



Functionalities in the model which were not used in the current study, but are described here as a matter of completeness and full disclosure of current functionality for potential users, include the relationship between predator foraging success and survival (Eq. A.16), and the relative competitive abilities of different predators and the fishery (Eqs. A.11 and A.12). We simplified these functions in the risk analysis by parameterizing the model so that adult survival rates of krill predators were constant and the competitive abilities of all predators and the fishery were equal. Our description of management measures includes only those considered in the current study. We refer readers to Watters et al. (2006, 2008) for a more complete description and evaluation of the alternative Catch Allocation Options.

### *Trophic, spatial and temporal structure*

The model represents one forage species (hereafter prey, which, in the current context, is synonymous with krill), its predators and fishery. The main spatial unit of the model is the small scale management unit (SSMU) in which predator, prey and fishery dynamics are explicitly modeled. There can be up to four predator groups per SSMU. The parameters of prey and predator groups can be defined specifically for each SSMU. There are also boundary areas, the main purpose of which is to represent prey outside the SSMUs that interacts with prey and predators inside the SSMUs. Boundary areas therefore have a simple representation of prey abundance and no explicit representation of predator or fishery dynamics. SSMUs can interact with other SSMUs and boundary areas through the movement of prey between areas and the foraging of predators that are assigned to a given SSMU in other areas.

The model has nested temporal structure, intended to represent seasons within years (typically 2 seasons per year). Most input parameters can be assigned different values for each season within the year. The basic time step is therefore one season and outputs can be sampled as either annual aggregates (sums or averages) or seasonally resolved snapshots.

### *Prey dynamics*

Prey dynamics are described by delay-difference equations. The abundance of prey in SSMU  $i$  at time  $t+1$  ( $K_{i,t+1}$ ) is a function of the total mortality during the preceding time step ( $Z_{i,t}$ ), recruitment ( $R_{i,t+1}$ ), and a set of season-specific (where season is identified by the subscript  $s$ ) instantaneous movement rates that describe movement among pairs of SSMUs  $i$  and  $j$  (individual rates in this set are designated  $v_{i \rightarrow j,s}$ ).

$$K_{i,t+1} = K_{i,t} \exp\left(-Z_{i,t} - \sum_{j \neq i} v_{i \rightarrow j,s}\right) + R_{i,t+1} + \sum_{j \neq i} \left( K_{j,t} \frac{v_{j \rightarrow i,s}}{Z_{j,t} + \sum_{h \neq j} v_{j \rightarrow h,s}} \left(1 - \exp\left(-Z_{j,t} - \sum_{h \neq j} v_{j \rightarrow h,s}\right)\right) \right) \quad (\text{A.1})$$

Three instantaneous mortality rates are components of the SSMU- and time-specific total mortality rate ( $Z_{i,t}$ ): natural, non-predation mortality in season  $s$  ( $M0_{i,s}$ ); predation mortality ( $M2_{i,t}$ ); and fishing mortality ( $F_{i,t}$ ).

$$Z_{i,t} = M0_{i,s} + M2_{i,t} + F_{i,t} \quad (\text{A.2})$$

All three mortality rates and all the instantaneous movement rates are  $\geq 0$ . We use season-specific transition matrices (one matrix per season) to contain the movement rates. These matrices are square with dimensions equal to the total number of areas (SSMUs plus boundary areas) being considered in an implementation of the model. An element in row  $i$  and column  $j$  of the matrix for season  $s$  describes the instantaneous rate of movement from area  $i$  to area  $j$  ( $v_{i \rightarrow j,s}$ ), and the diagonal elements of the transition matrix are equal to zero. The first term on the right side of Eq. A.1 describes the proportion of the population that remains after losses due to mortality and emigration from SSMU  $i$ . The third term describes net immigration into SSMU  $i$ . Note that our parameterization of movement allows prey to be exchanged between non-adjacent areas. Prey that transit through an area within a single time step are not subjected to additional predation or fishing mortality while *en route* to their destination.

Recruitment of prey in SSMU  $i$  at time  $t$  ( $R_{i,t}$ ) is an asymptotic function of the adult abundance in a previous time period, and the lag is determined by the age at which prey recruit to the adult stock ( $\rho$ ).

$$R_{i,t} = \frac{\alpha_{i,s} K_{i,t-\rho}}{\beta_{i,s} + K_{i,t-\rho}} \exp(\phi_{i,s} X_t + \varepsilon_t) \quad (\text{A.3})$$

$$\varepsilon_t \sim \text{N} \left( \frac{-\sigma^2}{2}, \sigma^2 \right) \quad (\text{A.4})$$

$\alpha_{i,s}$  is the maximum recruitment in SSMU  $i$  during season  $s$ , and  $\beta_{i,s}$  is the season- and SSMU-specific adult abundance that produces half that maximum. The recruitment of prey can also be influenced by a time-varying anomaly that describes environmental conditions influencing all SSMUs ( $X_t$ ), but the effect of these conditions is mediated by a season- and SSMU-specific scale parameter ( $\phi_{i,s}$ ). If the set  $\{X_t\}$  is not a normalized series of environmental anomalies, the recruitment deviates will be biased. Lognormal variation in prey recruitment is introduced through a time varying error term ( $\varepsilon_t$ ) that applies to all SSMUs and whose variance (in log space,  $\sigma^2$ ) is fixed.

Time-series of prey abundance in boundary areas are provided to the model as inputs. These time-series can be used in conjunction with the time-varying anomaly ( $X_t$ ) to implement hypotheses about bottom-up forcing of prey abundance. In Monte Carlo simulations intended to represent stochastic variability in krill recruitment it will be necessary to generate time-series with a unique sequence of random deviates for each trial.

### *Predator consumption*

Since predators and prey interact via the consumption process and predator dynamics can be affected indirectly by fishery catches, we first describe the predator consumption and catch components of the model. We compute the stock-, SSMU-, and time-specific per-capita potential consumption of prey from a function that is sufficiently flexible to model both Holling Type II and Type III functional responses.

$$\Omega'_{k,i,t} = \frac{Q_{k,i,s}^* \left( \sum_j [p_{k,i \leftarrow j,s} \cdot K_{i,t}/A_i] \right)^{q_{k,i,s}+1}}{\kappa_{k,i,s}^{q_{k,i,s}+1} + \left( \sum_j [p_{k,i \leftarrow j,s} \cdot K_{i,t}/A_i] \right)^{q_{k,i,s}+1}} \quad (\text{A.5})$$

Predators can forage in any SSMU, and  $p_{k,i \leftarrow j,s}$  is the proportion of energy that predators from stock  $k$  which breed in SSMU  $i$  obtain from SSMU  $j$  during season  $s$ .  $K_{i,t}/A_i$  is the density of prey in SSMU  $i$  ( $A_i$  is the area of SSMU  $i$ ), and, therefore, the term inside parentheses is the mean prey density encountered by predators that breed in SSMU  $i$  and feed throughout the arena of SSMUs during season  $s$ .  $Q_{k,i,s}^*$  is the maximum potential per-capita consumption that predators from stock  $k$  which breed in SSMU  $i$  can achieve during season  $s$ ; and  $\kappa_{k,i,s}$  is the prey density at which these predators can achieve half of  $Q_{k,i,s}^*$ . The parameter  $q_{k,i,s}$  determines the general type of the functional response. When  $q_{k,i,s} = 0$ , the functional response is a Type II response; when  $q_{k,i,s} > 0$ , the functional response is a Type III response.

The potential total consumption of prey by predators from stock  $k$  feeding in SSMU  $i$  during time  $t$  ( $\Omega_{k,i,t}$ ) is the product of the expected, potential per-capita consumption ( $\Omega'_{k,i,t}$ ) by these predators and the number of predators of group  $k$  feeding in SSMU  $j$ ,  $P_{k,j,t}P_{k,j \leftarrow i,s}$ ; note that subscript  $j$  here refers to the SSMU that predators are assigned to forage in and not the SSMU in which they breed, generally indexed by  $i$ .

$$\Omega_{k,i,t} = \sum_j \Omega'_{k,j,t} P_{k,i,t} P_{k,j \leftarrow i,s} \quad (\text{A.6})$$

Thus, Eq. A.6 describes the potential consumption by predators feeding in SSMU  $i$  regardless of whether they breed in that SSMU.

We then compute a measure of the relative, time-specific, mean per-capita foraging performance of the animals from stock  $k$  that breed in SSMU  $i$ .

$$\bar{Q}_{k,i,t} = \Omega'_{k,i,t} \sum_j (p_{k,i \leftarrow j,s} \cdot \lambda_{i,t} \cdot c_{k,i}) / Q_{k,i,s}^* \quad (\text{A.7})$$

$\bar{Q}_{k,i,t}$  represents an index of relative foraging success in the interval  $[0,1]$ , which is used to scale adult mortality as a function of foraging success (see Eq. A.16), and the proportion of the adult population that breed as a function of foraging success (see Eq. A.22), and recruitment of predators as a function of foraging success during the first winter of life (see Eq. A.23).  $\lambda_{i,t}$  is a factor that prorates potential consumption to calculate the realized consumption. The coefficients  $c_{k,i}$  describe the relative, competitive strengths of the predators from stock  $k$  that forage in SSMU  $i$ . When a predator that breeds in SSMU  $i$  feeds in SSMU  $j$ , that predator adopts the competition coefficient  $c_{k,j}$ . We set  $\lambda_{i,t} = c_{k,i} = 1$  when the available abundance of prey is not limiting. Note that relative foraging performance is computed across all areas in which the predators from stock  $k$  that breed in SSMU  $i$  feed (where feeding SSMUs are indexed by  $j$ ).

### Catch

Allocated catches,  $\Theta_{i,t}$ , are determined by the selection of an allocation option. These options represent a variety of candidates for allocating an overall catch limit for prey among SSMUs.

$$\Theta_{i,t} = (B_0 \cdot \gamma \cdot p_{i,t} / \bar{w}_i) \cdot f_{i,s} \quad (\text{A.8})$$

$B_0$  is the initial biomass of prey in all SSMUs combined (this can be input by the analyst or taken from a previous run, see Appendix B: *Initial Conditions*), and  $\gamma$  is the overall exploitation rate for the entire set of SSMUs being considered. The analyst can input  $\gamma$  or it can be computed from the ratio  $L/B_0$ , where  $L$  is a catch limit that is input by the analyst. Since our accounting of prey population dynamics is in abundance (e.g., Eq. A.1) and we do not model prey growth, we use an SSMU-specific estimate of average weight ( $\bar{w}_i$ ) to convert between prey biomass and numbers. The parameters  $f_{i,s}$  set the proportion of the annual catch allocated for SSMU  $i$  that is to be taken, as far as possible given the possibility of limiting prey abundance and competition with predators, in season  $s$ . The parameters  $f_{i,s}$  facilitate extreme flexibility for setting up fishing scenarios. For example these parameters enable the analyst to model temporal mismatches between the potential consumption of prey by predators and catches that are allocated to the fishery.

SSMU-specific allocation fractions,  $p_{i,t}$ , are determined in a two step process. First, initial SSMU-specific allocation fractions,  $p'_i$ , are prescribed by a Catch Allocation Option that is selected by the analyst. For the current study, we compared three of the five options suggested by Hewitt et al. (2004): allocate catch on the basis of historical catches (Catch), allocate catch on the basis of estimates of predator demand (Demand), and allocate catch on the basis of estimates of prey standing stock (Stock). Note that three other options, including one based on the difference between standing stock and predator demand (Hewitt et al. 2004), one that involves adjusting the allocation among areas on the basis of an ongoing monitoring program, and one that allocates catch among SSMUs on an arbitrary rotating basis, are also implemented in the model but not described here.

$$p'_i = \begin{cases} C_{H,i} / \sum_i C_{H,i} & \text{Catch} \\ \bar{w}_i \sum_k \Omega_{k,i,0} / \sum_i \left( \bar{w}_i \sum_k \Omega_{k,i,0} \right) & \text{Demand} \\ B_{i,0} / B_0 & \text{Stock} \end{cases} \quad (\text{A.9})$$

$C_{H,i}$  is the historical catch in SSMU  $i$ ,  $\sum_k \Omega_{k,i,0}$  is the initial demand for prey (in numbers) by all predator stocks that feed in SSMU  $i$ .  $B_{i,0}$  is the initial standing stock of prey (in biomass) in SSMU  $i$ , and  $\sum B_{i,0} = B_0$ .

The final SSMU-specific allocation fractions,  $p_i$ , can be calculated with both trial-specific log-normal observation error,  $\exp(a_t)$  and bias,  $b$ :

$$p_{i,t} = b \cdot p'_i \cdot \exp(a_t), \text{ where } a_t \sim N\left(\frac{-\sigma^{2'}}{2}, \sigma^{2'}\right) \quad (\text{A.10})$$

Note that in our analysis, we set  $b = 1$ , so bias was not simulated. The CV on the observation error was set to 20%. We also used the approach described for the Catch option to implement our Current option (allocate catch to represent current management), using the  $C_{H,t}$  values in Table B4 (Appendix B).

We discriminate both between allocated and realized catches and between the predators' potential and realized consumption of prey. The state variables  $\Theta_{i,t}$  and  $\sum_k \Omega_{k,i,t}$  respectively describe the allocated catch and total potential consumption of prey in SSMU  $i$  during time  $t$  by all predators foraging in SSMU  $i$ , and we use these state variables as the basis for computing the realized catch and consumption. The state variables  $C_{i,t}$  and  $\sum_k Q_{k,i,t}$  respectively describe the realized catch and realized consumption (where the sum is across the predator stocks indexed by  $k$ , and the maximum value of this index may be as large as four times the number of SSMUs being considered in the application) in SSMU  $i$  during time  $t$ .

Such discrimination between potential removals and actual removals of prey is necessary because the abundance of prey in any given SSMU at any given time may not be sufficient to support both the allocated catch (the catch prescribed by one of the candidate management procedures) and the potential consumption (the consumption prescribed by various functional response curves). When the sum of the allocated catch and potential consumption is less than the available abundance of prey in an SSMU, we set the realized catch equal to the allocated catch and the realized consumption equal to the potential consumption. When that sum of the allocated catch and potential consumption is greater than the available abundance of prey, realized catch may be less than the allocated catch and predators may consume less than their potential, depending on the relative competitive strengths of the fishery and the predators.

Importantly, we do not reduce removals due to non-predation mortality and movement when predator demand and the allocated catch exceed prey availability. Rather, the "balance" of prey that would remain after natural mortality and movement occur (if such a balance exists) is divided between realized catch and realized consumption on the basis of an SSMU-specific set of competition coefficients.

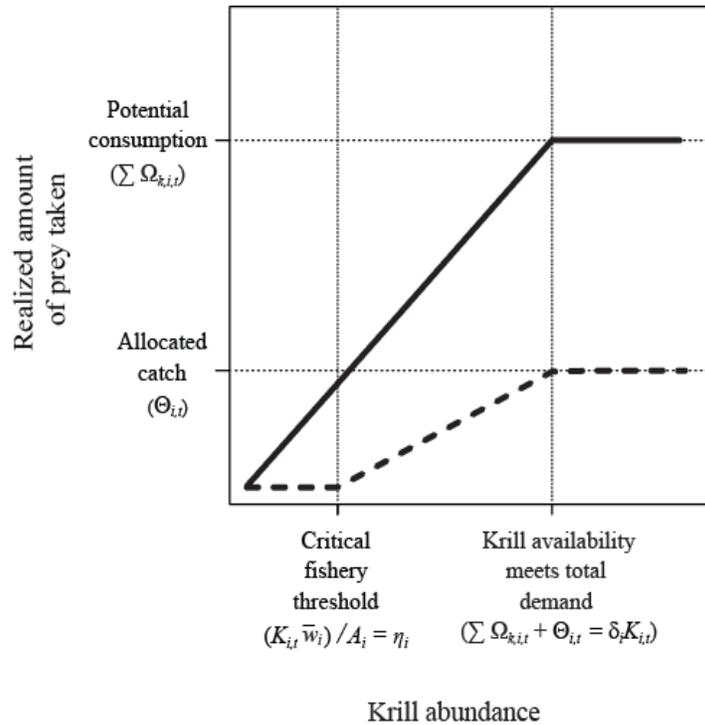
$$C_{i,t} = \begin{cases} \Theta_{i,t} & \text{if } \left( \Theta_{i,t} + \sum_k \Omega_{k,i,t} \right) \leq \left( \delta_i \cdot K_{i,t} \right) \\ 0 & \text{if } \left( K_{i,t} \cdot \bar{w}_i \right) / A_i < \eta_i \\ \lambda_{i,t} \cdot c_{F,i} \cdot \Theta_{i,t} & \text{otherwise} \end{cases} \quad (\text{A.11})$$

$$\sum_k Q_{k,i,t} = \begin{cases} \sum_k \Omega_{k,i,t} & \text{if } \left( \Theta_{i,t} + \sum_k \Omega_{k,i,t} \right) \leq (\delta_i \cdot K_{i,t}) \\ \lambda_{i,t} \sum_k (c_{k,i} \cdot \Omega_{k,i,t}) & \text{otherwise} \end{cases} \quad (\text{A.12})$$

$$\lambda_{i,t} = \frac{\delta_i \cdot K_{i,t}}{\Theta_{i,t} + \sum_k \Omega_{k,i,t}} \quad (\text{A.13})$$

Here,  $\delta_i$  is the proportion of prey present in SSMU  $i$  that are actually available for harvest and predation. Setting  $\delta_i = 1$  amounts to assuming that all prey in an SSMU are available for harvest and consumption, subject to the constraint that non-predation mortality and movement will out compete fishing and predation mortalities when prey are limiting.  $\eta_i$  is the SSMU-specific threshold prey density (in  $\text{g} \cdot \text{m}^{-2}$ ) below which the fishery stops operating.  $\lambda_{i,t}$  is a factor that prorates the allocated catch and potential consumption to calculate the realized catch and consumption.  $c_{F,i}$  is a coefficient that describes the competitive strength of the fishery relative to the competitive strengths of other predators that forage in SSMU  $i$ . The coefficients  $c_{k,i}$  describe the relative, competitive strengths of the predators that forage in SSMU  $i$ . Fig. A2 graphically represents how realized catch and consumption deviate from the allocated catch and potential consumption.

**FIG. A2.** Illustration of how realized catch and consumption changes with available prey abundance (Eqs. A11–13). The thick black line represents realized consumption; the thick dashed line represents realized catch. Below the critical density, the fishery catch is 0. When prey availability exceeds total demand, realized consumption and catch equal potential consumption and allocated catch. In between, realized catch and consumption decline based on the ratio of prey availability to demand for prey. For example if demand is 10 but availability is 5, predator consumption and realized catch are reduced by 50% (assuming equal competitive abilities).



Since we account for both realized catch and consumption in numbers of prey and model mortality and movement as competing, continuous risks (e.g., Eq. A.1), we use an iterative root finder (Brent 1973) to solve for the sum  $M2_{i,t} + F_{i,t}$  in an analog to the Baranov catch equation.

$$C_{i,t} + \sum_k Q_{k,i,t} = \frac{M2_{i,t} + F_{i,t}}{Z_{i,t} + \sum_{j \neq i} v_{i \rightarrow j,s}} \left( 1 - \exp\left(-Z_{i,t} - \sum_{j \neq i} v_{i \rightarrow j,s}\right) \right) K_{i,t} \quad (\text{A.14})$$

### Predator dynamics

The current implementation of the model allows up to four stocks of predators to occur in each SSMU and the equations governing the dynamics of each stock are the same (with abundance trajectories determined by stock-specific parameter values). The abundance of adult predators from stock  $k$  that breed in SSMU  $i$  at time  $t+1$  ( $P_{k,i,t+1}$ ) is a function of mortality during the preceding season ( $M_{k,i,s}$ ) and recruitment ( $R''_{k,i,t+1}$ ). Note that  $i$  identifies the SSMU in which predators breed or to which they recruit.

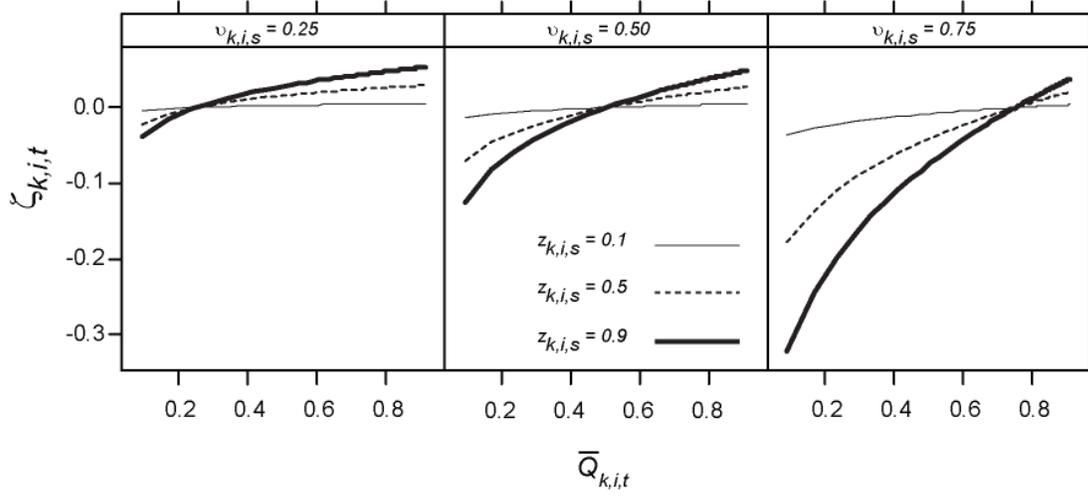
$$P_{k,i,t+1} = P_{k,i,t} \left( \exp(-\bar{M}_{k,i,s}) + \zeta_{k,i,t} \right) + R''_{k,i,t+1} \quad (\text{A.15})$$

$\bar{M}_{k,i,s}$  is the mean, instantaneous natural mortality rate for predators from stock  $k$  in season  $s$  and SSMU  $i$ , and  $\zeta_{k,i,t}$  is a survival anomaly for stock  $k$  that occurs in SSMU  $i$  at time  $t$ .

$$\zeta_{k,i,t} = z_{k,i,s} \left( \bar{Q}_{k,i,t}^{\left(\frac{-\bar{M}_{k,i,s}}{\log(v_{k,i,s})}\right)} \right) + z_{k,i,s} \exp(-\bar{M}_{k,i,s}). \quad (\text{A.16})$$

The survival anomalies,  $\zeta_{k,i,t}$ , are determined as a function of two parameters: the season-specific proportion of potential temporal variation in survival that is explained by variations in mean, per-capita foraging performance of the animals from stock  $k$  that breed in SSMU  $i$ ,  $z_{k,i,s}$ , and the level of foraging performance that distinguishes a “good” year from a “bad” year,  $v_{k,i,s}$ . A relative foraging success greater than  $v_{k,i,s}$  results in a positive survival anomaly while relative foraging success less than  $v_{k,i,s}$  results in a negative survival anomaly. The magnitude of the anomaly is scaled by  $z_{k,i,s}$ , with greater values resulting in larger anomalies as the relative foraging performance departs from the switch point ( $v_{k,i,s}$ ).

The parameters  $z_{k,i,s}$  and  $v_{k,i,s}$  should be set on the interval  $[0,1]$ , but note that the model is implemented so that if the analyst sets either  $z_{k,i,s} = 0$  or  $v_{k,i,s} = 0$ , then survival is constant at the mean level  $\bar{M}$ . For our simulations, the survival anomaly was set to 0. Note that Eq. A.16 was developed from the assumption that the relative amount of variation in survival explained by foraging performance is proportionally symmetric on either side of the mean survival. For reference, its functional form is shown in Fig. A3.

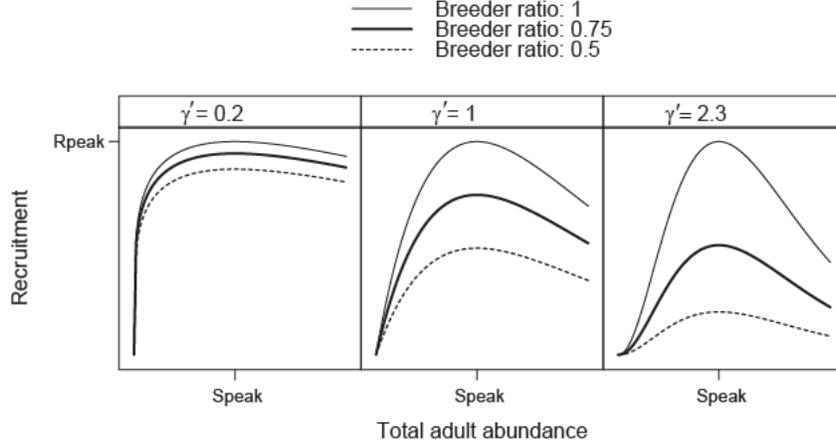


**FIG. A3.** Functional form of the survival anomaly implemented in the model. Positive survival anomalies occur when foraging performance is greater than the switch point ( $v$ ). The magnitude of the anomaly is then scaled by  $z$ , with greater values resulting in larger survival anomalies as foraging performance departs from the switch point. Survival anomalies will be larger (1) when the difference between foraging performance and the switch point grows and (2) if the proportion of annual survival that is attributable to foraging performance is large. For the figure, the mean mortality rate was set to 0.066, a typical value used for penguins in the current implementation of the model.

We use a “gamma” stock-recruitment model (e.g., Quinn and Deriso 1999) for predators. The recruitment of predators from stock  $k$  in SSMU  $i$  at time  $t$  ( $R'_{k,i,t}$ ) is a function of both the total abundance of adults that could breed ( $P_{k,i,t-\rho'_{k,i}}$ ) and the effective number of reproductively active adults ( $\tilde{P}_{k,i,t-\rho'_{k,i}}$ ) that were present during a previous time. The lag is again determined by the age at which individuals recruit to the adult stock, but, for predators, the age at recruitment is stock- and SSMU-specific ( $\rho'_{k,i}$ ).

$$R'_{k,i,t} = \alpha'_{k,i,s} \left( \tilde{P}_{k,i,t-\rho'_{k,i}} \right)^{\gamma'_{k,i,s}} \exp\left(-\beta'_{k,i,s} \cdot P_{k,i,t-\rho'_{k,i}}\right) \quad (\text{A.17})$$

For a given value of the ratio  $\tilde{P}_{k,i,t}/P_{k,i,t}$ , the stock-recruitment function is dome-shaped, and the stock-, season-, and SSMU-specific rate at which recruitment both approaches and departs from its peak level is determined by an interaction among the three parameters  $\alpha'_{k,i,s}$  (the maximum per-capita production of offspring at low adult abundance when all adults breed),  $\beta'_{k,i,s}$  (the level of density dependence at high adult abundance regardless of breeding status), and  $\gamma'_{k,i,s}$ . As  $\gamma'_{k,i,s}$  approaches zero, the recruitment function becomes more similar to a Beverton-Holt model, with less overcompensation at high adult abundances. When  $\gamma'_{k,i,s} = 1$ , the recruitment function is a Ricker model. When  $\gamma'_{k,i,s} > 1$ , the recruitment function is depensatory (i.e., the recruitment declines strongly with decreasing adult abundance when adult abundance is low). If  $\gamma'_{k,i,s} \leq 0$ , the model is not a valid stock-recruitment function because the curve does not go through the origin (Fig. A4).



**FIG. A4.** Example stock-recruit relationships from the gamma model, including a Beverton-Holt-like model ( $\gamma' = 0.2$ ), a Ricker model ( $\gamma' = 1$ ), and a depensatory model ( $\gamma' = 2.3$ ). The effect of three different breeder ratios on the stock-recruitment function is demonstrated.

In practice, it can be difficult to identify plausible values for  $\beta'_{k,i,s}$  and  $\gamma'_{k,i,s}$ . We have, therefore, implemented an alternative parameterization of Eq. A.17. This parameterization is motivated by noting that, when  $\beta'_{k,i,s} > 0$ ,  $\gamma'_{k,i,s} > 0$ , and  $\tilde{P}_{k,i,t}/P_{k,i,t} = 1$ , there is an analytical solution for the  $x$ - $y$  pair of adult abundance that produces the peak recruitment to stock  $k$  in season  $s$  and SSMU  $i$  ( $Speak_{k,i,s}$ ) and the peak recruitment when all adults breed ( $Rpeak_{k,i,s}$ ).

$$Speak_{k,i,s} = \frac{\gamma'_{k,i,s}}{\beta'_{k,i,s}} \quad (\text{A.18})$$

$$Rpeak_{k,i,s} = \alpha'_{k,i,s} \left( \frac{\gamma'_{k,i,s}}{\beta'_{k,i,s}} \right)^{\gamma'_{k,i,s}} \cdot \exp(-\gamma'_{k,i,s}) \quad (\text{A.19})$$

Eqs. A.18 and A.19 thus imply an alternative parameterization that requires the analyst to specify  $\alpha'_{k,i,s}$ ,  $Speak_{k,i,s}$ , and  $Rpeak_{k,i,s}$ ; we then compute  $\beta'_{k,i,s}$  and  $\gamma'_{k,i,s}$  from these inputs.

$$\gamma'_{k,i,s} = \frac{\ln(Rpeak_{k,i,s}/\alpha'_{k,i,s})}{\ln(Speak_{k,i,s}) - 1} \quad (\text{A.20})$$

$$\beta'_{k,i,s} = \frac{\gamma'_{k,i,s}}{Speak_{k,i,s}} \quad (\text{A.21})$$

The model explicitly separates each adult stock of predators into two categories: breeders and non-breeders. This separation is provided by modeling recruitment as a function of the effective number of reproductively active adults ( $\tilde{P}_{k,i,t}$ ). We use a relative measure of foraging performance to scale the total number of adult predators from stock  $k$  that breed in SSMU  $i$  and compute  $\tilde{P}_{k,i,t}$ .

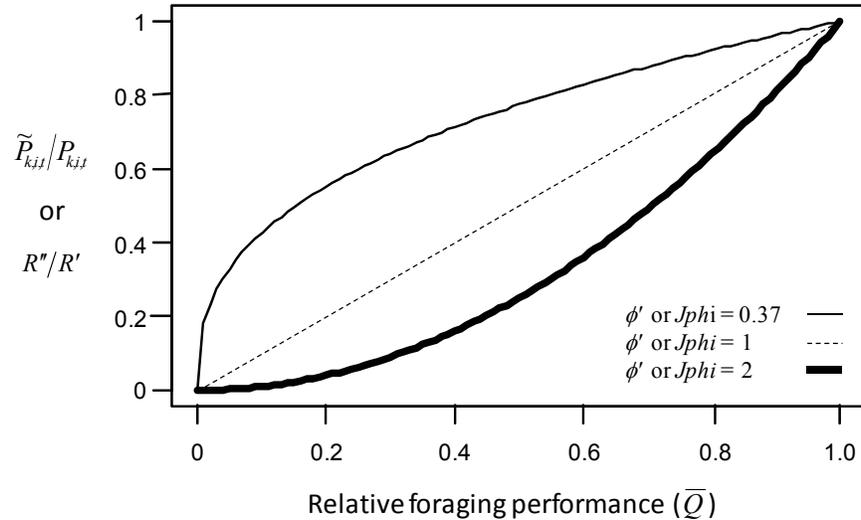
$$\tilde{P}_{k,i,t} = P_{k,i,t} (\bar{Q}_{k,i,t})^{\phi'_{k,i,s}} \quad (\text{A.22})$$

The parameter  $\phi'_{k,i,s}$  determines the shape of the scaling function relating  $\tilde{P}_{k,i,t}$  to  $P_{k,i,t}$ . When  $\phi'_{k,i,s} < 1$ , relative per-capita consumption has an hyper-stabilizing effect on the relationship between  $\tilde{P}_{k,i,t}$  and  $P_{k,i,t}$  (i.e., the ratio  $\tilde{P}_{k,i,t}/P_{k,i,t}$  decreases slower than  $\bar{Q}_{k,i,t}$  as the latter decreases from 1 to 0). Setting  $\phi'_{k,i,s} < 1$  can be used to describe diet switching by the predators or to describe situations in which the predators forage where external factors (e.g., oceanography) concentrate prey regardless of their abundance at the SSMU scale. When  $\phi'_{k,i,s} > 1$ , the ratio  $\tilde{P}_{k,i,t}/P_{k,i,t}$  decreases faster than  $\bar{Q}_{k,i,t}$  (an effect known as hyper-depletion). Setting  $\phi'_{k,i,s} > 1$  might, for example, be used to describe a situation in which predator foraging requires a threshold level of prey patchiness and this threshold is rapidly crossed as prey abundance changes. When  $\phi'_{k,i,s} = 1$ , the ratio  $\tilde{P}_{k,i,t}/P_{k,i,t}$  is equal to  $\bar{Q}_{k,i,t}$ , and, thus, the effective number of breeding adults from stock  $k$  in SSMU  $i$  during season  $s$  is proportional to the mean relative foraging performance of the individuals in that stock. Figure A5 demonstrates how the ratio  $\tilde{P}_{k,i,t}/P_{k,i,t}$  changes for different values of  $\phi'_{k,i,s}$  across the range of foraging success,  $\bar{Q}_{k,i,t}$ .

Finally, a shape parameter,  $Jphi$ , is used to modify predator recruitment.  $Jphi$  scales potential recruitment on the basis of the mean, per-capita foraging success ( $\bar{Q}_{k,i,t}$ ) during the first winter of life.

$$R'' = R' (\bar{Q}_{k,i,t})^{Jphi} \quad (\text{A.23})$$

When  $Jphi < 1$ , realized recruitment will decline slower than foraging performance, a hyper-stable condition. When  $Jphi = 1$ , realized recruitment will decline in direct proportion to declines in foraging performance. When  $Jphi > 1$ , realized recruitment will decline faster than foraging performance, a hyper-depleting condition. Figure A5 demonstrates how the ratio  $R''/R'$  changes for different values of  $Jphi$  across the range of foraging success,  $\bar{Q}_{k,i,t}$ .



**FIG. A5.** Effect of  $\phi'_{k,i,s}$  on the ratio of effective breeding population size to total population ( $\tilde{P}_{k,i,t}/P_{k,i,t}$ ) and the effect of  $Jphi$  on the ratio of realized to potential recruitment ( $R''/R'$ ). A stable relationship is illustrated for parameter values equal to 0.37. The linear relationship results from parameter values equal to 1. A hyper-depleting relationship arises when the parameter values exceed 1.

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