac <- rep(2001:2017, each=12) + seq(1,12)/12
save(y.raw, file=paste0(data.path,"DC_raw_nests_month.Rdata"))

years <- rep(2001:2017, each = 12)
n.years <- 17

# for estimating U  ######
n.timeseries <- ncol(y)
###--------------------------------------------------
```

```
#                    JAGS Implementation
###---------------------------------------------------

        jags.data <- list(y = y,
      m = rep(1:12, times = n.years),
      n.steps = nrow(y),
      n.months = 12,
      pi = pi,
      period = c(period.JM, period.W),
      n.timeseries = n.timeseries,
      n.years = n.years)

        jags.params <- c("c", "beta.cos", "beta.sin",
      'sigma.X', "sigma.y", "N",
       "y", "X", "deviance")

        MCMC.params <- list(n.chains = 5,
n.samples = 100000,
n.burnin = 50000,
n.thin = 5)

         jm <- jags(jags.data,
         inits = NULL,
         parameters.to.save= jags.params,
         model.file = paste0(main.folder,'model_norm_norm_Four_imputation.txt'),
         n.chains = MCMC.params$n.chains,
         n.burnin = MCMC.params$n.burnin,
         n.thin = MCMC.params$n.thin,
         n.iter = MCMC.params$n.samples,
         DIC = T, parallel=T)

         save(jm, file=paste0(imput.path,"JAGS_model_run.Rdata"))
###---------------------------------------------------
```

```
#                    Summary of JAGS model
###------------------------------------------------------

        Ns.stats.JM <- data.frame(time = year.begin.JM:year.end,
                low = as.vector(t(jm$q2.5$N[,1])),
                median = as.vector(t(jm$q50$N[,1])),
                high = as.vector(t(jm$q97.5$N[,1])))
        Ns.stats.JM$location <- "Jamursba-Medi"

        Ns.stats.W <- data.frame(time = year.begin.JM:year.end,
                low = as.vector(t(jm$q2.5$N[,2])),
                median = as.vector(t(jm$q50$N[,2])),
                high = as.vector(t(jm$q97.5$N[,2])))
        Ns.stats.W$location <- "Wermon"

        Ns.stats <- rbind(Ns.stats.JM, Ns.stats.W)

        save(Ns.stats.JM, Ns.stats.W, file=paste0(imput.path, "N_imput.Rdata"))
    }else{
        load(paste0(imput.path, "N_imput.Rdata"))
    }
###------------------------------------------------------
#           Historical ANE (led by Zach Siders)
###------------------------------------------------------
    check.prerun <- file.exists(paste0(data.path,"historical_ANE.csv"))
    if(!check.prerun | redo){
        ###------------------------------------------------------
        #                Take Demographics Data
        ###------------------------------------------------------
            #-------
            # Historical Take

            td.dat <- read.csv(paste0(data.path,"turtle_l_m.csv"), stringsAsFactors=FALSE)
```

```
colnames(td.dat) <- c("Year", "Spp", "M.low", "M.high", "Len")

td.dat <- td.dat[td.dat$Spp!="" & td.dat$Year != 2019,]
td.dat <- td.dat[td.dat$Spp %in% c("Leatherback", "Loggerhead"),]

DC.VBGF <- list(Linf = 142.7, K = 0.2262, tknot=-0.17, Amat = 16.1)
CC.VBGF <- list(Linf = 80.4473850, K = 0.1396317, Lknot=4.7363329, Amat = 26.4950786)

DC.Pj <- 0.81
DC.Pa <- 0.893
CC.Pj <- 0.8
CC.Pa <- 0.895

DC.PF <- 0.73
CC.PF <- 0.65
###-------------------------------------------------
#                 Individual Characteristics
###-------------------------------------------------

pred.Age <- seq(0,100, by=0.01) #sequence of ages to back calculate over
DC.Lpred <- with(DC.VBGF, Linf * (1-exp(-K*(pred.Age-tknot))))
CC.Lpred <- with(CC.VBGF, Linf - (Linf-Lknot)*exp(-K*pred.Age))

td.dat$Len[is.na(td.dat$Len) & td.dat$Spp == "Leatherback"] <- median(td.dat$Len[td.dat$Spp ==
"Leatherback"], na.rm=T)
td.dat$Len[is.na(td.dat$Len) & td.dat$Spp == "Loggerhead"] <- median(td.dat$Len[td.dat$Spp ==
"Loggerhead"], na.rm=T)

td.dat$M.mu <- rowMeans(td.dat[,c("M.low","M.high")], na.rm=T)
td.dat$M.mu[is.nan(td.dat$M.mu)] <- mean(td.dat$M.mu[!is.nan(td.dat$M.mu) & td.dat$Spp ==
td.dat$Spp[is.nan(td.dat$M.mu)]])
```

```
td.dat$Age <- NA
td.dat$Age[td.dat$Spp == "Leatherback"] <- sapply(td.dat$Len[td.dat$Spp == "Leatherback"], function(x)
{pred.Age[which.min(abs(x - DC.Lpred))]})
td.dat$Age[td.dat$Spp == "Loggerhead"] <- sapply(td.dat$Len[td.dat$Spp == "Loggerhead"], function(x)
{pred.Age[which.min(abs(x - CC.Lpred))]})

#determine the animals stage based on maturity
td.dat$Stage <- NA
td.dat$Stage[td.dat$Spp == "Leatherback"] <- ifelse(td.dat$Age[td.dat$Spp == "Leatherback"] >
DC.VBGF$Amat, "A", "J")
td.dat$Stage[td.dat$Spp == "Loggerhead"] <- ifelse(td.dat$Age[td.dat$Spp == "Loggerhead"] >
CC.VBGF$Amat, "A", "J")

#calculate the number of years until maturity
td.dat$YatLarge <- NA
td.dat$YatLarge[td.dat$Spp == "Leatherback"] <- DC.VBGF$Amat - td.dat$Age[td.dat$Spp == "Leatherback"]
td.dat$YatLarge[td.dat$Spp == "Loggerhead"] <- CC.VBGF$Amat - td.dat$Age[td.dat$Spp == "Loggerhead"]
###-------------------------------------------------
#                 back project for the Remigration Interval
###-------------------------------------------------

#back project the RI
td.dat$YatLargeR <- round(td.dat$YatLarge)
td.dat$YatLargeR[td.dat$YatLargeR < 0] <- 0

td.dat$Nest1 <- td.dat$Year + td.dat$YatLargeR
td.dat$Nest2 <- td.dat$Nest1 + 3
td.dat$Nest3 <- td.dat$Nest2 + 3
td.dat$Nest4 <- td.dat$Nest3 + 3
td.dat$Nest5 <- td.dat$Nest4 + 3
td.dat$Nest6 <- td.dat$Nest5 + 3
td.dat$Nest7 <- td.dat$Nest6 + 3
###-------------------------------------------------
```

```r
                #               Convert to ANEs
            ###-------------------------------------------------

                    ANEyr <- td.dat[,paste0("Nest",1:7)] - td.dat$Year
                    ANEproj <- ANEyr
                    ANEproj$Nest1 <- (ifelse(td.dat$Spp == "Leatherback", DC.Pj, CC.Pj) ^ ANEproj$Nest1) * ifelse(td.dat$Spp
== "Leatherback", DC.PF, CC.PF) * td.dat$M.mu
                    ANEproj[,-1] <- ifelse(td.dat$Spp == "Leatherback", DC.Pa, CC.Pa) ^ ANEproj[,-1] * ANEproj$Nest1

                    ANEproj.nFD <- ANEyr
                    ANEproj.nFD$Nest1 <- (ifelse(td.dat$Spp == "Leatherback", DC.Pj, CC.Pj) ^ ANEproj.nFD$Nest1)
                    ANEproj.nFD[,-1] <- ifelse(td.dat$Spp == "Leatherback", DC.Pa, CC.Pa) ^ ANEproj.nFD[,-1] *
ANEproj.nFD$Nest1

                    ANEp <- data.frame(nestyr = unlist(td.dat[,paste0("Nest",1:7)]),
                            ANE = unlist(ANEproj),
                            Spp = rep(td.dat$Spp, 7))

                    ANEtab <- aggregate(ANE ~ Spp + nestyr, data=ANEp, FUN=sum)

                    write.csv(ANEtab, file=paste0(data.path,"historical_ANE.csv"), row.names=FALSE)
        }else{
            ANEtab <- read.csv(paste0(data.path,"historical_ANE.csv"))
        }


check.prerun <- file.exists(paste0(data.path, "take_demo_mvn.Rdata"))

if(!check.prerun | redo){
        ###-------------------------------------------------
        #               Fit multivariate take demographics
        ###-------------------------------------------------
                tab.spp <- as.data.frame(with(td.dat, table(Year, Spp)))
```

```
DC.td.df <- na.omit(td.dat[td.dat$Spp=="Leatherback",])

DC.td.tab <- tab.spp[tab.spp$Spp=="Leatherback",c("Year","Spp","Freq")]

DC.td.dat <- list(N = nrow(DC.td.df),
        x = cbind(log(DC.td.df$L), boot::logit(DC.td.df$M.mu)),
        nyear = nrow(DC.td.tab),
        year = as.integer(factor(DC.td.df$Year)),
        rtl = DC.td.tab$Freq)
DC.td.fit <- stan(model_code = mvnorm,
        data = DC.td.dat,
        init = mv.DC.init,
        warmup = 5000,
        iter = 7500)
DC.td.sims <- rstan::extract(DC.td.fit)


###@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
        # LOGGERHEADS

CC.td.df <- na.omit(td.dat[td.dat$Spp=="Loggerhead",])
CC.td.df$M.mu[CC.td.df$M.mu==1] <- 0.999

CC.td.tab <- tab.spp[tab.spp$Spp=="Loggerhead",c("Year","Spp","Freq")]

CC.td.dat <- list(N = nrow(CC.td.df),
        x = cbind(log(CC.td.df$L), boot::logit(CC.td.df$M.mu)),
        nyear = nrow(CC.td.tab),
        year = as.integer(factor(CC.td.df$Year)),
        rtl = CC.td.tab$Freq)

CC.td.fit <- stan(model_code = mvnorm,
```

```
                        data = CC.td.dat,
                        init = mv.CC.init,
                        warmup = 5000,
                        iter = 7500)
            CC.td.sims <- rstan::extract(CC.td.fit)
###--------------------------------------------------
#              Summarize take Demographics
###--------------------------------------------------
            DC.mu0 <- median(DC.td.sims$mu0)
            DC.beta0 <- median(DC.td.sims$beta0)
            DC.beta1 <- median(DC.td.sims$beta1)
            DC.sigma <- apply(DC.td.sims$sigma, 2, median)
            DC.rho <- median(DC.td.sims$rho)
            DC.cov <- matrix(c(DC.sigma[1]^2, DC.sigma[1]*DC.sigma[2]*DC.rho, DC.sigma[1]*DC.sigma[2]*DC.rho,
DC.sigma[2]^2),2,2)


            CC.mu0 <- median(CC.td.sims$mu0)
            CC.beta0 <- median(CC.td.sims$beta0)
            CC.beta1 <- median(CC.td.sims$beta1)
            CC.sigma <- apply(CC.td.sims$sigma, 2, median)
            CC.rho <- median(CC.td.sims$rho)
            CC.cov <- matrix(c(CC.sigma[1]^2, CC.sigma[1]*CC.sigma[2]*CC.rho, CC.sigma[1]*CC.sigma[2]*CC.rho,
CC.sigma[2]^2),2,2)



            save(DC.mu0, DC.beta0, DC.beta1, DC.cov, CC.mu0, CC.beta0, CC.beta1, CC.cov,
file=paste0(data.path,"take_demo_mvn.Rdata"))
      }else{
            load(paste0(data.path,"take_demo_mvn.Rdata"))
      }
###----------------------------------------------------
#              Trend Analysis (led by Summer Martin)
###----------------------------------------------------
```

```
check.prerun <- all(file.exists(c(paste0(trend.path,"Historical.ANE.Scenarios/Dc_JM&W_MEDIAN_sUQ"),
                paste0(trend.path,"Historical.ANE.Scenarios/Dc_JM&W_LOW_sUQ"),
                paste0(trend.path,"Historical.ANE.Scenarios/Dc_JM&W_HIGH_sUQ"),
                paste0(trend.path,"Historical.ANE.Scenarios/Cc_Yakushima_sUQ"))))
if(!check.prerun | redo){
        ###------------------------------------------------
        #               Data Read In
        ###------------------------------------------------
                #-------
                # Yakushima 3 beaches (Loggerheads)

                CC.dat <- read.csv(paste0(data.path,"Yakushima_data_for_BiOp.csv"), header=T)

                clutch.freq <- 3          # clutch frequency = nests per female in a season (for converting nests to females)
                CC.dat[ ,c("Females_Mae", "Females_Inak", "Females_Yotsu")] <- CC.dat[ , 2:4]/clutch.freq   # use CF to
convert from nests to females that nest each year


                #-------
                # Jamursba-Medi & Wermon (Leatherbacks)


                #-------
                # Jamursba-Medi

                JM.dat <- Ns.stats.JM   # only keep specific data years per group discussions
                JM.dat[,2:4] <- exp(JM.dat[,2:4])
                clutch.freq <- 5.5    # clutch frequency =nests per female in a season; Tapilatu etal 2013 = mean CF 5.5 +/- 1.6
                JM.dat$Females_median <- JM.dat$median/clutch.freq   # use CF to convert from nests to females that nest
each year

                JM.dat$Females_low <- JM.dat$low/clutch.freq   # use CF to convert from nests to females that nest each year
                JM.dat$Females_high <- JM.dat$high/clutch.freq   # use CF to convert from nests to females that nest each year

                #-------
```

```
# Wermon
analysis.yrs <- c(2006:2017)
W.dat <- Ns.stats.W   # only keep specific data years per group discussions
W.dat[,2:4] <- exp(W.dat[,2:4])
W.dat <- W.dat[W.dat$time %in% analysis.yrs,]
W.dat$Females_median <- W.dat$median/clutch.freq   # use CF to convert from nests to females that nest each
year
W.dat$Females_low <- W.dat$low/clutch.freq   # use CF to convert from nests to females that nest each year
W.dat$Females_high <- W.dat$high/clutch.freq   # use CF to convert from nests to females that nest each year

colnames(JM.dat)[1] <- colnames(W.dat)[1] <- "Season"

#-------
# Combine

DC.dat.med <- merge(x=JM.dat[,c("Season", "Females_median")], y=W.dat[,c("Season", "Females_median")],
by="Season", all.x=TRUE, all.y=TRUE)

DC.dat.low <- merge(x=JM.dat[,c("Season", "Females_low")], y=W.dat[,c("Season", "Females_low")],
by="Season", all.x=TRUE, all.y=TRUE)

DC.dat.high <- merge(x=JM.dat[,c("Season", "Females_high")], y=W.dat[,c("Season", "Females_high")],
by="Season", all.x=TRUE, all.y=TRUE)

DC.raw.dat <- merge(x=JM.dat[,c("Season","low","median","high")], y =
W.dat[,c("Season","low","median","high")], by="Season", all.x=TRUE, all.y=TRUE, suffixes=c(".JM",".W"))


CC.dat.iT <- CC.dat
DC.dat.med.iT <- DC.dat.med
DC.dat.low.iT <- DC.dat.low
DC.dat.high.iT <- DC.dat.high
###--------------------------------------------------
```

```
#                    Adding the historical ANE
###--------------------------------------------------


    #-------
    # ANE Loggerheads

        CC.ANE <- ANEtab[ANEtab$Spp == "Loggerhead",]
        #proportion by beach
        prop.CC1 <- CC.dat[,5]/rowSums(CC.dat[5:7], na.rm=T)
        prop.CC2 <- CC.dat[,6]/rowSums(CC.dat[5:7], na.rm=T)
        prop.CC3 <- CC.dat[,7]/rowSums(CC.dat[5:7], na.rm=T)

        #tack it back in
        CC.dat[CC.dat$Year %in% CC.ANE$nestyr, 5] <- CC.dat[CC.dat$Year %in% CC.ANE$nestyr, 5] +
CC.ANE[CC.ANE$nestyr %in% CC.dat$Year,"ANE"] * prop.CC1[CC.dat$Year %in% CC.ANE$nestyr]
        CC.dat[CC.dat$Year %in% CC.ANE$nestyr, 6] <- CC.dat[CC.dat$Year %in% CC.ANE$nestyr, 6] +
CC.ANE[CC.ANE$nestyr %in% CC.dat$Year,"ANE"] * prop.CC2[CC.dat$Year %in% CC.ANE$nestyr]
        CC.dat[CC.dat$Year %in% CC.ANE$nestyr, 7] <- CC.dat[CC.dat$Year %in% CC.ANE$nestyr, 7] +
CC.ANE[CC.ANE$nestyr %in% CC.dat$Year,"ANE"] * prop.CC3[CC.dat$Year %in% CC.ANE$nestyr]


    #-------
    # ANE Leatherbacks
        DC.ANE <- ANEtab[ANEtab$Spp == "Leatherback",]

        prop.DC <- DC.dat.med[,2]/rowSums(DC.dat.med[,2:3], na.rm=T)

        DC.dat.med[DC.dat.med$Season %in% DC.ANE$nestyr, 2] <- DC.dat.med[DC.dat.med$Season %in%
DC.ANE$nestyr, 2] + DC.ANE[DC.ANE$nestyr %in% DC.dat.med$Season,"ANE"] * prop.DC[DC.dat.med$Season %in%
DC.ANE$nestyr]
        DC.dat.med[DC.dat.med$Season %in% DC.ANE$nestyr, 3] <- DC.dat.med[DC.dat.med$Season %in%
DC.ANE$nestyr, 3] + DC.ANE[DC.ANE$nestyr %in% DC.dat.med$Season,"ANE"] * (1-prop.DC[DC.dat.med$Season %in%
DC.ANE$nestyr])
```

DC.dat.low[DC.dat.low$Season %in% DC.ANE$nestyr, 2] <- DC.dat.low[DC.dat.low$Season %in% DC.ANE$nestyr, 2] + DC.ANE[DC.ANE$nestyr %in% DC.dat.low$Season,"ANE"] * prop.DC[DC.dat.low$Season %in% DC.ANE$nestyr]

DC.dat.low[DC.dat.low$Season %in% DC.ANE$nestyr, 3] <- DC.dat.low[DC.dat.low$Season %in% DC.ANE$nestyr, 3] + DC.ANE[DC.ANE$nestyr %in% DC.dat.low$Season,"ANE"] * (1-prop.DC[DC.dat.low$Season %in% DC.ANE$nestyr])

DC.dat.high[DC.dat.high$Season %in% DC.ANE$nestyr, 2] <- DC.dat.high[DC.dat.high$Season %in% DC.ANE$nestyr, 2] + DC.ANE[DC.ANE$nestyr %in% DC.dat.high$Season,"ANE"] * prop.DC[DC.dat.high$Season %in% DC.ANE$nestyr]

DC.dat.high[DC.dat.high$Season %in% DC.ANE$nestyr, 3] <- DC.dat.high[DC.dat.high$Season %in% DC.ANE$nestyr, 3] + DC.ANE[DC.ANE$nestyr %in% DC.dat.high$Season,"ANE"] * (1-prop.DC[DC.dat.high$Season %in% DC.ANE$nestyr])

```
###-------------------------------------------------
#                 Running the Trend analysis
###-------------------------------------------------


###@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
### Historical ANE added in

hist.scen.path <- paste0(trend.path,"Historical.ANE.Scenarios/")
if(!dir.exists(hist.scen.path)) dir.create(hist.scen.path)
# ---------------------------------------------
# 1 - Loggerheads - using 3 beaches from Yakushima, Japan
# ---------------------------------------------
scenario <- "Cc_Yakushima_sUQ"
thedata.loggers <- CC.dat
remigLH <- 3.3
clutch.freqLH <- 4.6
CC.file.tag <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(hist.scen.path, scenario)
source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
```

```
# ----------------------------------------------

# ----------------------------------------------
# 2A - Leatherbacks. Using MEDIAN annual nest count estimates Tomo's imputation model output.
# ----------------------------------------------
scenario <- "Dc_JM&W_MEDIAN_sUQ"
thedata.leathers <- DC.dat.med
remigLB <- 3.06
clutch.freqLB <- 5.5
DC.file.tag <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(hist.scen.path, scenario)
source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
# ----------------------------------------------

# ----------------------------------------------
# 2B - Leatherbacks. Using LOW (lower 95% CI value) annual nest count estimates from Tomo's imputation
```
model output.
```
# ----------------------------------------------
scenario <- "Dc_JM&W_LOW_sUQ"
thedata.leathers <- DC.dat.low
remigLB <- 3.06
clutch.freqLB <- 5.5
DC.file.tag.low <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(hist.scen.path, scenario)
source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
# ----------------------------------------------

# ----------------------------------------------
# 2C - Leatherbacks. Using HIGH (upper 95% CI value) annual nest count estimates from Tomo's imputation
```
model output.
```
# ----------------------------------------------
```

```
scenario <- "Dc_JM&W_HIGH_sUQ"
thedata.leathers <- DC.dat.high
remigLB <- 3
clutch.freqLB <- 5.5
DC.file.tag.high <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(hist.scen.path, scenario)
source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))



###@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
            ### No Historical ANE added in

            include.hist.take.path <- paste0(trend.path,"Include.Hist.Take.Scenarios/")
            if(!dir.exists(include.hist.take.path)) dir.create(include.hist.take.path)
            # --------------------------------------------
            # 1 - Loggerheads - using 3 beaches from Yakushima, Japan
            # --------------------------------------------
            scenario <- "Cc_Yakushima_sUQ"
            thedata.loggers <- CC.dat.iT
            remigLH <- 3.3
            clutch.freqLH <- 4.6
            CC.file.tag <- paste(scenario,"_", Sys.Date(), sep="")
            rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
            save.dir <- paste0(include.hist.take.path, scenario)
            source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
            # --------------------------------------------


            # --------------------------------------------
            # 2A - Leatherbacks. Using MEDIAN annual nest count estimates Tomo's imputation model output.
            # --------------------------------------------
            scenario <- "Dc_JM&W_MEDIAN_sUQ"
            thedata.leathers <- DC.dat.med.iT
```

```
remigLB <- 3.06
clutch.freqLB <- 5.5
DC.file.tag <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(include.hist.take.path, scenario)
source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
# ---------------------------------------------


# ---------------------------------------------
# 2B - Leatherbacks. Using LOW (lower 95% CI value) annual nest count estimates from Tomo's imputation
```

model output.

```
# ---------------------------------------------
scenario <- "Dc_JM&W_LOW_sUQ"
thedata.leathers <- DC.dat.low.iT
remigLB <- 3.06
clutch.freqLB <- 5.5
DC.file.tag.low <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(include.hist.take.path, scenario)
source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
# ---------------------------------------------


# ---------------------------------------------
# 2C - Leatherbacks. Using HIGH (upper 95% CI value) annual nest count estimates from Tomo's imputation
```

model output.

```
# ---------------------------------------------
scenario <- "Dc_JM&W_HIGH_sUQ"
thedata.leathers <- DC.dat.high.iT
remigLB <- 3
clutch.freqLB <- 5.5
DC.file.tag.high <- paste(scenario,"_", Sys.Date(), sep="")
rsel <- "rdyn"   # future predictions: choose "rdyn" (dynamic) or "rstat" (static) for future predictions
save.dir <- paste0(include.hist.take.path, scenario)
```

```
                    source(paste0(trend.path,"singleUQ_indeptUQs_PROJECTIONS.R"))
        }else{
                    hist.scen.path <- paste0(trend.path,"Historical.ANE.Scenarios/")
                    scenario <- "Cc_Yakushima_sUQ"
                    file.date <-
gsub("_0_data_used.csv","",gsub(paste0(scenario,"_"),"",grep("_data_used.csv",list.files(paste0(hist.scen.path,scenario)), value=T)))
                    file.date <- file.date[length(file.date)]
                    CC.file.tag <- paste(scenario,"_", file.date, sep="")
                    scenario <- "Dc_JM&W_MEDIAN_sUQ"
                    DC.file.tag <- paste(scenario,"_", file.date, sep="")
                    scenario <- "Dc_JM&W_LOW_sUQ"
                    DC.file.tag.low <- paste(scenario,"_", file.date, sep="")
                    scenario <- "Dc_JM&W_HIGH_sUQ"
                    DC.file.tag.high <- paste(scenario,"_", file.date, sep="")
                    include.hist.take.path <- paste0(trend.path,"Include.Hist.Take.Scenarios/")
        }


###----------------------------------------------------
#               Take Model (led by Zach Siders)
###----------------------------------------------------
        ###----------------------------------------------------
        #               Initialization
        ###----------------------------------------------------
                    #store DC MVN Take Demographic Parameters
                    TD_DC_MVN = list(mu0 = DC.mu0, beta0 = DC.beta0, beta1 = DC.beta1, cov = DC.cov)
                    #store CC MVN Take Demographic Parameters
                    TD_CC_MVN = list(mu0 = CC.mu0, beta0 = CC.beta0, beta1 = CC.beta1, cov = CC.cov)

                    #Conway-Maxwell Poisson parameters for 3 year segements
                    #Anticipated Take Level from Marti McCracken's model for Dc
                    DC_ATL <- list(mu1 = 2.124568, nu1 = 0.4805365, mu2 = 2.344938, nu2 = 0.141262, mu3 = 0.03930914, nu3 =
0.1149811)
                    #Anticipated Take Level from Marti McCracken's model for Cc
```

```
        CC_ATL = list(mu1 = 3.444104, nu1 = 0.06451325, mu2 = 7.506372e-05, nu2 =  0.01686626, mu3 = NULL, nu3 =
NULL)


        #Lontoh (2014) Dissertation on Dc; # of animals with a given remigration interval
        DC.RI <- c(1, 13, 7, 6, 4, 1)
        #Fit a Conway-Maxwell Poisson to the data
        DC.CMP <- com.fit(matrix(c(1:6, DC.RI), ncol=2))
    ###---------------------------------------------------
    #                 Loading the simulations
    ###---------------------------------------------------
        #read in the U, Q, and final years N
        DC.trend.sims <-
read.csv(paste0(hist.scen.path,"Dc_JM&W_MEDIAN_sUQ/Posteriors_U_and_AbundFinalYrs_",DC.file.tag,".csv"), header=T)
        DC.trend.sims.low <-
read.csv(paste0(hist.scen.path,"Dc_JM&W_LOW_sUQ/Posteriors_U_and_AbundFinalYrs_",DC.file.tag.low,".csv"), header=T)
        DC.trend.sims.high <-
read.csv(paste0(hist.scen.path,"Dc_JM&W_HIGH_sUQ/Posteriors_U_and_AbundFinalYrs_",DC.file.tag.high,".csv"), header=T)
        #includes historical take in U estimate
        DC.trend.sims.iT <-
read.csv(paste0(include.hist.take.path,"Dc_JM&W_MEDIAN_sUQ/Posteriors_U_and_AbundFinalYrs_",DC.file.tag,".csv"),
header=T)
        DC.trend.sims.iT.low <-
read.csv(paste0(include.hist.take.path,"Dc_JM&W_LOW_sUQ/Posteriors_U_and_AbundFinalYrs_",DC.file.tag.low,".csv"),
header=T)
        DC.trend.sims.iT.high <-
read.csv(paste0(include.hist.take.path,"Dc_JM&W_HIGH_sUQ/Posteriors_U_and_AbundFinalYrs_",DC.file.tag.high,".csv"),
header=T)


        CC.trend.sims <-
read.csv(paste0(hist.scen.path,"Cc_Yakushima_sUQ/Posteriors_U_and_AbundFinalYrs_",CC.file.tag,".csv"), header=T)
        CC.trend.sims.iT <-
read.csv(paste0(include.hist.take.path,"Cc_Yakushima_sUQ/Posteriors_U_and_AbundFinalYrs_",CC.file.tag,".csv"), header=T)
```

```
###--------------------------------------------------------
#                    Simulation Summary
###--------------------------------------------------------
        nsims <- nrow(DC.trend.sims)
        dc.trend <- DC.trend.sims[,c("U","Q","N_fym0")]
        colnames(dc.trend)[3] <- "N0"
        dc.trend.low <- DC.trend.sims.low[,c("U","Q","N_fym0")]
        colnames(dc.trend.low)[3] <- "N0"
        dc.trend.high <- DC.trend.sims.high[,c("U","Q","N_fym0")]
        colnames(dc.trend.high)[3] <- "N0"

        cc.trend <- CC.trend.sims[,c("U","Q","N_fym0")]
        colnames(cc.trend)[3] <- "N0"

    #-------
    # Write out Current Abundance

            write.csv(curr.abund.fn(DC.trend.sims, 3.06), file=paste0(table.path,"DC.Curr.Abund.csv"))
            write.csv(curr.abund.fn(DC.trend.sims.low, 3.06), file=paste0(table.path,"DC.Curr.Abund.LOW.csv"))
            write.csv(curr.abund.fn(DC.trend.sims.high, 3.06), file=paste0(table.path,"DC.Curr.Abund.HIGH.csv"))

            write.csv(curr.abund.fn(CC.trend.sims, 3.3), file=paste0(table.path,"CC.Curr.Abund.csv"))

    #-------
    # Write out U summary
        dc.u.sum <- data.frame(notake = sum.fn(dc.trend$U),
                take = sum.fn(DC.trend.sims.iT$U))
        dc.u.sum.low <- data.frame(notake = sum.fn(dc.trend.low$U),
                take = sum.fn(DC.trend.sims.iT.low$U))
        dc.u.sum.high <- data.frame(notake = sum.fn(dc.trend.high$U),
                take = sum.fn(DC.trend.sims.iT.high$U))

        cc.u.sum <- data.frame(notake = sum.fn(cc.trend$U),
```

```
                      take = sum.fn(CC.trend.sims.iT$U))

         write.csv(round(dc.u.sum,3), file=paste0(table.path,"DC.U_summary.csv"))
         write.csv(round(dc.u.sum.low,3), file=paste0(table.path,"DC.U_summary.LOW.csv"))
         write.csv(round(dc.u.sum.high,3), file=paste0(table.path,"DC.U_summary.HIGH.csv"))
         write.csv(round(cc.u.sum,3), file=paste0(table.path,"CC.U_summary.csv"))

#-------
# Plot overlapping U's

         pdf(file=paste0(fig.path, "U_Leatherbacks.pdf"), width=4, height=4)
         par(mar=c(4,4,1,1))
                  u.den(dc.trend$U, DC.trend.sims.iT$U)
                  fig.lab("W. Pac.\nLeatherbacks", xscale=0.8, yscale=0.9, cex=1)
                  abline(v=0, col='grey80')
         dev.off()

         pdf(file=paste0(fig.path, "U_Leatherbacks.LOW.pdf"), width=4, height=4)
         par(mar=c(4,4,1,1))
                  u.den(dc.trend.low$U, DC.trend.sims.iT.low$U)
                  fig.lab("W. Pac.\nLeatherbacks", xscale=0.8, yscale=0.9, cex=1)
                  abline(v=0, col='grey80')
         dev.off()

         pdf(file=paste0(fig.path, "U_Leatherbacks.HIGH.pdf"), width=4, height=4)
         par(mar=c(4,4,1,1))
                  u.den(dc.trend.high$U, DC.trend.sims.iT.high$U)
                  fig.lab("W. Pac.\nLeatherbacks", xscale=0.8, yscale=0.9, cex=1)
                  abline(v=0, col='grey80')
         dev.off()

         pdf(file=paste0(fig.path, "U_Loggerheads.pdf"), width=4, height=4)
         par(mar=c(4,4,1,1))
```

```
                        u.den(cc.trend$U, CC.trend.sims.iT$U)
                        fig.lab("N. Pac.\nLoggerheads", xscale=0.8, yscale=0.9, cex=1)
                        abline(v=0, col='grey80')
                dev.off()


        #-------
        # Plot Joint
                plot.joint(dc.trend, "DC", 6)
                plot.joint(dc.trend.low, "DC.LOW", 6)
                plot.joint(dc.trend.high, "DC.HIGH", 6)
                plot.joint(cc.trend, "CC", 6)
###----------------------------------------------------
#               Define Scenarios (Parameter Read In)
###----------------------------------------------------
        DC.scenario <- list(
            n_y = 100, #number of years in scenario
            VBGF = list(model="tknot",Linf = 142.7, K = 0.2262, tknot=-0.17, Amat = 16.1), #VBGF parameters
            TD_MVN = TD_DC_MVN, #take demographics MVN parameters
            PjV = list(mu = 0.81, sd = 0.03), #juvenile survival
            PaV = list(mu = 0.893, sd = 0.013), #adult survival
            RI.dist = c("CMP"), #distribution of RI
            RV = list(RI = com.mean(DC.CMP$lambda, DC.CMP$nu), RI_sd = DC.CMP$nu, CF = 5.5, CF_sd = 1.6, CS =
77.9, CS_sd = 2.35, PF = 0.73, PF_sd = 0), #reproductive values
            ATLp = list(mu1 = 2.124568, nu1 = 0.4805365, mu2 = 2.344938, nu2 = 0.141262, mu3 = 0.03930914, nu3 =
0.1149811),
            ANE_dyn = FALSE, #whether ANE is dynamic
            Surv_dyn = FALSE,
            dynUQ = TRUE,
            ATL_scale = FALSE,
            grim.reaper=FALSE)

        CC.scenario <- list(
            n_y = 100, #number of years in scenario
```

```
            VBGF = list(model="Lknot",Linf = 80.4473850, K = 0.1396317, Lknot=4.7363329, Amat = 26.4950786), #VBGF
parameters
            TD_MVN = TD_CC_MVN, #take demographics MVN parameters
            PjV = list(mu = 0.8, sd = 0.031), #juvenile survival
            PaV = list(mu = 0.895, sd = 0.028), #adult survival
            RI.dist = "normal",
            RV = list(RI = 3.3, RI_sd = 2.3, CF = 4.6, CF_sd = 1.1, CS = 122, CS_sd = 18.4, PF = 0.65, PF_sd = 0),
#reproductive values
            ATLp = list(mu1 = 3.444104, nu1 = 0.06451325, mu2 = 7.506372e-05, nu2 =  0.01686626, mu3 = NULL, nu3 =
NULL),
            ANE_dyn = FALSE, #whether ANE is dynamic
            Surv_dyn = FALSE,
            dynUQ = FALSE,
            ATL_scale = FALSE,
            grim.reaper=FALSE)
        DC.scenario.GR <- list(
            n_y = 100, #number of years in scenario
            VBGF = list(model="tknot",Linf = 142.7, K = 0.2262, tknot=-0.17, Amat = 16.1), #VBGF parameters
            TD_MVN = TD_DC_MVN, #take demographics MVN parameters
            PjV = list(mu = 0.81, sd = 0.03), #juvenile survival
            PaV = list(mu = 0.893, sd = 0.013), #adult survival
            RI.dist = c("CMP"), #distribution of RI
            RV = list(RI = com.mean(DC.CMP$lambda, DC.CMP$nu), RI_sd = DC.CMP$nu, CF = 5.5, CF_sd = 1.6, CS =
77.9, CS_sd = 2.35, PF = 0.73, PF_sd = 0), #reproductive values
            ATLp = list(mu1 = 2.124568, nu1 = 0.4805365, mu2 = 2.344938, nu2 = 0.141262, mu3 = 0.03930914, nu3 =
0.1149811),
            ANE_dyn = FALSE, #whether ANE is dynamic
            Surv_dyn = FALSE,
            dynUQ = TRUE,
            ATL_scale = FALSE,
            grim.reaper=TRUE)

        CC.scenario.GR <- list(
```

```
            n_y = 100, #number of years in scenario
            VBGF = list(model="Lknot",Linf = 80.4473850, K = 0.1396317, Lknot=4.7363329, Amat = 26.4950786), #VBGF
parameters
            TD_MVN = TD_CC_MVN, #take demographics MVN parameters
            PjV = list(mu = 0.8, sd = 0.031), #juvenile survival
            PaV = list(mu = 0.895, sd = 0.028), #adult survival
            RI.dist = "normal",
            RV = list(RI = 3.3, RI_sd = 2.3, CF = 4.6, CF_sd = 1.1, CS = 122, CS_sd = 18.4, PF = 0.65, PF_sd = 0),
#reproductive values
            ATLp = list(mu1 = 3.444104, nu1 = 0.06451325, mu2 = 7.506372e-05, nu2 =  0.01686626, mu3 = NULL, nu3 =
NULL),
            ANE_dyn = FALSE, #whether ANE is dynamic
            Surv_dyn = FALSE,
            dynUQ = FALSE,
            ATL_scale = FALSE,
            grim.reaper=TRUE)


    ###----------------------------------------------------
    #               projection function
    ###----------------------------------------------------


        # Toggles:
            # dynUQ: toggles whether a static U and Q to a dynamic (annual) U and Q is used
            # ATL_scale: toggles whether the ATL scales along with the population

        # Included modes:
            # det. ... deterministic runs
            # sto. ... stochastic runs (RI, Pj)
            # by
            # nost ... sex and discard mortality are drawn with binomial


        ### DC
```

```
DC.l <- sim.fn(dc.trend, DC.scenario, 10000, fn=pva.proj)
save(DC.l, file=paste0(sim.path,"DC_median_sim.Rdata"))
DC.l.low <- sim.fn(dc.trend.low, DC.scenario, 10000, fn=pva.proj)
save(DC.l.low, file=paste0(sim.path,"DC_low_sim.Rdata"))
DC.l.high <- sim.fn(dc.trend.high, DC.scenario, 10000, fn=pva.proj)
save(DC.l.high, file=paste0(sim.path,"DC_high_sim.Rdata"))
####

### CC
CC.l <- sim.fn(cc.trend, CC.scenario, 10000, fn=pva.proj)
save(CC.l, file=paste0(sim.path,"CC_sim.Rdata"))
#####

#-------
# Grim reaper

### DC
DC.l <- sim.fn(dc.trend, DC.scenario.GR, 10000, fn=pva.proj)
save(DC.l, file=paste0(sim.path,"DC_median_sim.GR.Rdata"))
DC.l.low <- sim.fn(dc.trend.low, DC.scenario.GR, 10000, fn=pva.proj)
save(DC.l.low, file=paste0(sim.path,"DC_low_sim.GR.Rdata"))
DC.l.high <- sim.fn(dc.trend.high, DC.scenario.GR, 10000, fn=pva.proj)
save(DC.l.high, file=paste0(sim.path,"DC_high_sim.GR.Rdata"))
####

### CC
CC.l <- sim.fn(cc.trend, CC.scenario.GR, 10000, fn=pva.proj)
save(CC.l, file=paste0(sim.path,"CC_sim.GR.Rdata"))
#####
###----------------------------------------------------
#               projection summary
###----------------------------------------------------
thres.pop <- c(.5, .25, .125)
```

```
thres.yr <- c(5, 10, 25, 50, 100)


        DC.sum <- proj.summ.fn(DC.l, dc.trend, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp="DC",
mode="MEDIAN")
        DC.sum.low <- proj.summ.fn(DC.l.low, dc.trend.low, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp="DC",
mode="LOW")
        DC.sum.high <- proj.summ.fn(DC.l.high, dc.trend.high, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12),
spp="DC", mode="HIGH")
        CC.sum <- proj.summ.fn(CC.l, cc.trend, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp="CC")

        #grim reaper
        DC.sum <- proj.summ.fn(DC.l, dc.trend, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp="DC",
mode="MEDIAN.GR")
        DC.sum.low <- proj.summ.fn(DC.l.low, dc.trend.low, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp="DC",
mode="LOW.GR")
        DC.sum.high <- proj.summ.fn(DC.l.high, dc.trend.high, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12),
spp="DC", mode="HIGH.GR")
        CC.sum <- proj.summ.fn(CC.l, cc.trend, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp="CC",
mode="GR")


    ###-----------------------------------------------------
    #            plot raw
    ###-----------------------------------------------------
        load(paste0(data.path,"DC_raw_nests_month.Rdata"))

        pdf(file=paste0(fig.path,"Raw_nest_data_monthly.pdf"))
            layout(matrix(c(rep(1:3,each=3),4,4,4,5,0,6,6,6,7),ncol=2))

            par(mar=c(2,5,0.1,1),cex.axis=1.2, oma=c(1,1,2,3))
            with(CC.dat, plot(Year, Maehama.Beach, ylim=range(pretty(range(CC.dat[,2:4], na.rm=T))), xlab="", ylab="",
type="b", pch=16, las=1, xaxt='n'))
            axis(1, pretty(CC.dat$Year), labels=FALSE)
```

```r
                mtext("N. Pac. Loggerheads", side=3, line=0.5)
                fig.lab("Maehama", xscale=0.025, yscale=0.975, adj=c(0,1))
                with(CC.dat, plot(Year, Inakahama.Beach, ylim=range(pretty(range(CC.dat[,2:4], na.rm=T))), xlab="", ylab="",
type="b", pch=16, las=1, xaxt='n'))
                fig.lab("Inakahama", xscale=0.025, yscale=0.975, adj=c(0,1))
                axis(1, pretty(CC.dat$Year), labels=FALSE)
                with(CC.dat, plot(Year, Yakushima.Yotsuse, ylim=range(pretty(range(CC.dat[,2:4], na.rm=T))), xlab="",
ylab="", type="b", pch=16, las=1, xaxt='n'))
                fig.lab("Yotsuse", xscale=0.025, yscale=0.975, adj=c(0,1))
                axis(1, pretty(CC.dat$Year), labels=TRUE, xpd=NA)

                ### DC
                with(DC.raw.dat, {
                        plot(Season, median.JM, ylim=range(pretty(range(DC.raw.dat[,2:7], na.rm=T))), xlab="", ylab="",
type="n", pch=16, las=1, xaxt='n', xlim=range(Season))
                                polygon(c(Season, rev(Season)),
                                    c(low.JM, rev(high.JM)),
                                    col=col2rgbA('gray50',0.25), border='gray50')
                                points(Season, median.JM, type='b', pch=16)})
                fig.lab("Jamursba-Medi", xscale=0.975, yscale=0.975, adj=c(1,1))
                mtext("W. Pac. Leatherbacks", side=3, line=0.5)
                axis(1, pretty(DC.raw.dat$Season), labels=FALSE)


                plot(y.raw$year.frac, y.raw$JM, ylim=range(pretty(range(y.raw[,1:2],na.rm=T))), type='l', col='black', pch=16,
las=1, xlab="", ylab="", xlim=range(DC.raw.dat$Season), xaxt='n', yaxt='n', lwd=1.2)
                axis(1, pretty(DC.raw.dat$Season), labels=FALSE)
                axis(2, pretty(range(y.raw[,1:2],na.rm=T))[seq(1,6,by=2)], las=1)
                fig.lab("Monthly", xscale=0.99, yscale=0.95, adj=c(1,1), cex=1)


                with(DC.raw.dat, {
```

```r
                    plot(Season, median.W, ylim=range(pretty(range(DC.raw.dat[,2:7], na.rm=T))), xlab="", ylab="",
type="n", pch=16, las=1, xaxt='n')
                        polygon(c(Season, rev(Season)),
                            c(low.W, rev(high.W)),
                            col=col2rgbA('gray50',0.25), border='gray50')
                        points(Season, median.W, type='b', pch=16)})
                fig.lab("Wermon", xscale=0.975, yscale=0.975, adj=c(1,1))
                axis(1, pretty(DC.raw.dat$Season), labels=FALSE)

                    plot(y.raw$year.frac, y.raw$W, ylim=range(pretty(range(y.raw[,1:2],na.rm=T))), type='l', col='black', pch=16,
las=1, xlab="", ylab="", xlim=range(DC.raw.dat$Season), xaxt='n', yaxt='n', lwd=1.2)
                fig.lab("Monthly", xscale=0.99, yscale=0.95, adj=c(1,1), cex=1)
                axis(1, pretty(DC.raw.dat$Season), labels=TRUE)
                axis(2, pretty(range(y.raw[,1:2],na.rm=T))[seq(1,6,by=2)], las=1)

                mtext("# of Nests", side=2, outer=T, line=-0.75, cex=1.4)
            dev.off()
```

B.   Helper Function

```r
data.extract <- function(location, year.begin,year.end, season.begin = year.begin, season.end = year.end, file.path = NULL){
    # In March 2019, we received new data for 2018. So, the raw data file
    # has been updated.
    # On 16 April 2019, the last few data points for 2019 were received
    # so the data files have been updated.
    if (is.null(season.begin)) season.begin <- year.begin
    if (is.null(season.end)) season.end <- year.end

    if (location == "JM"){
        data.0 <- read.csv(paste0(file.path,"JM_nests_April2019.csv"))

        data.0 %>%
            select(Year_begin, Month_begin, JM_Nests) %>%
            mutate(Nests = JM_Nests) -> data.0
```

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```r
} else if (location == "W"){
        data.0 <- read.csv(paste0(file.path,"W_nests_April2019.csv"))
        data.0 %>%
                select(Year_begin, Month_begin, W_Nests) %>%
                mutate(Nests = W_Nests) -> data.0
}

# create regularly spaced time series:
data.2 <- data.frame(Year = rep(min(data.0$Year_begin, na.rm = T):max(data.0$Year_begin, na.rm = T),each = 12),
                                                Month_begin = rep(1:12, max(data.0$Year_begin,
na.rm = T) - min(data.0$Year_begin, na.rm = T) + 1)) %>%
                mutate(begin_date = as.Date(paste(Year, Month_begin, '01', sep = "-"), format = "%Y-%m-%d"), Frac.Year = Year +
(Month_begin-0.5)/12) %>%
                select(Year, Month_begin, begin_date, Frac.Year)

# also make "nesting season" that starts April and ends March

data.0 %>% mutate(begin_date = as.Date(paste(Year_begin, Month_begin, '01', sep = "-"),format = "%Y-%m-%d")) %>%
        mutate(Year = Year_begin,
                        Month = Month_begin,
                        f_month = as.factor(Month),
                        f_year = as.factor(Year),
                        Frac.Year = Year + (Month_begin-0.5)/12) %>%
        select(Year, Month, Frac.Year, begin_date, Nests) %>%
        na.omit() %>%
        right_join(.,data.2, by = "begin_date") %>%
        transmute(Year = Year.y,
                                Month = Month_begin,
                                Frac.Year = Frac.Year.y,
                                Nests = Nests,
                                Season = ifelse(Month < 4, Year-1, Year),
                                Seq.Month = ifelse(Month < 4, Month + 9, Month - 3)) %>%
```

```
        reshape::sort_df(.,vars = "Frac.Year") %>%
        filter(Season >= season.begin & Season <= season.end) -> data.1

    data.1 %>% filter(Month > 3 & Month < 10) -> data.summer
    data.1 %>% filter(Month > 9 | Month < 4) %>%
        mutate(Seq.Month = Seq.Month - 6) -> data.winter

    jags.data <- list(y = log(data.1$Nests),
                                                        m = data.1$Seq.Month,
                                                        T = nrow(data.1))

    y <- matrix(log(data.1$Nests), ncol = 12, byrow = TRUE)

    jags.data2 <- list(y = y,
                                                        m = matrix(data.1$Seq.Month, ncol = 12, byrow = TRUE),
                                                        n.years = nrow(y))

    y.summer <- matrix(log(data.summer$Nests),
                                                        ncol = 6, byrow = TRUE)

    y.winter <- matrix(log(data.winter$Nests),
                                                        ncol = 6, byrow = TRUE)

    jags.data2.summer <- list(y = y.summer,
                                                        m =
matrix(data.summer$Seq.Month,ncol = 6, byrow = TRUE),
                                                        n.years = nrow(y.summer))

    jags.data2.winter <- list(y = y.winter,
                                                        m =
matrix(data.winter$Seq.Month, ncol = 6, byrow = TRUE),
                                                        n.years = nrow(y.winter))
```

```r
        out <- list(jags.data = jags.data,
                                        jags.data2 = jags.data2,
                                        jags.data.summer = jags.data2.summer,
                                        jags.data.winter = jags.data2.winter,
                                        data.1 = data.1,
                                        data.summer = data.summer,
                                        data.winter = data.winter)

        return(out)
}
sum.fn <- function(U){
        meanU <- mean(U)
        varU <- var(U)
        qU <- quantile(U, probs=c(0.5,0.025, 0.975))

        lamb <- exp(U)
        meanL <- mean(lamb)
        varL <- var(lamb)
        qL <- quantile(lamb, probs=c(0.5, 0.025, 0.975))

        summ <- matrix(c(meanU, qU[1], varU, qU[2:3], meanL, qL[1], varL, qL[2:3]), ncol=1)
        rownames(summ) <- c("meanU", "medianU", "varU", "L95U", "U95U", "meanl", "medianl", "varl", "L95l", "U95l")

        return(summ)
}
pva.proj <- function(sim, trend, scenario){
        with(scenario, {


        #convert U to lambda
                lambda <- rep(1, n_y) #exp of U
                Q.sd <- rep(NA, n_y) #std. dev. of Q (is variance)
                #toggle for dynamic or static U & Q
                if(dynUQ){
```

```
                samp.sim <- sample(1:length(trend$U), n_y-1, replace = FALSE)
                lambda[1] <- exp(trend$U[sim])
                lambda[2:n_y] <- exp(trend$U[samp.sim])
                Q.sd[1] <- sqrt(trend$Q[sim])
                Q.sd[2:n_y] <- sqrt(trend$Q[samp.sim])
        }else{
                lambda[1:n_y] <- exp(trend$U[sim])
                Q.sd[1:n_y] <- sqrt(trend$Q[sim])
        }


###-----------------------------------------------------
#draw a ATL
        #ATL_scale is a logical flag for scaling the ATL at the same rate as the population growth rate
        if(ATL_scale){
                ATL_segments <- matrix(0, n_y, 3)
                for(i in 1:n_y){
                        if(!is.null(ATLp$mu1)){
                        ATL_segments[i,1] <- rCMP(1, mu = ATLp$mu1*cumprod(lambda)[i], nu = ATLp$nu1)
                        }
                        if(!is.null(ATLp$mu2)){
                                ATL_segments[i,2] <- rCMP(1, mu = ATLp$mu2*cumprod(lambda)[i], nu = ATLp$nu2)
                        }
                        if(!is.null(ATLp$mu3)){
                                ATL_segments[i,3] <- rCMP(1, mu = ATLp$mu3*cumprod(lambda)[i], nu = ATLp$nu3)
                        }
                }

                ATL <- rowSums(ATL_segments)
        }else{
                ATL_segments <- matrix(0, n_y, 3)
                if(!is.null(ATLp$mu1)){
                        ATL_segments[,1] <- rCMP(n_y, mu = ATLp$mu1, nu = ATLp$nu1)
                }
```

```
            if(!is.null(ATLp$mu2)){
                    ATL_segments[,2] <- rCMP(n_y, mu = ATLp$mu2, nu = ATLp$nu2)
            }
            if(!is.null(ATLp$mu3)){
                    ATL_segments[,3] <- rCMP(n_y, mu = ATLp$mu3, nu = ATLp$nu3)
            }
            ATL <- rowSums(ATL_segments)
        }

    #draw a Size and Mortality based on ATL
        mu.l <- TD_MVN$beta0 + TD_MVN$beta1*ATL #linear model for mean lengths in take (log)
        mu.m <- rep(TD_MVN$mu0, n_y) # mean discard mortality in take (logit)

        pred.Age <- seq(0,100, by=0.01) #sequence of ages to back calculate over
        Lpred <- ifelse(VBGF$model =="tknot",with(VBGF, Linf * (1-exp(-K*(pred.Age-tknot)))), with(VBGF, Linf - (Linf -
Lknot)*(1-exp(-K*pred.Age)))) #lengths over those ages

        det.TD.draw.raw <- rep(list(NA),n_y) #storage list of MVN draws
        det.TD.draw <- rep(list(NA), n_y) #storage list
        det.Take <- rep(0, n_y) #storage vector of take
        det.Take.nost <- rep(0, n_y) #storage vector of take

        sto.TD.draw.raw <- rep(list(NA),n_y) #storage list of MVN draws
        sto.TD.draw <- rep(list(NA), n_y) #storage list
        sto.Take <- rep(0, n_y) #storage vector of take
        sto.Take.nost <- rep(0, n_y) #storage vector of take

        #draw a proportion female in the Take for each year
        PF.sto <- rnorm(n_y, RV$PF, RV$PF_sd)
        PF.det <- RV$PF

        for(i in 1:n_y){
```

```
if(ATL[i] > 0){
        #draw from MVN log(length) and logit(discard mortality)
        det.TD.draw.raw[[i]] <- sto.TD.draw.raw[[i]] <- rmvnorm(ATL[i], c(mu.l[i], mu.m[i]), TD_MVN$cov)
        #convert to length and discard mortality (prob. space)
        det.TD.draw[[i]] <- sto.TD.draw[[i]] <- data.frame(l = exp(sto.TD.draw.raw[[i]][,1]), m =
boot::inv.logit(sto.TD.draw.raw[[i]][,2]))
        #get an anticpated Age from the VBGF
        det.TD.draw[[i]]$Age <- sto.TD.draw[[i]]$Age <- sapply(sto.TD.draw[[i]]$l, function(x)
{pred.Age[which.min(abs(x - Lpred))]})
        #calculate the number of years until maturity
        det.TD.draw[[i]]$YatLarge <- sto.TD.draw[[i]]$YatLarge <- VBGF$Amat - sto.TD.draw[[i]]$Age
        #determine the animals stage based on maturity
        det.TD.draw[[i]]$Stage <- sto.TD.draw[[i]]$Stage <- ifelse(sto.TD.draw[[i]]$Age > VBGF$Amat, "A",
"J")


        #### Stochastic
        #draw a remigration interval for every animal based on a specified distribution (normal or CMP)
        if(RI.dist =="normal"){
                sto.TD.draw[[i]]$RI <- rtruncnorm(nrow(sto.TD.draw[[i]]), a=0, mean=RV$RI, sd=RV$RI_sd)
#remigration interval
        }else if(RI.dist =="CMP"){
                sto.TD.draw[[i]]$RI <- rCMP(nrow(sto.TD.draw[[i]]), mu=RV$RI, nu=RV$RI_sd) #remigration
interval
                while(any(sto.TD.draw[[i]]$RI==0)){
                        sto.TD.draw[[i]]$RI[sto.TD.draw[[i]]$RI==0] <- rCMP(sum(sto.TD.draw[[i]]$RI==0),
mu = RV$RI, nu = RV$RI_sd)
                }
        }else{
                sto.TD.draw[[i]]$RI <- RV$RI
                #error handling
                print("Distribution was not specified as normal or CMP")
        }
        #draw a juvenile survival for every animal
```

```
                    sto.TD.draw[[i]]$Pj <- rnorm(nrow(sto.TD.draw[[i]]), PjV$mu, PjV$sd) #juvenile survival
                    #Calculate the Adult Nester Equivalency
                    sto.TD.draw[[i]]$ANEj <- (sto.TD.draw[[i]]$Pj^sto.TD.draw[[i]]$YatLarge) * (1/sto.TD.draw[[i]]$RI)
#ANE

                    #Draw whether the animal is M/F based on yearly proportion
                    sto.TD.draw[[i]]$Sex <- rbinom(nrow(sto.TD.draw[[i]]), 1, PF.sto[i])
                    #Draw whether the animal lived or died based on discard mortality
                    if(grim.reaper){
                            sto.TD.draw[[i]]$Fdead <- 1
                    }else{
                            sto.TD.draw[[i]]$Fdead <- rbinom(nrow(sto.TD.draw[[i]]), 1, sto.TD.draw[[i]]$m)
                    }


                    #Fill in Adult ANE
                    sto.TD.draw[[i]]$ANEa <- 1
                    #Calculate the realized ANE
                    sto.TD.draw[[i]]$rANE <- ((sto.TD.draw[[i]]$ANEj * as.integer(sto.TD.draw[[i]]$Stage=="J")) +
(sto.TD.draw[[i]]$ANEa * as.integer(sto.TD.draw[[i]]$Stage=="A"))) * (sto.TD.draw[[i]]$Sex * sto.TD.draw[[i]]$Fdead)
                    #Calculate the realized ANE w/o stochastic Sex or Discard Mortality draws
                    sto.TD.draw[[i]]$rANE.nost <- ((sto.TD.draw[[i]]$ANEj * as.integer(sto.TD.draw[[i]]$Stage=="J")) +
(sto.TD.draw[[i]]$ANEa * as.integer(sto.TD.draw[[i]]$Stage=="A"))) * (PF.sto[i] * sto.TD.draw[[i]]$m)



                    #### Deterministic
                    det.TD.draw[[i]]$RI <- RV$RI
                    det.TD.draw[[i]]$Pj <- PjV$mu
                    det.TD.draw[[i]]$Pa <- PaV$mu
                    det.TD.draw[[i]]$ANEj <- (det.TD.draw[[i]]$Pj^det.TD.draw[[i]]$YatLarge) * (1/det.TD.draw[[i]]$RI)
                    det.TD.draw[[i]]$Sex <- rbinom(length(det.TD.draw[[i]]$Stage), 1, PF.det)
                    if(grim.reaper){
                            det.TD.draw[[i]]$Fdead <- 1
                    }else{
```

```
                    det.TD.draw[[i]]$Fdead <- rbinom(nrow(det.TD.draw[[i]]), 1, det.TD.draw[[i]]$m)
        }

        det.TD.draw[[i]]$ANEa <- 1

        det.TD.draw[[i]]$rANE <- ((det.TD.draw[[i]]$ANEj * as.integer(det.TD.draw[[i]]$Stage=="J")) +
(det.TD.draw[[i]]$ANEa * as.integer(det.TD.draw[[i]]$Stage=="A"))) * (det.TD.draw[[i]]$Sex * det.TD.draw[[i]]$Fdead)
        det.TD.draw[[i]]$rANE.nost <- ((det.TD.draw[[i]]$ANEj * as.integer(det.TD.draw[[i]]$Stage=="J")) +
(det.TD.draw[[i]]$ANEa * as.integer(det.TD.draw[[i]]$Stage=="A"))) * (PF.det * det.TD.draw[[i]]$m)



        det.Take[i] <- sum(det.TD.draw[[i]]$rANE)
        det.Take.nost[i] <- sum(det.TD.draw[[i]]$rANE.nost)
        sto.Take[i] <- sum(sto.TD.draw[[i]]$rANE)
        sto.Take.nost[i] <- sum(sto.TD.draw[[i]]$rANE.nost)
    }
}

### deterministic
det.nost.Nt_take <- det.Nt_take <- det.Nt <- det.nost.Nt_take.iQ <- det.Nt_take.iQ <- det.Nt.iQ <- rep(0, n_y)

det.Nt_take.iQ[1] <- rnorm(1,(trend$N0[sim] - det.Take[1])*lambda[1], Q.sd[1])
det.nost.Nt_take.iQ[1] <- rnorm(1,(trend$N0[sim] - det.Take.nost[1])*lambda[1], Q.sd[1])
det.Nt.iQ[1] <- rnorm(1, trend$N0[sim] * lambda[1], Q.sd[1])
det.Nt_take[1] <- (trend$N0[sim] - det.Take[1])*lambda[1]
det.nost.Nt_take[1] <- (trend$N0[sim] - det.Take.nost[1])*lambda[1]
det.Nt[1] <- trend$N0[sim] * lambda[1]
for(i in 2:n_y){
    #include process variance Q
    det.Nt_take.iQ[i] <- rnorm(1,(det.Nt_take.iQ[i-1] - det.Take[i])*lambda[i], Q.sd[i])
    det.nost.Nt_take.iQ[i] <- rnorm(1,(det.Nt_take.iQ[i-1] - det.Take.nost[i])*lambda[i], Q.sd[i])
    det.Nt.iQ[i] <- rnorm(1, det.Nt.iQ[i-1] * lambda[i], Q.sd[i])
```

```
                #drop process variance Q
                det.Nt_take[i] <- (det.Nt_take[i-1] - det.Take[i])*lambda[i]
                det.nost.Nt_take[i] <- (det.Nt_take[i-1] - det.Take.nost[i])*lambda[i]
                det.Nt[i] <-  det.Nt[i-1] * lambda[i]
        }


        ### stochastic
        sto.nost.Nt_take <- sto.nost.Nt <- sto.Nt_take <- sto.Nt <- sto.nost.Nt_take.iQ <- sto.nost.Nt.iQ <-sto.Nt_take.iQ <-
sto.Nt.iQ <- rep(0, n_y)

        sto.Nt_take.iQ[1] <- rnorm(1,(trend$N0[sim] - sto.Take[1])*lambda[1], Q.sd[1])
        sto.nost.Nt_take.iQ[1] <- rnorm(1,(trend$N0[sim] - sto.Take.nost[1])*lambda[1], Q.sd[1])
        sto.Nt.iQ[1] <- rnorm(1, trend$N0[sim] * lambda[1], Q.sd[1])
        sto.Nt_take[1] <- (trend$N0[sim] - sto.Take[1])*lambda[1]
        sto.nost.Nt_take[1] <- (trend$N0[sim] - sto.Take.nost[1])*lambda[1]
        sto.Nt[1] <-  trend$N0[sim] * lambda[1]
        for(i in 2:n_y){
                #include process variance Q
                sto.Nt_take.iQ[i] <- rnorm(1,(sto.Nt_take.iQ[i-1] - sto.Take[i])*lambda[i], Q.sd[i])
                sto.nost.Nt_take.iQ[i] <- rnorm(1,(sto.Nt_take.iQ[i-1] - sto.Take.nost[i])*lambda[i], Q.sd[i])
                sto.Nt.iQ[i] <- rnorm(1, sto.Nt.iQ[i-1] * lambda[i], Q.sd[i])
                #drop process variance Q
                sto.Nt_take[i] <- (sto.Nt_take[i-1] - sto.Take[i])*lambda[i]
                sto.nost.Nt_take[i] <- (sto.Nt_take[i-1] - sto.Take.nost[i])*lambda[i]
                sto.Nt[i] <-  sto.Nt[i-1] * lambda[i]
        }

    return(as.matrix(
     data.frame(det.nost.Nt_take = det.nost.Nt_take,
           det.Nt_take = det.Nt_take,
           det.Nt = det.Nt,
           det.nost.Nt_take.iQ = det.nost.Nt_take.iQ,
           det.Nt_take.iQ = det.Nt_take.iQ,
```

```
                    det.Nt.iQ = det.Nt.iQ,
                    sto.nost.Nt_take = sto.nost.Nt_take,
                    sto.Nt_take = sto.Nt_take,
                    sto.Nt = sto.Nt,
                    sto.nost.Nt_take.iQ = sto.nost.Nt_take.iQ,
                    sto.Nt_take.iQ = sto.Nt_take.iQ,
                    sto.Nt.iQ = sto.Nt.iQ)))
        })
}
curr.abund.fn <- function(dat, RI, round=TRUE){
        curr.abund <- matrix(c(quantile(dat$N_fym0, probs=c(0.5,0.025,0.975)), quantile(dat$N_fym1, probs=c(0.5,0.025,0.975)),
quantile(dat$N_fym2, probs=c(0.5,0.025,0.975)), quantile(dat$N_fym3, probs=c(0.5,0.025,0.975)),
quantile(rowSums(dat[,c("N_fym0","N_fym1","N_fym2","N_fym3")]),probs=c(0.5,0.025,0.975))*(RI/4)), nrow=5, byrow=T)
        rownames(curr.abund) <- c("N0","N-1","N-2","N-3","Sum")
        colnames(curr.abund) <- c("Median","L95%","U95%")
        if(round) curr.abund <- round(curr.abund)
        return(curr.abund)
}
sim.fn <- function(trend, scenario, nsim, fn){
        pva.proj <- fn
        UseCores <- detectCores() - 2
        cl <- makeCluster(UseCores)
        registerDoParallel(cl)
        nst <- ceiling(seq(from=1, to = nsim, length.out=(UseCores+1)))[-(UseCores+1)]
        nen <- ceiling(seq(from=1, to = nsim, length.out=(UseCores+1)))[-1] - c(rep(1,(UseCores-1)),0)

        df <- foreach(i = 1:length(nst), .packages=c("CMP", "mvtnorm","truncnorm")) %dopar% {

                iseq <- seq(nst[i],nen[i])
                arr <- array(NA, dim=c(100, 12, length(iseq)))

                for(j in 1:length(iseq)){
                        arr[,,j] <- pva.proj(iseq[j], trend, scenario)
```

```r
                    }

                    return(arr)
            }
            stopCluster(cl)
            return(df)
}
bootCI <- function(dt, R){
            samps <- replicate(R, sample(1:length(dt), floor(0.9*length(dt))))
            q <- apply(samps, 2, function(v) {sum(dt[v]/length(v))})
            return(q)
}
fig.lab <- function(i, xscale=0.05, yscale, cex=1.4, adj=c(0.5,0.5)){
            text(x = par('usr')[1] + abs(diff(par('usr')[1:2]))*xscale,
                y = par('usr')[3] + abs(diff(par('usr')[3:4]))*yscale,
                ifelse(is.numeric(i),LETTERS[i],i), xpd=NA, cex=cex, adj=adj)
}
u.den <- function(notake, take){
            d1 <- density(notake, adj=2)
            d2 <- density(take, adj=2)
            d1$y <- d1$y/max(d1$y)
            d2$y <- d2$y/max(d2$y)

            plot(d1$x, d1$y, xlab="r", ylab="Relative Density", ylim=c(0,1.01), las=1, col='chartreuse4', type='l', lwd=3)
            lines(d2$x, d2$y, col='dodgerblue4', lwd=3, lty=2)
            legend("topleft", legend=c(expression(N[j]), expression(N[j]-F)), lwd=3, col=c('chartreuse4', 'dodgerblue4'), bty='n')
}
col2rgbA<-function(color,transparency)
{
  rgb(t(col2rgb(color))/255,alpha=transparency)
}
proj.summ.fn <- function(sim.l, trend, thres.pop, thres.yr, alpha=0.05, keepers=c(5,6,11,12), spp, mode=NULL){
```

```
lci <- alpha/2
uci <- 1-(alpha/2)

arr <- abind(sim.l, along=3)

### Summary arrays
#dims = length(thres.pop), 12 modes from pva.proj, 4 summary metrics (mean, median, LCI, UCI)
tab.yr <- array(NA, dim=c(length(thres.pop),12, 4))
#dims = length(thres.yr), length(thres.pop), 12 modes from pva.proj, 3 summary metrics (median, LCI, UCI)
tab.prob <- array(NA, dim=c(length(thres.yr), length(thres.pop), 12, 3))

### Storage arrays
#dims = length(thres.pop), 12 modes from pva.proj, nsims
yr <- array(NA, dim=c(length(thres.pop), 12, dim(arr)[3]))
#dims = length(thres.yr), length(thres.pop), 12 modes from pva.proj, nsims
prob <- array(NA, dim=c(length(thres.yr), length(thres.pop), 12, dim(arr)[3]))

#duplicate array to fill in extinct years with 0's
arr2 <- arr

for(i in 1:dim(arr)[3]){
        N0 <- trend$N0[i]
        N0.thres <- N0*thres.pop

        #fills in zeros for extinct runs
        arr2[,,i] <- apply(arr2[,,i], 2, function(x) {if(any(x < 0)){ d <- min(which(x < 0)); x[d:100] <- 0}; return(x)})

        #first year to fall below threshold
        yr[,,i] <- apply(arr2[,,i], 2, FUN = function(x) {sapply(N0.thres, function(v) ifelse(min(which((x < v)==1))==Inf, NA,
min(which((x < v)==1))))})

        # prob[,,,i] <- array(apply(arr2[,,i], 2, function(x) {sapply(N0.thres, function(v){ sapply(thres.yr, function(y)
sum(x[1:y] < v)/y)})}), dim=c(5,3,12))
```

```
        prob[,,,i] <- array(apply(arr2[,,i], 2, function(x) {sapply(N0.thres, function(v){ sapply(thres.yr, function(y)
as.integer(any(x[1:y] < v)))})}), dim=c(5,3,12))
        }

        #Summarize Years to threshold
        tab.yr[,,1] <- apply(yr, c(1,2), mean, na.rm=T)
        tab.yr[,,2] <- apply(yr, c(1,2), median, na.rm=T)
        tab.yr[,,3] <- apply(yr, c(1,2), quantile, prob = lci, na.rm=T)
        tab.yr[,,4] <- apply(yr, c(1,2), quantile, prob = uci, na.rm=T)

        #Summarize probability of falling below threshold
        tab.prob[,,,1] <- apply(prob, c(1,2,3), function(x) {sum(x)/length(x)})
        bootci.prob <- apply(prob,c(1,2,3), bootCI, R=1000)
        tab.prob[,,,2] <- apply(bootci.prob, c(2,3,4), quantile, prob=lci)
        tab.prob[,,,3] <- apply(bootci.prob, c(2,3,4), quantile, prob=uci)

        # Table 1
                tab1.det.NT <- matrix(c(1-aperm(tab.prob[,,keepers[2],], c(2,1,3))[,5,1], aperm(tab.prob[,,6,], c(2,1,3))[,5,1],
tab.yr[,6,]), nrow=3)
                tab1.det.T <- matrix(c(1-aperm(tab.prob[,,keepers[1],], c(2,1,3))[,5,1], aperm(tab.prob[,,5,], c(2,1,3))[,5,1], tab.yr[,5,]),
nrow=3)
                tab1.sto.NT <- matrix(c(1-aperm(tab.prob[,,12,], c(2,1,3))[,5,1], aperm(tab.prob[,,keepers[4],], c(2,1,3))[,5,1],
tab.yr[,12,]), nrow=3)
                tab1.sto.T <- matrix(c(1-aperm(tab.prob[,,11,], c(2,1,3))[,5,1], aperm(tab.prob[,,keepers[3],], c(2,1,3))[,5,1],
tab.yr[,11,]), nrow=3)

                rownames(tab1.det.NT) <- rownames(tab1.det.T) <- rownames(tab1.sto.NT) <- rownames(tab1.sto.T) <-
paste0(thres.pop*100, "%")
                colnames(tab1.det.NT) <- colnames(tab1.det.T) <- colnames(tab1.sto.NT) <- colnames(tab1.sto.T) <-
c("Prob.Above","Prob.Below","MeanYr","MedYr","L95Yr","U95Yr")

                write.csv(round(tab1.det.NT,2), file=paste0(table.path,"Table1.",spp, mode,".det.NT.csv"))
                write.csv(round(tab1.det.T,2), file=paste0(table.path,"Table1.",spp, mode,".det.T.csv"))
```

```
        write.csv(round(tab1.sto.NT,2), file=paste0(table.path,"Table1.",spp, mode,".sto.NT.csv"))
        write.csv(round(tab1.sto.T,2), file=paste0(table.path,"Table1.",spp, mode,".sto.T.csv"))


    # Table 2
        tp.det.NT <- apply(aperm(tab.prob[,,keepers[2],], c(2,1,3)),2,c)[c(1,4,7,2,5,8,3,6,9),]
        tp.det.T <- apply(aperm(tab.prob[,,keepers[1],], c(2,1,3)),2,c)[c(1,4,7,2,5,8,3,6,9),]
        tp.sto.NT <- apply(aperm(tab.prob[,,keepers[4],], c(2,1,3)),2,c)[c(1,4,7,2,5,8,3,6,9),]
        tp.sto.T <- apply(aperm(tab.prob[,,keepers[3],], c(2,1,3)),2,c)[c(1,4,7,2,5,8,3,6,9),]

        rownames(tp.det.NT) <- rownames(tp.det.T) <- rownames(tp.sto.NT) <- rownames(tp.sto.T) <-
paste0(rep(paste0(thres.pop*100,"%"),each=3),  c("", "L95","U95"))
        colnames(tp.det.NT) <- colnames(tp.det.T) <- colnames(tp.sto.NT) <- colnames(tp.sto.T) <- paste0(thres.yr,'yr')

        write.csv(round(tp.det.NT,3), file=paste0(table.path,"Table2.",spp, mode,".det.NT.csv"))
        write.csv(round(tp.det.T,3), file=paste0(table.path,"Table2.",spp, mode,".det.T.csv"))
        write.csv(round(tp.sto.NT,3), file=paste0(table.path,"Table2.",spp, mode,".sto.NT.csv"))
        write.csv(round(tp.sto.T,3), file=paste0(table.path,"Table2.",spp, mode,".sto.T.csv"))

    #Median Projections
        proj.med <- apply(arr2, c(1,2), quantile, probs=c(lci, 0.5, uci))
        proj.log.med <- apply(arr2, c(1,2), function(x) {quantile(log(x), probs=c(lci, 0.5, uci))})
        proj.log.med[is.infinite(proj.log.med)] <- min(proj.log.med[!is.infinite(proj.log.med)]) * 5
        diff.det <- arr2[,keepers[1],] - arr2[,keepers[2],]
        diff.sto <- arr2[,keepers[3],] - arr2[,keepers[4],]
        proj.diff.det <- apply(diff.det, 1, quantile, probs=c(lci, 0.5, uci))
        proj.diff.sto <- apply(diff.sto, 1, quantile, probs=c(lci, 0.5, uci))
        if(spp=="DC"){
            pdf(file=paste0(fig.path,spp,mode,"proj100.pdf"))
                ###PROJECT 100
                par(mfrow=c(2,1), mar=c(3,4,2,1))
                # Deterministic
                plot(2018:2117, proj.med[2,,keepers[1]],
                    xlim=c(2017,2118),
```

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```
                        ylim=c(0,max(proj.med[,,keepers])),
                        type='n', las=1, xlab="Years",
                        xaxt='n', ylab="Annual Nesters",
                        yaxs='i', xaxs='i')
                polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.med[1,,keepers[1]],
rev(proj.med[3,,keepers[1]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.med[1,,keepers[2]],
rev(proj.med[3,,keepers[2]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                lines(2018:2117, proj.med[2,,keepers[1]], col="dodgerblue4", lwd=3)
                lines(2018:2117, proj.med[2,,keepers[2]], col="chartreuse4", lwd=3)
                yrpretty <- pretty(2018:2118)[pretty(2018:2118)>2018 & pretty(2018:2118) < 2118]
                axis(1, yrpretty, yrpretty)
                mtext("Deterministic", side=3, font=3)
                fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)

                # Stochastic
                par(mar=c(4,4,1,1))
                plot(2018:2117, proj.med[2,,keepers[3]],
                        xlim=c(2017,2118),
                        ylim=c(0,max(proj.med[,,keepers])),
                        type='n', las=1, xlab="Years",
                        xaxt='n', ylab="Annual Nesters",
                        yaxs='i', xaxs='i')
                polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.med[1,,keepers[3]],
rev(proj.med[3,,keepers[3]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.med[1,,keepers[4]],
rev(proj.med[3,,keepers[4]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                lines(2018:2117, proj.med[2,,keepers[3]], col="dodgerblue4", lwd=3)
                lines(2018:2117, proj.med[2,,keepers[4]], col="chartreuse4", lwd=3)
                axis(1, yrpretty, yrpretty)
                mtext("Stochastic", side=3, font=3)
                fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)
```

```
                              legend("bottomright", legend=c(expression(paste(N[t] -F," Median")), expression(paste(N[j] -F,"
95%CI")),expression(paste(N[j]," Median")), expression(paste(N[j]," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA),
pch=c(NA,15,NA,15), col=c("dodgerblue4",col2rgbA("dodgerblue3",0.5),"chartreuse4", col2rgbA("chartreuse3", 0.5)), bty='n', pt.cex
= 2, inset = c(0,0.1))
                    dev.off()

                    pdf(file=paste0(fig.path,spp,mode,"logproj100.pdf"))
                              ###PROJECT 100
                              par(mfrow=c(2,1), mar=c(3,4,2,1))
                              # Deterministic
                              plot(2018:2117, proj.log.med[2,,keepers[1]],
                                  xlim=c(2017,2118),
                                  ylim=c(0.0001,max(proj.log.med[,,keepers])),
                                  type='n', las=1, xlab="Years",
                                  xaxt='n', ylab="Annual Nesters",
                                  yaxs='i', xaxs='i')
                              polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.log.med[1,,keepers[1]],
rev(proj.log.med[3,,keepers[1]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                              polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.log.med[1,,keepers[2]],
rev(proj.log.med[3,,keepers[2]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                              lines(2018:2117, proj.log.med[2,,keepers[1]], col="dodgerblue4", lwd=3)
                              lines(2018:2117, proj.log.med[2,,keepers[2]], col="chartreuse4", lwd=3)
                              yrpretty <- pretty(2018:2118)[pretty(2018:2118)>2018 & pretty(2018:2118) < 2118]
                              axis(1, yrpretty, yrpretty)
                              mtext("Deterministic", side=3, font=3)
                              fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)

                              # Stochastic
                              par(mar=c(4,4,1,1))
                              plot(2018:2117, proj.log.med[2,,keepers[3]],
                                  xlim=c(2017,2118),
                                  ylim=c(0.0001,max(proj.log.med[,,keepers])),
                                  type='n', las=1, xlab="Years",
```

```r
                xaxt='n', ylab="Annual Nesters",
                yaxs='i', xaxs='i')
        polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.log.med[1,,keepers[3]],
rev(proj.log.med[3,,keepers[3]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
        polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.log.med[1,,keepers[4]],
rev(proj.log.med[3,,keepers[4]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
        lines(2018:2117, proj.log.med[2,,keepers[3]], col="dodgerblue4", lwd=3)
        lines(2018:2117, proj.log.med[2,,keepers[4]], col="chartreuse4", lwd=3)
        axis(1, yrpretty, yrpretty)
        mtext("Stochastic", side=3, font=3)
        fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)
        legend("topright", legend=c(expression(paste(N[j] -F," Median")), expression(paste(N[j] -F,"
95%CI")),expression(paste(N[j]," Median")), expression(paste(N[j]," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA),
pch=c(NA,15,NA,15), col=c("dodgerblue4",col2rgbA("dodgerblue3",0.5),"chartreuse4", col2rgbA("chartreuse3", 0.5)), bty='n', pt.cex
= 2, inset = c(0,0.1))
            dev.off()

            pdf(file=paste0(fig.path,spp,mode,"proj10.pdf"))
                #### PROJECT 10
                par(mfrow=c(2,1), mar=c(3,4,2,1))
                # Deterministic
                plot(2018:2027, proj.med[2,1:10,keepers[1]],
                    xlim=c(2017.75,2027.25),
                    ylim=c(0,max(proj.med[,1:10,keepers])),
                    type='n', las=1, xlab="Years",
                    xaxt='n', ylab="Annual Nesters",
                    yaxs='i', xaxs='i')
        polygon(x = c(2018:2027, rev(2018:2027)), y = c(proj.med[1,1:10,keepers[1]],
rev(proj.med[3,1:10,keepers[1]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
        polygon(x = c(2018:2027, rev(2018:2027)), y = c(proj.med[1,1:10,keepers[2]],
rev(proj.med[3,1:10,keepers[2]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
        lines(2018:2027, proj.med[2,1:10,keepers[1]], col="dodgerblue4", lwd=3)
        lines(2018:2027, proj.med[2,1:10,keepers[2]], col="chartreuse4", lwd=3)
```

```r
yrpretty <- pretty(2018:2028)[pretty(2018:2028)>2018 & pretty(2018:2028) < 2028]
axis(1, yrpretty, yrpretty)
mtext("Deterministic", side=3, font=3)
fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)

# Stochastic
par(mar=c(4,4,1,1))
plot(2018:2027, proj.med[2,1:10,keepers[3]],
    xlim=c(2017.75,2027.25),
    ylim=c(0,max(proj.med[,1:10,keepers])),
    type='n', las=1, xlab="Years",
    xaxt='n', ylab="Annual Nesters",
    yaxs='i', xaxs='i')
polygon(x = c(2018:2027, rev(2018:2027)), y = c(proj.med[1,1:10,keepers[3]],
rev(proj.med[3,1:10,keepers[3]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
polygon(x = c(2018:2027, rev(2018:2027)), y = c(proj.med[1,1:10,keepers[4]],
rev(proj.med[3,1:10,keepers[4]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
lines(2018:2027, proj.med[2,1:10,keepers[3]], col="dodgerblue4", lwd=3)
lines(2018:2027, proj.med[2,1:10,keepers[4]], col="chartreuse4", lwd=3)
axis(1, yrpretty, yrpretty)
mtext("Stochastic", side=3, font=3)
fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)
legend("bottomleft", legend=c(expression(paste(N[j] -F," Median")), expression(paste(N[j] -F,"
95%CI")),expression(paste(N[j]," Median")), expression(paste(N[j]," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA),
pch=c(NA,15,NA,15), col=c("dodgerblue4",col2rgbA("dodgerblue3",0.5),"chartreuse4", col2rgbA("chartreuse3", 0.5)), bty='n', pt.cex
= 2)
dev.off()

pdf(file=paste0(fig.path,spp,mode,"diff100.pdf"))
###PROJECT 100
par(mfrow=c(2,1), mar=c(3,4,2,1))
# Deterministic
plot(2018:2117, proj.diff.det[2,],
```

```
                    xlim=c(2017,2118),
                    ylim=range(pretty(range(proj.diff.det))),
                    type='n', las=1, xlab="Years",
                    xaxt='n', ylab="Annual Nesters",
                    yaxs='i', xaxs='i')
             polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.diff.det[1,], rev(proj.diff.det[3,])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
             lines(2018:2117, proj.diff.det[2,], col="darkorchid4", lwd=3)
             yrpretty <- pretty(2018:2118)[pretty(2018:2118)>2018 & pretty(2018:2118) < 2118]
             axis(1, yrpretty, yrpretty)
             mtext("Deterministic", side=3, font=3)
             fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)

             # Stochastic
             par(mar=c(4,4,1,1))
             plot(2018:2117, proj.diff.sto[2,],
                    xlim=c(2017,2118),
                    ylim=range(pretty(range(proj.diff.sto))),
                    type='n', las=1, xlab="Years",
                    xaxt='n', ylab="Annual Nesters",
                    yaxs='i', xaxs='i')
             polygon(x = c(2018:2117, rev(2018:2117)), y = c(proj.diff.sto[1,], rev(proj.diff.sto[3,])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
             lines(2018:2117, proj.diff.sto[2,], col="darkorchid4", lwd=3)
             yrpretty <- pretty(2018:2118)[pretty(2018:2118)>2018 & pretty(2018:2118) < 2118]
             axis(1, yrpretty, yrpretty)
             mtext("Stochastic", side=3, font=3)
             fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)
             legend("bottomleft", legend=c(expression(paste(N[j] - (N[j]-F)," Median")), expression(paste(N[j] -
(N[j]-F)," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA), pch=c(NA,15,NA,15),
col=c("darkorchid4",col2rgbA("darkorchid",0.5)), bty='n', pt.cex = 2, inset = c(0,0.1))
                        dev.off()
```

```
pdf(file=paste0(fig.path,spp,mode,"diff10.pdf"))
#### PROJECT 10
par(mfrow=c(2,1), mar=c(3,4,2,1))
# Deterministic
plot(2018:2027, proj.diff.det[2,1:10],
    xlim=c(2017.75,2027.25),
    ylim=range(pretty(range(proj.diff.det[,1:10]))),
    type='n', las=1, xlab="Years",
    xaxt='n', ylab="Annual Nesters",
    yaxs='i', xaxs='i')
polygon(x = c(2018:2027, rev(2018:2027)), y = c(proj.diff.det[1,1:10], rev(proj.diff.det[3,1:10])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
lines(2018:2027, proj.diff.det[2,1:10], col="darkorchid4", lwd=3)
yrpretty <- pretty(2018:2028)[pretty(2018:2028)>2018 & pretty(2018:2028) < 2028]
axis(1, yrpretty, yrpretty)
mtext("Deterministic", side=3, font=3)
fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)

# Stochastic
par(mar=c(4,4,1,1))
plot(2018:2027, proj.diff.sto[2,1:10],
    xlim=c(2017.75,2027.25),
    ylim=range(pretty(range(proj.diff.sto[,1:10]))),
    type='n', las=1, xlab="Years",
    xaxt='n', ylab="Annual Nesters",
    yaxs='i', xaxs='i')
polygon(x = c(2018:2027, rev(2018:2027)), y = c(proj.diff.sto[1,1:10], rev(proj.diff.sto[3,1:10])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
lines(2018:2027, proj.diff.sto[2,1:10], col="darkorchid4", lwd=3)
yrpretty <- pretty(2018:2028)[pretty(2018:2028)>2018 & pretty(2018:2028) < 2028]
axis(1, yrpretty, yrpretty)
mtext("Stochastic", side=3, font=3)
fig.lab("W. Pac. Leatherbacks", xscale=0.85, yscale=0.925, cex = 1)
```

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                      legend("bottomleft", legend=c(expression(paste(N[j] - (N[j]-F)," Median")), expression(paste(N[j] -
(N[j]-F)," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA), pch=c(NA,15,NA,15),
col=c("darkorchid4",col2rgbA("darkorchid",0.5)), bty='n', pt.cex = 2, inset = c(0,0.1))
                      dev.off()

            }else{
                  pdf(file=paste0(fig.path,spp,mode,"proj100.pdf"))
                      ###PROJECT 100
                      par(mfrow=c(2,1), mar=c(3,4,2,1))
                      # Deterministic
                      plot(2016:2115, proj.med[2,,keepers[1]],
                          xlim=c(2015,2116),
                          ylim=c(0,max(proj.med[2,,keepers])),
                          type='n', las=1, xlab="Years",
                          xaxt='n', ylab="Annual Nesters",
                          yaxs='i', xaxs='i')
                      polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.med[1,,keepers[1]],
rev(proj.med[3,,keepers[1]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                      polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.med[1,,keepers[2]],
rev(proj.med[3,,keepers[2]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                      lines(2016:2115, proj.med[2,,keepers[1]], col="dodgerblue4", lwd=3)
                      lines(2016:2115, proj.med[2,,keepers[2]], col="chartreuse4", lwd=3)
                      yrpretty <- pretty(2016:2116)[pretty(2016:2116)>2016 & pretty(2016:2116) < 2116]
                      axis(1, yrpretty, yrpretty)
                      mtext("Deterministic", side=3, font=3)
                      fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)

                      # Stochastic
                      par(mar=c(4,4,1,1))
                      plot(2016:2115, proj.med[2,,keepers[3]],
                          xlim=c(2015,2116),
                          ylim=c(0,max(proj.med[2,,keepers])),
                          type='n', las=1, xlab="Years",
```

```r
                          xaxt='n', ylab="Annual Nesters",
                          yaxs='i', xaxs='i')
                    polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.med[1,,keepers[3]],
rev(proj.med[3,,keepers[3]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                    polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.med[1,,keepers[4]],
rev(proj.med[3,,keepers[4]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                    lines(2016:2115, proj.med[2,,keepers[3]], col="dodgerblue4", lwd=3)
                    lines(2016:2115, proj.med[2,,keepers[4]], col="chartreuse4", lwd=3)
                    axis(1, yrpretty, yrpretty)
                    mtext("Stochastic", side=3, font=3)
                    fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)
                    legend("topleft", legend=c(expression(paste(N[j] -F," Median")), expression(paste(N[j] -F,"
95%CI")),expression(paste(N[j]," Median")), expression(paste(N[j]," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA),
pch=c(NA,15,NA,15), col=c("dodgerblue4",col2rgbA("dodgerblue3",0.5),"chartreuse4", col2rgbA("chartreuse3", 0.5)), bty='n', pt.cex
= 2, inset = c(0,0.1))
                 dev.off()

                 pdf(file=paste0(fig.path,spp,mode,"logproj100.pdf"))
                    ###PROJECT 100
                    par(mfrow=c(2,1), mar=c(3,4,2,1))
                    # Deterministic
                    plot(2016:2115, proj.log.med[2,,keepers[1]],
                          xlim=c(2015,2116),
                          ylim=c(0.0001,max(proj.log.med[,,keepers])),
                          type='n', las=1, xlab="Years",
                          xaxt='n', ylab="Annual Nesters",
                          yaxs='i', xaxs='i')
                    polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.log.med[1,,keepers[1]],
rev(proj.log.med[3,,keepers[1]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                    polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.log.med[1,,keepers[2]],
rev(proj.log.med[3,,keepers[2]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                    lines(2016:2115, proj.log.med[2,,keepers[1]], col="dodgerblue4", lwd=3)
                    lines(2016:2115, proj.log.med[2,,keepers[2]], col="chartreuse4", lwd=3)
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yrpretty <- pretty(2016:2116)[pretty(2016:2116)>2016 & pretty(2016:2116) < 2116]
axis(1, yrpretty, yrpretty)
mtext("Deterministic", side=3, font=3)
fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)

# Stochastic
par(mar=c(4,4,1,1))
plot(2016:2115, proj.log.med[2,,keepers[3]],
    xlim=c(2015,2116),
    ylim=c(0.0001,max(proj.log.med[,,keepers])),
    type='n', las=1, xlab="Years",
    xaxt='n', ylab="Annual Nesters",
    yaxs='i', xaxs='i')
polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.log.med[1,,keepers[3]],
rev(proj.log.med[3,,keepers[3]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.log.med[1,,keepers[4]],
rev(proj.log.med[3,,keepers[4]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
lines(2016:2115, proj.log.med[2,,keepers[3]], col="dodgerblue4", lwd=3)
lines(2016:2115, proj.log.med[2,,keepers[4]], col="chartreuse4", lwd=3)
axis(1, yrpretty, yrpretty)
mtext("Stochastic", side=3, font=3)
fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)
legend("topleft", legend=c(expression(paste(N[j] -F," Median")), expression(paste(N[j] -F,"
95%CI")),expression(paste(N[j]," Median")), expression(paste(N[j]," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA),
pch=c(NA,15,NA,15), col=c("dodgerblue4",col2rgbA("dodgerblue3",0.5),"chartreuse4", col2rgbA("chartreuse3", 0.5)), bty='n', pt.cex
= 2, inset=c(0,0.1))
dev.off()

pdf(file=paste0(fig.path,spp,mode,"proj10.pdf"))
#### PROJECT 10
par(mfrow=c(2,1), mar=c(3,4,2,1))
# Deterministic
plot(2016:2025, proj.med[2,1:10,keepers[1]],
```

```
                        xlim=c(2015.75,2025.25),
                        ylim=c(0,max(proj.med[,1:10,keepers])),
                        type='n', las=1, xlab="Years",
                        xaxt='n', ylab="Annual Nesters",
                        yaxs='i', xaxs='i')
                polygon(x = c(2016:2025, rev(2016:2025)), y = c(proj.med[1,1:10,keepers[1]],
rev(proj.med[3,1:10,keepers[1]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                polygon(x = c(2016:2025, rev(2016:2025)), y = c(proj.med[1,1:10,keepers[2]],
rev(proj.med[3,1:10,keepers[2]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                lines(2016:2025, proj.med[2,1:10,keepers[1]], col="dodgerblue4", lwd=3)
                lines(2016:2025, proj.med[2,1:10,keepers[2]], col="chartreuse4", lwd=3)
                yrpretty <- pretty(2016:2026)[pretty(2016:2026)>2016 & pretty(2016:2026) < 2026]
                axis(1, yrpretty, yrpretty)
                mtext("Deterministic", side=3, font=3)
                fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)

                # Stochastic
                par(mar=c(4,4,1,1))
                plot(2016:2025, proj.med[2,1:10,keepers[3]],
                        xlim=c(2015.75,2025.25),
                        ylim=c(0,max(proj.med[,1:10,keepers])),
                        type='n', las=1, xlab="Years",
                        xaxt='n', ylab="Annual Nesters",
                        yaxs='i', xaxs='i')
                polygon(x = c(2016:2025, rev(2016:2025)), y = c(proj.med[1,1:10,keepers[3]],
rev(proj.med[3,1:10,keepers[3]])), border=FALSE, col=col2rgbA("dodgerblue3", 0.5))
                polygon(x = c(2016:2025, rev(2016:2025)), y = c(proj.med[1,1:10,keepers[4]],
rev(proj.med[3,1:10,keepers[4]])), border=FALSE, col=col2rgbA("chartreuse3", 0.5))
                lines(2016:2025, proj.med[2,1:10,keepers[3]], col="dodgerblue4", lwd=3)
                lines(2016:2025, proj.med[2,1:10,keepers[4]], col="chartreuse4", lwd=3)
                axis(1, yrpretty, yrpretty)
                mtext("Stochastic", side=3, font=3)
                fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)
```

```
                    legend("topleft", legend=c(expression(paste(N[j] -F," Median")), expression(paste(N[j] -F,"
95%CI"))),expression(paste(N[j]," Median")), expression(paste(N[j]," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA),
pch=c(NA,15,NA,15), col=c("dodgerblue4",col2rgbA("dodgerblue3",0.5),"chartreuse4", col2rgbA("chartreuse3", 0.5)), bty='n', pt.cex
= 2, inset = c(0,0.1))
                    dev.off()

                    pdf(file=paste0(fig.path,spp,mode,"diff100.pdf"))
                         ###PROJECT 100
                         par(mfrow=c(2,1), mar=c(3,4,2,1))
                         # Deterministic
                         plot(2016:2115, proj.diff.det[2,],
                             xlim=c(2015,2116),
                             ylim=range(pretty(range(proj.diff.det))),
                             type='n', las=1, xlab="Years",
                             xaxt='n', ylab="Annual Nesters",
                             yaxs='i', xaxs='i')
                         polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.diff.det[1,], rev(proj.diff.det[3,])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
                         lines(2016:2115, proj.diff.det[2,], col="darkorchid4", lwd=3)
                         yrpretty <- pretty(2016:2116)[pretty(2016:2116)>2016 & pretty(2016:2116) < 2116]
                         axis(1, yrpretty, yrpretty)
                         mtext("Deterministic", side=3, font=3)
                         fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)

                         # Stochastic
                         par(mar=c(4,4,1,1))
                         plot(2016:2115, proj.diff.sto[2,],
                             xlim=c(2015,2116),
                             ylim=range(pretty(range(proj.diff.sto))),
                             type='n', las=1, xlab="Years",
                             xaxt='n', ylab="Annual Nesters",
                             yaxs='i', xaxs='i')
```

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                polygon(x = c(2016:2115, rev(2016:2115)), y = c(proj.diff.sto[1,], rev(proj.diff.sto[3,])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
                lines(2016:2115, proj.diff.sto[2,], col="darkorchid4", lwd=3)
                yrpretty <- pretty(2016:2116)[pretty(2016:2116)>2016 & pretty(2016:2116) < 2116]
                axis(1, yrpretty, yrpretty)
                mtext("Stochastic", side=3, font=3)
                fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)
                legend("topleft", legend=c(expression(paste(N[j] - (N[j]-F)," Median")), expression(paste(N[j] - (N[j]-
F)," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA), pch=c(NA,15,NA,15), col=c("darkorchid4",col2rgbA("darkorchid",0.5)),
bty='n', pt.cex = 2, inset = c(0,0.1))
                dev.off()

        pdf(file=paste0(fig.path,spp,mode,"diff10.pdf"))
                #### PROJECT 10
                par(mfrow=c(2,1), mar=c(3,4,2,1))
                # Deterministic
                plot(2016:2025, proj.diff.det[2,1:10],
                    xlim=c(2015.75,2025.25),
                    ylim=range(pretty(range(proj.diff.det[,1:10]))),
                    type='n', las=1, xlab="Years",
                    xaxt='n', ylab="Annual Nesters",
                    yaxs='i', xaxs='i')
                polygon(x = c(2016:2025, rev(2016:2025)), y = c(proj.diff.det[1,1:10], rev(proj.diff.det[3,1:10])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
                lines(2016:2025, proj.diff.det[2,1:10], col="darkorchid4", lwd=3)
                yrpretty <- pretty(2016:2026)[pretty(2016:2026)>2016 & pretty(2016:2026) < 2026]
                axis(1, yrpretty, yrpretty)
                mtext("Deterministic", side=3, font=3)
                fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)

                # Stochastic
                par(mar=c(4,4,1,1))
                plot(2016:2025, proj.diff.sto[2,1:10],
```

```r
                                            xlim=c(2015.75,2025.25),
                                            ylim=range(pretty(range(proj.diff.sto[,1:10]))),
                                            type='n', las=1, xlab="Years",
                                            xaxt='n', ylab="Annual Nesters",
                                            yaxs='i', xaxs='i')
                                    polygon(x = c(2016:2025, rev(2016:2025)), y = c(proj.diff.sto[1,1:10], rev(proj.diff.sto[3,1:10])),
border=FALSE, col=col2rgbA("darkorchid", 0.5))
                                            lines(2016:2025, proj.diff.sto[2,1:10], col="darkorchid4", lwd=3)
                                            yrpretty <- pretty(2016:2026)[pretty(2016:2026)>2016 & pretty(2016:2026) < 2026]
                                            axis(1, yrpretty, yrpretty)
                                            mtext("Stochastic", side=3, font=3)
                                            fig.lab("N. Pac. Loggerheads", xscale=0.15, yscale=0.925, cex = 1)
                                            legend("topleft", legend=c(expression(paste(N[j] - (N[j]-F)," Median")), expression(paste(N[j] - (N[j]-
F)," 95%CI"))), lty=c(1,NA,1,NA), lwd=c(3,NA,3,NA), pch=c(NA,15,NA,15), col=c("darkorchid4",col2rgbA("darkorchid",0.5)),
bty='n', pt.cex = 2, inset = c(0,0.1))
                                    dev.off()
                            }

                    return(list(tab.yr = tab.yr,
                            tab.prob = tab.prob))
        }
cor.lab <- function(x, y, xscale, yscale, cex=1.2, adj=c(0.5,0.5)){
            xpt <- par('usr')[1]+abs(diff(par('usr')[1:2]))*xscale
            ypt <- par('usr')[3]+abs(diff(par('usr')[3:4]))*yscale

            cor <- round(cor(x,y),2)

            text(xpt, ypt, cor, xpd=NA, cex=cex, adj=adj)
        }
kde.plot <- function(x, y, n=100){
            kde <- MASS::kde2d(x, y, n=n)
            kde$z <- kde$z/max(kde$z)
            contour(kde, levels=c(0.05, 0.5), col='black', drawlabels=FALSE, add=TRUE, lwd=c(1,3))
```

```r
}
plot.joint <- function(trend, spp, graph){
        d.u <- density(trend$U, adj=2)
        d.N0 <- density(trend$N0, adj=2)
        d.Q <- density(trend$Q, adj=2)

        d.u$y <- d.u$y/max(d.u$y)
        d.N0$y <- d.N0$y/max(d.N0$y)
        d.Q$y <- d.Q$y/max(d.Q$y)

        samp <- sample(1:nrow(trend), floor(0.5*nrow(trend)))
        pdf(file=paste0(fig.path,spp,"joint_post.pdf"))
                par(mfrow=c(3,3), mar=c(4,4,1,1), cex.axis=1.1, cex.lab=1.1)
        for(i in 1:9){
                if(i ==1) {
                        #1
                        plot(d.u$x, d.u$y, type='l', xlab='U', ylab='Rel. Density', ylim=c(0,1), yaxt='n', las=1)
                        axis(2, at=pretty(c(0,1)), las=1)
                }
                if(i==2){
                        #2
                        plot(trend$U, trend$N0, pch=".", col='grey80', xlab='U', ylab=expression(N[0]), las=1)
                        kde.plot(trend$U[samp], trend$N0[samp], n=100)
                }
                if(i==3){
                        #3
                        plot(trend$U[samp], trend$Q[samp], pch=".", col='grey80',xlab='U', ylab='Q', las=1)
                        kde.plot(trend$U, trend$Q, n=100)
                }
                if(i==4){
                        #4
                        plot.new()
                        box()
```

```
                cor.lab(trend$U, trend$N0, xscale=0.5, yscale=0.5, cex=1.4)
                fig.lab(expression(paste("U, ",N[0])), xscale=0.15, yscale=0.1, cex=1.1)
        }
        if(i==5){
                #5
                plot(d.N0$x, d.N0$y, type='l', xlab=expression(N[0]), ylab='Rel. Density', ylim=c(0,1), yaxt='n', las=1)
                axis(2, at=pretty(c(0,1)), las=1)
        }
        if(i==6){
                #6
                plot(trend$N0[samp], trend$Q[samp], pch=".", col='grey80',xlab=expression(N[0]), ylab='Q', las=1)
                kde.plot(trend$N0, trend$Q, n=100)
        }
        if(i==7){
                #7
                plot.new()
                box()
                cor.lab(trend$U, trend$Q, xscale=0.5, yscale=0.5, cex=1.4)
                fig.lab("U, Q", xscale=0.15, yscale=0.1, cex=1.1)
        }
        if(i==8){
                #8
                plot.new()
                box()
                cor.lab(trend$N0, trend$Q, xscale=0.5, yscale=0.5, cex=1.4)
                fig.lab(expression(paste(N[0],", Q")), xscale=0.15, yscale=0.1, cex=1.1)
        }
        if(i==9){
                #9
                plot(d.Q$x, d.Q$y, type='l', xlab='Q', ylab='Rel. Density', ylim=c(0,1), yaxt='n', las=1)
                axis(2, at=pretty(c(0,1)), las=1)
        }
        if(i==graph) legend("topright", legend=c("0.05", "0.5"), lwd=c(1,3), bty='n')
```

```
        }
        dev.off()
}
mvnorm <- "
        functions {
                matrix cov_matrix_2d(vector sigma, real rho) {
                    matrix[2,2] Sigma;
                    Sigma[1,1] = square(sigma[1]);
                    Sigma[2,2] = square(sigma[2]);
                    Sigma[1,2] = sigma[1] * sigma[2] * rho;
                    Sigma[2,1] = Sigma[1,2];
                    return Sigma;
                 }
        }
        data {
                int<lower=1> N; //number of obs
                vector[2] x[N]; //lengths and mortality
                int<lower=1> nyear; //number of years
                int<lower=1> year[N]; //year pointer
                vector[nyear] rtl; // realized take
        }
        parameters {
                real<lower=-1, upper=1> rho; //correlation
                vector<lower=0>[2] sigma; //sigma of mus
                real beta0; //int for rtl
                real beta1; //slope for rtl
                real mu0; //mu for m
        }
        transformed parameters{
                vector[2] mu[nyear];
                for(y in 1:nyear){
                        mu[y,1] = beta0 + beta1*rtl[y];
                        mu[y,2] = mu0;
```

```
                    }
            }
            model {
                    mu0 ~ normal(0,2);
                    beta0 ~ normal(0,2);
                    beta1 ~ normal(0,2);
                    sigma ~ normal(0,2);
                    (rho + 1) / 2 ~ beta(2, 2);

                    for(n in 1:N){
                            x[n] ~ multi_normal(mu[year[n]], cov_matrix_2d(sigma, rho));
                    }
            }"
mv.DC.init <- function(chain_id){
        lm <- lm(log(Len)~Year, data=DC.td.df)

        beta0 <- rnorm(1, coef(lm)[1], abs(coef(lm)[1]*0.1))
        beta1 <- rnorm(1, coef(lm)[2], abs(coef(lm)[2]*0.1))

        mu0 <- rnorm(1, 0, 1)

        sigma <- rtruncnorm(2, a=0, mean = apply(DC.td.dat$x, 2, sd), sd = apply(DC.td.dat$x, 2, sd)*0.1)
        rho <- rtruncnorm(1, a=-1, b=1, cor(DC.td.dat$x)[1,2], abs(cor(DC.td.dat$x)[1,2]*0.1))

        return(list(beta0 = beta0,
                    beta1 = beta1,
                    mu0 = mu0,
                    sigma = sigma,
                    rho = rho))
}
mv.CC.init <- function(chain_id){
        lm <- lm(log(Len)~Year, data=CC.td.df)
```

```r
        beta0 <- rnorm(1, coef(lm)[1], abs(coef(lm)[1]*0.1))
        beta1 <- rnorm(1, coef(lm)[2], abs(coef(lm)[2]*0.1))

        mu0 <- rnorm(1, 0, 1)

        sigma <- rtruncnorm(2, a=0, mean = apply(CC.td.dat$x, 2, sd), sd = apply(CC.td.dat$x, 2, sd)*0.1)
        rho <- rtruncnorm(1, a=-1, b=1, cor(CC.td.dat$x)[1,2], abs(cor(CC.td.dat$x)[1,2]*0.1))

        return(list(beta0 = beta0,
                beta1 = beta1,
                mu0 = mu0,
                sigma = sigma,
                rho = rho))
}
vbgm_stan_l0_ln <- "
        data{
                int<lower=1> n_obs; //number of observations
                vector<lower=0>[n_obs] age; //ages of fish
                vector<lower=0>[n_obs] l; //length of fish
                int<lower=1> nseq;
                vector<lower=0>[nseq] seq_ages;
                int<lower=1> n_hatchlings;
                vector<lower=0>[n_hatchlings] hatchling_size;
                real<lower=0> nester_size;
                real<lower=0> nester_sd;
        }
        parameters{
                real<lower=0> Linf; //L infinity
                real<lower=0> K; //vb K
                real<lower=0> Lknot; //t knot

                real<lower=0> sigma_obs; //sigma_obs
                real<lower=0> sigma_Lknot; //sigma_obs
```

```
        }
        model{
                vector[n_obs] Lpred;
                Linf ~ normal(nester_size, nester_sd);
                K ~ normal(0.1, 0.5);
                Lknot ~ normal(4, 0.2);

                sigma_obs ~ normal(0, 1);
                sigma_Lknot ~ normal(0, 1);

                for(i in 1:n_obs){
                        Lpred[i] = Linf - (Linf-Lknot)*exp(-K*age[i]);
                         target += lognormal_lpdf(l[i]|log(Lpred[i]), sigma_obs);
                }
                for(i in 1:n_hatchlings){
                        target += lognormal_lpdf(hatchling_size[i]|log(Lknot),sigma_Lknot);
                }
        }
        generated quantities{
                real Amat;
                real tknot;
                vector[nseq] Lage;
                Amat = (1/K)*log((Linf-Lknot)/(Linf*(1-0.975)));
                tknot = (1/K)*log((Linf-Lknot)/Linf);

                for(i in 1:nseq){
                        Lage[i] = Linf - (Linf-Lknot)*exp(-K*seq_ages[i]);
                }
}"
init.vbgm.l0 <- function(chain_id){
        return(list(Linf = rtruncnorm(1, a=0, mean=nester_size, sd=nester_sd),
                        K = rtruncnorm(1, a=0, mean=0.1, sd=0.01),
                        Lknot = rtruncnorm(1,a=0, mean=hatchling_size,sd=hatchling_sd),
```

```
                      sigma_obs = rtruncnorm(1, a=0, mean=1, sd=0.01),
                          sigma_Lknot = rtruncnorm(1, a=0, mean=1, sd=0.01)))
}
```

C.   Projections

```
### Bayesian state-space model for estimating long-term trend in nest count time series data
### Original model estimation code adapted from Boyd et al. (2016) paper; code provided by C. Boyd
### Future projections and evaluation of probabilities code by S. Martin
### with input from T. Eguchi, B. Langseth, A. Yau, J. Baker, T. Jones, R. Ahrens, Z. Siders, N. Ducharme-Barth

#setwd(save.dir)
require(ggplot2)

##==================================================================================
# SELECT MODELING OPTION BELOW depending on what model we're using (**FINAL** options only here for this script):
##==================================================================================
# -------------------------------------
# 1. Set up Loggerheads Model = singleUQ (using 3 time series of nest counts from Yakushima)
# -------------------------------------
if(scenario=="Cc_Yakushima_sUQ"){
  # name of file directory to save model results into
 if (file.exists(save.dir)){                     # if file directory exists, set wd to it
   setwd(file.path(save.dir))
 } else {                              # if file directory doesn't exist, create it, then set wd to it
   dir.create(file.path(save.dir))
   setwd(file.path(save.dir))
 }
 rdatafile <- paste(scenario, ".RData", sep="")      # can use load(file=rdatafile) if you've already run code and want to re-load results
 file.tag <- paste(scenario,"_", Sys.Date(), sep="")   # to add to output file names below
 thedata <- thedata.loggers[2:31, c(1,6,5,7)] # remove first row due to all NAs; put beach w/ first year of data in first data column
 data.cols <- 2:4              # columns of Annual Females data to analyze
 data.rows <- 1:30                 # rows=Years of data to analyze; must start with a value rather than NA for at least 1 time series
```

```
  write.csv(thedata[data.rows , c(1,data.cols)], file=paste(file.tag,"_0_data_used.csv",sep=""),quote=FALSE, row.names=FALSE) #
export actual data feeding into model
  modl <- "singleUQ"
  data.type <- "Annual_Females"            # this is from when we were testing variants of Annual vs. Total Femals vs. Nests
  pop.name <- c("Inakahama", "Maehama", "Yotsuse")   # code below uses these population names, e.g., for plots
  pop.name.combo <- "N. Pacific Loggerheads - Yakushima 3 beaches"   # code below uses for plots
  remig <- remigLH
  clutch.freq <- clutch.freqLH
}


# ---------------------------------------
# 2. Set up Leatherbacks Model = singleUQ (with JM and W separate time series BUT *same* trend/process)
# 2A. Uses ** MEDIAN ** nest count estimates from Tomo's imputation model output
# 2B. Uses ** LOW ** (lower 95% CI) nest count estimates from Tomo's imputation model output
# 2C. Uses ** HIGH ** (upper 95% CI) nest count estimates from Tomo's imputation model output
# ---------------------------------------
if(scenario=="Dc_JM&W_MEDIAN_sUQ"|scenario=="Dc_JM&W_LOW_sUQ"|scenario=="Dc_JM&W_HIGH_sUQ") {
  if (file.exists(save.dir)){
    setwd(file.path(save.dir))
  } else {
    dir.create(file.path(save.dir))
    setwd(file.path(save.dir))
  }
  rdatafile <- paste(scenario, ".RData", sep="")      # can use load(file=rdatafile) if you've already run code and want to re-load results
  file.tag <- paste(scenario,"_", Sys.Date(), sep="")  # to add to output file names below
  thedata <- thedata.leathers
  data.cols <- 2:3            # columns of Annual Females data to analyze
  data.rows <- 1:17           # need to start with a value rather than NA for at least 1 time series
  write.csv(thedata[data.rows , c(1,data.cols)], file=paste(file.tag,"_0_data_used.csv",sep=""),quote=FALSE, row.names=FALSE) #
export actual data feeding into model
  modl <- "singleUQ"
  data.type <- "Annual_Females"   # this is from when we were testing variants of Annual vs. Total Femals vs. Nests
  pop.name <- c("Jamursba Medi Leatherback Turtles", "Wermon Leatherback Turtles")
```

```
   pop.name.combo <- "Western Pacific Leatherback Turtles"
   remig <- remigLB          # remigration interval in years (for run sum period)
   clutch.freq <- clutch.freqLB
}
##===============================================================================


##===============================================================================
# PLOT DATA
##===============================================================================

# SINGLE TIME SERIES:
# --------------------------------------
if(length(pop.name)==1) {
 png(filename=paste(file.tag,"_0", "_data_rawNests.png", sep=""), width=650, height=575, units="px")
 par(mfrow=c(1,1), mar=c(5, 5, 4, 2) + 0.1)
 plot(thedata[,1], clutch.freq*thedata[ ,data.cols], pch=19,
     ylim=range(clutch.freq*thedata[ ,data.cols], na.rm=T), xlab="Season", ylab="Nest Counts", main=pop.name,
     cex.lab=1.5, cex.axis=1.5, cex.main=2, cex=1.75)
 lines(thedata[,1], clutch.freq*thedata[ ,data.cols], lwd=2, cex=1.5)
 dev.off()

 png(filename=paste(file.tag,"_1", "_data_lnFemales.png", sep=""), width=650, height=575, units="px")
 par(mfrow=c(1,1), mar=c(5, 5, 4, 2) + 0.1)
 plot(thedata[,1], log(thedata[ ,data.cols]), pch=19, ylim=range(log(thedata[ ,data.cols]), na.rm=T),
     xlab="Season", ylab="Ln(Annual Females)", main=pop.name,
     cex.lab=1.5, cex.axis=1.5, cex.main=2, cex=1.75)
 lines(thedata[,1], log(thedata[ ,data.cols]), lwd=2, cex=1.5)
 dev.off()
}
```

```
# MULTIPLE TIME SERIES:
# ---------------------------------------
if(length(pop.name)>1) {
  for (i in 1:length(pop.name)) {
    png(filename=paste(file.tag,"_0.", i, "_data_rawNests.png", sep=""), width=650, height=575, units="px")
    par(mfrow=c(1,1), mar=c(5, 5, 4, 2) + 0.1)
    plot(thedata[,1], clutch.freq*thedata[,i+1], pch=19,
        ylim=range(clutch.freq*thedata[,i+1], na.rm=T), xlab="Season", ylab="Nest Counts", main=pop.name[i],
        cex.lab=1.5, cex.axis=1.5, cex.main=2, cex=1.75)
    lines(thedata[,1], clutch.freq*thedata[,i+1], lwd=2, cex=1.5)
    dev.off()
  }

  for (i in 1:length(pop.name)) {
    png(filename=paste(file.tag,"_1.", i, "_data_lnFemales.png", sep=""), width=650, height=575, units="px")
    par(mfrow=c(1,1), mar=c(5, 5, 4, 2) + 0.1)
    plot(thedata[,1], log(thedata[,i+1]), pch=19, ylim=range(log(thedata[,i+1]), na.rm=T),
        xlab="Season", ylab="Ln(Annual Females)", main=pop.name[i],
        cex.lab=1.5, cex.axis=1.5, cex.main=2, cex=1.75)
    lines(thedata[,1], log(thedata[,i+1]), lwd=2, cex=1.5)
    dev.off()
  }
}
##===========================================================================
```

```
##=================================================================
# TRANSFORM DATA: into natural log (Ln) space for the model
##=================================================================
log.data <- log(thedata[data.rows , data.cols])     # Ln(TOTAL NUMBER OF FEMALES)
data.mat <- t(log.data)    # tranpose to have rows = time series and cols = years of data
data.mat
##=================================================================



##=================================================================
## Model setup definitions and priors
##=================================================================
# Model options:
# 1: single population process (singleUQ)
# 2: independent trend, independent variance, covariance
# 3: independent population processes

# Data
dat <- data.mat     # matrix with rows = different time series and cols = years of data within those time series
n.yrs <- ncol(dat)
n.timeseries <- nrow(dat)
Y <- rbind(dat, NA)   # add a row (ie time series of data) to trick jagsUI into NOT converting single time series matrix to vector
Y

# Set priors
a_mean <- 0
a_sd <- 4

u_mean <- 0
u_sd <- 0.05

q_alpha <- 8
q_beta <- 2
```

```
r_alpha <- 8
r_beta <- 2


# Note: The initial state, x0, is treated as a model parameter.
# the prior matters for Wermon - setting mean to first JM data point skews Wermon to JM trend due to poor W data
# making it specific to each time series for independentUQ

# for singleUQ, set mean of X0 based on first time series (first data point of it)
if(modl=="singleUQ") {
  x0_mean <- dat[1,1]    # take the first data point of first time series (JM for leathers)
  x0_sd <- 10            # we went with wide sd by testing for both JM and W for leathers; 10 works to make it super wide so as to not
influence Wermon
}


# Set MCMC parameters
n.samples <- 10000   # 1000; bumped up to 5000 per CB after geweke.diag for deviance in chain 1 looked high at 2.1830; gives
10,000 across the 2 chains
mcmc.chains <- 2     # 2 is min; AY uses 3
mcmc.thin <- 50      # 50-100 is more than safe; 500 seems excessive per AY
mcmc.burn <- 5000    # 1000; also bumped up to 5000 (same as n.samples) per CB after geweke.diag for deviance in chain 1 still
looked high at 2.2
samples2Save <- (mcmc.burn + n.samples) * mcmc.thin
##=====================================================================================
```

```
##=================================================================================
# Model 1:  'singleUQ' ... multiple time series -> single population process (trend)
# This is the final one we are using (7/31/19), not the Independent UQ model below, but left that in for now
##=================================================================================
if(modl=="singleUQ"){

  # Model-specific parameters
  whichPop <- rep(1,n.timeseries) # multiple time series -> single population process
  n.states <- max(whichPop)

  Z <- matrix(0,n.timeseries+1,n.states+1)   # matrix with rows as n.timeseries and cols as n.states (pops)
  Z[n.timeseries+1, ] <- NA            # add a row of NAs to keep jagsUI from converting single time series matrix into vector
  Z[ , n.states+1] <- NA            # add a col of NAs to keep jagsUI from converting single state matrix into vector
  for(i in 1:length(whichPop)) Z[i,whichPop[i]] <- 1
  Z

  jags.data <-
list("Y","n.yrs","n.timeseries","Z","a_mean","a_sd","u_mean","u_sd","q_alpha","q_beta","r_alpha","r_beta","x0_mean","x0_sd")
  jags.params <- c("A", "U", "Q", "R", "X0", "X")
  model.loc <- paste(main.folder, "singleUQ.txt", sep="")

  # Run model
  set.seed <- 132
  jags.model <- jags(jags.data,
              inits = NULL,
              parameters.to.save= jags.params,
              model.file=model.loc,
              n.chains = mcmc.chains,
              n.burnin = mcmc.burn*mcmc.thin,
              n.thin = mcmc.thin,
              n.iter = samples2Save,
              DIC = T,
              parallel=T,
```

```
                seed=set.seed)
  print(jags.model)
}
##============================================================================


##============================================================================
# DIAGNOSTICS: Trace plots - CB didn't like the ones from jagsUI so these were her own...
##============================================================================
labpar<-c("U", "Q", "R", "X0", "deviance")
xx <- 1:n.samples

outs <- array(NA, c(n.samples, 2, length(labpar)))  # order is: rows, cols, matrices: 5 matrices w/ nrows=n.samples, ncols=5)
# row, col, matrix
outs[,1,1] <- jags.model$sims.list$U[1:n.samples]
outs[,2,1] <- jags.model$sims.list$U[(n.samples+1):(n.samples*2)]
outs[,1,2] <- jags.model$sims.list$Q[1:n.samples]
outs[,2,2] <- jags.model$sims.list$Q[(n.samples+1):(n.samples*2)]
outs[,1,3] <- jags.model$sims.list$R[1:n.samples]
outs[,2,3] <- jags.model$sims.list$R[(n.samples+1):(n.samples*2)]
outs[,1,4] <- jags.model$sims.list$X0[1:n.samples]
outs[,2,4] <- jags.model$sims.list$X0[(n.samples+1):(n.samples*2)]
outs[,1,5] <- jags.model$sims.list$deviance[1:n.samples]
outs[,2,5] <- jags.model$sims.list$deviance[(n.samples+1):(n.samples*2)]

png(filename=paste(file.tag,"_3_Trace_plots.png", sep=""), width=650, height=575, units="px")
par(mfrow=c(2, 3))
for(j in 1:length(labpar)) {
  plot(xx, outs[,1,j], xlab="cycle number", ylab=labpar[j],type='b',pch=16, ylim=range(outs[,,j]))
  lines(xx, outs[,2,j], type='b',pch=16, col="gray50")
}
dev.off()
##============================================================================
```

```
##=====================================================================
# MORE DIAGNOSTICS - export to files
##=====================================================================
McmcList <- vector("list",mcmc.chains)
for(i in 1:length(McmcList)) McmcList[[i]] <- as.mcmc(outs[,i,])

# Write model diagnostics to txt file
sink(paste(file.tag,"_4_model_diagnostics_", modl, ".txt", sep="")) # open file
print("effectiveSize(McmcList[[1]])")
print(effectiveSize(McmcList[[1]]))
cat("\n")

print("effectiveSize(McmcList[[2]])")
print(effectiveSize(McmcList[[2]]))
cat("\n")

print("geweke.diag(McmcList[[1]])")
print(geweke.diag(McmcList[[1]])) # the test statistic is the standard z score for the equality of two means - value greater than 1.96
(p<0.05) two-tailed
#cat("\n")

print("geweke.diag(McmcList[[2]])")
print(geweke.diag(McmcList[[2]]))
#cat("\n")

print("gelman.diag(McmcList)")
print(gelman.diag(McmcList)) # values of the statistic should be small for each parameter (i.e. 1.00-1.05).
sink()   # close file
##=====================================================================
```

```
##=========================================================================
# WRITE the model file"jags.model" to a txt file
##=========================================================================
file.jags <- paste(file.tag,"_2_Jags_model_", modl, ".txt", sep="")
sink(file.jags) # open file
print(jags.model)
sink()   # close file
##=========================================================================




##=========================================================================
# PLOT MODEL FIT GRAPH: with data points, median model predicted counts, 95% CI band shading
##=========================================================================
# Define a color for confidence interval bounds on plot
col2rgb("gray", alpha=TRUE) # get specs on gray color to use in polygon and tweak transparency
mygray <- rgb(red=190, green=190, blue=190, alpha=200, maxColorValue=255)

# PLOT model fit line (estimated trend line) on top of the data  with 95% CI shading
jags.model$q50$X   # median
length(jags.model$q50$X)  # should be number of years of data

# SINGLE TIME SERIES:
# ---------------------------------------
if(length(pop.name)==1){
  png(filename=paste(file.tag,"_6_model_fit_med95.png", sep=""), width=650, height=575, units="px")
  par(mfrow=c(1,1), mar=c(5, 5, 4, 2) + 0.1)
  #ylim.specs <- c(range(log.data, na.rm=T)[1]*.95, range(log.data, na.rm=T)[2]*1.05)  # add 5% to min & max values for y axis
  y.low <- min(min(jags.model$q2.5$X), min(log.data, na.rm=T))        # min of data or CI
  y.hi <- 1.05*max(max(jags.model$q97.5$X), max(log.data, na.rm=T))  # max of data or CI
  ylim.specs <- c(y.low, y.hi)

  plot(thedata[data.rows,1], log.data, pch=19, ylim=ylim.specs, xlab="Year", ylab="Ln(Annual Females)", main=pop.name,
```

```r
      cex.lab=1.5, cex.axis=1.5, cex.main=2, cex=1.75)
  polygon(x= c(thedata[data.rows,1][1], thedata[data.rows,1], rev(thedata[data.rows,1])),            # add 95% CI shading from
JAGS model output
        y= c(jags.model$q2.5$X[1], jags.model$q97.5$X, rev(jags.model$q2.5$X)),
        col=mygray, lty=0)
  lines(thedata[data.rows,1], jags.model$q50$X, col="blue", lwd=2)        # plot median fit line (better than mean for Bayes)
  points(thedata[data.rows,1], log.data, lwd=2, type="p", pch=16, cex=1.75) # add points back over CI shading
  dev.off()
}

# MULTIPLE TIME SERIES:
# ---------------------------------------
if(length(pop.name)>1){
  y.vec.low <- jags.model$q2.5$X   # create vector with lower 95% values for X
  y.vec.hi <- jags.model$q97.5$X   # create vector with upper 95% values for X

  for (i in 2:length(pop.name)){   # for each time series, the X values are really X+A; put all in one vec to find min & max for plot
limits
    y.vec.low <- c(y.vec.low,  jags.model$q2.5$X + jags.model$q2.5$A[i])
    y.vec.hi <- c(y.vec.hi, jags.model$q97.5$X + jags.model$q97.5$A[i])
  }

  y.low <- min(min(y.vec.low), min(log.data, na.rm=T))        # plot limits; min of data or CI
  y.hi <- 1.05*max(max(y.vec.hi), max(log.data, na.rm=T))     # plot limits; max of data or CI
  ylim.specs <- c(y.low, y.hi)

  for (i in 1:length(pop.name)){
    png(filename=paste(file.tag,"_6.", i, "_model_fit_med95.png", sep=""), width=650, height=575, units="px")
    par(mfrow=c(1,1), mar=c(5, 5, 4, 2) + 0.1)
    plot(thedata[data.rows,1], log.data[data.rows,i], pch=19, ylim=ylim.specs, xlab="Year", ylab="Ln(Annual Females)",
main=pop.name[i],
        cex.lab=1.5, cex.axis=1.5, cex.main=2, cex=1.75)
```

```
  # Add in 'A' scaling factor from the model estimates
    polygon(x= c(thedata[data.rows,1][1], thedata[data.rows,1], rev(thedata[data.rows,1])),              # add 95% CI shading from
JAGS model output
        y= c(jags.model$q2.5$X[1]+jags.model$q2.5$A[i], jags.model$q97.5$X+jags.model$q97.5$A[i],
rev(jags.model$q2.5$X+jags.model$q2.5$A[i])),
        col=mygray, lty=0)
    lines(thedata[,1], jags.model$q50$X+jags.model$q50$A[i], col="blue", lwd=2)        # plot median fit line (better than mean for
Bayes)

    points(thedata[,1], log.data[,i], lwd=2, type="p", pch=16, cex=1.75) # add points back over CI shading
    dev.off()
  }
}
# Save output
saveRDS(jags.model, paste(file.tag, ".rds", sep=""))   # SLM: this is an R workspace file to re-load work thus far if needed
##==================================================================================
fy <- length(thedata[data.rows,1])      # final year of observed data; 22 for loggerheads; 17 for leatherbacks (JM)
yrf=100                     # 100 = years into the future
nsim=10000                      # number of sim runs; length(jags.model$sims.list$X[ ,fy])

Umed=jags.model$q50$U                # for reporting results, median is best
Umean=jags.model$mean$U                 # but for simulations, use mean, sd in distribution
Usd=jags.model$sd$U
Uvar=Usd^2
Uci=c(jags.model$q2.5$U, jags.model$q97.5$U)

lambda.mean=exp(Umean)
lambda.med=exp(Umed)
lambda.var=exp(Uvar)
lambda.ci=exp(Uci)

Qmed=jags.model$q50$Q
Qmean=jags.model$mean$Q
```

```
Qsd=jags.model$sd$Q

X.len <- length(jags.model$sims.list$X[,fy-0])
X.thin <- seq(from=1, to=X.len, by = X.len/nsim)  # make length of the X estimate vectors same as nsim, (thin by every other value
from MCMC samples)

# **SINGLE** time series
# --------------------------------------
if(length(pop.name)==1){
  X.fym0 <- exp(jags.model$sims.list$X[,fy-0][X.thin])  # Number of Annual Females in final data year
  X.fym1 <- exp(jags.model$sims.list$X[,fy-1][X.thin])  # final data year minus one
  X.fym2 <- exp(jags.model$sims.list$X[,fy-2][X.thin])
  X.fym3 <- exp(jags.model$sims.list$X[,fy-3][X.thin])
}

# **MULTIPLE TIME SERIES** (e.g., for leatherbacks, need to account for X representing JM since A=0 and X+A representing W
since A!=0)
# e.g., Annual Females estimate for JM & W combined = exp(X) + exp(X+A), where first part is JM and second is for W.
# --------------------------------------
if(length(pop.name)>1){
  X.fym0 <- exp(jags.model$sims.list$X[,fy-0][X.thin])  # Number of Annual Females in final data year
  X.fym1 <- exp(jags.model$sims.list$X[,fy-1][X.thin])  # final data year minus one
  X.fym2 <- exp(jags.model$sims.list$X[,fy-2][X.thin])
  X.fym3 <- exp(jags.model$sims.list$X[,fy-3][X.thin])

  for (i in 2:length(pop.name)){
    X.fym0 <- X.fym0 + exp(jags.model$sims.list$X[,fy-0][X.thin] + jags.model$sims.list$A[,i][X.thin])  # rescaling to correct
magnitude
    X.fym1 <- X.fym1 + exp(jags.model$sims.list$X[,fy-1][X.thin] + jags.model$sims.list$A[,i][X.thin])
    X.fym2 <- X.fym2 + exp(jags.model$sims.list$X[,fy-2][X.thin] + jags.model$sims.list$A[,i][X.thin])
    X.fym3 <- X.fym3 + exp(jags.model$sims.list$X[,fy-3][X.thin] + jags.model$sims.list$A[,i][X.thin])
  }
}
```

```
###@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
## plot the fit

X.total <- apply(cbind(jags.model$sims.list$X0,jags.model$sims.list$X), 2, function(v) rowSums(apply(jags.model$sims.list$A[,], 2,
function(x) exp(v+x))))

X0.total <- rowSums(apply(jags.model$sims.list$A[,], 2, function(x) exp(jags.model$sims.list$X0+x)))

X.total.med <- apply(log(X.total),2,median)

# X.fit <- apply(sapply(jags.model$sims.list$U, function(x) {x * seq(0,nrow(thedata))}), 1, function(x) x + log(X0.total))

X.q <- apply(log(X.total), 2, quantile, probs=c(0.025, 0.5, 0.975))
#X0
den.X0 <- density(log(X0.total),adj=2)
den.X0$y2 <- (den.X0$y/max(den.X0$y))
q.X0 <- quantile(log(X0.total), probs=c(0.025,0.975))
xid<- sapply(q.X0, function(x) {which.min(abs(x-den.X0$x))})
#N0
den.N0 <- density(log(X.total[,ncol(X.total)]),adj=2)
den.N0$y2 <- (den.N0$y/max(den.N0$y))
q.N0 <- quantile(log(X.total[,ncol(X.total)]), probs=c(0.025,0.975))
xid.n0<- sapply(q.N0, function(x) {which.min(abs(x-den.N0$x))})

yrange <- range(c(log(rowSums(thedata[,2:ncol(thedata)], na.rm=T)), den.X0$x))

png(filename=paste(file.tag,"_model_fit_U.png", sep=""), width=7, height=4.62, units="in", res=300)
  layout(matrix(1:2,1,2),width=c(1,0.23))
  par(mar=c(4,4,1,1))

  plot(thedata[,1], log(rowSums(thedata[,2:ncol(thedata)], na.rm=T)), pch=16, type="n", las=1, ylab="log(Annual Nesters)",
xlab="Season", ylim=range(pretty(yrange)), xlim=c(min(thedata[,1])-1.1, max(thedata[,1]+0.25)), xaxs='i')
```

```
polygon(c(c(min(thedata[,1])-1,thedata[,1]), rev(c(min(thedata[,1])-1,thedata[,1]))),
    c(X.q[1,], rev(X.q[3,])),
    col='grey85',
    border=FALSE)

lines(c(min(thedata[,1])-1,thedata[,1]), X.q[2,], lwd=3, col='gray50')

polygon(x = c(rep((thedata[1,1]-1), length(xid[1]:xid[2])),rev(den.X0$y2[xid[1]:xid[2]]+(thedata[1,1]-1))),
    y = c(den.X0$x[xid[1]:xid[2]],rev(den.X0$x[xid[1]:xid[2]])),
    lwd=2, border=FALSE,
    col=col2rgbA("dodgerblue3", 0.3))

polygon(x = c(rep(thedata[nrow(thedata),1], length(xid.n0[1]:xid.n0[2])),rev(-
den.N0$y2[xid.n0[1]:xid.n0[2]]+thedata[nrow(thedata),1])),
    y = c(den.N0$x[xid.n0[1]:xid.n0[2]],rev(den.N0$x[xid.n0[1]:xid.n0[2]])),
    lwd=2, border=FALSE,
    col=col2rgbA("darkorchid3", 0.3))

lines(den.X0$y2[xid[1]:xid[2]]+(thedata[1,1]-1), den.X0$x[xid[1]:xid[2]], lwd=2, col='dodgerblue3')
lines(-den.N0$y2[xid.n0[1]:xid.n0[2]]+thedata[nrow(thedata),1], den.N0$x[xid.n0[1]:xid.n0[2]], lwd=2, col='darkorchid3')

points(thedata[,1], log(rowSums(thedata[,2:ncol(thedata)], na.rm=T)), pch=16)
points(c(min(thedata[,1])-1,thedata[,1]), X.total.med, pch=16, col=c('dodgerblue3',rep('red',length(X.total)-2), "darkorchid3"))

par(mar=c(0,0,0,0))
plot.new()
legend("center", legend=c(expression(sum(N[list(obs,j)],j,"")), expression(sum(T[j]+a[j],j,"")), "Median r", "95% r",
expression(paste(T[0]," (95%CI)")), expression(paste(N[final]," (95% CI)"))), pch=c(16,16,NA,15,NA,NA),
lwd=c(NA,NA,3,NA,2,2), pt.cex=c(1,1,NA,3,NA,NA), col=c("black","red","gray50","gray85","dodgerblue3","darkorchid3"),
bty="n", y.intersp = 0.9, xpd=NA)
pop.name.combo2 <- gsub("Pacific ","Pac.\n",pop.name.combo)
if(grepl("Leatherback",pop.name.combo2)){
  pop.name.combo2 <- gsub("Western","W.",pop.name.combo2)
```

```
    pop.name.combo2 <- gsub(" Turtles","\n(JM & W)",pop.name.combo2)
  }else{
    pop.name.combo2 <- gsub(" 3 beaches","\n(3 beaches)",pop.name.combo2)
    pop.name.combo2 <- gsub(" - ","\n",pop.name.combo2)
  }

  fig.lab(pop.name.combo2, xscale=0.5, yscale=0.85, cex=1)
dev.off()

# POSTERIORS for Zach to input into the projections and take model component now (7/24/19)
posts.out <- cbind("U"=jags.model$sims.list$U, "Q"=jags.model$sims.list$Q, "N_fym0"=X.fym0, "N_fym1"=X.fym1,
"N_fym2"=X.fym2, "N_fym3"=X.fym3)
head(posts.out)
write.csv(posts.out, paste("Posteriors_U_and_AbundFinalYrs_", file.tag, ".csv", sep=""), row.names=FALSE)
```

Appendix IV: Loggerhead von Bertalanffy Growth Model

To estimate the von Bertalanffy Growth Model (von Bertalanffy 1934) (Eq. 26) parameters for loggerheads, the data from Tomaszewicz et al. (2015) of loggerhead ages and SCLs were used. The mean and standard deviation of nesting female sizes in Minabe, Japan from Hatase et al. (2002) was used to generate an informative normal prior on L_∞ due to the limited number of adults in the Tomaszewicz data set (Eq. 27). Additionally, observations of L_0, based on the hatchling size measured by Dodd Jr (1988), were assumed to come from a log-normal likelihood (Eq. 28). The age at maturity was derived from the von Bertalanffy growth model using Eq. 29.

$$L_t = L_\infty - \left(L_\infty - \hat{L}_0\right)e^{-kt}$$

Eq. 26

$$L_\infty \sim N\left(\mu_{L_{\text{nesters}}}, \sigma_{L_{\text{nesters}}}\right)$$

Eq. 27

$$L_0 \sim logNormal\left(\log\left(\hat{L}_0\right), \sigma_{L_0}\right)$$

Eq. 28

$$t_{0.975} = \left(\frac{1}{k}\right)\log\left(\frac{L_\infty - \hat{L}_0}{L_\infty(1 - t_{0.975})}\right)$$

Eq. 29

Where L_t is the length at time t and k is the Brody growth rate coefficient. The model was implemented in STAN using RStan (Stan Development Team 2018) with 7,500 simulations per chain (5,000 discarded burnin and 2,500 kept) for 10,000 total simulations. All chains converge with $\hat{R} < 1.1$ for all parameters (Gelman and Rubin 1992). The posteriors are shown in Figure A1.
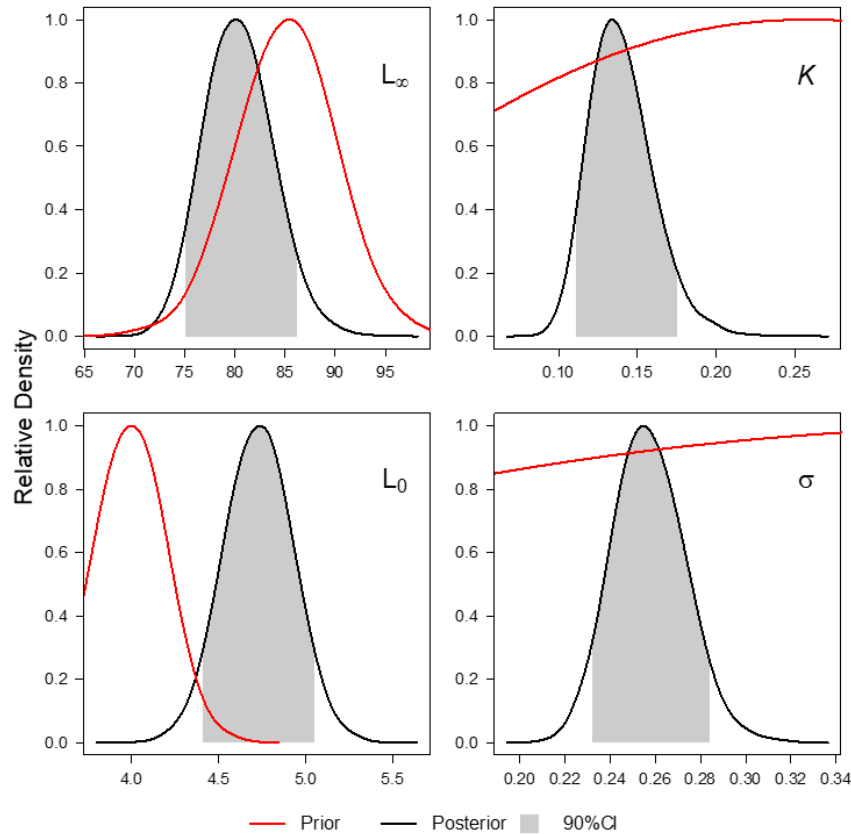
Figure A1. Von Bertalanffy growth model parameters for North Pacific loggerhead turtles. Priors (in red) and posteriors (in black) with the 90% credible intervals in gray for the four parameters: three from the VBGM (*estimated values*: $L_\infty = 80.4\ cm$, $k = 0.14$, $L_0 = 4.7\ cm$) **and the fourth is the standard deviation of the observations, σ.**

References

Bertalanffy Lv. 1934. Untersuchungen über die gesetzlichkeit des wachstums. I allgemeine grundlagen der theorie, mathematische und physiologische gesetzlichkeiten des wachstums bei wassertieren. Roux'archiv für entwicklungsmechanik 131, 613-652. The relationships between gill surface area and growth performance in fish. 279.

Dodd Jr CK. 1988. Synopsis of the biological data on the loggerhead sea turtle Caretta caretta (Linnaeus 1758). Florida Cooperative Fish and Wildlife Research Unit Gainesville.

Gelman A, Rubin DB. 1992. Inference from iterative simulation using multiple sequences. Statist Sci. 7(4):457-472.

Hatase H, Goto K, Sato K, Bando T, Matsuzawa Y, Sakamoto W. 2002. Using annual body size fluctuations to explore potential causes for the decline in a nesting population of the loggerhead turtle Caretta caretta at Senri Beach, Japan. Mar Ecol Prog Ser. 245:299-304.

Stan Development Team. 2018. Rstan: The R interface to stan. R package version 2.17.3.

Tomaszewicz CNT, Seminoff JA, Avens L, Goshe LR, Peckham SH, Rguez-Baron JM, Bickerman K, Kurle CM. 2015. Age and residency duration of loggerhead turtles at a north Pacific bycatch hotspot using skeletochronology. Biol Cons. 186:134-142.