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DRAFT Programmatic Environmental Impact Statement Appendices A-L

Hawaiian Monk Seal Recovery Actions

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Appendix J
Hawaiian Monk Seal Stochastic
Model

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The monk seal stochastic simulation model is one of the primary tools used by the PIFSC of the NFMS to perform quantitative analyses for research and management of the species. Historically, the model has been used for a variety of applications. The most common applications are: to make predictions about the future status of the population based on current demography, to evaluate the significance of specific mortality sources (such as shark predation or male aggression), and to evaluate the sensitivity and likely benefits derived from candidate interventions. Details of the model structure and mechanics are provided in Harting (2002), with the fundamental features summarized below.

At its core, the model is a mechanistic, stochastic, metapopulation model with provisions for handling uncertainties in input parameters and modeled processes. The model is heavily data driven, capitalizing on the demographic and life history data collected over more than two decades in the NWHI and, more recently, the incipient demographic data set for the MHI. Necker and Nihoa Islands (NWHI) are relatively data poor and have historically comprised a small portion of total abundance, and are therefore not included in simulations. The demographic data (reproductive, survival, and migration rates) used by the model are derived primarily from resightings of known-aged (or “cohort”) seals first tagged as pups.

Demographic data are evaluated separately for each of the 7 breeding sites handled by the model. For the NWHI sites, Jolly-Seber survival estimates (Jolly 1965; Seber 1965) are calculated using the cohort resighting data as input, with separate estimates for two time periods: all years pooled, and most recent three years pooled. The latter estimates were used for all projections described in this PEIS. Siler’s five-parameter competing risk model (Siler 1979, 1983) is then fit to the observed (Jolly-Seber) rates. For the model, parameter uncertainty is handled by random sampling Siler parameters from the variance/covariance matrix from the parameter fitting.

Age-specific reproductive rates are estimated from pooling pupping data from 1990 to the present using methods described in Harting *et al.* (2007). As with survival rates, parameter uncertainty is handled by randomly sampling a unique set of correlated parameters from the fitted distributions. In the model, survival and reproduction are determined stochastically for each individual in the population by binomial sampling (testing a uniform random number in the range [0,1] against the age-specific survival rate). Migration is also determined stochastically for each individual according to the fitted movement rate for each age class.

As compared to the NWHI, data from which to estimate vital rates and population composition are much more limited for the MHI. A detailed description of the methods used to fit both survival and reproductive rates for

the MHI are provided in Baker *et al.* (in press). Where data are lacking (*e.g.*, reproductive rates of older MHI females), some inference and extrapolation is necessary based on patterns observed in the NWHI. Uncertainty in parameter estimates is handled in the same manner as for the NWHI, with unique parameters drawn from their fitted distributions at the start of each simulation.

Each simulation is initialized with the most recent starting age/sex distribution for each site, as compiled from the most recent year's observations. Ages are ascribed different degrees of confidence depending on the age at which a seal was first identified. At the start of each simulation, the model randomly assigns all minimum-aged seals (those first identified as adults) a working age for initializing that simulation. The random age assignment is consistent with the estimated survival schedule for each site. Interatoll movement rates are also calculated from the annual resighting data, with different rates for each pups, juveniles, subadults, and adults..

The primary sequence of events during each simulation year are survival and reproduction, specific natural perturbations, migration between subpopulations, and management actions. The model provides multiple options for simulating natural perturbations (survival catastrophes, birth catastrophes, shark predation, and aggressive male interactions) and management interventions (captive rearing/release, translocations, shark removals, and other). The only perturbations and management actions to be included in the projections described in this PEIS were removal of aggressive males, removal (death) of females, and translocation. For the translocations, the model transfers the desired number of seals from the donor site to the recipient site, and tracks their annual survival until they are transferred back to the donor site. Survival rate decrements are applied to these seals as specified in the modeled scenario.

The model produces a diverse array of outputs suitable for evaluating simulation outcomes including abundance, realized growth rate, multiple demographic descriptors, and assorted metrics specific to whatever intervention scenario was executed. The primary output is site-specific, with summary diagnostics for the entire system and the two main regions (NWHI and MHI).

For the purposes of this analysis, certain other model components were disabled, including the option for density dependent adjustment of demographic rates. While that feature of the model is certainly important when performing long-term projections, the precise manner in which density dependence operates on the monk seal population is unknown and its influence can overwhelm and obscure the effects of all other factors included in the simulation scenario.